

MANAGING LIFE'S FUTURE: SPECIES ESSENTIALISM AND EVOLUTIONARY
NORMATIVITY IN CONSERVATION POLICY,
PRACTICE, AND IMAGINARIES

by

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A DISSERTATION

Presented to the Environmental Studies Program
and the Division of Graduate Studies of the University of Oregon
in partial fulfillment of the requirements
for the degree of
Doctor of Philosophy

June 2023

DISSERTATION APPROVAL PAGE

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Title: Managing Life's Future: Species Essentialism and Evolutionary Normativity in Conservation Policy, Practice, and Imaginaries

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Degree awarded June 2023

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DISSERTATION ABSTRACT

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Doctor of Philosophy

Environmental Studies Program

June 2023

Title: Managing Life's Future: Species Essentialism and Evolutionary Normativity in Conservation Policy, Practice, and Imaginaries

Folk essentialist and normative understandings of species are not only prevalent in popular layperson communities, but also end up undergirding United States conservation policy and practice due to the simplistic clarity they afford the notoriously knotty scientific debate of “the Species Problem” that recognizes over 26 in-use species definitions. Popular views of species typically see species as static and clearly bounded entities, a view reinforced by the need for species clarity in the legal frameworks of powerful conservation policy such as the Endangered Species Act of 1973 (ESA). These static views are thus taken up into conservation policy and practice and species in the field are managed as such—a circumstance that not only fails to protect species as the constantly evolving entities they are, but also manages organismal agency by policing the boundaries between species and thereby creating materially specific species realities motivated by human-derived frameworks. This dissertation tracks normative views on species in conservation policy (e.g., the ESA) and practice, through contemporary debates over the place of biotechnology in threatened and endangered species conservation, and into speculative future imaginaries. It draws on a wide range of primary materials including U.S. Fish & Wildlife Service and non-governmental organization management plans; policy documents; scientist op-eds and studies; and speculative bestiaries for its interpretive and historical analysis of the development,

integration, and actualization of normative, essentialist species concepts in U.S. conservation. I argue that conservation is a fundamentally creative practice of *worldmaking* that brings materially specific species futures into being while preventing others. Attentiveness to who nonhuman animals and plants *themselves* identify as kin (through processes of mating and reproduction), rather than merely using human-structured frameworks of species-being is therefore paramount to account for nonhuman agency in conservation practice. Such attention will force us to rethink the place of hybrid individuals and processual, evolutionary models in our conservation practice. Deploying a further speculative method in the form of entries into a *Speculative Field Notes on the Pacific Northwest*, this project asks: *What unexpected evolutionary possibilities and species agency might emerge at the margins, in spite of “command and control” conservation methods?*

ACKNOWLEDGMENTS

I would like to express my deepest gratitude to my advisor, Stacy Alaimo, who was hugely supportive to me during the final stretch of completing my dissertation. In addition, I am extremely grateful to Nicolae Morar, who has been on this journey with me since my time as a Master's student—I couldn't imagine this project without your philosophy of biology insights! Sincere thanks to Emily Scott and her advising crew for our ongoing meetings over the course of the pandemic—keeping all of us sane and grounded in our research with virtual social gatherings. I am thankful also to Gordon Sayre and Nina Amstutz for bringing their dynamic and historical understanding to my work. And thank you always to my family and friends for bringing a splash of chaos and equal doses of fresh air into my life—always reminding me to take a break. Lastly, thanks must go to Stacie Rowan—you helped me through the loss of my two best friends and your steadying insights were always incredibly grounding. I am deeply grateful.

To Žižek and Roo.

You began the journey with me, and while not here physically at the end, I know you are with me nevertheless. Our story together will go on—with love unending...

TABLE OF CONTENTS

Chapter	Page
I. INTRODUCTION: THE SPECIES PROBLEM, ESSENTIALISM, AND CONSERVATION AS WORLDMAKING	14
Introduction	14
Background: The Essential Species Foundation	16
Taxonomy & The Species Problem.....	17
Species Concepts & Conservation.....	20
This Dissertation.....	26
Theoretical Orientations	26
Policing Species Boundaries in T&E Conservation (Research Questions).....	31
Chapter Outline	36
II. POLICING HYBRIDS & BOUNDARY-CROSSERS: U.S. CONSERVATION IN THE AGE OF THE ENDAGNERED SPECIES ACT	41
Introduction	41
How the U.S. Endangered Species Act Sees Species.....	43
The ESA, Species Concepts, & “Best Available Science” Mandate: A Model of Scientist Discretion?.....	44
Taxonomic Prioritization for Listing & Recovery: Minor or Significant?.....	51
The ESA Approach to Hybrids.....	56
Threatened & Endangered Border Crossers	65
A Debate Over the Red Wolf’s Origins: Questioned Species Status & Hybrid Policing	66

Chapter	Page
When your Differences are Only Feather Deep: Golden-winged & Blue-winged Warblers.....	80
Intentional Hybridization for Genetic Rescue: The Florida Panther & The Texas Puma	90
Conclusion: Hybridity, Agency, Power.....	101
SPECULATIVE FIELD NOTES ENTRY I: SPARRED OWL	106
III. NATURAL ENGINEERS, GENETIC INTEGRITY, & NATIVIST PURITY: HOW SCIENTISTS ARE MAKING THE CASE FOR TRANSGENICS IN CONSERVATION	107
Introduction	107
The Transgenic American Chestnut: Darling 58.....	109
History & Approaches to Blight Tolerance.....	109
The Chinese/American Backcross Program.....	115
Naturalness & Novelty Appeal.....	121
Minimal Human Intervention Appeal	125
Percentages Over Relatedness? The Genetic Integrity & Precision Appeal ...	131
Racial & Cultural Politics: The Nativist Purity Appeal	137
Discussion & Conclusion: What does the Prospect of Transgenics Conservation Reveal?	144
Darling 58's Public Support & Regulatory Path	144
Complications & Contradictions?	148
Overlaps and Slippages: Purist Conservationists in Biotech Clothing?	152

Chapter	Page
SPECULATIVE FIELD NOTES ENTRY II: MIGHTY ASH.....	155
IV. SPECULATIVE EVOLUTION & THE FUTURE OF LIFE.....	157
Introduction	157
Speculative Evolution Imaginaries.....	164
<i>After Man</i> : The Human-less Eden.....	164
The Desirable and the Undesirable: Battling Disgust in the Age of Weeds....	173
Building New Life Through Death: Agency & Speculative Evolutionary Process.....	195
Conclusion.....	210
V. CONCLUSION: NURTURING LIFE’S FUTURE	213
Conservation as Worldmaking	213
Looking Forward for Conservation.....	215
Evolution as a Story Without End.....	221
REFERENCES CITED	223

LIST OF FIGURES

Figure	Page
2.1. Hybridization types differentiated by natural or anthropogenic causes	57
2.2. Red wolf historic range, captive-breeding source population, and non-essential experimental population site map	67
2.3. Red wolf non-essential experimental population management zone map with sterilization line marked	74
2.4. Geographic range of <i>Vermivora</i> warblers and illustrations of phenotypes	81
2.5. Florida panther historic and contemporary ranges	91
2.6. Collection locations of <i>Puma concolor</i> specimens used in original 1946 subspecies boundary delineation	97
2.7. IUCN Cat Specialist Group revised <i>Puma concolor</i> 2 subspecies taxonomy map	98
SFN 1. Spurred owl Speculative Field Notes entry	106
3.1. Diagram of Oxalate oxidase converting oxalic acid into hydrogen peroxide and carbon dioxide	112
3.2. American Chestnut Foundation Chinese/American backcross program	117
3.3. Map of USFS lands in American chestnut range; hybrid chestnuts have Already been planted in some of the marked areas	118
3.4. Comparison images of blight cankers on first generation Darling 58 x WT American chestnut that did and did not inherit the OxO gene	127
3.5. Ranges of North American <i>Castanea</i> species	130
3.6. OxO gene leaps from wheat to chestnut. Screenshot from “American Chestnut Research” video	151
3.7. Happy people tend their transgenic chestnuts. Screenshot from “American Chestnut Research” video	151
SFN 2. “Mighty Ash” and Emerald Ash Borer Speculative Field Notes entry	155

Figure	Page
SFN 3. Ash swale over time; Speculative Field Notes entry	156
4.1. Falanx hunt Common Rabbuck, illustrations by Diz Wallis	167
4.2. Aquatic mammals of the tropical forests, illustrations by John Butler	168
4.3. “First Encounter” by Alexis Rockman	175
4.4. “Thylacine” (1997) by Alexis Rockman	176
4.5. “The Farm” (2000) by Alexis Rockman	177
4.6. Rotrap paper pop-up, paper art by Shawn Sheehy (2018).....	187
4.7. Rotrap description page, illustrations by Jordi Solano (2018)	188
4.8. “Stomaximus” by Pinar Yoldas (2014)	197
4.9. Stomaximus diagram by Pinar Yoldas (2014).....	201
4.10. General gameplay of <i>Evolution</i> , image by Florence Sullivan	205
5.1. Diagrams of Conventional Species Action Plans (SAP) & Process-Based SAP	219

LIST OF TABLES

Table	Page
1. USFWS listing & recovery prioritization protocol	52

CHAPTER I.

INTRODUCTION:

THE SPECIES PROBLEM, ESSENTIALISM, AND CONSERVATION AS WORLDMAKING

“[Conservation biology emerges with] a new right to ‘make live and let die’, manifest as the right and duty to catalog life at the level of the species, organism, and genome, make nonhuman species live, and preserve certain visions of nature—all this while allowing abnormal...populations to die off”
—Christine Biermann & Becky Mansfield 2014, 263

“In fact, there is no way of telling whether turtles (and most other animals, with some exceptions such as bees and ants) have a conception of themselves as a larger population or as a species, or care about the flourishing of the population or the species.”
—Krithika Srinivasan 2014, 512

Introduction

Species carry an unquestioned intrinsic value to many conservation biologists and laypeople seeking the protection of biodiversity—but what is the species to an individual animal within it? What is the species to the red wolf who mates with the coyote, passing on their genetics through viable “hybrid” young? What does such a wolf’s behavior tell us about species boundaries? And if conservationists were to prevent such a hybrid mating, what narrative of species is enacted through this management? The materiality of red wolves and their future possibilities as a species are altered through such interventions: new worlds are created while other pathways are closed. Through management practices, species conservation in the US constantly writes stories for the species it protects, participating in creative worldmaking practices that support particular species lifeworlds while discouraging others: “making live” the species that have been identified as worthy of such efforts, while “letting die” those that are not.

These projects are undoubtedly put forth *in the interest* of the species they seek to protect, while nonetheless reflecting human interpretations of species concepts and ideals and optimal outcomes—not all of which promote nonhuman agency in enacting conservation goals. In this dissertation I will explore the complex process of conservation worldmaking through Threatened & Endangered (T&E) species conservation efforts (such as the red wolf) and speculative creative projects, two areas that are particularly interested in the valuation of specific forms of life and the overall future of biodiversity. I hope to draw out the complexity of the species concept as a foundation for conservation due to its definitional uncertainty and evolutionary fluctuation as well as the import of considering the nonhuman beings themselves as potential partners for identifying meaningful units for conservation management. No concept has been more impactful on conservation practice on the ground than species—they are identified as biodiversity proxies and undergird contemporary conservation policy such as the Endangered Species Act. Understanding how conservation scientist narratives about species develop materially specific species realities through management is therefore of paramount importance if we are to assess conservation management practice clearly and honestly.

In what follows I will provide background on The Species Problem (the scientific and philosophical debate on how to define species), particularly as it presents problems for conservation and conservation policy broadly. This framework is essential for providing a background to contemporary conservation practice as such debates affect the listing of species as T&E and influence the perspective scientists take to management decision making. Second, I will outline my dissertation's theoretical underpinnings as it draws methodologically from feminist science studies and theoretically from material feminism, biopolitical theory, and multispecies studies. Lastly, I will outline my research questions and chapters of the dissertation,

discussing the thread of *creative worldmaking* as it weaves through my dissertation's conservation case studies and speculative media. As you will see, species are “made to live” in many ways over the course of this dissertation, not the least of which is how they are *conceptually* made to live as an essential definitional ideal—the foundation of our story.

Background: The Essential Species Foundation

As both the most commonly used unit for marking biodiversity and a widely accepted unit of evolution, species have long held a controversial yet vital place at the center of conservation efforts (Maclaurin and Sterelny 2008; Dupré 1999; Ereshefsky 2022). Species are counted in massive censuses; their populations are assessed and monitored for viability; and if they are deemed worthy, they become the recipients of intensive management operations intended to “make live” thereby preventing species extinction and biodiversity loss (Youatt 2015; Lorimer 2015; Biermann and Anderson 2017). These patterns of conservation management programs are all marked by intense emotional appeals linked to these rare species human communities have deemed valuable enough to fight for their survival (Heise 2016; Jørgensen 2019; van Dooren 2019). But alongside these passionate species conservation efforts comes uncertainty about the distinguishability of the very creatures we've identified as so vital to protect because species fundamentally are not clearly bounded entities with consistent definable characteristics. As Marc Ereshefsky notes, “biologists disagree on the definition of the term ‘species,’ and philosophers disagree over the ontological status of species” (2022). With over 26 definitions presently in use, and entire books dedicated to what is widely considered “The Species Problem” (e.g. Zachos 2016; Wilkins, Zachos, and Pavlinov 2022; Pavlinov 2023), it is clear that “species” are not as obvious as the average layperson might assume.

Taxonomy & The Species Problem

The most thoroughly structured attempt at species taxonomic organization dates to Carl Linnaeus, widely seen as the “father of modern taxonomy,” who designed the system of binomial scientific naming (a species’ genus and species name, e.g., *Castanea dentata*) which first appeared in his 1737 collection on plants and remains with us today. His view on species was founded in the belief that each species bore a fundamental essence that distinguished it from all others—a quality derived from their divine creation (Ereshefsky 2001). This form of essentialism, whether religious or otherwise, dominated biological taxonomy for centuries. Such essentialism has three main principles:

- (1) All and only the members of a kind share a common set of traits that is the real essence of that kind.
- (2) That essence makes an entity a particular kind of thing.
- (3) Knowing an entity’s essence is crucial for explaining the other properties typically associated with an entity of that kind. (Ereshefsky 2001, 95)

These essentialist ideas carried much sway because they were anchored in widespread, pancultural, “folk essentialist” logics where “biological species [are understood] as the manifestation of underlying ‘natures’ shared by all members of a species,” thus species all carry innate traits that distinguish them clearly from others (Griffiths 2002, 72). According to Griffiths (2002), “this is precisely the ‘typological’ perspective on species that Darwin had to displace in order to establish the gradual transformation of one species into another” (77). Thus, with the publication of Charles Darwin’s *On the Origin of Species* in 1859, such views of species as bearing static “essences” could no longer hold up under the new understanding of constant adaptive change and evolution (Darwin 1859; Dupré 1999). However, as Ereshefsky (2001) notes, while “essentialism concerning taxa” therefore “[fell] out of favor...many of Linnaeus’s original principles remain in place,” in particular, “the assumption that there is an essence to the species *category* is still widely held” (3-4; my emphasis). Thus, while biologists might, in

practice, acknowledge the untenability of an “essential” notion of a particular species taxa in Linnaean terms—that an organism will have a core “essence ... shared by all members of the species” (Griffiths 2002, 77)—the idea of a *species category*, or the ability to define species and select a single (essential) definition whereby one can do so, is nonetheless held as possible and desirable.

Attempts at defining species therefore abound in scientific and philosophical literature, with over 26 presently in circulation. I will address only the most widely used species concepts here, and particularly those that are most widely used in conservation practice. Without a doubt the Biological Species Concept (BSC), first described by Ernst Mayr in 1942, is the most in-use species concept today, which emphasizes sexual reproduction and isolation between populations: “species are groups of actually or potentially interbreeding natural populations which are reproductively isolated from other such groups” (Mayr 1942, 120). The BSC thus sees “species [as] genetic fortresses, protected by isolating mechanisms and held together by interbreeding” (Ereshefsky 1992, 4). A key component of this definition is a focus on *populations* of species, essentially groups of organisms grouped together by space, time, and reproductive connectivity. Where these different populations are only partially reproductively isolated, however, and species hybridize, a “strict application of the BSC” would require the hybridizing species to be “synonymized” and grouped as the same species (Sokal and Crovello 1992, 47; Fitzpatrick et al. 2015). However, in practice, many users of the BSC will arbitrarily accept some crossing while nonetheless asserting species distinction—this lends some uncertainty, and individual taxonomist judgement, to the *amount* of reproductive overlap that can be tolerated before the species are combined (Sokal and Crovello 1992; Carolan 2008). The Phylogenetic Species Concept (PSC) is the second-most in use species concept, defined by “the smallest diagnosable cluster of

individual organisms within which there is a parental pattern of ancestry and descent” (Cracraft 1983, 170). The PSC is especially popular with scientists embracing genetic technologies, as strategies such as “DNA barcoding” for example, can be used to differentiate cryptic species (those that appear to be morphologically the same) using the DNA sequencing of a standard gene region (i.e., “DNA barcoding”). Paul Hebert (considered the “father of DNA barcoding” (Greenfield 2020)) first used this technique to discover 10 cryptic two-barred flasher butterfly species hiding in one¹ in northwestern Costa Rica (Hebert et al. 2004). The PSC can also apply to asexually reproducing populations whereas the BSC is reliant on sexual reproduction as its unifying factor—making the PSC more expansive for the diversity of life. Phylogeny (or the study of the evolution and descent of a species group) as an organizing principle was particularly important theoretically as it helped better align species concepts with evolution—the process of speciation itself: “Because the most effective and natural classification systems are those that ‘capture’ the entities resulting from processes that generate the things being classified, the general biological classification system should be used to reflect the tree of life” (Mishler 1999, 309-310). The PSC is seen as an “operationalized” version of the earlier Evolutionary Species Concept (ESC) (Groves et al. 2017, 1249), a more theoretical definition that identified species as “a single lineage of ancestral-descendent populations which maintains its identity from other such lineages and which has its own evolutionary tendencies and historical fate” (Wiley 1978, 18). While a conceptually meaningful definition, the ESC wasn’t very functional in practice as it expected a long-term view that many taxonomists on the ground just couldn’t expect to glean in the short-term (George and Mayden 2005). And though many biologists hold out hope that a

¹ Notably, there were additional clues to the butterflies’ differences aside from genetics: the caterpillars both looked different, but also used different host plants. Typically, however, biologists of the period used adult butterfly genital morphology for taxonomic distinctions rather than these other differences (Greenfield 2020).

single, functional, correct species concept can be reached that can be used across *all* natural taxa (species monism), others believe that a pluralist approach to species is more realistic—thus a view where there is in fact no essential quality to the species category and different species concepts will be necessary to accommodate the diversity of life (Ereshefsky 2001).

Species Concepts & Conservation

The BSC and PSC see the most “action” in the context of conservation because they are two of the most operational species definitions: they are easy to put into practice on the ground. They are also two of the most conflicting definitions as they often place taxonomists in one of two camps: the “lumpers” (the BSC adherents) or the “splitters” (those that prefer the PSC). From scholarly articles to blog posts, the phenomena of “lumping and splitting” species is widely discussed and debated within conservation biology circles (Kell et al. 2009; Senn et al. 2014; Montgomerie 2018; Vaidya, Lepage, and Guralnick 2018). The language of “lumping” and “splitting” dates back to even Darwin’s time, where he remarked on the practice in an 1857 letter to the botanist J.D. Hooker: “Those who make many species are the ‘splitters,’ and those who make few are the ‘lumpers’” (Darwin n.d.). Due to the recent rise in genetic and genomic technologies—and particularly due to their now rapidly increasing speed and affordability—the PSC has been growing in popularity, leading to more “splits” than “lumps.” The recent shifts from using “broad-brush” species concepts such as the BSC to “fine-grained” ones like the PSC have thus led to accusations of “taxonomic inflation” that might even serve to hide extinction trends by creating a false image of stable or increasing species numbers and therefore no “loss” (Isaac, Mallet, and Mace 2004, 1). One study of North American bird taxonomy trends from 1889-2016 showed “lumping” of many species occurring in the 1930s-40s and then a reversal to

splitting of many taxa from the 1990s to 2016 (Vaidya, Lepage, and Guralnick 2018). Of course, debate rages on both sides for and against “lumping” and “splitting.”

On the one hand, some scholars see the PSC as potentially *excessively* splitting, often by an overuse of narrow differences in Mitochondrial DNA (mtDNA), for example, which is known for its high mutation rate—a trait that allows populations to delineate more quickly from parent populations. Such splitting can contribute to more species with fewer individuals with which to draw from genetically for conservation purposes—this lack of diversity can put these populations at risk when confronting environmental changes, including disease and climate change (Frankham et al. 2012). On the other hand, those concerned about “over-lumping” see the practice of lumping species together as “making species invisible to conservation and risking their extinction unnoticed” (Groves et al. 2017, 1249; Russello and Amato 2014). In particular, the BSC relies on subspecies to gain its “finer-grained” distinctions between populations, but the subspecies category has lately gained considerable pushback, with many believing the category lacks scientific rigor and might only reflect arbitrary distinctions (Haig et al. 2006; Groves et al. 2017; Padial and De la Riva 2021). Because the PSC uses the “smallest diagnosable cluster” to distinguish species, it also avoids the problems inherent in subspecies, though it still suffers under accusations of “arbitrariness” with what distinguishes significant difference between populations. For example, recently a new species of mouse lemur—Jonah’s mouse lemur—was added to a ballooning list of mouse lemur species which has now reached 25 from what was once believed to be a monotypic genus as recently as the 1970s (Yoder et al. 2000; Schüßler et al. 2020). Primarily mtDNA and an emphasis on the PSC has contributed to the massive increase in mouse lemur species whose populations, as they split, are deemed increasingly threatened with extinction. Such examples bear out the complexity of the problem for conservation, particularly

when species numbers are often increasing unevenly to favor the more highly studied taxa, such as primates. While undoubtedly scientists are identifying real difference in the lemur populations, is this *significant* difference for conservation, particularly when conservation funds are limited, and many species are threatened with extinction? And what impacts might there be to the lemur populations if they are managed separately, and genetic flow is prevented between populations? Could this produce future problems for the genetic diversity within the population? As you might notice based on the question I asked first—the question about taxonomy was translated into taxonomy in the context of conservation, and this becomes the further sticking point for taxonomy: whether conservation considerations should play a role in taxonomy at all.

Most biologists and taxonomists would argue No, taxonomy is a fundamentally objective and scientific endeavor that should be held separate from conservation considerations (and deserves more funding so it can remain so) (Dubois 2003; George and Mayden 2005; Jackson, Scherz, and Zona 2017). Others are less certain about such assertions, seeking closer alliances and working partnerships between taxonomists and conservationists, and even (in some cases) suggesting checks on taxonomists to accommodate conservation interests (Mace 2004; Holstein and Luebert 2017; Garnett and Christidis 2017). Adding further problems to the taxonomic situation is the evolutionary fact that species are constantly shifting—whether minutely or drastically—further problematizing their discernibility and provoking potentially unanswerable questions (empirically) about management directions (Hey et al. 2003). Fitzpatrick et al., (2015) explain the problems at hand for conservation and taxonomy succinctly:

Species based conservation is challenged by two major aspects of evolutionary biology. First, evolution has definitively rejected the typological view of species as fixed (unchanging) groups, each with a unique, distinct essence (Darwin, 1859; Mayr, 1982; Futuyma, 2013). ... Second, there is no universally accepted definition of ‘species’ or set of criteria for delimiting species taxa. This should not be surprising in light of the dynamic evolutionary view of biodiversity. (Fitzpatrick et al. 2015, 206-207)

While we understand the problems with no set definitions—why is the rejection of a typological (essentialist) view potentially challenging for species-based conservation? This particularly comes down to the policy foundation that relies on such typological and essentialist ideals. From a legal standpoint, species must appear stable (standing outside scientific consensus that species are in constant flux)—a view that ultimately corroborates the folk essentialist ideas I discussed earlier. As explained by Jason Scott Robert and Françoise Baylis in their influential article “Crossing Species Boundaries,” this folk approach to species is significant as “notwithstanding the claim that biologically species are fluid, people believe that species identities and boundaries are indeed fixed and in fact make every day moral decisions on the basis of this belief” (Robert and Baylis 2003, 6). And while Robert and Baylis are specifically interested in the human-nonhuman species boundaries (in the context of interspecies biotech research), their claim regarding moral decision-making holds just as true in the context of nonhuman species boundaries. The role of species lists and boundaries in conservation policy is indicative of this importance, as without clear boundaries between species then legal protections become unstable and uncertain: if we don’t “know” what species are, then how do we know what we are protecting? Legislation guiding conservation work must be, by necessity, as clear as possible and long-standing scientific debates that have no consensus will inevitably work against the ultimate goals of the policy. Some scholars such as Georgiana M. Mace (2004) have suggested a two-pronged approach that would, on the one hand, build species lists with clearly bounded entities for legal protections and, on the other, enact more malleable on the ground units as the *actual* “targets of conservation action”: “The challenge here is to break the assumed link between the entities that are listed in conservation plans and those that need to benefit from direct conservation actions” (717). Similarly, Hey et al. (2003) stress that distinctions should be made

between species taxa and actual evolutionary entities adapting and evolving in real time—a distinction that *could* hinder legal aspects of species conservation, but perhaps only due to the overreliance on “species” as the focus for conservation efforts. Indeed, despite the confusions arising from species definitionally, they are nonetheless still the principle anchor for most conservation efforts and the typical proxy used for biodiversity censuses (Maclaurin and Sterelny 2008; Youatt 2015; Morar, Toadvine, and Bohannan 2015). Our most powerful conservation policy in the U.S., the Endangered Species Act of 1973, one of my main focuses in this dissertation, is thus entirely centered on the subject of one of the thorniest debates in biology: species. And the need for clarity in such policies has resulted in an unspoken yet implicit assumption that species are clearly bounded and static entities. As Mace notes, it is unlikely a shift to other models will come anytime soon “because of the amount of expectation in policy-makers and legislators about the reality of the species concept. They really believe in it” (qtd. in Marris 2007, 253). Such beliefs in the “reality” of species also serve a further moral role, as suggested by Robert and Baylis above, especially when paired with the legal and value-oriented context of conservation policy.

In particular, conservation’s role as a “crisis discipline” (Soulé 1985; Russello and Amato 2014), which frames the issue ethically, reinforces the sense that species, as something of value worth protecting, are more than descriptive categories but are also moral in nature. Species boundaries, then, take on a normative bent in conservation practice: as something that must be policed in order to be protected. In addition, the progressive “ever expanding cone”² view on evolution that is widespread in the popular consciousness, expects constant diversification and

² Stephen Jay Gould called this “the straitjacket of linear advance” (32) that produced an iconography blending evolution with progress: more species equated with “better” and a species’ placement in time was correlated with their worth (Gould 1989).

splitting of species rather than merging—species merging is therefore seen as counterintuitive and “backwards”—which brings a further *normative* sense to maintaining species boundaries. The urgency of species conservation is therefore fueled, in part, by the sense of moral “rightness” afforded when a species is distinguished and protected from infiltration by other species around it. This is nowhere more obvious than in Threatened and Endangered species (T&E) conservation, as the coveted “listed” place on the Endangered Species Act (ESA) of 1973 brings such restrictions to lands designated as “critical habitat,” these listings often provoke conflict with private and corporate stakeholders. This contested landscape draws out species boundary anxiety, as the less certain a species’ status, the less likely it will maintain legal protections: such uncertainty will be capitalized upon in delisting petitions by private interests. Blurring along species borders for T&E species is therefore tolerated far less than in species under less extinction threat and *policing* these borders becomes an acute *need* of conservation in order to shore up a species’ conservation protections. Thus, the moral urgency of a crisis discipline; the moral sense of “rightness” in species identity and boundaries; and the moral tenor of law all reinforce one another, indicating that what from a policy or public perspective may initially seem to be merely a matter of “science” and “fact” is rather a deeply ethical issue. As Michael E. Soulé asserts, conservation biology has at its core a series of normative postulates that anchor the field as fundamentally ethical in nature: “*diversity of organisms is good, ...ecological complexity is good, ...evolution is good, ...[and] biotic diversity has intrinsic value*” (1985, 730-731). And because species have so frequently come to stand in as a kind of proxy for biodiversity, the importance of identifying, defending, and protecting the evolutionary potential of species is paramount to conservation work. Ironically, however, the bounded and static sense with which species are understood in conservation policy is what stands in the way

of adequately protecting them as the changing and adaptive entities that they are. A shortcoming that not only fails to live up to the postulates Soulé describes, but also might both restrict a species' agency and ability to survive on their own terms as well as the ability of conservation practitioners to protect the species innovatively and responsively.

This Dissertation

This dissertation, *Managing Life's Future: Species Essentialism and Evolutionary Normativity in Conservation Policy, Practice, and Imaginaries*, will intervene in this space where popular normative concepts of evolution, speciation, and species intersect with conservation policy and practice—specifically in T&E conservation in the US.

Theoretical Orientations

How might we orient ourselves around these questions of species agency, normative ideals of species and evolution, and restrictive managerial conservation methods impacted by policy? My thinking on these topics is informed by insights from feminist science studies and material feminism, biopolitics, and multispecies studies. As a method for identifying value judgments in scientific study, feminist science studies has long offered useful critical approaches for parsing objectivity and subjectivity in the sciences and attending to the ethical dimensions and androcentric biases of scientific study (Merchant 1980; D. J. Haraway 1991; Harding 2008). I draw particular methodological inspiration from Donna Haraway's early work in *Primate Visions* where she describes "looking at primatology, a branch of the life sciences, as a story-telling craft" therefore being "interested in the *narratives* of scientific fact—those potent fictions of science"(D. Haraway 1989, 4-5; my emphasis). What are the stories science tells, through

recovery plans and management practice, about species ideals? And how do these stories produce different material conditions for the species they describe? As Haraway notes, in these narratives, “possible worlds are constantly reinvented in the contest for very real, present worlds” (1989, 5). Thus, the *materiality* of these narratives of species, the epistemological frame of species concepts, is the key point of interest for my dissertation, and the key intersection for material feminist theory. As Karen Barad explains, this moves beyond a representational model and into a performative understanding, a frame she calls “agential realism”:

The point is not merely that knowledge practices have material consequences but that *practices of knowing are specific material engagements that participate in (re)configuring the world*. Which practices we enact matter—in both senses of the word. Making knowledge is not simply about making facts but about making worlds—not in the sense of making them up..., but in the sense of materially engaging as part of the world in giving it specific material form. (Barad 2007, 91)

Such a frame calls for attentiveness to the ways species concepts come to *matter*, and thereby enact processes of worldmaking for species in real time. Barad emphasizes that these practices of knowledge-making (and therefore worldmaking) must therefore be *accountable* to these processes, requiring “a methodology that is attentive to, and responsive/responsible to, the specificity of material entanglements in their agential becoming” (91). Barad’s interest in agency and “intra-action” within this process of meaning making and material reconfigurations is of particular importance to my project, as conservation biologists on the ground attempt to adapt their practice through new knowledge of the species they manage even while reconfiguring species worlds and possibilities through restrictive “command and control” management methods. “What” the species are materially is continually made anew through ongoing management even while management practice itself changes through new knowledge gained from their very interactions on the ground: an intra-active cycle of entangled agents. My dissertation seeks to expand upon the current feminist science studies and material feminist

purview of the sciences into the realm of policy to further explore how legal ways of knowing are interpolated into this material-discursive framework and play a role in the materialization of specific species futures.

To address the importance of governance in this process, I turn therefore to work applying Michel Foucault's lens of biopower to conservation and the management of nonhuman life. Foucault described such power as a modern governance "right to make live and to let die" in which contemporary governments manage human populations (Foucault 2003, 241), marking out certain communities to *make live* and others to *let die* through regulatory and disciplinary means in our hospitals, schools, prisons, etc. (Lemke 2011). Thus, according to Rutherford, "Governing becomes the construction of certain truths and their circulation via normalizing and disciplining techniques, methods, discourses and practices that extend beyond the state and stretch across the social body" (Rutherford 2007, 293)—practices that work both on populations and influence the behavior of individuals. While Foucault himself did not see such biopolitics as applying to nonhuman animals, scholars studying the management of nonhuman species have remarked on the considerable similarities between such practices, particularly in the context of contemporary conservation where extensive effort is expended on "*making nature live*" (Biermann and Mansfield 2014, 258). The emphasis on managing species *populations* and the differentiation between species worthy of protection (those we "make live") and those that can be sacrificed, contained, or merely not prioritized (those we "let die") are key factors that render conservation practice particularly applicable to biopolitical theory. As Biermann and Anderson explain:

Conservation biopolitics encompasses the logics, spatial practices, and political economies through which material and discursive distinctions are drawn between those life forms (genes, populations, species, etc.) to be fostered (made to live) and those to be "let die." Even as many conservation interventions are scientifically informed and technically derived, they are also value-laden projects in which particular human subjects

decide who or what is made to live and who or what is allowed to die. (Biermann and Anderson 2017, 3)

The inherent nature of valuation within conservation practice, a crisis-discipline that lists T&E species it will strive to protect and marks out other species (e.g., invasives) it deems unworthy of protection, makes clear some of the anchoring biopolitical logics in the discipline. Under the overall goal of maximizing benefits to “life,” “conservation science aims to control life—all the while drawing the line between biological threats and advantages—in order for life to proliferate freely” (Biermann and Mansfield 2014, 264). This practice seeks to “prescribe” certain futures while preventing others “less lively and less diverse”—a normative orientation on evolutionary processes that takes a managerial role in bringing such futures into being (264). In particular, certain forms of gene-flow between species and populations are viewed as less desirable and “in these ways, impure bodies are seen as not enhancing biodiversity but as threatening it” (266). Further, scholars such as Srinivasan (2014) stress the “entanglement of harm and care” (504) even on the populations identified as vulnerable: the T&E species themselves, as monitoring behaviors such as tagging and censuses carried out during periods such as turtle egg-laying can cause stress, harm and even death in some cases. Such management practices also weigh the benefits of and consider numbers of allowable individual deaths, a form of “agential subjectification” all “rooted in genuine motives of care for the ‘Other’” (510). Srinivasan sees such agential subjectification as the conservationist’s unquestioned focus on animal well-being at the population level which emerges out of the conservationist’s “human-oriented normative objectives” in pursuit of “win-win” solutions involving multiple stakeholders (humans and nonhumans) (511). The “true” (and therefore neutral) knowledge of species populations is thus forwarded by biopolitical structures of management to “enable harmful interventions on

individuals in the name of collective well-being” (512), whether such actions would be sought out or desired by the individual animals in such collections themselves or not.

The entanglements of nonhuman animals and conservationists provoke profoundly ethical questions about world-making and the interactions of different species in material communities. The field of multispecies studies offers some entry points of interest for me in this area, particularly in considering the importance of multispecies worldmaking and ethical configurations that encapsulate varied agencies other than the human. For Thom van Dooren, multispecies ethics “asks what ethics might look like if we take [nonhuman animals] seriously: not just what they *need* but what they can *do*. That is, not just as possible *subjects* of others’ ethical regard but as beings who are themselves shaping our shared worlds in consequential ways” (van Dooren 2019, 3). This reorientation to considering more than just *needs*, but also just another being’s way of living in the world can serve as a call to think of other species as more than just populations with biological needs and patterns, but also ways of living, communities, and kinship relations. It also reminds us to consider the *interactions* between humans and other species in the context of conservation as we influence one another—our management efforts developing and altering both biological and community possibilities for other species. These are ultimately processes of world-making:

“Making worlds is not limited to humans...all organisms make ecological living places, altering earth, air, and water. Without the ability to make workable living arrangements, species would die out. In the process, each species changes everyone’s world. ...world-making projects can overlap, allowing room for more than one species...Humans, pines and fungi make living arrangements simultaneously for themselves and for others: multispecies worlds.” (Tsing 2015, 22)

Work in multispecies studies attends closely to the interactions across and between species, the open-ended “assemblages,” that are constantly in flux: “some thwart each other; others work together to make life possible; still others just happen to find themselves in the same place”

(Tsing 2015, 22). Multispecies worldmaking also offers further entry points into considering kinship relations within and across species. Rather than tossing all species categorizations out the window and embracing a fully fluid movement across species borders, such a view recognizes the ways that nonhumans also regularly distinguish between those they deem kin or not, species that are food, good for shelter, etc. Thus, multispecies studies scholars ask: “How do entangled agents torque one another with their own practices of classification, recognition, and differentiation? How are different kinds of being enacted and sensed in the ongoing ebb and flow of agency in multispecies worlds?” (van Dooren, Kirksey, and Münster 2016, 5). Attentiveness to the agency of nonhuman animals themselves as they categorize and differentiate between who is a viable mate and who isn’t, for instance, could thus offer valuable information for developing more responsive conservation.

Policing Species Boundaries in T&E Conservation (Research Questions)

Bringing to bear insights from multispecies studies, material feminism, and biopolitics as well as methodologies from feminist science studies, this dissertation will interrogate the materiality of species concepts and normative understandings of evolution as they are operationalized through the Endangered Species Act (ESA) and T&E conservation and actualized in conservation practice. The practice of legally *policing* T&E species boundaries through an essentialist politics of purity ultimately produces materially specific species realities: fostering some futures while letting others die. The chapters will track ESA approaches to species and hybrids, debates on transgenics in T&E conservation, and speculative evolution imaginaries of future species worlds. My project will chart the following threads of inquiry as they trace through these different case studies: essentialist understandings of species; narratives

of genetic purity and hybridity; the role of the human in the evolution of other species; and futurity, or the future of life itself. Each of these threads are fundamentally ethical in nature as differential understandings of each can develop markedly different materialities, an issue that further undergirds the urgency evident in conservation biology and practice. It is this ability for conservation policy and practice to bring into being different species futures that requires not only an attentiveness to speculative evolutionary narratives, but also a speculative method that I will also interweave throughout the work. My dissertation ultimately seeks to better understand the materiality of essentialist species ideals as they are enacted through policy and made real through conservation practice as well as the interaction between this process and the managed species themselves (how do they inform the process? resist it? are molded by it? etc.). This approach will contribute to a more dynamic understanding of conservation policy and the material impacts of conservation in action.

To elucidate the materiality of these different processes, I will use case studies throughout the dissertation to ground my study in concrete projects with real material impacts for the species involved. In exploring the narratives of these case studies, I will ask the following questions:

- What kinds of management practices are selected? How are these justified?
- What role do value judgments play in the selection of particular management pathways? What role do ideals about species being play in these decisions (e.g., do management decisions hinge on a species' genetic integrity or to dissuade ESA delisting)?
- What is the material fallout of these human choices for the species in question?
- How is the agency of the organisms in the different populations supported or controlled?
- In creative imaginaries, how are speculative views on future evolution paired with value judgments of different forms of life? Who are represented as evolutionary agents: humans, other organisms, etc.?

In telling the story of each case study, the biopolitical reality of the management approaches will structure the production of materially specific species realities: they bring into being particular species futures while preventing others. Thus, as we explore the different case studies in this dissertation, a specter tracks every species on the landscape: the present/future species that *could* exist with different conservation management choices. Bearing this in mind provokes one to think critically about the types of interventions we make and to seek avenues that foster the agency of nonhuman beings wherever possible. Doing this therefore requires close attentiveness to the material entanglements of these nonhuman animals (and plants) on the ground: how do they interact with one another? What do their reproductive patterns (that play out both genetically over time and in short-term interactions between individuals) tell us about who they see as kin? These are questions I bear in mind as I look closely at the different case studies over the course of this dissertation. So, while the management practices themselves might come to the fore for much of the dissertation, keeping these questions in mind is essential for the overall project's attention to the materiality of species futurity and possibility: the species futures rendered both possible and impossible by management practice. These questions intersect well with Matthew Chrulew's translation of Foucault's approach to the Kantian question of human subjectivity (*Who am I, who are we today?*) for the animal subject: "*Who are they, these others, today? And Who might they—we—become?*"(Chrulew 2016, 236).

In furthering this speculative project of species possibility and futurity, I will also be interspersing my own speculative take on species futures throughout the dissertation. I will interweave entries into a *Speculative Field Notes on the Pacific Northwest* that explores different Pacific northwest species, or species relationships, in-between each chapter. My goal in this creative aspect of the dissertation will be to offer different methodological insight into how

policy and conservation practice sees species and helps actualize (or limits) particular species life-worlds. This speculative methodology finds inspiration from Ruha Benjamin's "Racial Fictions, Biological Facts: Expanding the Sociological Imagination through Speculative Methods," where her theoretical work is interwoven with theory of a different kind: fiction. As Benjamin asserts:

Fictions, in this sense, are not falsehoods but refashionings through which analysts experiment with different scenarios, trajectories, and reversals, elaborating new values and testing different possibilities for creating more just and equitable societies. Such fictions are not meant to convince others of *what is*, but to expand our own visions of what is *possible*. This is not to say that imagining alternatives is sufficient, or that all things possible are even desirable. But how will we know if we do not routinely push the boundaries of our own thinking...? (Benjamin 2016, 2)

I concur with Benjamin's call for speculative engagement and aim to take up this call by speculating into the futures that might be made manifest through the conservation policy and practice that I explore in my dissertation. My speculative approach will take the form of field notes—in the long tradition of scientists and naturalists writing and drawing in the field, witnessing nonhuman others in practice, and recording those moments on paper. Field notes are never finished, they are a practice in ongoingness: in being with, recording, and recording again. Nothing is erased; every observation carries meaning. Rather than a field guide that attempts to restrict a species with taxonomic certainty, field notes can dwell within the uncertain and explore questions alongside nonhuman-others. I intersperse these field note entries throughout the entire dissertation to make clear that the importance of a speculative method is not only present in the context of speculative fictions as explored in the final body chapter, but must be present in our engagements with policy and conservation practice on the ground as well. My field note entries will include watercolor illustrations, species descriptions and characteristics, as well as field note textual components. To ground each entry more clearly in the material reality that I draw on for

each species' inspiration, the water I will use for painting will be drawn from carefully selected regions connected with my own understanding of these speculative species. These entries inquire: *What species possibilities might emerge at the margins, in the fallout of human conservation efforts? What unexpected evolutionary agency exists in spite of "command and control" conservation methods?* As adrienne maree brown says, "If we want to bring new worlds into existence, then we need to challenge the narratives that uphold current power dynamics and patterns" (brown 2015, 279)—I hope the agency I see in these species' resistance can be such a form of "challenge" against current structures of power in conservation practice.

This project will be ongoing, and the species currently included in this dissertation are only the beginning of what will be an ongoing practice of speculative notetaking in the field. As the practice of field notes and developing new futures are both unfinished practices, this project will be an ongoing—ever in-flux—*practice* rather than final *product*. Presently included in the dissertation are two primary species entries: The Sparred Owl (Northern spotted owl x barred owl) and the "Mighty" Ash (GM/Oregon ash x Manchurian ash). The first hybrid species responds to the interbreeding of the native Northern spotted owl of the Pacific northwest to the barred owl of the Eastern U.S., speculating on how the owls might respond in the years following the USFWS's experimental lethal removal of barred owls (a project that will likely not remove *all* barred owls). This speculative entry imagines species adaptation through hybridization and resistance of conservation practice that seeks to keep two species apart. The second responds to the 2022 discovery of the emerald ash borer in Oregon (a nonnative beetle that decimates native ash trees), speculating on a combined genetic engineering and back breeding program to gain resistance to the beetle. This entry speculates on how ecosystems

might work alongside humans as partners in conservation—the Oregon ash being highly susceptible to the emerald ash borer without intervention.

Chapter Outline

Chapter 1, “Policing Hybrids & Boundary-Crossers: U.S. Conservation in the Age of the Endangered Species Act,” bears the primary thrust of my argument where I, first, evaluate the ESA’s understanding of species and hybrids and second, interrogate conservation case studies of hybridizing T&E species to assess different ways the U.S. Fish & Wildlife Service (USFWS) has responded to the blurring of species boundaries in practice. The ESA has a vague, mostly undefined understanding of species, relying on its “best available science” mandate, and therefore USFWS scientist discretion, to properly identify species and guide proper management decision making. While outside review of management plans is part of this process, and further peer review is encouraged to settle “uncertainty,” *discretion* is nonetheless still a part of selecting who participates in such reviews and therefore the judgment—and value-judgments—of USFWS scientists play a significant role in identifying species and determining what level of blurring across species borders is deemed acceptable. Typically, due to the intense controversy over species listing, *no* boundary blurring is accepted and genetic integrity of species is considered of paramount importance. The ESA has no current policy on hybrid species, but current precedent has determined hybrids to typically be identified as *threats* to the futurity of T&E species and their recovery. The first case study of this chapter, the red wolf, looks at one the principal cases of hybrid threat in US T&E conservation where USFWS biologists actively sterilize and euthanize hybridizing coyotes and hybrid coyote—red wolves to prevent the infiltration of coyote genes into the red wolf genome. In contrast, there are also rare, extreme, cases in which the USFWS will *use* hybridization for conservation purposes, but only in contexts controlled by

humans, as demonstrated by the Florida panther case study. In this case, the Florida panthers were so inbred their extinction seemed imminent without introducing outside diversity, thus the USFWS used controlled hybridization with Texas pumas for “genetic rescue” of the panthers. In both the red wolf and Florida panther case studies, *control* of hybridization is therefore central to the management practice, whether or not such hybridization is allowed to occur. The third case study considers a different trajectory (one not yet taken by the USFWS) wherein a group of wood warblers, the golden-winged and blue-winged warblers (and their many hybridized forms), might be managed as an evolving *complex* with genetic exchange across species boundaries. However, such a strategy would require the relinquishing of human control over genetic flow and a more responsive management approach that considers who the birds themselves perceive as kin.

Chapter 2, “Natural Engineers, Genetic Integrity, & Nativist Purity: How Scientists are Making the Case for Transgenics in Conservation,” turns to current debates about the place of biotechnology in T&E conservation through the case study of the transgenic American chestnut: Darling 58, which is presently under review by the US Department of Agriculture for potential wild release. Darling 58 is the transgenic option intended to bring the functionally extinct American chestnut back from the brink after billions of trees were reduced to stump sprouts by the chestnut blight—an introduced fungal pathogen from Asia. This chapter analyzes the different appeals proponents of the transgenic chestnut are using to support the tree’s wild release, particularly in contrast to the other primary conservation approach, a hybridized tree crossing the American chestnut with the Chinese chestnut which coevolved with the blight and has natural resistance. The transgenics scientists draw on a set of 4 primary appeals in their arguments: (1) a naturalness appeal, citing a natural gene engineer and natural sources for the

blight resistance gene; (2) a minimal human intervention appeal, both through promoting natural transgene inheritance and rejecting Chinese chestnut genetics as bearing thousands of years of human intentional breeding as an orchard tree; (3) a genetic purity/integrity appeal, as the *amount* of introduced genes is far less in the transgenic option than in the hybrid cross program; and (4) a nativist purity/cultural lens appealing to American heritage by rejecting the Chinese chestnut “foreign” genetics. In an interesting twist of logic, the scientists supporting the transgenics efforts both draw upon contemporary research in Horizontal Gene Transfer (HGT) that emphasizes the role of natural genetic engineers, and thus the porosity of species boundaries and the commonness of sharing genes in nature, as well as emphasize the way biotechnology’s “precision” can retain more genetic integrity of a species and avoid older, “messier,” tools such as breeding—an essentialist purity narrative. So, while there are opportunities for a new, less essentialist view of species, these scientists appear to be, rather, purist conservationists in new, biotech clothing—celebrating the benefits of biotechnology for *promoting* the retention of pure species even while allowing novel conservation strategies such as novel pathogen adaptation interventions.

In chapter 3, “Speculative Evolution & the Future of Life,” the focus moves to speculative evolution imaginaries developed through art installations, bestiaries, natural histories, pop-up books, and boardgames. In this chapter I consider the ways speculative imaginaries can operate as places to test out different modes of “ongoingness”—worlds not ending but continuing—wherein potential futures can be analyzed for their emergent ethics. Such imaginaries promote vastly different ethical configurations, however: some fostering organismal agency, others repulsed by and passing judgment on potential future life. Dougal Dixon’s *After Man: A Zoology of the Future* (1981/2018) imagines a world where future diversity and

abundance produces species uncannily familiar, but sees this future world as only possible through the removal of humans from Earth altogether: a human death fantasy producing a “new Eden.” Peter Ward’s *Future Evolution: An Illuminated History of Life to Come* (2001, illustrated by Alexis Rockman) and Shawn Sheehy’s *Beyond the Sixth Extinction: A Post-Apocalyptic Pop-up* (2018, illustrated by Jordi Solano) both reject such human death fantasies and imagine Anthropocene futures—deploying (in different ways) affects of disgust and revulsion as they depict species adapted to human refuse and toxic landscapes. The last section of the chapter moves away from book-bound imaginaries to explore organismal evolutionary agency with the boardgame *Evolution* (developed by Dominic Crapuchettes, Dimitri Knorre, & Sergey Machin; illustrated by Catherine Hamilton) and Pinar Yoldas’s art installation *An Ecosystem of Excess* (2014). It is in this final section where I consider the ways speculative endeavors can also bring insight to the ways nonhuman organisms themselves can play agential roles in bringing such potential evolutionary futures into being. Speculative evolution imaginaries are thus both practical tools for envisioning future multispecies worldmaking as well as theoretical undertakings which depict and promote differential normative configurations for human relationships with other species: emergent multispecies ethics through worldmaking.

Such creative projects might seem, at the surface, irrelevant to conservation practice, but I hope that over the course of the conservation case studies I explore in the coming chapters, the creative process of worldmaking through conservation will become evident. Through conservation decisions, species worlds are made—for better or for worse—and this is a fundamentally creative process. By analyzing speculative creative imaginaries alongside conservation projects that enact specific discourses regarding species ideals, genetic integrity, purity, the role of humans in species evolution, and so forth, I hope to tease out the ways these

projects (and the stories they tell) are therefore fundamentally projects of *worldmaking*.

Understanding policy's impact on such patterns of worldmaking is crucial, therefore it is with conservation policy, and the Endangered Species Act, where the story begins.

CHAPTER II.
POLICING HYBRIDS & BOUNDARY-CROSSERS: U.S. CONSERVATION IN THE AGE
OF THE ENDANGERED SPECIES ACT

“Species classification is a model—an idealized representation of nature
that does not describe all of the messy details and nuances.”
—Fitzpatrick et al. 2015 (207)

“living beings in knotted and dynamic ecologies are opportunistic,
not idealistic”
—Haraway 2011

Introduction

To fully understand how the folk essentialist and typological impulse toward genetic purity and principles of “genetic integrity” come to dominate U.S. conservation, it is essential to address the policy landscape of conservation and particularly the piece of conservation policy that has widely been deemed the most effective at conserving large swaths of the American landscape: the Endangered Species Act (ESA) of 1973. Policy is a vital part of the overall picture because it operates as on the one hand a kind of line of communication between public interests and scientific practice on the ground and on the other it also ultimately will shape, in return, particular scientific approaches and even layperson perceptions of conservation practice and the biology of species itself. The *legal* framework of policy such as the ESA also necessitates a definitive stance on species taxonomy—lines must be drawn in legal and biological terms to clearly delineate what is being protected and what is *not* being protected. This biopolitical frame ultimately passes judgment on which genetic lineages are valued and uses the power of policy and “best available science” to “make live” the worthy and “let die” the aberrant (Biermann and Mansfield 2014; Srinivasan 2014; Biermann and Anderson 2017). However, as the Species Problem elaborated in the introduction to this dissertation can attest, taxonomic lines cannot

always be so easily drawn, leading to uncertainty and shaky protections for the groups of organisms in question. The ultimate taxonomic uncertainty comes in the form of hybrids—those organisms who descend from parental lines crossing species, subspecies, or population boundaries. Because the ESA ultimately relies on clear delineation of species boundaries—a typological or essentialist model—hybrids wreak havoc on this system. It is for this reason hybrid case studies will be the primary policy focus for this chapter.

Hybrids offer entry points of inquiry for organismal agency: even in a narrow framework of perceiving nonhuman animals as reproduction oriented toward passing on genetic material, “species” fails to signify anything to an organism—why else would instances of hybrid offspring be so common (as will be clear in a moment)? Certainly hybrid matings have little to do with a concern for the future of a *species*, so how should we read these instances from conceptual view? What do the existence of hybrid offspring (both viable as well as sterile) tell us about what *matters* to nonhuman species and organisms? Can a reading of these hybrids be corroborated by the current ESA policy stance on species? And if the existence of hybrids cannot be aligned with current policy views, then perhaps a recalibration is necessary—a shift towards organismal flourishing and processual/evolutionary management rather than an untoward emphasis on species-as-such. In what follows I will first discuss the ESA understanding of species broadly understood, with particular attention to the role of the “best available science” mandate and U.S. Fish & Wildlife Service (USFWS or the Service)/Agency discretion, as this plays a role in all listing and taxonomic judgments in ESA policy-relevant management decisions. I will then look at the ESA policy history on hybrids including their current stance in the context of contemporary literature on hybridization and its ecological and evolutionary roles. The second half of the chapter will look at three case studies of Threatened and Endangered (T&E) species

that are either ESA listed or listing candidates that hybridize. Two of these cases, the red wolf and the golden-winged warbler, are species that hybridized in the wild “naturally,”³ the third, the Florida panther, is a case of intentional hybridization for genetic rescue—an interesting case of USFWS policy change in the extreme circumstance of looming extinction. As these cases will show, taxonomic uncertainty and the presence of hybrids are readily taken advantage of by private interests as opportunities for delisting species (and opening lands up for development) but also are sometimes overblown by USFWS scientists themselves as they lean on the debates and uncertainty paired with the “best available science” mandate to then support their own discretionary decision making. When taxonomic certainty vanishes, values more easily come to dominate conservation decisions—whether this is readily admitted by USFWS employees themselves or not. However, as will soon become clear, taxonomy itself is not devoid of value judgment—an inherent part of any policy-relevant decision. Thus, we will begin with the ESA and how it views species and taxonomy.

How the U.S. Endangered Species Act Sees Species

The U.S. Endangered Species Act (ESA) of 1973 was the result of concerted efforts over the course of the 1960s by Department of Interior employees and legislators, developing from its earliest form as the Endangered Species Preservation Act of 1966, to an amended Endangered Species Conservation Act of 1969 (that now included threatened species), to the 1973 version that largely remains in the same form we know it today (U.S. Fish and Wildlife Service n.d.). In 1969 President Nixon signed the National Environmental Policy Act (NEPA), another key

³ I put this in scare quotes as the red wolf hybridization with the coyote could be construed as anthropogenically induced due to the shifting ranges of coyotes and contraction of red wolf habitat and massive anthropogenic reduction of red wolf numbers. This will be clearer when I discuss the case in detail in a moment.

environmental policy of this era that requires federal agencies to produce environmental impact assessments and seek public feedback during decision making processes. Together, these policies have been central in shaping the practice of species conservation in the U.S. and the role of the public in that process. In this section I will first unpack the ESA's definitions and recommendations regarding species concepts and how these have been broadly interpreted (and debated) by the scientific literature. Key policy components we will consider are the ESA's stance on hybrids (as they naturally complicate species concepts), the taxonomic prioritization protocol, and the role of "best [available] scientific ...data" and scientist discretion in decision making (Department of Interior, U.S. Fish and Wildlife Service 1973, Section 4 [b][1][A]).

The ESA, Species Concepts, & "Best Available Science" Mandate: A Model of Scientist Discretion?

In the ESA section 3(16), they define species as follows: "The term species includes any subspecies of fish or wildlife or plants, and any distinct population segment⁴ of any species of vertebrate fish or wildlife which interbreed when mature" (Department of the Interior, U.S. Fish and Wildlife Service 1973). As some scholars have noted, "this definition does not define a species at all; it merely provides for protection of groups below the species level" (George and Mayden 2005, 374). Ultimately, leaving out a clear definition of species has practical implications:

This omission could be read as a deferment to allow for a scientific, not legal, judgment of species status. Instead, this language actually creates a loophole in which the

⁴ Distinct population segments refer (according to USFWS & National Oceanic and Atmospheric Administration [NOAA] policy) to specifically vertebrate populations of a species that meet specific "discreteness" and "significance" criteria such that the population is sufficiently separated from the rest of its larger species group (e.g. physically, ecologically, behaviorally, etc.) and contributes to the evolutionary futurity, overall diversity, or potential persistence of the species (Department of the Interior 1996b).

protection offered by the ESA is vulnerable because section 3 offers no guidelines to aid in identifying species. (George and Mayden 2005, 374-375)

How is this a loophole? It comes down to the ESA's key directive that all T&E species listing decisions must be made "solely on the basis of the best scientific and commercial data available" (Department of the Interior, U.S. Fish and Wildlife Service 1973, Section 4[b][1][A]). The Department of Interior information standards and peer review directives elaborating on this mandate only require USFWS employees "evaluate all scientific information that is used" to assure its "quality," to use primary data whenever possible, maintain records of their sources and reviews, and incorporate outside specialist peer review before finalizing listing or recovery plans or in special circumstances to resolve "unacceptable...scientific uncertainty"⁵ (Department of the Interior 1994b, 34271; 1994a, 34270). This ESA mandate, in the absence of clear definitions or policies in the legal framework itself, produces a setting whereby a massive array of conflicting scientific information can be taken up to promote various stakeholder interests. While this might seem like a disingenuous reading of the use of scientific data, our discussion of T&E hybrid case studies in a moment will illustrate just how slippery the slope can get when USFWS conservation biologists on the ground are put in the position of making tough, deeply ethical, calls regarding species taxonomy and subsequent management decisions (Haig et al. 2006). As Fitzpatrick et al. (2015) note, "the best science does not always lend itself to simple interpretations or clear cut recommendations" (213). The problem would not be so acute if the scientific literature weren't so torn over not only defining species in general (as discussed in the introduction to this dissertation), but also in the specifics of many different T&E species' cases.

⁵ While the "special circumstances" section allowed for peer review to step in if disagreement broke out, most often such peer reviews were only used (and intended) to corroborate USFWS scientist data collection methods and not to confirm accuracy of the data itself or to settle any scientific debate (Doremus 1997, 1147).

What constitutes the “*best* scientific ...data available” can therefore be fiercely contested, a window of opportunity that is frequently seized by corporate and private interests who, in an effort to turn land control away from conservation, will uplift data that sheds doubt on a T&E species’ taxonomic validity (as I will show in a moment with the red wolf). Just like the constant evolution of species, science itself is ever evolving and the eb and flow of criticism and review wherein scientific opinion can rapidly shift must be taken into account in adaptive conservation management decision making (Hill 1993; Doremus 2010). Indeed, some have argued that the USFWS and the National Oceanic and Atmospheric Administration’s (NOAA) National Marine Fisheries Service (the other agency that enacts the ESA), have regularly failed to uphold the “best available science” (BAS) mandate—but without clear definitions of what “best” means, it has been hard to prove such claims (Murphy and Weiland 2016). Higher courts have almost exclusively ruled in favor of the USFWS or NOAA over matters of BAS, even in cases where the science amounted to precedent, “declaring that the federal courts must accord ‘the highest deference’ to agency determinations,” perhaps “reflect[ing] the appreciation of individual judges that they themselves do not have a grasp of the science” (2).

While we cannot expect judges to become experts in any scientific field in addition to their legal expertise, numerous scholars do point to the need to create some legal or practical guidance for the BAS mandate (Doremus 2010; Murphy and Weiland 2016; Lowell and Kelly 2016). As George and Mayden stress,

determining species status is not a process that should occur in the courtroom. Instead, it should be an objective process, supported by scientific data and structured by a correct understanding of the various species concepts. Because conservation biology is a science, it is imperative that no decisions about species status are made with policy as the principal goal. Allowing any other discipline to intervene with taxonomic research will lead to bias and ethical dilemmas, neither of which will aid the goal of conservation. Although listing decisions are unavoidably political, such pressure must not affect the science involved in species identification. (George and Mayden 2005, 406)

But is it possible to separate taxonomic research so completely from policy decision making? How does the BAS mandate play out in practice within both a policy sphere and with such uncertain data? In their study of USFWS & NOAA Recovery Plans, Biological Opinions, and legal battles from 1980-2014, Lowell and Kelly (2016) have shown that while both agencies have won similar proportions of legal battles, the USFWS (which protects a considerably larger percentage of US T&E species) had, as compared overall to NOAA, less diverse authorship affiliation for their Species Recovery Plans and less frequently cited from literature published in high-quality journals. They note that NOAA's Fisheries branch (which manages its ESA oversight) operates on a similar budget as the USFWS but with considerably fewer species to protect—an institutional capacity that might allow NOAA to produce more thorough reviews of scientific literature in the development of their plans and other policy documents. In addition, NOAA has more extensive research and science centers that “are geographically and administratively separate from regional regulatory offices” (58). Lowell and Kelly stress that USFWS' lack of such separate science centers “does not directly imply a lesser use of science, but does at least somewhat increase the potential for regulatory capture—an agency acting in the interest of the industry that it regulates or political powers instead of in the public interest—due to the greater blurring of political and scientific lines of inquiry” (58). When compared to other government agencies such as the US Forest Service or Bureau of Land Management, industry interests work less in concert with the USFWS and the Service also less often *directly* regulates industry (as the Environmental Protection Agency or Animal and Plant Health Inspection Service do for instance), thus the blurring of industry interests with USFWS interests might be less of a concern. However, Lowell and Kelly's observation does emphasize how scientific and policy realms are brought into the same space—a blurring of interests that can lend itself to masking the

way scientists' own values can enter scientific decision making. And the problem of species definitional uncertainty creates fertile ground for values to enter scientific discourse.

When the species definitions scientists have to work with are theoretical concepts that can only loosely capture what exists in reality (or can capture it much of the time, but not always), then scientists must resort to their own judgments in difficult cases: “Thus the question becomes: when *should* the two populations be defined as distinct—when 99%, 98%, 97%, et cetera, are reproductively isolated?And while [answers to these questions] can be informed by science, such definitional acts are ultimately political, social, and moral pursuits” (Carolan 2008, 946-947). As the first epigraph to this chapter suggests, species classification becomes a kind of idealized model—one that,

that works very well most of the time, but is not always satisfactory. The problem for conservation is that agencies and organizations cannot always expect to receive a single true answer from scientists on questions about taxonomic status. Sometimes classification must be a policy decision to follow one of many scientifically sound conventions for delimiting taxa or identifying individuals. (Fitzpatrick et al. 2015, 207)

Therefore, despite some scholars (such as George and Mayden 2005 quoted in the above paragraph) preferring to see taxonomic decisions as a “purely” scientific endeavor devoid of bias and “ethical dilemmas”—this is clearly a pipe dream. Even George and Mayden (2005) themselves admit “data chauvinism,” or the preference of certain data collection methods to the exclusion of all others, to be a particular problem in current taxonomy (403). For instance, such chauvinistic views presently create division between those who prefer genetics (and its latest technological innovations) over morphological characters for separating lineages. These disputes in science indicate, on the one hand, perhaps a *scientific* debate over the superior method, but also a value orientation as most scientists will nevertheless disagree, and many still believe a combination of tools is the best approach. While such a debate can be informed by science (e.g.,

we can identify cryptic [not morphologically evident] species by their genes therefore genetics are better, etc.⁶), with many different goals for taxonomy, many different species definitions, and no actual clarity on species themselves...the debate is not likely to be resolved by the scientific method any time soon. As Holly Doremus (1997) notes, these kinds of subjective factors “may strongly influence the views of individual scientists, but they dominate community views only at the borders or frontiers of science, where lack of data leaves more room for subjective interpretation” (1067). As the scientific community learns more, the data is mulled over and the scientific method “exerts powerful checks” on potentially overly subjective forays into scientific practice. Of course, many of the species presently imperiled have very small population numbers, making them harder to study, and those that are not presently listed under the ESA might be harder to find research funding for—so for many of these candidate species, little is presently known about them. Therefore, in the case of species under consideration for ESA listing, USFWS employees can draw upon the “best available science” at their disposal, but if that science disagrees (or is lacking)—they will ultimately be making a policy-oriented decision undergirded by values on their species’ taxonomy (Shrader-Frechette and McCoy 1999). A decision with potentially huge consequences considering the “species” in question is one potentially on the brink of extinction.

The Preble’s meadow jumping mouse (*Zapus hudsonius preblei*) is one such subspecies whose taxonomic debate nearly meant losing its protections in the early 2000s. In 2003, then biologist for Denver Museum of Nature and Science Rob Ramey released a genetic, morphological, and ecological study suggesting that Preble’s does not represent a discrete

⁶ For example, strategies of “DNA barcoding” revealed ten novel butterfly species from a single species previously identified (Hebert et al. 2004). Of course, many debate whether such strategies are merely “taxonomic inflation” and over emphasize genetic differences as measures of distinctiveness.

subspecies and should be synonymized (i.e., considered the same species) as the Bear Lodge meadow jumping mouse (*Z. h. campestris*) (Carolan 2008; Ramey II et al. 2005). Practically following on the heels of this report, the USFWS began outside peer review of the study and, finding that Ramey's results seemed to have merit, began the process for delisting Preble's. Massive outcry followed this proposal, including a huge outpouring of scholarly articles all attempting to establish Preble's subspecies identity beyond question. But as Carolan (2008) notes, what the Preble's debate reveals is both the limits of the "best available science" mandate and the tenuous nature of our species concepts. He points to a Ramey quote in a Denver-based newspaper as particularly revealing of the undergirding values inherent in the debate. Ramey said:

"If you're willing to keep this [Preble's mouse] listed as a subspecies, then how far are you willing to go?" (Erikson 2006, A2). In short, Ramey's reason for denying Preble's mouse subspecies status is because 99.5% genetic similarity would constitute an ESA policy stance that is too precautionary for his liking. (948)

Carolan also notes the other side of the debate similarly approach the problem with different "shoulds"—theirs more concerned with protecting evolutionary potential and therefore populations such as the Preble's might have value in such a view. What is important to consider here, Carolan stresses (and I agree), is not so much a criticism that values are engaged in the debates but rather that values are often *masked* as scientific judgments and therefore glossed over and ignored: "By not explicitly acknowledging these value judgments, the scientists of the U.S. Fish and Wildlife Service (FWS) and National Oceanic and Atmospheric Administration (NOAA) Fisheries are being allowed to tacitly inject their own values into these decisions" (Carolan 2008, 947). Openly acknowledging even the value judgments inherent in determining what constitutes "best" in the "best available science" mandate would be itself an important step toward a more transparent process. And as Haig et al. (2006) note, subspecies designations

themselves have caused dispute in the scientific community, therefore leaving the USFWS to “evaluate highly esoteric disagreements among respected scientific experts with little expertise of their own” (1591). While Haig et al. assent that “some degree of interpretation of what is the ‘best available’ scientific information will always be required”—therefore value judgments are always part of the equation—they are of the opinion that “the scientific community can help ensure that interpretation of taxonomy is solely a scientific endeavor” (1591). The push and pull between acknowledging the unavoidable nature of valuation in listing decision-making and yet striving for the objective scientific ideal is evident in these science-policy intersections. And disagreement over the value of subspecies categorizations themselves and how to distinguish them foreshadow problems to come for the ESA’s taxonomic prioritization hierarchy put into place in 1983.

Taxonomic Prioritization for Listing & Recovery: Minor or Significant?

While receiving far less attention in the literature than the ESA species problem writ large, the ESA taxonomic prioritization protocol presents its own challenges that stack upon these other issues. In 1983, the ESA was amended to add a prioritization protocol targeted at appropriately directing limited conservation funding to species identified as the most deserving by measures of magnitude and immediacy of threat, their recovery potential, and taxonomic categorizations. In the latter category, the highest priority was given to monotypic genus species (a species that is the only in its genus), the second to species, and the third to subspecies or distinct population segments—though in the third category there was a finer distinction made if necessary, placing distinct population segments at the lowest level of priority. Overall, the prioritization schema creates a scale of 18 priority levels different species/subspecies

can be placed (see Table 1). The rough taxonomic categorization was aimed at quickly grasping and protecting the most genetic distinctness possible without requiring extensive analysis. The designation made ultimately value-based claims regarding the importance of protecting “genetic distinctness”:

Taxa that are most genetically distinct should receive priority within any given category of degree of threat. Monotypic genera will be given priority over species, subspecies, or populations. This last criterion is in recognition that the loss of the most genetically distinct taxa is of greater significance than the loss of less genetically distinct taxa. That is, for example, the loss of a full genus is of greater significance than the loss of a single species or population of that species. (Fish and Wildlife Service, Interior 1983, 43104)

The USFWS further emphasized that this distinctiveness was a way of capturing the species’ potential contribution to wider biodiversity: “the more isolated or distinctive a gene pool, the greater contribution its conservation is likely to make to the maintenance of ecosystem diversity”

Recovery Priority			
Degree of threat and recovery potential	Taxonomy	Priority	Conflict
High:			
High.....	Monotypic genus.....	1	1C, 1.
High.....	Species.....	2	2C, 2.
High.....	Subspecies.....	3	3C, 3.
Low.....	Monotypic genus.....	4	4C, 4.
Low.....	Species.....	5	5C, 5.
Low.....	Subspecies.....	6	6C, 6.
Moderate:			
High.....	Monotypic genus	7	7C, 7.
High.....	Species.....	8	8C, 8.
High.....	Subspecies.....	9	9C, 9.
Low.....	Monotypic genus.....	10	10C, 10.
Low.....	Species.....	11	11C, 11.
Low.....	Subspecies.....	12	12C, 12.
Low:			
High.....	Monotypic genus.....	13	13C, 13.
High.....	Species.....	14	14C, 14.
High.....	Subspecies.....	15	15C, 15.
Low.....	Monotypic genus.....	16	16C, 16.
Low.....	Species.....	17	17C, 17.
Low.....	Subspecies.....	18	18C, 18.

Table 1: USFWS listing & recovery prioritization protocol. "Conflict" refers to potential species conflict with development which bumps a species up in priority at the last stage. Table reproduced from Fish and Wildlife Service, Interior 1983.

(43103). While the taxonomic protocol was a sticking point for some during the public comment period, the Service asserted that the prioritization system was intended to be flexible as needed, so could be modified depending on the specifics of different circumstances. The Ecological Society of America was one concerned party, who noted that plants and invertebrates tended to have different taxonomic

standards than vertebrates, leading to far fewer monotypic genera—a difference that could lead to a deepening bias towards conservation protections for vertebrates (43099). Of course, under the ESA only vertebrates can be listed as “distinct population segments” whereas plants and fungi cannot be listed below the subspecies/variety level. This might indicate a potential balancing of the scale, but as Haig et al. (2006) note, “subspecific taxa are frequently described” among plants (1589) and one 1995 study of 104 monographs found 56% included taxa below the species level (McDade 1995).

The use of different species concepts can also have a significant impact on the way groups of organisms are distributed between the different taxonomic levels. Under the typical Phylogenetic Species Concept (PSC), because often minute differences can differentiate species, species are the “smallest, irreducible...units” and as such subspecies are not recognized under this model—this raises nearly all listable units to the species level, giving them a higher priority under the ESA’s prioritization schema (Haig et al. 2006, 1585). Under the Biological Species Concept (BSC), such groupings might be either lumped together (and potentially lose protections) or retain protections but at a lower priority level as they would then be given subspecies designations. Which species concept used, particularly when paired with the prioritization protocol, can therefore have real material consequences for recovery. It is easy to see how value judgments regarding different species concepts might bleed into conservation goals, as the selection of a species concept, paired with conservation intentions can easily lead a taxonomist to prefer the PSC over the BSC in practice. The accusations of “taxonomic inflation” as discussed in the introduction to this dissertation become an acute problem in this context (Padial and De la Riva 2021). And the functionality of the prioritization system differs greatly depending on the species concept in use. Where it might be easy to identify genetic

distinctiveness using taxonomic levels if the BSC is predominant (and therefore subspecies are regularly used), if the PSC is in use, then the “isolated or distinctive gene pool” that is deemed of value to the USFWS is not as readily graspable merely by glancing at Linnaean trinomials (i.e., the three-named system used by subspecies). Further complicating matters is the frequent lack of clearly stated methods by taxonomists or listing agencies on what species concept is in use. As Haig et al. stress, “Experts in each field are better able to judge the legitimacy of subspecies if the methodology, including the species concept used to determine classification, is stated explicitly in taxonomic publications”—a call that applies equally to listing and recovery planning where understanding the actual “genetic distinctiveness” of the group of organisms at hand will mean understanding the means by which they have been taxonomically grouped (Haig et al. 2006, 1590-1591).

As yet, the prioritization protocol has received an overall limited attention in the literature. However, some public critics have pointed out that the protocol doesn’t specify how much funding is strictly required to go to higher priority versus lower priority species—potentially diminishing its overall functionality. In an *Atlantic* piece, Charles C. Mann and Mark L. Plummer remarked that the dusky seaside sparrow, a species now extinct, shared its level 6 ranking with 38 species at the time, including the northeastern beach tiger beetle and the Florida panther: “In 1990 the service spent not one penny to bolster the beetle’s chances for survival...meanwhile, the Florida panther, a ‘higher’ life form, received \$3.8 million” (Mann and Plummer 1992). The protocol had been introduced in part to replace an earlier policy that actually favored such “higher life forms”—formerly requiring a priority of “mammals, birds, fishes, reptiles, amphibians, vascular plants, invertebrates”—as the legislators had now specifically stated “opposition to the adoption of any system that would give consideration to

whether species were ‘higher or lower life forms’” (Fish and Wildlife Service, Interior 1983, 43102). As Mann and Plummer suggest, however, the intent of the USFWS and the actual designation of funds are perhaps less aligned than the intent of the original policy—leading one to question the efficacy of the protocol’s ability to capture conservation values such as “genetic distinctiveness” and its overall impact on conservation in practice. One area it has had an undoubted impact, however, is on the speed with which some species are rushed through the listing process and others are thrown into a candidacy purgatory. Such species are deemed warranted for listing but are “precluded” by higher priority species bumping their spot on the list, keeping them perpetually in a state of “candidacy under review” without moving up to protected status as a listed species. Houck calls the “‘warranted but precluded’ category...a black hole for unlisted endangered species” (Houck 1993, 286). This is clearly a symptom of an underfunded and understaffed USFWS—with enough bodies on the ground there would be enough people to review such candidate cases. However, debate circulates around the USFWS use of candidate conservation agreements, typically used to avoid listing species altogether, many conservationists uncertain whether these agreements constitute adequate protection or “sound basis” for not pursuing ESA protections (Rosmarino 2002, 25). Organizations such as the Center for Biological Diversity pursue legal recourse by suing the USFWS to spur motion when they see the agency as being “too slow” to list a species (Center for Biological Diversity n.d.). Ultimately, the presence of *valuation* in the process of prioritization is clearly still at work, no matter how objective the USFWS hopes the process will be. On the one hand perception of threat is paramount, which is clearly a risk judgment that can only come with interpretive and value-based orientations, and on the other hand sits both the values inherent in species taxonomy and the evident preferences towards “higher-life forms” still biasing funding regimes. The priority

system, and its taxonomic foundation, are—for better or for worse—riddled with value-judgements. These values are therefore profoundly important for considering the ESA’s approach to cases where these species norms and values do not hold up: hybrids.

The ESA Approach to Hybrids

As might be already clear, uncertainty over species concepts, and therefore uncertainty over where one species ends and where another begins, can add fundamental complications to the question of when and where hybridization between species is occurring. However, hybridization has a broad definition that encompasses crossing between species, subspecies, and even distinct populations underneath the larger species umbrella, thus there are many naturally occurring “hybrid zones” that spring up where different populations of a species intersect. Sometimes hybridization can be a matter of just limited desirable partners in an organism’s own species—a circumstance that will trend upward when there are dwindling numbers in a T&E species. As Maclaurin and Sterelny (2008) quip, “whether you are in with a chance depends on who else is at the party” (28). Hybridization is typically described as “genetic introgression⁷” from one species into another, which, as the Cambridge textbook definition asserts, is “a threat to the genetic integrity of a range of canid, fish plant, etc. species” (Frankham, Ballou, and Briscoe 2010, 532). The “genetic integrity” appeal deployed here is a normative concept that is frequently called upon in conservation biology as a value “so intuitive as to go unjustified” (Rohwer and Marris 2015, 235). And while many biologists will loosely frame hybridization as an overall “threat” to genetic integrity, there are still attempts made to further determine “good versus bad” hybridization, particularly when making conservation decisions. As always there is

⁷ Introgression refers to the transfer of genetic material from one species into the gene pool, or genome, of another.

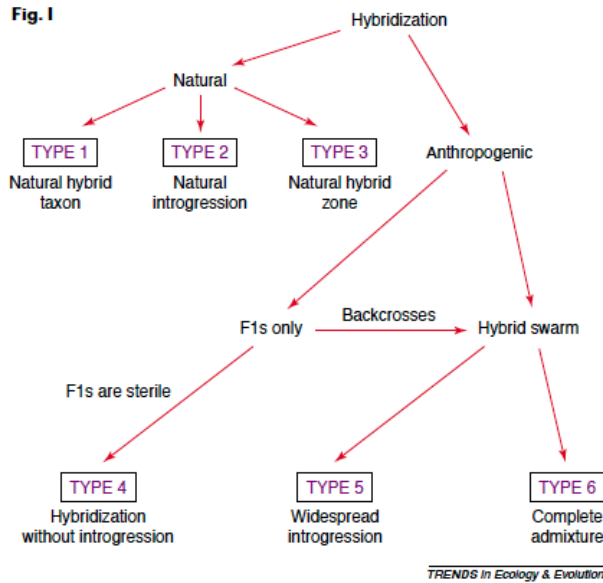


Figure 2.1: Hybridization types differentiated by natural or anthropogenic causes. Figure from Allendorf et al. 2001

disagreement, but many biologists nonetheless typically draw the line at “natural versus anthropogenic” hybridization (Allendorf et al. 2001; Jackiw, Mandil, and Hager 2015). On the one side are naturally occurring fully hybrid taxa and hybrid zones where the parent species can maintain their source populations and separation, on the other extreme are often human-introduced species that rapidly hybridize with native species, quickly producing widespread introgression and ultimately creating “hybrid swarms” of completely admixed organisms (see Figure 2.1). This is a difference some see as of particular importance in the context of management. As one widely cited article on the topic states:

We appreciate how difficult it can be to distinguish between natural and anthropogenic hybridization. Nevertheless, this distinction is of primary importance. The alternative is to either not allow protection of natural hybrids or to protect anthropogenic hybrids that could contribute to extinction of parental species and waste limited resources available for conservation. (Allendorf et al. 2001, 618)

Some recent literature seeks to break this dichotomy, however, stressing that it can downplay the agency of other-than-human beings, uplift Western conceptions of Nature, and maintain an overly anthropocentric orientation (Donfrancesco and Luque-Lora 2022). Rethinking hybridization as a conservation management tool that might forward biodiversity goals in the Anthropocene are widely under debate (Chan, Hoffmann, and van Oppen 2019; Ottenburghs 2021; Draper, Laguna, and Marques 2021). Fitzpatrick et al. (2015) suggest an enhanced understanding of evolutionary processes in particular would go a long way to supporting

conservation practice as it would better capture the “messiness” of species that are hard to classify, hybridizing, or just not quite separate (yet) from other populations as they near speciation. The process of “speciation can be very fast or quite slow, but a fundamental prediction of evolutionary biology is that there will almost always be a period of uncertain or incomplete separation” (Fitzpatrick et al. 2015, 207)—it is these moments of uncertainty that make species even more difficult to capture with essentialist or typological concepts.

Adding even more complications to the already messy endeavor of taxonomy, hybrids make for decidedly confusing territory when protecting T&E species—where do hybrid progeny of a listed species land? Should they receive protections? Or be viewed as a threat? The ESA’s conflicting and unclear policies on hybrids have therefore received extensive attention and debate over the years (Allendorf et al. 2001; 2004; Haig et al. 2004; Lind-Riehl et al. 2016; Erwin 2017; Willis 2020). Initially, the ESA took a strict stance against extending protections to hybrid young of listed parents, asserting that such young could not conceivably have a role in furthering the “continued existence of that species,” however the policy was withdrawn in 1990 as genetic research of the era began to call into question such rigid standards, seeking a case-by-case approach instead (Allendorf et al. 2001, 614). It is often suggested that the ESA’s early “no tolerance” policy is what spelled the demise of the dusky seaside sparrow—whose restoration funding dried up in the late 1980s as only male duskies remained and a hybrid breeding program was the species’ last chance (Avisé and Nelson 1989; Mann and Plummer 1992). In 1996, an “intercross”⁸ policy was proposed, where USFWS might manage intercross (i.e., hybrid) individuals in their overall effort to protect the T&E parent species,

⁸ As defined by the Department of Interior, “intercross” referred to “any mating, fertilization, or other means of exchange of genetic material between different species, subspecies, or distinct vertebrate population segments within a taxonomic species” (Department of the Interior 1996a, 4713).

by protecting and conserving intercross progeny, eliminating intercross progeny if their presence interferes with conservation efforts for a listed species, and fostering intercrossing when this would preserve remaining genetic material of a listed species....these actions [would only be sanctioned] where recommended in an approved recovery plan, supported in an approved genetics management plan, ... and undertaken to compensate for a loss of genetic viability in listed taxa that have been genetically isolated in the wild as a result of human activity. (Department of the Interior 1996a, 4710)

The policy focused on overall genetic viability of the listed species paired with human *fault* as the cause for its genetic isolation. However, the policy would have primarily emphasized intercrosses that “closely resemble” their listed parent species, a measure that some scholars emphasized was not always a good marker for genetic similarity (Department of the Interior 1996a, 4710; Lind-Riehl et al. 2016). And, like our species “precluded” into candidacy purgatory, the ESA Intercross Policy never made its way beyond the stage of “proposed rule”—a perpetual limbo that has left contemporary approaches to hybrid individuals mixed, confused, hotly debated, and rife with value-judgments. The only presently existing official policy regarding hybrids or intercrosses remains in the policy on propagation—or captive breeding—programs where it is “not considered for use” *unless* specifically recommended in approved recovery plans (usually for genetic rescue), using identical language as listed in the above, defunct, intercross policy. However, it goes further to require formal approval from the USFWS Director if any intercross individuals will be used in breeding recovery programs for species conservation (Department of the Interior 2000, 56920). And while US policy is ultimately vague on hybrids, the international authority on conservation, The International Union for the Conservation of Nature (IUCN) sees hybridization as a threat to species extinction comparable to pollution, competition and parasites, all “classified as threats for the survival of species [which]... means that evaluators of the extinction risk of species might declare hybridization as a threat even without a specific quantification of its impacts” (Draper, Laguna, and Marques 2021,

2). IUCN also asserts hybrids cannot be proposed for Red List assessments as they do not fit the “pure species” criteria.⁹ In the absence of clear guidance by ESA policy, falling back on precedent such as IUCN policies or general scientist sentiment regarding hybrids is not uncommon—particularly when scientist discretion under the “best available science” directive has such sway.

A 2016 study interviewed USFWS employees to better understand their knowledge base in ESA hybrid policy, hybrid science, and how they approached hybridization in practice. It noted that, “in general, the less work experience respondents had with unclear species boundaries and hybridization (natural or human-mediated) issues, the more likely they were to view hybridization as broadly negative in a conservation context” (Lind-Riehl et al. 2016, 1292). As one USFWS employee expressed, for “the purposes of the ESA, we tend to view hybridization as a threat because of its potential to cause the appropriation of the species or loss of the species due to introgression and outbreeding and depression...” (qtd in. Lind-Riehl et al. 2016, 1292).

However, many biologists emphasized human mediated as different than natural:

I might only call [hybridization] a threat if it’s something that’s obviously human induced. [T]hat would be my one bias... I know there’s some [natural] hybridization that is going on ... [for example] prairie bush clover ... hybridizes with round-headed clover, and it seems like that only happens in some places..., so I don’t think we would call it a threat at this point. (qtd. in Lind-Riehl et al. 2016, 1292-1293)

Another claimed, “hybridization is only a problem because of human intervention” (1293).

Significantly, the USFWS scientists seemed to have a large amount of personal discretion in how they “interpret[ed] policy and work[ed] to identify, assess, and interpret data sources regarding

⁹ This policy has created its own problems as assessors have ended up following a binary approach where hybrid populations are assigned to one parent species or the other, rather than identified as hybrid—a situation that can have conservation implications on the ground. For instance for elephant conservation when a population is described as a “forest elephant” or “savanna elephant” when the hybrid population in fact uses both areas, preventing regional governments from effectively engaging in international conservation policy debates (Bauer et al. 2021).

candidate species” (1291). As one interviewee expressed, “I do my literature review...and make my assessment and talk to the management, and they may have questions [for me to clarify], but generally it’s my assessment” (1291). While final decision making and approval isn’t made until proposals reach headquarters, and recommendations *are* peer reviewed, the interviewees emphasized their early conversations and discretion in selecting collaborators done to avoid any “surprises” later on. But how are these views, and present gaps in hybrid policy, matching up with literature on hybridization?

The current genomic turn has had a significant impact on an outpouring of literature attempting to turn the tide on negative views regarding hybridization (Dowling and Secor 1997; Draper, Laguna, and Marques 2021; Hirashiki, Kareiva, and Marvier 2021). As vonHoldt et al. (2018) discuss, this research indicates that “evolutionary relationships more closely resemble a web-of-life (WOL), whereby hybridization is often as important as the TOL [tree-of-life] evolutionary process of reproductive isolation...[and] this revelation of frequent gene flow among taxa necessitates a new outlook for conservation” (1). Seeing hybrids as not just threats, but as opportunities for supporting the future evolutionary potential of imperiled species is one way vonHoldt et al. stress we need to be rethinking hybrid conservation potential. Hybridization events can thus provide,

a platform on which selection can act by way of stable hybrid forms that contribute to distinct evolutionary change.... The natural emergence of these nascent genomes can be evolutionarily successful because they have a new capacity to respond to changing conditions and environments. (2)

They point to an example of admixture and subsequent adaptive speciation events of Lake Victoria cichlids (a kind of fish)—thus a hybrid swarm and initial outwardly “homogenizing” gene pool was the catalyst for an array of diverse, branching events. Such evolutionary oriented views argue that “the ultimate goal of management should not be to conserve species purity in

and of itself, but rather dynamic ecoevolutionary processes (e.g., gene flow and adaptation)”—a potentially difficult proposal under the ESA’s restrained view on species (Donfrancesco and Luque-Lora 2022, 2). As many scholars point out, overcoming the present negative conservation views on hybrids is a key problem that needs to be dealt with if such “evolutionary enlightened management” practices are to be put into place (Jackiw, Mandil, and Hager 2015; vonHoldt et al. 2018; Draper, Laguna, and Marques 2021; Donfrancesco and Luque-Lora 2022).

So why not open the floodgates altogether and freely accept hybridization wherever it occurs? There are added complications to such a stance as well. As might already be clear from above, there is the concern in the field of T&E conservation of species extinction, or namely, *genetic* extinction, as a species will only live on through admixed progeny and pure specimens will no longer remain (Rhymer and Simberloff 1996). If the numbers of the hybridizing species are large enough, even that genetic signature might disappear through a process of genetic swamping. A further concern is what is called “outbreeding depression,” or reduced reproductive fitness in hybrid individuals that can be caused by genetic incompatibility or reduced adaptation to the environment (Allendorf et al. 2001). Concern is frequently voiced over the impacts of introduced rainbow trout (for sport fishing) and their subsequent hybridization with native cutthroat trout as the two fish are adapted to different stream temperature ranges in addition to other sets of local and regional adaptations (Allendorf et al. 2004; Campton and Kaeding 2005; McKelvey et al. 2016). Similar problems arise when wild salmon interbreed with hatchery salmon potentially resulting in a subsequent reduced overall fitness (Grant 2012). And while all these are legitimate concerns, and many scholars have raised the alarms over hybridization as a major extinction threat for T&E species in the past (e.g. Rhymer and Simberloff 1996; Allendorf et al. 2001; Todesco et al. 2016), a 2021 evaluation of 959 extinct species reports by the IUCN

found hybridization to only be a factor in 0.07% of the cases (Draper, Laguna, and Marques 2021). Thus, the threat to complete *extinction* of a species could be overstated while nonetheless some caution about the impacts of hybridization on the potential loss of local adaptations is warranted. An evolutionary view on management would help keep such a focus on adaptive optimization in the forefront.

Within the present ESA paradigm scholars have proposed a couple of strategies for recognizing and protecting hybrids. One approach is through the ESA's similarity of appearance clause (Section 4[e]) under which hybrids could gain the same protections as their parent T&E species (Haig et al. 2004). The original intent of the similarity of appearance clause is to avoid unintentional take of a T&E species by presuming it was a similar looking but different species (therefore the similar looking species will receive protections as well to avoid mistakes). To receive such protections, ultimately being treated *as if* the non-listed species was listed, it must be a species that "so closely resembles in appearance ... a species which has been listed ... that enforcement personnel would have substantial difficulty in attempting to differentiate" (Department of the Interior, U.S. Fish and Wildlife Service 1973, Section 4[e][A]). But for hybrids who sufficiently differ in appearance from their T&E parents this clause would not apply. For example, the complex of golden-winged—blue-winged warbler hybrids (which I will discuss later in this chapter) are so different from their parent species that they were named as their own species when originally described by Western taxonomists in the 19th century. Such hybrids would not find recourse under the similarity of appearance clause. vonHoldt et al. also

suggest that even an interpretation within the ESA’s loose species definition¹⁰ allows for recognition of hybridization, as it could:

(1) recognize that a species or subspecies can be the result of hybridization or reflect past or ongoing hybridization and (2) allow natural hybridization to be one of the factors that makes a vertebrate population distinct. Imperiled species that happen to have a hybrid origin should not be denied protection because of their origin: list the entity because the contemporary understanding of speciation recognizes that new species can arise out of hybridization. (vonHoldt et al. 2018, 4)

This approach helps expand upon contemporary understandings of species to allow for hybridization to be a source of species origin (a potential factor in our red wolf case study in a moment), and even a source of *distinctiveness* for “distinct population segments”—thus recognizing the role that hybrid zones can have in supporting future adaptation and evolution (a consideration in the golden-winged—blue-winged warbler case). Though they do note that “controversy ... arises ... where the hybrid species is backcrossing with a parental species,” suggesting that *ongoing* hybridization that maintains its connection with a parent species (continuing to cross “back” by breeding with “pure” parent individuals) might be more than the present ESA species definition can handle (4). The backcrossing problem will come up clearly in a moment with our wood warbler case study. Unfortunately, however, without a clear hybrid policy from the USFWS, and the only current policy of genetic rescue through hybridization requiring USFWS Director approval, enacting these hybrid management recommendations from the literature in practice seem unlikely without strong USFWS scientist will. To explore how hybridity is presently managed, and what scientist discretion and the enacting of “best available science” has looked like in practice, we’ll turn now to our hybrid case studies.

¹⁰ “any subspecies of fish and wildlife or plants, and any distinct population segment of any species of vertebrate fish or wildlife which interbreeds when mature” ESA, section (3)(15)

Threatened & Endangered Border Crossers

I will look here at a set of different case studies where T&E species are crossing boundaries—the borders between species are being blurred by the species/organisms themselves who are ultimately complicating how conservation can be approached in practice. I say species/organisms because, rather than just considering species as a whole, what is most interesting about hybrid case studies (I think), is the way individual organisms *within* the different categories of species make their own reproductive decisions. It is, ultimately, their choices as individuals that complicate matters for conservationists and then produce the hybrid population dynamics we see unfolding. If the individual organisms did not recognize a non-species member as a viable reproductive partner, we wouldn't have hybrid populations at all, and consequently no case studies to consider. As Donfrancesco and Luque-Lora (2022) emphasize, remembering the agency independent of humans in hybridization cases is essential to avoiding an anthropocentric view and to remembering the *coproduction* of environmental conditions shared across species. While conservation biologists talk and operate at the level of populations for good management reasons, I don't want us to forget about the agency of individual organisms within these species we seek to protect. For it is ultimately *their* behaviors that might create the overall patterns we can tease out, question, and consider. But at the root—there was something an individual organism recognized as *familiar* in another organism that transcended species boundaries; that is always the place stories of hybrids begin. In the cases that follow, we will track narratives of threat and taxonomic uncertainty through the story of the red wolf; questions of cause and management for evolutionary complexity through the golden-winged—blue-winged warbler complex; and intentional hybridization for genetic rescue with the Florida panther—where the specter of extinction renders hybridity a functional tool. Together, these cases tell a

complex and evolving story of hybrid management in US T&E conservation, and one that helps reveal how species—the conceptual foundation of the ESA—proves an ultimately soft and tenuous surface to tread.

A Debate Over the Red Wolf's Origins: Questioned Species Status & Hybrid Policing

First listed under the Endangered Species Preservation Act in 1967, the red wolf (*Canis rufus*) has been a flagship species of T&E species conservation in the U.S. since its inception. However, controversy has dogged the canid's protection nearly as long due to extensive documentation of the wolf's ongoing interbreeding with coyotes (*C. latrans*). Primary concerns this interbreeding provoked initially were regarding hybrid introgression from the coyote into the red wolf genome. With such small numbers of red wolves remaining (diminished mostly due to anthropogenic predator reduction campaigns—a familiar story in the history of wolves globally), the fear of genetic swamping from the much larger numbers of coyotes and eventual complete absorption of the red wolf genes into the coyote genome seemed imminent. In 1973 conservationists had to act quickly, and they began capturing wild canids in a small coastal region of Texas and Louisiana where the species had been reduced (see Figure 2.2, next page). Even the species' low point in numbers is hard to estimate due to the blurring across species borders that was occurring during this period. As noted by the USFWS, from the animals captured “it was clear that red wolves had already experienced significant hybridization with local coyotes. From 1973 to 1980, over 400 canids were captured; only 43 met the criteria for inclusion in the breeding/certification program” (U.S. Fish and Wildlife Service 2018, 13).

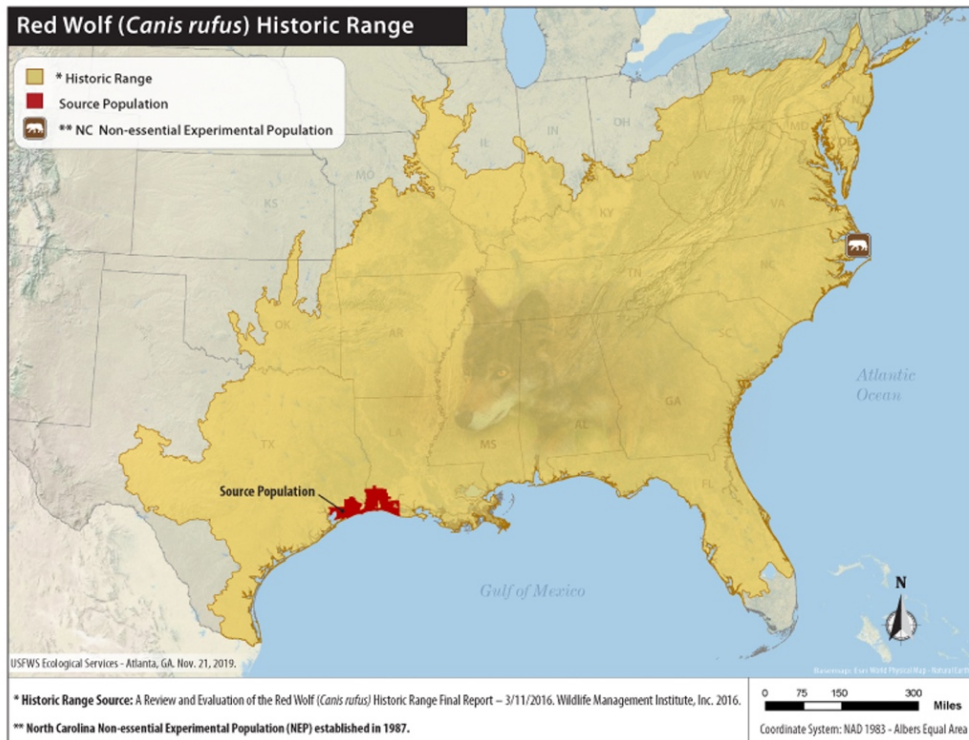


Figure 2.2: Red wolf historic range (in yellow), source population site for captive breeding program (in red), and Non-essential Experimental Population reintroduction site (brown wolf sign). Image USFWS.

Unfortunately, as this breeding program was one of the first of its kind, it met with numerous difficulties and only 12 of those original individuals now have living descendants in red wolf populations—a consideration for overall genetic diversity of the red wolf species. Red wolves were officially declared extinct in the wild in 1980, with captive breeding programs managed through their Species Survival Plan in Zoos across the US. Formal reintroduction efforts began at Alligator River National Wildlife Refuge (ARNWR, eastern North Carolina) in 1987 with what is called a “Non-essential Experimental Population” (NEP) (marked in Figure 2.2). NEPs are populations of T&E species established under Section 10(j) of the ESA and reintroduced on federal lands (e.g. National Wildlife Refuges or National Parks) within their historic range. As “non-essential” populations, their take¹¹ provisions are different than other populations of their

¹¹ The ESA defines “take” as “to harass, harm, pursue, hunt, shoot, wound, kill, trap, capture, or collect, or to attempt to engage in any such conduct” (Department of the Interior, U.S. Fish and Wildlife Service 1973, Section 3 [19]).

species, allowing more flexibility to adjacent private landowners in land use and management of offending T&E individual animals than would typically be acceptable. For example, if particular red wolves begin showing undue interest in livestock or domestic pets as prey, landowners can harass them away to deter the behavior; if even USFWS active capture and removal is unsuccessful in discouraging the wolf (i.e. it returns to the same location), then private landowners can be written approval by the USFWS to take (i.e. kill) the offending animal (Fish and Wildlife Service, Interior 1995b). Such policies are put in place to help bolster public support of reintroduction efforts outside a species' present range—particularly when considering the predominant negative reputation T&E conservation has with private landowners. Wolf conservation is especially in need of such support as predator restoration draws considerable pushback for those fearful for the protection of their livestock, pets, and children. Therefore, when controversy started to arise in the 1990s over red wolf species status, it should come as no surprise that this was capitalized upon by agricultural and private landowner interests who wished to see the red wolf reintroduction program ended.

With the development of continually more advanced genetic technologies in the late 1980s and early 1990s, DNA analysis of the red wolf began to call into question its status as a species. The most notable researchers were Robert K. Wayne and Susan M. Jenks whose 1991 mitochondrial DNA (mtDNA) analysis of captive red wolves, red wolf skins (collected 1905-1930), and blood samples from canids collected during the initial capture of the source population in Louisiana and Texas (samples collected 1974-1976) indicated contemporary red wolves bear either coyote or grey wolf mtDNA genotypes (Wayne and Jenks 1991). Even of the historical red wolf skins, they noted that they were “similar or identical to those of the grey wolf or coyote” whereas “grey wolves and coyotes are very distinct” (566). They argue their results

suggest the “red wolf could have been a distinct species with unique mtDNA genotypes that were missed in [their] survey or became extinct through genetic drift” which then hybridized throughout the majority of its range, or it is a phenotype¹² “derived entirely from hybridization between coyotes and grey wolves” (566). That same year, 1991, the American Sheep Industry Association drew upon Wayne and Jenks’s results and filed a petition to delist the red wolf, claiming it is a wolf/coyote hybrid and therefore not eligible for protections (Fish and Wildlife Service, Interior 1992). The USFWS’s finding on the petition ultimately rejects the delisting proposal, but they discuss in detail Wayne and Jenks’s results, considering different potential interpretations of the mtDNA data. Important for us to consider is that mtDNA is exclusively passed on through the maternal line—it is separate from the bulk of our genes collected in the nucleus of our cells that are paired and traded during sexual reproduction with a mate. Because mtDNA exists separately from our nuclear DNA, it is passed on directly without any exchange or loss through paternal lines. This makes mtDNA useful for identifying lines of direct descent (matrilineally, or through the maternal line), but it also offers important considerations for hybrids. As the USFWS notes in their response to the petition, it creates another interpretation of Wayne and Jenks’s results that might go beyond a narrative of extensive hybridization or hybrid origins:

[mtDNA] frequency depends solely upon the survival and spread of the matriline in the population. In contrast, any nuclear DNA that is subject to selection and is received from coyotes can be ‘bred out’ by natural or artificial selective pressures over succeeding generations.... This suggest [sic] that female offspring from any past hybridizations were successfully backcrossed with male red wolves, and their offspring did the same. These backcrossings may have produced decreasing proportions of any coyote nuclear DNA in individual wolves, while maintaining the entire mtDNA complement. Thus, any coyote traits coded by nuclear DNA have disappeared from the red wolf population, even though the mtDNA persisted. (Fish and Wildlife Service, Interior 1992, 1249)

¹² A phenotype is the collection of observable traits and characteristics of an organism; these can be derived from genes but are also the result of interactions between an organism and their environment and developmental processes. The phenotype is therefore different from the “genotype,” or genetic makeup of an organism.

Indeed, it might not take very many red wolf—coyote matings for coyote mtDNA to potentially leave its mark, particularly as wolf numbers diminished. A handful of coyote mothers could quickly alter the mtDNA dynamics of a red wolf population in flux. In their findings the USFWS also draws upon additional key research in this period to refute the hybrid origin narrative which comes from morphological and paleontological work by Ron Nowak and colleagues. Their skull measurements of coyotes, gray wolves, and red wolves indicate each group within their own populations and none overlap with the other—aligning with the argument for the three species theory (Nowak 1992).

In 1996, Roy et al. (including Wayne), published further genetic analysis of pre-1940 red wolf specimens, this time looking at both mtDNA and nuclear DNA, with the assumption that red wolves during this period *should* show unique genotypes from gray wolves and coyotes if they represent their own distinct species. As this analysis also included a larger grouping of pre-1940s specimens than Wayne and Jenks’s 1991 study, it was presumed unique red wolf mtDNA genotypes would surface with this group if there were any to be found. However, the 1996 study seemed to corroborate the 1991 findings—showing pre-1940s red wolf mtDNA grouping predominantly with coyote mtDNA and nuclear DNA having very few unique alleles¹³ when compared to gray wolves or coyotes. At the same time this work was being published, the second delist petition for the red wolf was filed by Rob Gordon of the National Wilderness Institute (NWI) in 1995, again marking the red wolf’s status as a gray wolf/coyote hybrid (Fish and Wildlife Service, Interior 1997). Now defunct, NWI was a “wise management” organization whose mission was to “unleash the creative forces of the free market, protect or extend private

¹³ For every gene you receive two copies—one from each parent. When the copies differ (often producing recessive versus dominant versions of a trait), these copies are called alleles. Because alleles appear consistently at the same location on a chromosome, and alleles will differ between populations, they can be useful tools for tracking patterns in population genetics.

property rights, and reduce the inefficient and counterproductive effect of government regulations” (“National Wilderness Institute” n.d.). Gordon co-founded NWI in 1989 and is now serving as President of Responsible Resources at the Heartland Institute (“Robert Gordon – The Heartland Institute” n.d.). In light of NWI’s mission, the motivations behind Gordon and the NWI’s delisting efforts should be relatively clear, but I mark them to note the way that controversy over the red wolf’s status as a species was regularly used over the course of the early 1990s to further private property and agricultural interests hoping for its delisting. The ESA had always been controversial policy for private and corporate interests, and any opportunity to restrict its scope or delist a particularly troublesome species is typically taken up by the relevant stakeholders. Maintaining management of the flagship red wolf as a fully-fledged species and asserting barriers between it and other species therefore has ulterior motives beyond just protection of red wolves—this status keeps funding lines open to the project and region and helps reassert the validity and necessity of the ESA’s strict policy guidelines. Therefore, NWI’s petition was found without merit in a relatively short response by the USFWS, mostly referring back to their 1992 findings with some additional reference to the Roy et al. research that had emerged over the intervening time (Fish and Wildlife Service, Interior 1997). In the USFWS’ words, “these studies suggest past hybridization, but provide no support for continuing hybridization in the existing red wolf populations,” seeking to assert the Service’s full capability to enact the “elimination of such coyote nuclear DNA from existing red wolves” (64800).

During this same period citizen organizations were forming in opposition of red wolf presence on private land and North Carolina passed legislation allowing for the trapping and killing of red wolves by private land owners (House Resources Committee, 104th Congress 1996; General Assembly of North Carolina Session 1993 1994). It was clear by now that

something needed to be done regarding the hybrid controversy in order to deter future delist petitions. In 1999 a population and habitat viability assessment workshop was held gathering together 40 scientific and management experts to assess the future prospects of the red wolf program. While the workshop initially had split into 5 working groups (e.g., wild population monitoring, new population site selection, etc.), “the hybridization/genetics group quickly realized that the immediacy and significance of the hybridization threat superseded all other issues. ... By noon on the second day of the workshop, it was clear that each of the working groups began to focus on hybridization as the primary issue driving discussion on red wolf conservation” (Kelly, B.T., Miller, and Seal 1999, 4). Debates in the hybrid working group included questions such as “How do you place the red wolf in an evolutionary context, should we preserve it in captivity, is the red wolf a species or sub-species, is hybridization a natural process, are hybrids red wolf more adapted to current conditions (i.e., have we interfered with a natural evolutionary process that may not be constructive?)” (12). These questions offer a compelling window into their conversations, particularly in the face of the clear “hybrid threat” narrative with which hybridization is being framed in the overall document and workshop. While questions about the red wolf’s status as a species come up in this working group (and notably both Wayne and Nowak are present in this group—so certainly disagreement will be imminent), there is more interest in the practical evolutionary trajectory of the wolf. What might hybridization mean for the red wolf’s evolutionary path? Is coyote interbreeding supporting it in some way? However, in the end, the group settled on an ultimately more conservative overarching statement that reflected the “collective feelings” of the working group: **“Hybridization that affects the genetic and phenotypic integrity of the red wolf is the primary issue facing its recovery. How we proceed with red wolf recovery is dependent**

upon how we assess, and if possible, manage hybridization” (14; bold original). Legal scholar Holly Doremus has argued that knowledge gaps and moments of uncertainty like that faced by the red wolf working group provide spaces for managers to make their own interpretive judgments under the guise of the “best available science” ESA mandate: “They can often conceal those judgments, and the reasons for specific choices made, from public oversight with claims that they are simply following the science.... Uncertainty may, therefore, in effect, maximize management discretion”(Doremus 2011, 1463). The questions that were raised in the red wolf working group over the potential *value* of hybrid red wolf—coyote individuals suggests there were interpretive judgments made in the moment of uncertainty, but ultimately the group decided upon the moral stance that hybridization was “bad” for the red wolf species.

Adaptive management, or flexible management decision making that changes in response to shifting data or conditions, is often taken up as a strategy for dealing with such “knowledge gaps” as it allows for “action in the face of uncertainty in the short run while information gaps are filled in over the long term” (Doremus 2011, 1464). Following the workshop, the USFWS developed the Red Wolf Adaptive Management Work Plan (RWAMWP, first ed. 2000) to respond to the uncertainties and threats of hybrid introgression in the red wolf:

The RWAMWP includes 1) the placeholder concept (removal/sterilization of coyotes and hybrids), 2) the release of red wolves from the captive breeding program, 3) genetic testing of litters, 4) cross-fostering of captive pups born to wild parents, and 5) public relations to promote recovery. (U.S. Fish and Wildlife Service 2018, 34)

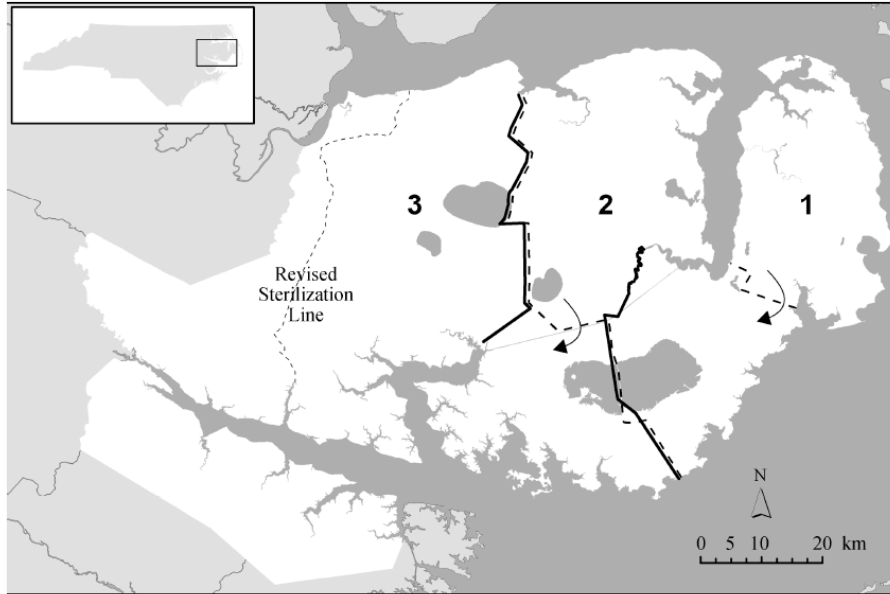


Figure 2.3: Red wolf non-essential experimental population management zones; coyote & hybrid sterilization line marked by grey dotted line. Map from Gese et al, 2015

The RWAMWP thus proposed an active management of the hybrid threat by drawing a sterilization line around the red wolf reintroduction zone: coyotes maintaining breeding territory inside that zone were captured, sterilized, and re-released (see Figure 2.3). “Removal” of coyotes and hybrids in management documents refers to euthanasia: *lethal* removal (Gese and Terletzky 2015). It is also noted that not all coyotes within the restoration zone are captured and sterilized due to the impracticality of such an endeavor, therefore the *territorial* “placeholder” concept is emphasized (Gese and Terletzky 2015). The USFWS explains:

The RWAMWP describes techniques to capture and sterilize hormonally intact coyotes via vasectomy or tubal ligation, then releases the sterile canid at its place of capture to act as a territorial ‘placeholder’ until the animal is replaced by wild red wolves. Sterile coyotes are not capable of breeding with other coyotes, effectively limiting the growth of the coyote population, nor are they capable of interbreeding with wild red wolves, limiting hybridization events. In addition, the sterile canid will exclude other coyotes from its territory.... Ultimately, the placeholder coyotes are replaced by the larger red wolves either naturally by displacing the coyote or via management actions (e.g., removal of the coyote followed by insertion of wild or translocated wolves). (U.S. Fish and Wildlife Service 2018, 35)

Operating as a “territorial ‘placeholder,’” sterilized coyotes both prevent fertile coyotes from entering the red wolf recovery zone as well as prevent the reproduction of coyotes and hybrids in the region. “Replacement” of such sterile coyotes can occur through the coyote’s death, harassment away by the larger red wolf as it is introduced, or through active lethal removal of the sterile animal to make way for the insertion of wolves. But the project went beyond sterilizing just coyotes to prevent coyote introgression into red wolves, they also captured hybrids for sterilization and rereleased them to act as placeholders (Gese et al. 2015; Gese and Terletzky 2015). When the program began an evident hybrid had to have at least 75% red wolf ancestry to pass the threshold for sterilization; the bar was raised to 87.5% red wolf ancestry in 2002 (Gese et al. 2015, 195). While the raising of the sterilization bar is, in part, a factor of the program’s goal to remove previously introgressed genes and gain a purer population, it nonetheless suggests the ways species boundaries can have arbitrary value-based standards. Thus, species boundary crossing for red wolves had very direct consequences—sterilization (or euthanasia) would effectively cease all reproductive contributions hybrids could bring to the population and indicated that the USFWS had ultimately taken a clear stance on the evolutionary value of coyote hybridization. Studies of the project emphasize that “sterilization was not used to control or manage the coyote population in the recovery area, but to create non-reproductive territories with sterile animals that were incapable of successful reproduction (i.e., hybridization)” (Gese and Terletzky 2015, 17). Keeping the sterile animals alive to be *used* is therefore a key facet of the project. Their labor as territorial reproductive voids are seen as essential “biological means by which zones of ignorance [territory with no present canids] can be systematically assessed and eliminated, a critical intermediate step in the transition to a landscape occupied predominantly by red wolf breeding groups” (U.S. Fish and Wildlife Service 2013, 7). As the USFWS attempts to

develop a kind of barrier between the red wolf genome and that of the coyote, they deploy a kind of genetic void to serve as that barrier in the form of the sterile coyote and hybrid coyote-wolf. In a further effort to prevent potentially hybrid individuals from reaching breeding age, monitoring of denning females and subsequent genetic testing of litters after whelping allowed for immediate “removal” of “non-wolf” litters from the population (9).¹⁴

Despite early mishaps where 3 red wolves were misidentified as hybrids and sterilized (before genetic testing became part of the protocol, 1999-2000), the “placeholder” concept has been lauded as a success in preventing continued coyote introgression into the red wolf genome and has been recommended for other carnivore conservation applications (Gese et al. 2015; Gese and Terletzky 2015). Gese et al. (2015) did note, however, that there are still questions to ask about the program’s ability to support overall red wolf recovery. If the RWAMP project proceeds as intended, they consider, *theoretically* coyote sterilization wouldn’t need to be practiced long-term as red wolves would now occupy all the available territory in the recovery area and have no trouble finding desirable red wolf mates, “Under such conditions...coyotes immigrating to the area would be naturally excluded by resident wolves” (200):

However, we believe this scenario is unlikely because wolf habitat is discontinuous within the recovery area and anthropogenic habitat changes will continue to favor coyotes because of their ability to more effectively colonize landscapes in closer proximity to human activity (Benson et al., 2012; Gese et al., 2012; Benson and Patterson, 2013). Further, there is little evidence red wolves naturally control the coyote population through strife, which is a core prediction derived from the competitive exclusion hypothesis (Murray et al., 2015). (200)

In essence, Gese et al. suggest that, to succeed in preventing coyote introgression into red wolves long-term, sterile coyote and hybrid placeholders will likely be part of an ongoing conservation

¹⁴ During whelping captive bred “pure” red wolf pups were often inserted into wild litters to be raised by wild mothers. While I can’t corroborate this hypothesis based on the RWAMP, it is my hope these captive bred litters might replace the “removed” litters, therefore not leaving wild mothers completely bereft.

effort rather than a short-term fix as the red wolves regain their dominance. The ongoing anthropogenic impact on habitats in the region and the well-known coyote adaptability to such conditions will naturally give the smaller canid a leg up—whether small numbers are being sterilized or not. Indeed, recent increases in wolf anthropogenic mortality (e.g., gunshots and vehicle strikes) have started to once again drive red wolves to look for heterospecific mates (i.e., coyotes or hybrids), making rapid mid breeding season switches after losing their red wolf mates (U.S. Fish and Wildlife Service 2018, 37). From the experimental population’s high point in 2012 of as many as 120 animals, the population has taken a massive downturn in recent years to only between 15 to 17 estimated animals in the wild today. The mortality rate rose in 2021 to 20-25% and in 2022 to as high as 29-32%. Many of these deaths have been due to vehicular strikes, a small few to unknown reasons, but the rest are under investigation by law enforcement—often the wolves found dead on private property (U.S. Fish and Wildlife Service 2022). These deaths have caused clear disruptions to red wolf reproduction and 2022 was the first year since 2018 that a red wolf litter was born in the wild. It does not bode well for the red wolf program’s long-term success that continued escalating tensions with local private landowners are quite likely fueling the increased gunshot mortalities and subsequent hybrid matings (thus ultimately failed matings and diminished population numbers if the mate is sterile).

The plummeting population numbers have also recently brought more attention to the problem of genetic diversity within the red wolf population and its potential long-term impacts on the species’ fertility and health. As noted earlier, the red wolf experimental population is the result of a breeding program developed from 14 founder individuals, of which only 12 are genetically represented in the current captive and wild populations. Such a narrow gene pool presents its own challenges for the managers of the Species Survival Plan (SSP) captive breeding

program and with the increasing mortality rates of introduced wolves, the problem has only become more acute. Small gene pools can cause what is called “inbreeding depression”—with less genetic variability comes less individual reproductive fitness¹⁵ and less potential to adapt to changing environmental conditions (U.S. Fish and Wildlife Service 2018, 33). Such small bottleneck populations are especially vulnerable to “genetic drift,” a process where harmful or nonbeneficial alleles gain dominance in the population due to the individuals with these alleles, by chance, reproducing more than others. Because the population is small, these chance events can have outsized effects in the long-term—effectively sidestepping natural selection as these alleles are not predictively supportive of reproductive fitness. Studies of the wild red wolf population has shown the average yearly inbreeding coefficients of wild born litters since 1988 to be increasing drastically. 99% of the wild population is inbred, with the coefficient range from 0—0.383. The mean value is 0.154—indicating a greater than half-sibling mating (Brzeski et al. 2014). So far, the deleterious effect of inbreeding has only an overall reduction in wolf body size, but this amount of inbreeding is a troubling trend for the wolves long-term, particularly as the “true effects of inbreeding are generally greater than those observed, not less” (4251).

However, recent genetic work to better understand the history of coyote—red wolf admixture in the South has posed questions about the potential role coyotes might play in the future of red wolf conservation. Geneticists Bridgett M. vonHoldt, Kristin E. Brzeski, and colleagues performed DNA analyses of coyotes trapped throughout the Southern US (primarily Texas and Louisiana), finding significant percentages of cryptic (i.e., not evident through visible traits) red wolf genes in coyote populations local to the red wolf recovery source population

¹⁵ “Fitness” is the measure of an individual’s reproductive success, therefore ability to pass on its genes to the next generation.

(marked in red in Figure 2.2). Some coyotes in the Louisiana Gulf coast region showed as much as 69% red wolf parentage while appearing to be (evidently) coyotes (vonHoldt, Hinton, et al. 2022). vonHoldt et al. emphasize their results could have profound implications for the SSP-lineage (Species Survival Plan; descent from captive bred wolves) which “continues to become more inbred through time” because the “coyotes continue to be a significant reservoir of ghost and SSP-lineage red wolf ancestry... [and] the longer-term viability of the red wolf relies heavily upon the potential for the SSP to incorporate novel and variable red wolf genomic content” (vonHoldt et al. 2022, 5449). Such individual coyotes might carry red wolf genetic diversity not represented in the present red wolf recovery population, and considering its current threat from inbreeding, such genetic diversity might be more valuable than the potential threat of hybridization (or so vonHoldt and colleagues suggest). As the vonHoldt, Hinton, et al. (2022) article asserts:

When a coyote is estimated to carry a predominant estimate of red wolf genomic ancestry proportion (i.e., >50%), we argue such individuals are a crucial component for the persistence of the endangered red wolf... We encourage conservation practitioners to go beyond species concepts and pioneer a vision that leverages admixture to provide endangered genomes with the best possible probability for survival in our rapidly changing world. (9)

Current red wolf conservation has ultimately pivoted around the hybrid-as-threat narrative, funneling mass amounts of funding to create reproductive voids and barriers around the sacred (and now divinely inbred) red wolf genome. After 50 years of captive breeding, the red wolf is still critically endangered and a deeply conservation-reliant species. Undoubtedly it is because the wolf has had its species identity questioned so thoroughly over the years that such a program of hybrid conservation strategy might seem controversial, but, interestingly, alongside the proposal of admixture-as-restoration, vonHoldt et al. (2022) also stress that their studies present “genetic evidence that the red wolf is indeed a distinct species, supported through the

identification of putative barrier or resistance loci, primarily on the X chromosome ... a characteristic typically found in distinct species” (5448). Therefore, asserting the red wolf is indeed its own distinct species—separate from the coyote—does not mean admixed coyotes must lose value to red wolf restoration. An innovative restoration approach will consider all resources of red wolf genetic variation available, whether they are cryptic “ghost alleles” tucked away in Louisiana coyotes, or those in the current SSP-lineage red wolves. Presently, the USFWS’s stance on red wolf taxonomy is as follows:

The debate over the taxonomic status of the red wolf has continued for more than 30 years.... There are three main theories on the origin of the red wolf: (1) the red wolf originated from ancient hybridization between gray wolves and coyotes, (2) the red wolf originated from recent (post European colonization) hybridization between gray wolves and coyotes, and (3) the red wolf evolved from a common ancestor with the coyote, but is of a lineage divergent from coyotes.... The most recent scientific publications continue to provide conflicting interpretations and support for different theories of origin, specifically theories 2 and 3 above; therefore, USFWS continues to recognize the red wolf as the species *Canis rufus*. (U.S. Fish and Wildlife Service 2018, 17)

As this admixed coyote research and genomic evidence for red wolf species status is extremely recent (2022), it is unclear yet how USFWS conservationists will (or will not) consider adopting new hybrid policies into their red wolf conservation practice. Hybridization for genetic rescue, however, *does* have precedent in US T&E conservation and I will discuss one of the most relevant famous case studies, the Florida panther, later in the chapter. First, however, we will consider further how hybrid “threat” is unsettled and questioned through the case of the *Vermivora* complex of wood warblers.

When your Differences are only Feather Deep: Golden-winged & Blue-winged Warblers

At the same time the red wolf is undergoing intense scrutiny and, perhaps, upheaval over its conservation status due to its questioned origins, another threatened species’ hybridizing ways

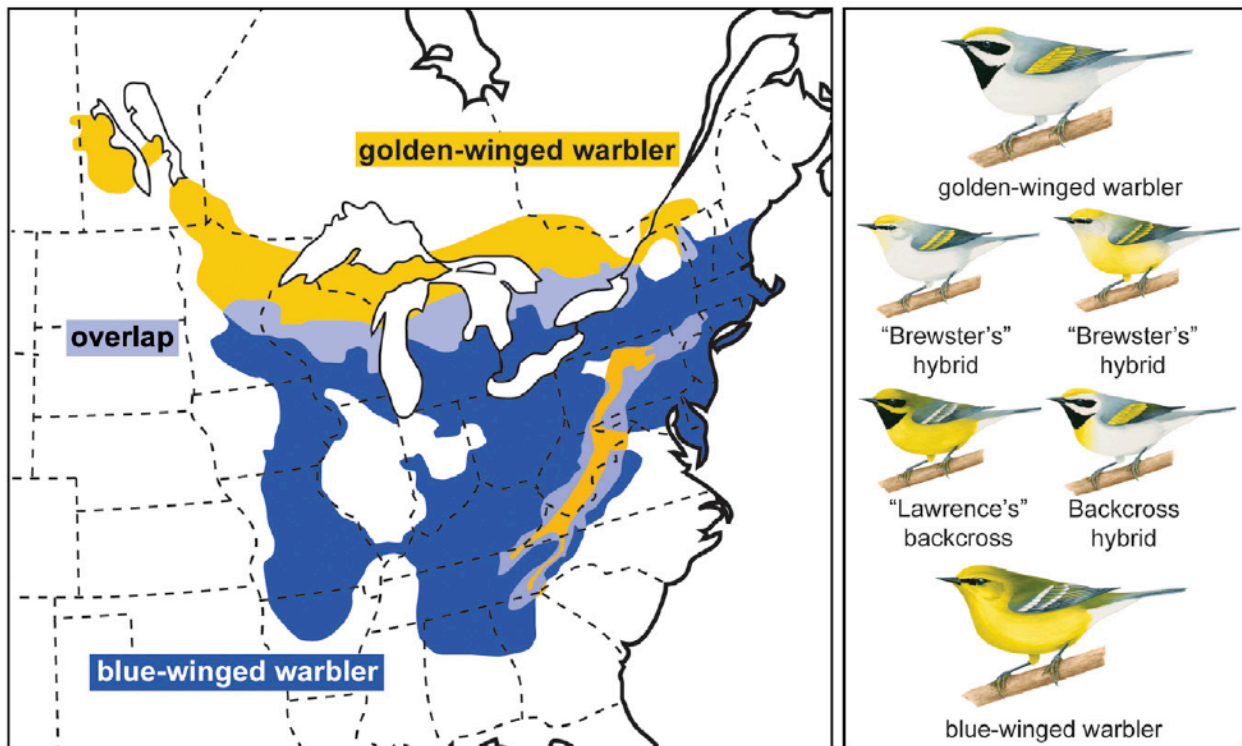


Figure 2.4: Left: Geographic range of golden-winged (yellow) and blue-winged (blue) warblers; overlap (light blue) have both parental phenotypes and hybrid birds. Right: Illustrations of parental and several hybrid phenotypes; illustrations by Liz Clayton Fuller. Figures from Toews et al. (2016).

are also getting a closer genomic look. Golden-winged warblers (*Vermivora chrysoptera*) are listed in Canada and are under review for listing in the US. Where their range overlaps with a closely related species, the blue-winged warbler (*V. cyanoptera*), the two interbreed resulting in a set of distinctive hybrids, called the Brewster's and Lawrence's warblers, as well as a backcross, sometimes called "intergrade,"¹⁶ hybrid (see Figure 2.4). It had long been believed that the mixing of the two warbler parent species (golden-winged & blue-winged) had been precipitated recently due to European colonization and settling of the region—leading to logging and contraction of the warbler's nesting grounds (Roth et al. 2019). The perception of the

¹⁶ As I will note in a moment, all the hybrids are far more complex hybridizations than first generation crosses and, in fact, include backcrosses into their parent species (golden-winged and blue-winged), therefore the "backcross" name for the third hybrid is a bit of a misnomer (they are all really backcrosses). This third hybrid is therefore often called the "intergrade." The other two hybrids have true names because they were initially misidentified as their own species due to their distinctive appearances before a clearer understanding of the complex hybridization relationship between golden-winged and blue-winged warblers was obtained.

interbreeding of the two warblers, and resultant hybrid mixing, was therefore viewed as a threat to the less numerous golden-winged species—and a threat brought on through human fault. The outsized menace of blue-winged genetic introgression into the golden-winged genome was regularly stated in early literature as the blue-winged warblers spread north and “replaced” the golden-winged warblers (Confer, Larkin, and Allen 2003; Gill 2004; Buehler et al. 2007; Wood et al. 2016). The risk was never taken to extreme measures (e.g. lethal), but some researchers did recommend “developing management strategies that favor Golden-winged Warblers over Blue-winged Warblers where [their distributions overlap]” (Buehler et al. 2007, 1442-1443); a somewhat difficult prospect to imagine, considering the birds’ considerable genetic overlaps (as will become clear in a moment). The Golden-Winged Warbler Working Group¹⁷ has so far developed the most comprehensive conservation plan for the species, the *Golden-winged Warbler Status Review and Conservation Plan* (1st ed. published in 2012, 2nd ed. 2019; Roth et al. 2019), which has been widely taken up by natural resource professionals.¹⁸ The plan offers detailed updates of golden-winged warbler status for each state and province in its range, including threats present in each state/province; of the states and provinces for which they were able to obtain specific threat-relevant data, 13 specifically mentioned hybridization, genetic introgression, or genetic replacement as blue-winged warbler threats to the golden-winged warbler; 3 mentioned blue-winged warblers as either a competitive or replacement threat only; and 7 either did not mention blue-winged warblers at all or specifically noted they weren’t a threat in that location. Overall, attentiveness to blue-winged warblers as a specific threat or a

¹⁷ The Golden Winged Warbler Working Group is a collaborative of over 200 NGO, federal & state agency, and industry scholars, conservationists, and land managers in Canada, the US and Latin America (where golden-winged warblers over winter) that coordinates golden-winged warbler research and conservation. The plan was published with support from the Cornell Lab of Ornithology, USFWS, and the National Fish and Wildlife Foundation.

¹⁸ The Working Group has also developed a set of management best practices that are regionally specific (e.g. Appalachia, Canada, Great Lakes, etc.) and for non-breeding season conservation (in Latin America).

potential threat is evident throughout the document; a view corroborated by the 2010 petition to list golden-winged warblers as a threatened or endangered species (Sewell 2010)¹⁹.

Despite this current conservation view, recent whole genome studies of the golden-winged, blue-winged, Brewster's and Lawrence's have uncovered a far more complex history of hybrid mixing than previously believed. A 2016 study found the difference between the different warbler species might first, be only feather-deep, and second, might not be the "fault" of humans at all. Using whole genome analyses of 10 golden-winged and 10 blue-winged warblers, Toews et al. (2016) showed that the two species' "divergent sites represent <0.03% of the polymorphic regions of the genome," meaning the only sites where the birds' genetic makeups differed were on 6 small clustered regions relating to phenotypic traits (i.e. observable traits) such as feather pigmentation (2314). The bulk of the two species' genomes, around 99.97%, are pretty much identical. A key site they identified where the two species differed was the *agouti signaling protein*, or *ASIP*, a promoter that is known to recessively pass on dark pigment—all birds in their sample presenting the black throat were also the only birds homozygous for the *ASIP* promotor (2316). In other words, these birds received a copy of this gene from both of their parents, thus presenting the black throat trait phenotypically (black throat is a recessive trait). The intermixing that occurs through the Brewster's and Lawrence's hybrids is also highly dynamic, and not the result of just F₁ (first generation) crosses between golden- and blue-winged parents. A 2020 genome-wide study of Brewster's, Lawrence's, and backcross or "intergrade" hybrid warblers indicates far more complex genetic ancestries, and even extensive pigmentation variation in the Brewster's individuals. Using "hybrid indices" to identify predominant ancestry from blue-

¹⁹ The 90-day finding by the USFWS from this 2010 petition asserted ESA listing for the golden-winged warbler "may be warranted," therefore prompting thorough scientific review. That review is still underway and it is unclear when it will be complete (Fish and Wildlife Service, Interior 2011).

winged or golden-winged warbler parents,²⁰ the hybrid categorizations (pictured in Figure 2.4) showed variable ancestry, Lawrence's with predominant blue-winged parentage, backcross/intergrade hybrids with larger golden-winged percentages, and Brewster's showing a wide variability, "suggesting the Brewster's phenotype can result as a consequence of backcrossing into either parental species" (Baiz et al. 2020, 6). The study noted that, in fact, "any categorization of hybrids into discrete types is based primarily on one discrete trait (throat patch), whereas there is continuous variation in carotenoid-based [yellow] pigmentation and considerable underlying genomic variation in hybrids" (8). Ultimately, based on these genetic analyses, it appears that golden-winged and blue-winged warblers as well as hybrids in the *Vermivora* complex's genomes diverge just based on their plumage. This is a highly significant finding as many arguments against hybrid mixing of species often hinges on diminished local adaptations, or other key features that might result in less overall fitness in hybrid populations. If the birds have largely identical genomes aside from plumage, and might learn certain regional behaviors from parents, arguments regarding adaptive fitness have less weight.

The second key finding from the 2016 study, and a key one I want to address in this section, is the matter of *timeline*—when did the hybridization first occur? Knowing when the birds began to hybridize helps us speculate on some reasons *why* they did (or at least cut out some options). Because prior research (and conservation) has assumed golden-winged—blue-winged hybridization has been a recent phenomenon brought on by colonial settlement of the region, there has long been a narrative of human fault in the hybridization story. The Toews et al. (2016) study, however, overturns this narrative, finding "the best model [for hybridization

²⁰ A hybrid index scores a hybrid's genome to indicate the amount of "backcrossing" by hybrid individuals into pure blue-winged or golden-winged individuals occurred, resulting in larger percentages of those genetics in their progeny (the scored hybrid). Thus a first generation (F1) hybrid would have a 0.5 score, golden-winged backcrosses will have hybrid index scores of >0.5, and blue-winged backcrosses will have hybrid index scores of <0.5.

histories] included an old and continuous movement of genes, as opposed to only recent gene flow. This result is consistent with humans facilitating *some* recent admixture via 19th-century habitat change but *also* shows hybridization has likely occurred over many millennia” (2317; my emphasis). In contrast to the hybridization story previously told, this complicates matters: if hybridization has occurred “over many millennia,” then something other than just anthropogenic forces are at work here. How do we view blue-winged warblers as a hybrid-threat if hybridization has such an extensive history where full warbler agency cannot be doubted? Toews et al. draw a series of implications from these findings for warbler conservation:

On the one hand, the low and restricted genomic divergence between these taxa—likely resulting from extensive hybridization—makes their classification as distinct species less certain; on the other hand, these distinct phenotypes appear to have persisted despite this extreme genomic similarity and despite a protracted period of hybridization. Both regulatory frameworks [Canadian Species at Risk Act & the ESA] support the conservation of evolutionary significant variation with species, and we recommend focusing on managing the genetic and phenotypic diversity within the warbler complex as a whole. (2317)

They acknowledge here the slipperiness of drawing species boundaries in the case of these two warblers but seek to draw upon regulatory tools that might consider more innovative conservation approaches adaptive to their particular case.

The ESA does recognize “Evolutionarily Significant Units” as a population measure for protection—currently predominantly used for the protection of specific fish populations (e.g. salmon runs)—though these approaches typically *narrow* the scope rather than widen it to focus on potential future evolutionary branches developed using a larger-than-species complex (Waples 1995). Such typical conservation approaches seek to capture local adaptations of a specific population *within* a species, for example, that could be important for the evolutionary future of the species. Sometimes these local variations are marked by subspecies designations, but not always. This is particularly why the strategy has been taken up in fisheries for the

protection of, for example, spring-run versus winter-runs of different salmon species.²¹ Presently, the model isn't designed to build back up beyond the lines of species to consider the ways evolutionarily pathways aren't *just* the "ever expanding cone" that continually diversifies "forward," but might also share genes in less obviously progress-oriented ways. I think this example hits against some of the normative thinking around evolution that is essential to start resisting: what does it mean to consider species that diverged evolutionarily millennia ago might converge again, continue to share genes, and split off (or not) in the future? How does this change the way we think about conservation? If present "Evolutionarily Significant Units" operate at the population level—therefore below the species—we aren't presently accounting for the way this type of gene sharing across species borders might be evolutionarily significant. As Toews et al. suggest, to truly take biodiversity conservation seriously in the case of the golden-winged warblers is to take their *behavior* seriously, as is made evident through the genetic admixture their genome demonstrates. Therefore, to protect the golden-winged warbler, we must also protect those they consider kin: the broader *Vermivora* complex of species and hybrids they share genes with. Like Nancy Tuana's concept of "viscous porosity," the species adhere, congeal, and connect, flowing into one another, but resisting complete admixture and retaining some distinguishable key differences (Tuana 2008). In light of findings like the Toews et al. study, it seems less probable to achieve *Vermivora* conservation through suggestions such as the management strategy I mentioned earlier that prioritized approaches favoring golden-winged warblers over blue-winged warblers (Buehler et al. 2007). What would it even look like to favor one over the other when they are so intimately connected?

²¹ Spring-run and winter-run (or summer or fall) refer to the time of year the salmon "run" up the river from the ocean, migrating to spawn. These stocks are genetically linked groups, with the instinct to run the river at that particular time, creating a specific population unit.

Interestingly, despite the considerable public interest in the golden-winged—blue-winged genetic similarity²², the Golden-Winged Warbler Working Group’s 2019 2nd edition conservation plan did not incorporate any contemporary research on golden-winged genetics—nor even seem to have updated relevant sections from their 2012 edition. On the working group’s website, they state that “significant new research has produced insights into Golden-winged Warbler nesting and post-fledging habitat use, migratory connectivity, and habitat segregation among the sexes on the wintering groups,” indicating aspects of the plan relevant to these topics were updated by the Steering committee and science experts in the revision; no commentary was made on novel genetic research (Golden-Winged Warbler Working Group n.d.). Using data from the late 1990s and early 2000s, the plan still asserts hybridization is “more disadvantageous for Golden-winged Warbler than Blue-winged Warbler” (Roth et al. 2019, 1-30). In dramatic terms, they even describe the extreme threat to “the only pure genetic populations of Golden-winged Warbler throughout the breeding range” presently identified in Manitoba due to the capture of a single blue-winged warbler in the region in 2010 (1-68). They stress “these discoveries suggest that introgression of Blue-winged Warbler DNA into the [last] pure Golden-winged Warbler population may be imminent” (1-68). However, it does include the following passage I will quote in full, as it offers insight into the tensions presently at play in golden-winged conservation:

Whereas virtually all researchers would agree that introgression of Blue-winged Warbler genes (whether visually apparent or cryptic) into the Golden-winged Warbler population threatens the continued existence of a pure Golden-winged Warbler phenotype, many researchers and conservationists are transitioning from a position of regarding Blue-winged Warbler as a direct threat to Golden-winged Warbler per se to a position that recognizes a strategy of maintaining, to the greatest extent possible, the full genetic diversity represented within the *Vermivora* complex. Such a strategy includes

²² The popular Cornell Bird Lab site even posted an article discussing the results of the 2016 study in terms understandable for the broader public (Axelson 2016).

maintaining populations of pure Golden-winged Warbler genotypes where allopatry [geographic species separation] or habitat segregation in sympatry [shared geographic range] appears to facilitate genetic isolation. (1-31)

On the one hand, the working group seeks to assert that “virtually all researchers would agree” there is a threat to pure golden-winged warblers represented by the hybridization events with blue-winged while simultaneously undercutting the idea by trying to pay their dues to a likely growing group of scholars hoping to see past such a purist ideology for the “*Vermivora* complex.”

The “complex” terminology here is useful, as it offers an innovative way of considering the dynamic record of hybridization within the *Vermivora* genus. Despite the extensive interbreeding and its long history, the two species are able to maintain stronghold populations of their parent species—how loosely we define the genomic boundaries of those species (and how they might shift over time) could be up for debate (as suggested by Toews et al. above). As Tom Will, USFWS Midwest Region Migratory Bird Coordinator noted,

for humans to say, ‘Well, I want to protect golden-wings from blue-wings,’ that seems to be a largely aesthetic judgment, and not really justifiable from a wildlife or evolutionary standpoint.... We need to think of these two species as an evolving complex.... This system of golden-wings and blue-wings sharing genes may be a much better way of adapting to environmental change than we as humans could possibly figure out, I think that we should let it happen. It’s a good example of the beauty of evolution. And apparently, it’s been going on for a long time. (qtd. in Axelson 2016)

For Will, thinking about the *Vermivora* species “complex” is to consider how they are evolving and adapting to environmental change through a complicated strategy of “sharing genes” that, perhaps, we may not fully understand yet. “Protecting” one species from another, in this view, is not only “aesthetic,” but also short-sighted and ignores the actual materiality of how the birds are experiencing environmental change and responding to it. Some researchers disagree with this stance, such as Confer et al. (2020) who drew on previously published data to argue for the

maintenance of the two species as strictly separate—suggesting low hybrid fitness and considerable breeding habitat preference differences as barriers. However, Confer et al. readily admit their “estimates of reproductive isolation might underestimate the actual level of gene flow between Golden-winged and Blue-winged Warblers” as their primary interest was “whether divergent plumage phenotypes contribute to nonrandom mating” rather than genes (10642). Interestingly, Confer et al. (2020) draw a conclusion of “significant hybrid reduced fitness” due to plumage based on the same studies that Baiz et al. (2020) observe “little evidence for reduced hybrid fitness”—clearly there is disagreement across the literature and perhaps some of the lack of clarity is due to less overall research focus on the hybrids themselves. To truly understand the *Vermivora* complex as an evolving group, more attention to the hybrid individuals in the research would be advantageous. In any case, continuing narratives of hybrid “threat” or desires for “pure” golden-wing populations is certainly counter to contemporary genetic knowledge that sees the *Vermivora* complex as hybridizing over millennia—with or without human impact. To capture this contemporary research in conservation practice might mean rethinking how we draw boundaries around what is deemed “evolutionarily significant” to expand beyond narrow species concepts and normative evolutionary ideals. It will also mean overcoming a policy landscape that requires strict boundaries to be drawn between species in order for adequate protections to be put into place. While the golden-winged warbler’s ESA listing is still under review, and it is unclear how much longer it will be in “warranted but precluded” limbo, it is certain that the *Vermivora* complex hybridization will have to be addressed one way or another in order for the warbler to gain coveted listed status.

Intentional Hybridization for Genetic Rescue: The Florida Panther & The Texas Puma

Hybridization hasn't *always* been framed by the USFWS in strictly negative terms, however, and in extremely rare cases has even been taken up in T&E conservation as a tool for genetic rescue. The Florida panther (*Puma concolor coryi*) case is one such widely talked about and frequently praised hybridization-as-genetic-rescue project. It is this case that demonstrates the ways hybridization will become acceptable to contemporary US conservation in dire circumstances when extinction looms. Like the red wolf discussed earlier, the Florida panther (I will refer to Florida panthers as “panthers” and other subspecies as “pumas” as per USFWS vernacular) has been a flagship ESA species from the beginning, first listed in 1967 under the Endangered Species Preservation Act. The Eastern cougar (*P. c. cougar*), declared officially extinct by the USFWS in 2011, had likely already been extinct since the 1930s, leaving the Florida panthers the only puma subspecies extant East of the Mississippi (U.S. Fish and Wildlife Service 2011). Before 1949, Florida panthers were killed year-round in Florida, drastically reducing their numbers; they were briefly regulated as a game animal between 1950-1958 before receiving legal protections in 1958. As of 1978, Florida State Law now makes it a felony to kill a panther (U.S. Fish and Wildlife Service 2008). Like the red wolf, the early unregulated hunting paired with anthropogenic development throughout their historic range led to a protraction of their habitat (see Figure 2.5, next page) and plummeting population numbers, reaching an estimated all-time low of 10 animals (Bodine 2022). For the panthers, however, these diminished numbers did not come with any viable heterospecific breeding partners—a population bottleneck resulting in high levels of inbreeding throughout the small population. The inbreeding demonstrated itself in a number of ways, some benign and others more malignant for the future of the species. Less concerning were the morphological features such as a high frequency of

kinked tails (94% frequency) and cowlicks (88%) appeared among the population— features that appeared in other puma subspecies but at much lower frequencies (9% & 27% respectively) (Roelke, Martenson, and O’Brien 1993, 342). The more troubling outcomes were the cause of inbreeding depression and diminished overall fitness for the panthers. These features included the male panthers showing “some of the poorest seminal

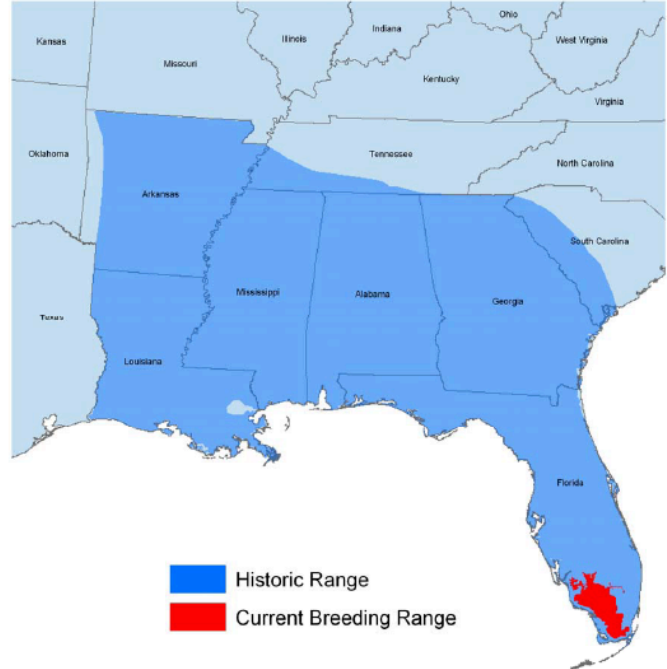


Figure 2.5: Florida panther contemporary range (in red) is less than 5% of its historic (in blue). Image from U.S. Fish & Wildlife Service 2008.

quality traits ever recorded for any felid species or subspecies,” including malformed and less motile sperm (capable of motion) than is typical (344). Cryptorchidism, or one or more undescended testicles, also skyrocketed from 0% incidence in males born pre-1975 to 90% in those born post-1989—22% of these males were bilateral and therefore sterile, the rest showing decreased sperm motility (346). Heart defects and compromised immune systems were also shown to impact panther mortality (346-347). For a population already small and at risk, inbreeding depression seemed poised to quickly tip the scales and potentially take the panthers past the point of no return; it was clear that something drastic needed to be done.

In May 1991 and later in October 1992, the USFWS, IUCN Captive Breeding Specialist Group, and partners gathered to consider potential genetic management strategies for the panther. A 1989 population viability assessment had already found the panther to be at “high risk of extinction” within the next 25-40 years and analysis had shown a 6% loss of genetic variation

every generation if the population wasn't increased—a clear death knell when inbreeding was already causing such dire impacts (Seal 1992). The workshop consensus was “the reinstatement of historic gene flow between the Florida panther and adjoining *Felis concolor*^[23] subspecies, i.e., genetic augmentation, is needed to reverse these effects of inbreeding depression, that effective action needs to be taken quickly and that the amount of introgression required may reach 20%” (3). At the time, the USFWS had only recently (1990), and informally, retracted their previous strict “no hybrids” policy and had not yet drafted their 1996 intercross policy proposal. Surmounting the precedent of “hybrid threat” to support introgression as a tool for recovery would therefore not be a simple task. A 1991 perspective piece in *Science* by Stephen O'Brien and Ernst Mayr directly addressed the Florida panther's plight, and potential need for introgression, remarking on the problem of the ESA's “Hybrid Policy” (an informal opinion, but nonetheless treated as a policy) in this context:

The genetic advantages of introducing some additional genetic material into a population suffering from inbreeding would have been comforting except for one detail. Three [Department of Interior] opinions ... have ruled with the force of precedent that hybrids between endangered species, subspecies, or populations cannot be protected. ... The current status of the Florida panther as endangered could be challenged or even revoked under a strict interpretation of [these opinions]. (O'Brien and Mayr 1991, 1187)

In order to assure, without a doubt, future admixed panthers would not create easy prey for delisting from private interests—particularly as the panther's habitat is already constantly under threat from development²⁴—a clear ruling from the Service on the status of the admixed panthers was required. Ultimately, the USFWS “made the determination that any resulting offspring would receive the full protections of the ESA. This determination was the result of a rigorous

²³ At the time of the workshop, panthers were not yet grouped as a monotypic genus (*Puma*) and were still in the subgenus *Felis*. *Felis* was assigned full genus status and *Puma* the new subgenus in 1993 (U.S. Fish and Wildlife Service 2008).

²⁴ The panther's priority rating is a 6C—the “C” attesting to the high threat from development conflict to panther habitat.

policy and legal review at the highest levels of the agency”—including a formal 1994 opinion from the USFWS Director Beattie, approving the regional director to move forward with the plan (U.S. Fish and Wildlife Service 2008, 10).

In 1994, a genetic restoration plan was developed through a collaboration between numerous experts and policymakers including the Florida Game and Freshwater Fish Commission, the USFWS, various Zoos, the IUCN Conservation Breeding Specialist Group, and panther specialists and geneticists. In the plan they assert “an initial release will be made of 8 non-pregnant young adult females from the Texas population”—the panther’s closest neighboring subspecies: the Texas puma (*Puma concolor stanleyana*) (Seal 1994, 2). They emphasize that the Florida panther’s range was contiguous with the Texas puma before the twentieth century when settlement and development severed the connection and therefore “it is likely that genetic exchange occurred between these groups because there were no dispersal barriers between their ranges” (2). The historic connection between the two subspecies allowed for additional justification of the intentional introgression, as it merely operated off historical precedent, effectively *restoring* historical patterns of genetic flow rather than creating an entirely new genetic link. Opposition to the project primarily attempted to claim the panther population was presently stable—and therefore didn’t require such drastic intervention at all. Such arguments could typically be traced back to a single paper on panther demographics (Maehr and Caddick 1995) which asserted that, despite low genetic variability, births actually outpaced deaths since 1987 and therefore “perhaps the perceived dangers of inbreeding depression... have been overemphasized” (1296). The paper went on to speculate on future negative impacts of the introgression project, stressing that, due to the panthers’ period of separation from other puma subspecies, “outbreeding depression [could] stem from [a loss of] genetic adaptation to the local

environment” (1296). However, the paper’s method has been widely discredited since due to sloppy inferences (e.g., no common population base for birth to death ratios) and data gaps (e.g., kitten annual survival rate inferred without adequate data) (Beier et al. 2006; Gross 2005). Nonetheless, Maehr’s role as the former leader of the USFWS panther project, and therefore a foremost panther expert of the period, lent credibility to his arguments and his continued assertions over the years for caution on the project and even removal of introgressed panthers have gained some support (Maehr and Lacy 2002). Some very recent studies, which I will discuss in a moment, have also lent some credibility to his concerns about outbreeding depression.

Despite some resistance, however, the USFWS released its formal Environmental Assessment in January 1995, supporting the proposed translocation action wherein they emphasized “existing data indicate that the Florida panther will likely go extinct without actions to restore genetic health to the population”—the immediate threat of extinction was a key impetus for the seemingly drastic conservation action of introgression (Fish and Wildlife Service, Interior 1995a, 478). Later that year, the USFWS went forward with the project and translocated the 8 female Texas pumas, 5 of which went on to produce 20 hybrid offspring (U.S. Fish and Wildlife Service 2008). Almost immediately the population massively increased, from 1996 to 2003 each year increasing by 14% and producing 26.6 kittens annually (Johnson et al. 2010). In 2003, managers removed the last two surviving Texas pumas from the population to avoid a “genomic sweep” (van de Kerk et al. 2019).²⁵ A long-term study of the male panthers showed improvement in sperm quality and lower rates of cryptorchidism, the former correlated

²⁵ I have been unable to confirm what was done with these Texas pumas after removal, if they were relocated back to their original Texas habitat or brought into captivity. Based on the initial genetic restoration plan, it is not suggested they planned to euthanize removed cougars (Seal 1994).

with larger body size—a trait that was most common in admixed panthers (Penfold et al. 2022). Throughout the population, by 2019, the panthers showed a threefold increase in heterozygosity (i.e., inheritance of two different alleles), a measure of genetic diversity, when compared to the Florida panther predecessors—indicating huge success in the program’s support for the population’s diverse gene pool (an essential foundation for future evolutionary adaptation and change) (Ochoa et al. 2019). However, the same team of scientists later found potentially concerning evidence of “deleterious alleles”—much like those causing inbreeding depression in the previous pure populations, but this time in the admixed populations, suggesting a potential future outbreeding depression effect (Ochoa et al. 2022). They note,

Florida panthers succeeding the 1995 genetic rescue program possibly inherited substantial Texas ancestry (Hedrick 2010), which might have established a burden of introduced novel deleterious alleles with increased chances of becoming fixed by means of drift and with increased chances of becoming overrepresented in homogenous genotypes by inbreeding. Furthermore, the reproductive success of introduced Texas pumas and subsequent admixed panthers could have resulted in the erosion of Florida panther adaptive variation (Hedrick 2010). (Ochoa et al. 2022, 496)

Because the population is still small, they noted, any introduced deleterious alleles could therefore still be reinforced through patterns of inbreeding in the population. Already by 2000, one Florida panther father had mated with his hybrid offspring, producing a backcross litter with a high inbreeding coefficient despite the added genetic diversity the initial outcross brought to the gene pool (Land and Lacy 2000). In addition, the majority of the introgressed genes only came from 3 of the 5 Texas pumas who reproduced and 40% came from a single cat who contributed the most progeny (103). Such reproductive patterns suggest the ways small populations are particularly at risk to *ongoing* threat from inbreeding concerns such as genetic drift and raise questions about whether there may be only short-term benefit from the introgression due to the limited scope of genetic contribution from the Texas founders (104). As

one of the lead scientists on the Ochoa et al. 2022 project, Robert R. Fitak, noted, "Until recently, most studies of wildlife genomes have focused on their adaptations, in other words, those traits that are beneficial and specific to the species... Now, we are flipping the question around and asking what about the bad, or 'deleterious,' traits?" (University of Central Florida 2022). Ochoa et al. stress that carefully assessing the source population for genetic rescue programs so individuals with the "lowest mean mutation load" are selected is therefore paramount to avoid, as much as possible, the introduction of deleterious alleles (2022, 497). Finding a donor population as closely related as possible and thorough consideration of potential negative consequences—offset by including experimental captive crossbreeding before wild release if possible—should be a part of any genetic rescue project (Hedrick and Fredrickson 2010). Notably, the initial USFWS genetic restoration plan included a suggested captive introgression breeding program which would monitor any maladaptive traits or potential sterility, but the Service seemed to scrap the plan for unknown reasons (perhaps due to increasing time-sensitive pressure to rescue the dwindling panthers in the wild) (Seal 1994).

But how different are the Florida panthers from other North American pumas really? Are such outbreeding depression concerns a factor of just overall small populations and selecting the wrong Texas founding individuals for translocation? Ultimately this is a question for taxonomists—is hybridity really a concern for these subspecies or is their taxonomy up for debate? As biotech nonprofit Revive & Restore casually comments on their website about the project, "both [Texas pumas and Florida panthers] are different names of the same species, *Puma concolor*"—which is perhaps just truth by omission (of the subspecies conversation) (Revive & Restore n.d.). As discussed earlier, subspecies designations are often considered suspect due to their frequently arbitrary geographic nature. Indeed, recent reevaluation of the original 1946

Florida panther description data and its justification for range found the scientists baldly stated the boundaries between subspecies were “arbitrarily drawn along lines representing the nearest approach to accuracy” (Young and Goldman 1946, 185). Further, the justification for the Florida panther’s historic distribution into Arkansas (as shown in Figure 2.5) was given no justification, as the museum specimens used only represented populations in Florida and Louisiana (see Figure 2.6; U.S. Fish and Wildlife Service 2020, 28). Despite these inaccuracies, some scholars have even suggested that all North American cougars should just be a single subspecies (*P. c. cougar*)²⁶ as mtDNA and microsatellite data²⁷ indicate “little support” for the previous 32

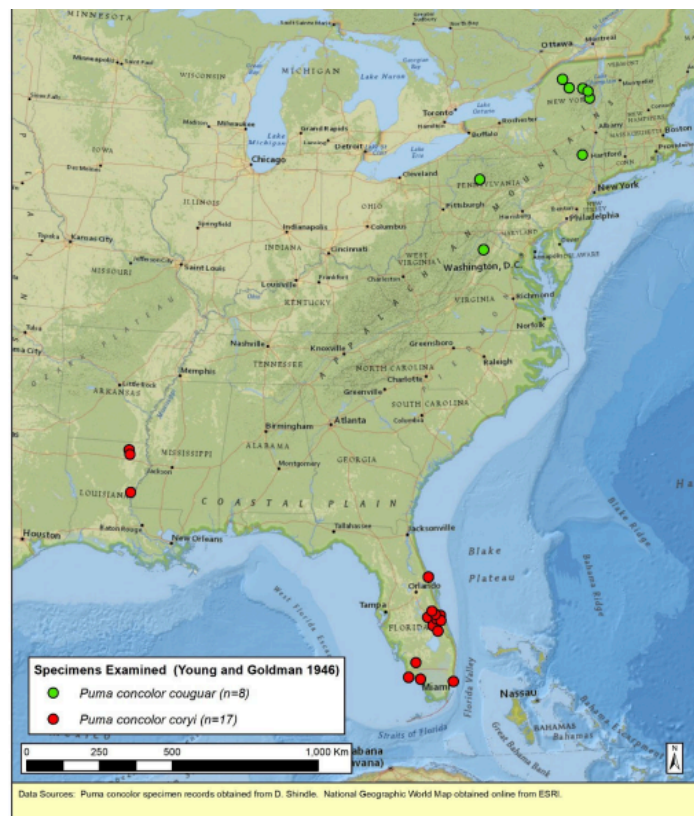


Figure 2.6: Collection locations (approximate) of *Puma concolor* specimens used in Young & Goldman (1946) delineation of subspecies boundaries and historic distributions for *Puma concolor coryi* and *P. c. cougar* (Eastern cougar, extinct). Figure from USFWS 2020.

²⁶ You may recognize this scientific name as that of the extinct subspecies, the Eastern cougar—its usage presents compelling questions about what extinction means in the face of constantly shifting taxonomy: if the North American subspecies were to all be combined into a single subspecies, is the Eastern cougar no longer extinct?

²⁷ Short repeating segments of DNA widely distributed throughout a species’ genome that making for easy DNA “fingerprinting,” identifying parentage, etc. —sometimes called simple sequence repeats (SSRs) (Putman and Carbone 2014).

subspecies division altogether and instead call for 6 phylogeographic subspecies in the genus (Culver et al. 2000). The 2000 study showed only a few scattered populations with unique features, the Florida population being one—its severe inbreeding being one aspect that made the panthers stand out. In 2017 the IUCN Cat Specialist Group put out a revised Felidae



Figure 2.7: IUCN Cat Specialist Group revised 2 subspecies taxonomy for *Puma concolor*: *P. c. cougar* (yellow) in North America and *P. c. concolor* (green) in South America. Figure from Kitchener et al. 2017

taxonomy that drew upon more contemporary mtDNA data to further “lump” the pumas into only 2 main geographic groupings, the North American *P. c. cougar*, and a South American *P. c. concolor*—though they recognized their final taxonomy as nonetheless “tentative” (the borders between the subspecies in Central America being so far speculative; see Figure 2.7) (Kitchener et al. 2017, 33). But the value of genetic data in puma taxonomy is still up for debate (according to the USFWS) and certainly is not the only measure with which to determine taxonomic difference (U.S. Fish and Wildlife Service 2008). On morphological grounds, others have emphasized the Florida panthers’ unique cranial features (Wilkins et al. 1997) that have even been retained through outbreeding with Texas pumas, though there continues to be disagreement on whether the slight cranial variation is significant enough to delineate subspecies (Finn et al. 2013). When it comes to such taxonomic uncertainty in listed species, the USFWS often leans into the uncertainty as a factor of “best available science” and suggests “more research” as the perpetual antidote. Their statement on the debate in the current panther recovery plan is as follows:

The degree to which the scientific community has accepted the use of genetics in puma taxonomy is not resolved at this time. ... Additional research is needed to understand genetic and morphological similarities and differences of puma across North America. The Florida panther is listed under the ESA and any change in its listing status based on best available science would require completing the formal rulemaking process pursuant to the ESA. (U.S. Fish and Wildlife Service 2008, 12)

Without considerable research capacity of their own, the USFWS is effectively sidestepping the problem through the assertion that “best available science” presently is not resolved on the panther’s taxonomy. In their 2020 Species Status Assessment, the USFWS tracked the IUCN’s classification and further remarked on an overall “absence of scientific debate” about the “single North American puma subspecies concept,” noting it has been in common usage since its proposal *except* in the case of populations of conservation concern, “such as the Florida panther” (U.S. Fish and Wildlife Service 2020, 18-19). The USFWS maintained that “best available information and expert opinion supports a single North American subspecies of puma” therefore they assessed the panther as “the only breeding population of puma in the eastern United States” (19). Thus, even if the panther were to formally lose its subspecific status, its role as the last remaining panther population East of the Mississippi and its unique subtropical ecoregion in the Florida Everglades should be sufficient to maintain its listed status as a “Distinct Population Segment” (DPS) (Crooks et al. 2017; Padial and De la Riva 2021), key relevant components of which can include the following:

1. Persistence of the [DPS] in an ecological setting unusual or unique for the taxon, [and]
2. Evidence that loss of the [DPS] would result in a significant gap in the range of the taxon (Department of the Interior 1996b, 4725)

The Florida population of panthers could easily fall under both categories²⁸ even without full subspecies status—therefore maintaining its ESA protections.

While the Florida panther’s taxonomic status as a subspecies is questionable, and the USFWS has even gone so far as to consider delisting the cat due to the uncertainty (though nothing definitive has happened yet), the significance of the Service’s initial decision to enact the

²⁸ However, if the IUCN 2 subspecies classification holds, the “ecoregion” category might have less validity as the *P. c. couguar* range (figure 7) has a clear distribution through other subtropical habitats.

hybridization for genetic rescue program should not be diminished (Department of the Interior 2022). This was especially significant during the early 1990s when the USFWS had barely turned away from a strict “no hybrids” policy that had recently nixed funding for the now extinct dusky seaside sparrow’s hybrid recovery program (admittedly another species whose subspecies status was under debate even at the time). For hybridization to be rendered “acceptable” in the panther’s case, the Service had to first reject the “no hybrids” policy—a key factor for this rejection being the booming field of genetics in the late 1980s showing hybridity was far more common than previously believed—and second, see the panther as absolutely on the brink of extinction. While panthers and red wolves both dropped down to similar numbers—the red wolf even going fully into captivity before returning to the wild—the key distinction between these two cases that allows one to maintain hybridity as a threat and a potential boon for the other is where the threat of extinction comes from and the overall magnitude of extinction threat. For the red wolf, inbreeding may have been present, but it wasn’t causing severe problems for them the way it was for the panthers; inbreeding was a death sentence for the panthers. And hybridity for the red wolf presented a more complex challenge as it was potentially leaping across a conceptually larger boundary (species rather than subspecies) as well as the fact that the hybridizer in question (coyotes) were far more numerous, widespread, and successful. For panthers, the potential hybridizer had hundreds of miles of separation and could therefore be easily contained before anything got out of hand. Human control was clearly readily enforceable in this case and was eventually invoked through the removal of the Texas pumas in 2003 once they had provided what was needed.

Conclusion: Hybridity, Agency, Power

These case studies offer three disparate entry points into hybrid “problems” and USFWS/conservationist responses. The first is a classic case of the “hybrid threat” through a flagship ESA species, the red wolf which hybridizes with coyotes. Debate has raged over the taxonomic validity of the red wolf, and whether it might just be a coyote-gray wolf hybrid, which has added additional fodder to the managerial debate. Ultimately, however, scientific discretion landed upon a policy of strict boundary policing through strategies of coyote and hybrid sterilization and euthanasia. The second case study queries how we respond to genomic data indicating only minute differences between two hybridizing parent species, the golden-winged and blue-winged warblers, particularly when such data indicates hybridization has occurred across the span of millennia rather than caused recently by human impact. What might innovative conservation responses look like that think about an evolving *complex* of wood warbler species, accepting blurring across species boundaries even as one species within the complex is a candidate species for ESA listing? The final case study turns to active human intervention in the classic case of the Florida panther, a notoriously inbred population of panthers that was “genetically rescued” in the 1990s by USFWS introduced Texas pumas, a related subspecies. Policy navigations included preemptive planning to assure protections for the hybrid offspring and it was specifically supported due to a *historic* precedent of continuity between the two subspecies. Together, these case studies offer an overarching window into the range of USFWS responses to border-crossing species, and while they differ a thread can be drawn between them—the managerial desire to establish control on where and when boundary crossing can occur.

Wherever hybridity occurs, the USFWS managerial conservation approach emphasizes containment and control as much as possible, restricting the spread of hybridizing actors. As Youatt notes, “[nonhumans’] governability rests solely on whether they can be controlled indirectly through the patterned grids of scientific prediction” (Youatt 2015, 56). Or, when they “escape” prediction, more direct controls and interventions are therefore necessary. In some cases, as in the red wolf, these hybridizers are thus contained through decisive measures such as sterility and even lethal control. The agency of the individual organisms engaged in hybrid matings is therefore contained and restricted by conservation policy and practice. Even in the dire cases such as the Florida panther where hybridity is deemed a functional tool, these are *controlled* measures of genetic rescue, undertaken only if human agency drives them and with the knowledge that human action can cull unwanted outcomes if necessary. Just as the last remaining Texas cats were removed from the population in 2003 once they had served their purpose—their physical presence on the landscape and continued genetic contributions were no longer needed and were deemed now unworthy and unwanted. As Biermann and Mansfield stress, current conservation science is a fundamentally biopolitical endeavor invested in a “logic of abnormality” which “*requires* judgment about what parts of nature to make live and what to let die in the name of making live. Not all life has intrinsic value” (Biermann and Mansfield 2014, 269). Even acts of harm to individuals such as the euthanized hybrid red wolves are framed in support of the health of populations and can thus be deemed “care” in this conservation framework (Srinivasan 2014). The *Vermivora* wood warbler complex presents the knottiest problem for this kind of control-oriented approach. If we are to take conservation measures that see them as an evolving complex seriously, control over the viscous flow of genes from blue-winged to golden-winged to Brewster’s and back again...this must all be relinquished

to the agency of the 0.35 ounce birds themselves. Rethinking conservation as the management of evolutionary *process* (e.g., adaptation, speciation, etc.) rather than the management of evolutionary *products* (i.e., species) might be a useful orientation shift for allowing such blurring across species boundaries to exist in practice and to support nonhuman agency in conservation management. However, the domineering force of the ESA, its powerful ability to protect habitats, and its reliance on *Species* (I capitalize jokingly, but their importance becomes so hyperbolic it seems accurate) suggest that species (and therefore taxonomy) as a conservation tool won't be leaving us anytime soon.

So, perhaps to address the taxonomic elephant in the room? As you might have noticed from the hybrid case studies explored above, I never explicitly stated what species concept was used in the delineation of the different species. This is because no scientists or policymakers *do* state which species concept (e.g. phylogenetic, biological, etc.) they are using, just (if you are lucky) some of the reasons why they believe the population counts as a species, sometimes using genetic data, sometimes morphological, phylogenetic, geographic, or combinations of the above. Even in debates over taxonomic status, rarely do actual species concepts come up, except to occasionally draw attention to the discrepancy between the Biological Species Concept (which uses ability to interbreed as a primary determination) and the existence of hybrid species populations. Some scholars have gone so far as to call this problem “taxonomy anarchy” seeking restrained and responsible taxonomy and the development and application of uniform definitions²⁹ guided by the International Union of Biological Sciences (Garnett and Christidis 2017). Such scholars emphasize the problem with a “single taxonomic paper...affect[ing] whole conservation programmes”(26):

²⁹ Though they leave open the possibility that taxon-specific definitions may be necessary in some cases.

Take the proposal in 2000 to lump the Florida panther (*Puma concolor coryi*) with the widespread North American cougar. Had it been universally accepted, it would have threatened the subspecies' conservation. (26)

While I think the threat to the panther's ESA protections might be overblown (as I discussed above, it would likely still find recourse as a DPS), the way small numbers of taxonomic papers can incite massive outrage and even numerous delisting petitions is clearly supported by the cases I have discussed here. Whether USFWS discretion crumbles under the pressure from private stakeholders with vested interest in species delistings or maintains a "waiting on best available science" stance and keeps the species listed—both approaches might ultimately have more to do with discretionary value judgments than taxonomic accuracy (Lind-Riehl et al. 2016).

The view on species hybrids in USFWS T&E conservation thus ranges from a severe hybrid threat with drastic reproductive voids as measures to prevent introgression, to controlled hybridization as genetic rescue—but only in *dire* circumstances when lack of genetic diversity threatens a species with extinction. As Allendorf et al. (2001) note, when considering the amount of admixture acceptable in a management population, a key factor to consider is the number of pure populations remaining: "the smaller the number of pure populations, the greater the conservation and restoration value of any hybridized populations" (619). Hybrids therefore would "warrant protection when [they] contain the only remaining genetic information from a taxon that has otherwise been lost by genetic mixing" (621). This idea is clearly under consideration by innovative geneticists even in the case of red wolves (e.g., vonHoldt, Hinton, et al. 2022), though only time will tell if the USFWS sees the red wolf's situation dire enough to consider admixed coyotes as viable conservation populations. The acceptance of hybridization seems to go up overall as a species nears extinction (or genetic extinction in this case as pure populations disappear) as a last-ditch effort to avoid that fate. In this sense, then, hybridization

becomes just another tool in the conservation toolbox (albeit a risky one) with which a species can be recovered. In the next chapter we will look at a case study of another controversial conservation tool that blurs species boundaries and only seems to become viable as a species reaches the brink of extinction: biotechnology, specifically transgenics, for adaptive T&E recovery.

SPECULATIVE FIELD NOTES ENTRY I:
SPARRED OWL

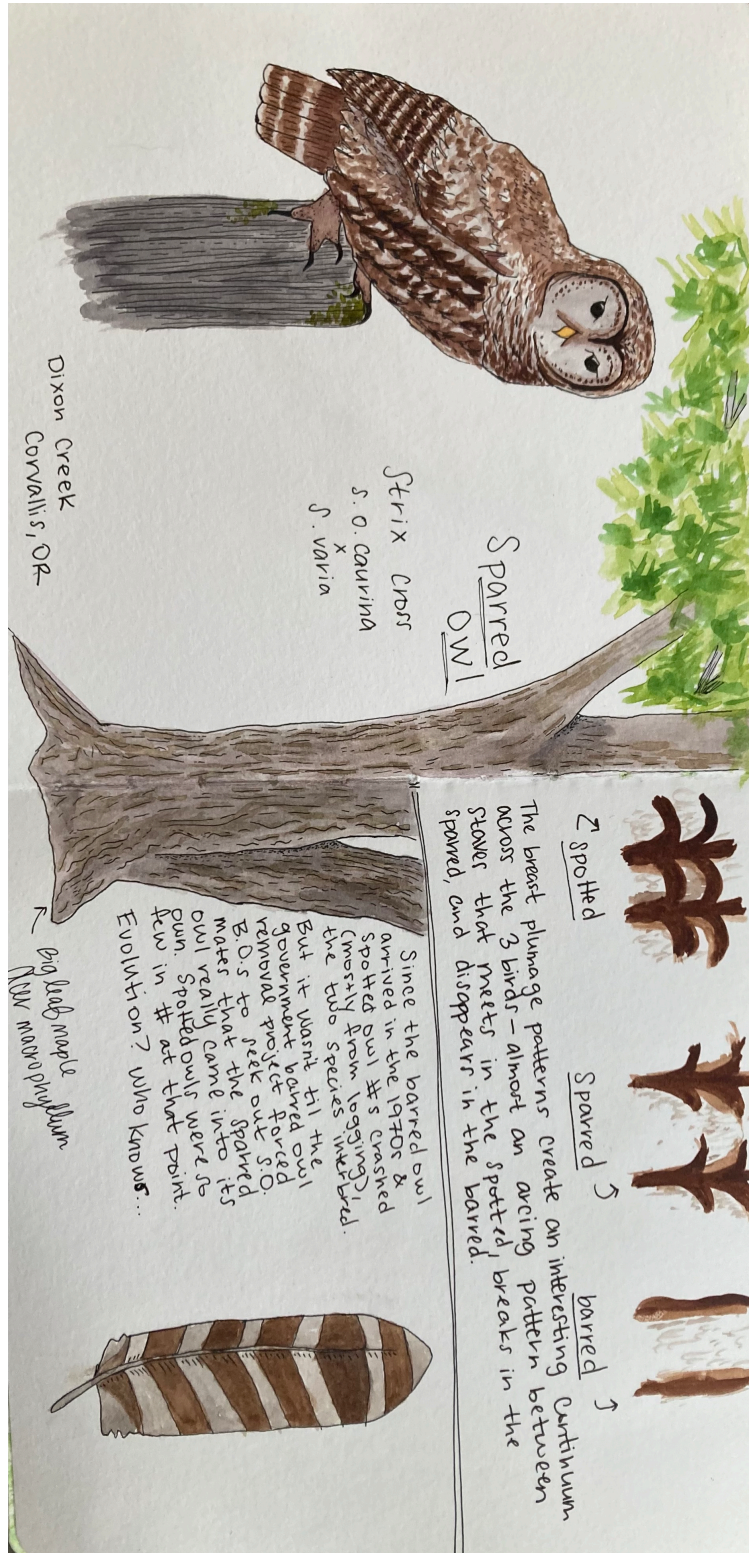


Figure SFN1: Spurred Owl field notes entry, Katrina Maggiulli 2023

CHAPTER III.

NATURAL ENGINEERS, GENETIC INTEGRITY, & NATIVIST PURITY: HOW SCIENTISTS ARE MAKING THE CASE FOR TRANSGENICS IN CONSERVATION

“Mary Douglas [has] suggested that ‘dirt’ be defined as ‘matter out of place.’ ...how should we imagine a gene out of place?”(200)
—Kent H. Redford & William M. Adams,
*Strange Natures: Conservation in the Era of Synthetic
Biology*

Introduction

As species conservation increasingly confronts an uphill battle under rapidly changing climate altered conditions, some biologists are beginning to look to biotechnology as a potential option to stem the tide of biodiversity loss (Piaggio et al. 2017; Breed et al. 2019; Phelps, Seeb, and Seeb 2020). The International Union for Conservation of Nature (IUCN), which brings together governments and civil society organizations on topics such as the development of the Threatened and Endangered Species “Red List,” recently produced a nearly 200-page assessment of synthetic biology and biodiversity conservation (“Genetic Frontiers for Conservation: An Assessment of Synthetic Biology and Biodiversity Conservation” 2019). Some applications they discuss include those that mitigate threats (e.g., interventions to remove invasive species or diminish impact of disease through genetic alterations) and those that support adaptation of threatened species—particularly considering the rapid changes underway due to anthropogenic climate change. Whether or not individual biologists, organizations, or nations support the technology, the assessment’s existence suggests that a windfall of change is coming to species conservation. What interests me about the work introducing biotech to conservation efforts—especially in threatened and endangered (T&E) species conservation—is how it begins to blur

what we deem to be acceptable ranges for species purity or integrity and how we see the role of humans in the evolution of other species.

In Ronald Sandler's 2020 piece on the topic, he notes that technologies such as gene drives, which bypass Mendelian inheritance to promote the rapid inheritance of an edited gene into a population, might change the way we think about conservation altogether—seeing the goal of our work as “fixing” the problems found in the genetic makeup of the species we seek to protect rather than in human restraint (Sandler 2020). Sandler notes we must consider if modification to our conservation philosophies might be necessary: “Should restoration involve greater forward-looking design and creativity? ... Or, should recoveries involve less human design and control, and provide more space for ecological systems to reconfigure on their own...?” (Sandler 2020, 382). Sandler's questions here ally with my own interests in species agency in relation to conservation work, though I would push back against the idea that such prospect of creativity and design is a completely novel one for conservation. As indicated in chapter 1 of this dissertation, even more “traditional” conservation work seeks to bring particular species futures into being and structures species agency. What I do see as more novel about this work, and what we will explore in this chapter, is the way scientists use biotechnology “precision” arguments to bolster their purity species rhetoric and avoid the “messier” species hybrid methods that might previously have been deemed acceptable in a handful of cases. The “cleanliness” of precision biotech gene selection for adaption work, rather than breeding projects that carry large amounts of “foreign” genetic material, trade on familiar purity rhetoric but in surprising ways—considering genetically modified organisms have traditionally been perceived as the *most* “alien.” At the same time purity is maintained, naturalness of transgenic organisms is also supported using contemporary genetic knowledge of Horizontal Gene Transfer (HGT)—

thus the transgenic organism is both *more pure* than other options as well as decidedly *natural*. As might already be clear, the rhetorical framing of both of these ideas together is somewhat ironic as admitting HGT to be natural (and therefore common) would actually upset the fundamental idea of species as pure and essentialist—nonetheless, species-as-conservation-ideal have always managed to operate somewhat outside of biological reality in order to maintain their conservation value. To explore these ideas, we will look at the contemporary case of the transgenic American chestnut presently under review for deregulated status by the USDA Animal and Plant Health Inspection Service (APHIS): Darling 58.³⁰

The Transgenic American Chestnut: Darling 58

History & Approaches to Blight Tolerance

One of the most widely referenced examples of genetic engineering applications in T&E species conservation is the case of the American chestnut (*Castanea dentata*, listed as critically endangered on the IUCN red list³¹) and the chestnut blight fungus (*Cryphonestria parasitica*). The chestnut blight is believed to have first arrived in the United States in the late 19th century by way of imported Japanese chestnut (*Castanea crenata*) trees destined for nurseries and home orchards (Anagnostakis n.d.). Continued imports of Japanese chestnuts and then Chinese chestnuts (*Castanea mollissima*) in the early 20th century purchased via mail order across the Eastern United States allowed the fungus to quickly establish itself and spread rapidly to the

³⁰ USDA APHIS released its draft Plant Pest Risk and Environmental Impact Statements in 2022—both approving the tree for deregulated status. The tree will still need to be approved by the Environmental Protection Agency and the Food and Drug Administration for wild planting in the U.S.

³¹ While the American chestnut is listed by the IUCN and in several U.S. states as well as Canada, it is *not* federally listed in the U.S.—I assume this is due to the tree’s association with the agricultural and orchard industry (where numerous American chestnut crosses are still grown and sold in orchards). I have been unable to corroborate this hypothesis or find any information on this matter after extensive research.

vulnerable native trees (Anagnostakis n.d.). Whereas Chinese and Japanese chestnut trees had coevolved with the fungus, so had a reasonable amount of resistance to its attacks, the American chestnut was completely unprepared for this new pathogen and its populations were swiftly decimated. It went from being one of the most common trees in the Eastern U.S. forests to functionally extinct in only 50 years (Berry 1978). In the wild the tree primarily exists today at the root level, producing shrubby sprouts before they are attacked by the blight; only small holdouts of healthy adult American chestnuts remain. As a foundation species upon which numerous organisms relied for its stable and consistent nut crop as well as a key economic fixture for the human populations of the Northeast, the loss of the American chestnut has had long term cascading effects. The numerous interests in the tree (biological, ecological, cultural, economic, etc.) has made it the natural focus for a variety of different restoration efforts. Three *main* paths unfolded in the course of this restoration: hybrid backcrosses, all-American back breeding, and transgenics. A fourth (failed) path I will discuss briefly due to its interconnected reasoning with transgenics is radiation-induced mutagenesis.

In 1909, the U.S. Department of Agriculture Division of Forest Pathology began breeding for blight resistance by crossing different American chestnuts with other chestnut species (both European and Asian species)—the greatest successes came from crosses with Chinese chestnuts (Berry 1978). While developing a hybrid tree called the “Clapper” saw some success (named for Russell B. Clapper, who bred chestnuts for the USDA), it did eventually succumb to blight and the USDA project was abandoned in 1960 (Berry 1978). Even before all hybrid projects were abandoned, reports on the trees stressed their lack of equivalency to the true American chestnut. As one historian notes, “a 1963 report about hybrid chestnuts described the revival of the ‘lordly American chestnut’ in glowing terms, but it reminded readers that the comeback was ‘as a

hybrid’ and the likely candidates were just ‘kissing cousin relations’ to the former ‘king of the hardwoods’” (Curry 2014, 231). As doubts over the hybrid project and the atomic era coincided, a new project began in the 1960s attempting radiation-induced mutagenesis to speed up chestnut adaptation to the blight (Curry 2014; A. E. Newhouse and Powell 2021). Albert Dietz, chestnut enthusiast who collaborated on the mutagenesis project and planted irradiated chestnuts on his property, stoutly asserted that “The American chestnut program deserves the effort of a ‘Manhattan Project’ or a ‘moon Landing Project.’ A blight-resistant American chestnut would be a valuable resource” (Curry 2014; Dietz 1978, 20). While these projects would ultimately fail, the set of logics that supported them were the same that would go on to support transgenics projects in the future: mutagenesis avoided concerns over hybrid mixing of genetics and the trees’ characteristic suitability as an *American* chestnut (Curry 2014).

With the failure of mutagenesis projects, renewed attention through nonprofit resources was brought to bear on the hybrid backcrossing projects. In 1983, a non-profit, The American Chestnut Foundation (TACF) was established and built off the USDA’s prior work breeding blight tolerant hybrids to backcross to original American stock and produce 15/16ths American chestnut trees that still retained blight resistance (J. W. Westbrook, Zhang, et al. 2020). Another non-profit, The American Chestnut Cooperators’ Foundation (ACCF, est. 1984) sets itself apart from hybrid breeding programs by (in their words) “not using Oriental genes for blight resistance, but intercrossing among American chestnuts selected for native resistance to the blight” (American Chestnut Cooperators’ Foundation n.d.).^{32 33} The nativist and racial discourse

³² ACCF combines its American chestnut “pure” breeding program with hypovirulence (i.e. blight strains infected with fungal viruses causing a reduced ability to infect/colonize the tree) blight control inoculation developed from blight strains of European origin. Cankers are inoculated through infection by fungal viruses in the family of Hypoviridae, which increases the tree’s tolerance and typically keeps the tree alive (Griffin 2000; Milgroom and Cortesi 2004).

³³ ACCF has updated their website as of 11/6/2022 and no longer describes the hybrid program as “Oriental,” the quote above was collected from their website on 4/4/2022. They still breed their trees for resistance from all-American lines.

of the ACCF’s desire to prevent genes of “Oriental” origin from entering the American chestnut gene pool might seem like a troubling outlier, but these narratives are also mirrored in some of the rhetoric used to garner support for the third (and reputedly most successful) path for a blight tolerant American chestnut: transgenics.

The transgenic American Chestnut project is a collaboration between the State University of New York’s College of Environmental Science & Forestry (SUNY-ESF) and the New York Chapter of The American Chestnut Foundation (NY-TACF) that began in 1990. While other chapters of TACF continued the USDA’s former work on Chinese/American hybrid chestnuts, the SUNY-ESF/NY-TACF collaboration focused specifically on the transgenics approach. The team had identified Oxalate oxidase (OxO), a common enzyme many plants (e.g. barley, beet, sorghum) produce to protect themselves from attackers that create oxalic acid (a common strategy of many fungal pathogens). The enzyme takes oxalic acid and converts it into its component parts: hydrogen peroxide and carbon dioxide, two harmless compounds—thus disabling the attacker and protecting the plant (see Figure 3.1). A unique characteristic of OxO in relation to the blight that, the SUNY-ESF/NY-TACF team believes, might impart long-term tolerance is that it doesn’t kill the pathogen—it allows it to continue feeding on dead tissues but prevents it from killing living parts of the tree. The hope, then, is that this approach could

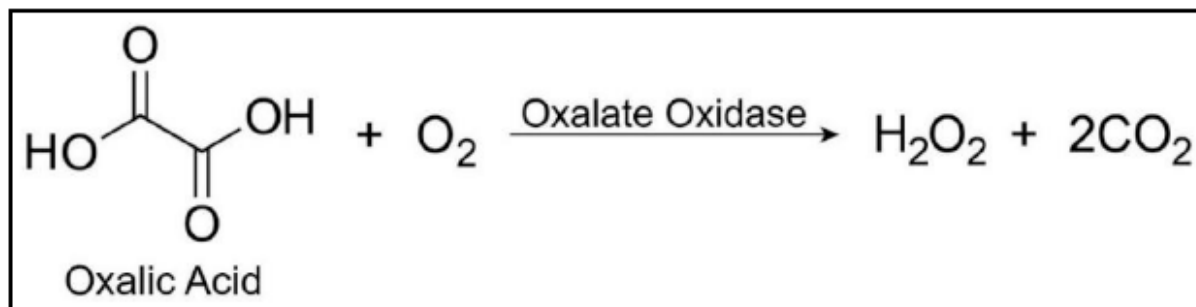


Figure 3.1: Oxalate oxidase is the catalyst that converts oxalic acid into hydrogen peroxide and carbon dioxide. Figure from (A. Newhouse et al. 2020).

facilitate “coexistence” of the tree and the pathogen—allowing the blight to continue feeding on any cracks or branches that have died naturally but preventing it from killing the entire tree (A. Newhouse et al. 2020, 22). By appeasing the blight in this way, this approach might also prevent the blight from evolving a work-around to the tree’s tolerance—one that the team of engineers would have to eventually respond to in kind. Much like in contemporary “Roundup Ready” crops, for example, weeds have quickly adapted to the increased amounts of herbicides we have thrown at them (Brookes 2022). Scientists in the transgenic chestnut project hope that by allowing the blight to continue thriving on limited terms, this same problem might be avoided (A. E. Newhouse and Powell 2021). A familiar plant carrying the OxO gene is wheat, and after some trial and error, it eventually became the “donor” from which the SUNY-ESF team isolated the gene for transfer to the American chestnut (A. Newhouse et al. 2020).

Because of the early timeframe in which they began this project, the technologies for introduction of the OxO gene with which they began their work are also more familiar to GMO agriculture work. They first experimented with the “gene gun”(first designed by John Stanford at Cornell University in 1984)—a somewhat clumsy tool where metal pellets are coated with the desired genetic material, are directed at the cells where they want them to go and are fired into them (Klein and Jones 1999, 21). In a video interview, one of the lead scientists on the project, Charles Maynard (now retired), seemed to laugh at the mere idea that they tried it, saying, “that’s a fifteen-thousand-dollar air pistol, um, and that didn’t work” (Alliance for Science 2016). However, the gene gun has seen success in many other GMO applications primarily in crops such as wheat, soybeans, and maize—as the tool could blast quite readily through cell walls that other transgenic applications were less able to affect (Klein and Jones 1999, 22). The gene gun is still undoubtedly a clumsy tool—the transfer DNA (T-DNA) ending up higgledy-piggledy

wherever in the genome they land—even ending up in organelles rather than the cell nucleus—as the scientists ultimately have little control over where it will land (Low et al. 2018, 51). The tool the SUNY-ESF team ended up finding success with was a natural gene-transferring agent: *Agrobacterium tumefaciens* known to plant growers as the crown gall disease. In natural conditions, this pathogen has a fascinating strategy for attacking its host plants: it enters them through a wound in the plant, transfers DNA into the plant cell causing abnormal cell division and growth of tumors—developing the characteristic cankers of the disease (Kado 2002). But the T-DNA also does one more thing, it has the plant produce opines which the bacterium uses as a source of energy, carbon and nitrogen, in other words: dinner (Kado 2002). In the early 1980’s scientists “tamed” *A. tumefaciens*’s DNA transferring skills, and by removing its tumor-causing side-effects have produced numerous transgenic agricultural products using this method (Herrera-Estrella, Simpson, and Martínez-Trujillo 2005, 5; Low et al. 2018, 47). While still a less precise method than the more recent development of CRISPR-Cas9, it is still a tried-and-true method of transgenic work (Low et al. 2018, 55).

I will first spend some time here teasing out the *material* similarities and differences between the transgenic’s primary competitor as a restoration pathway, the hybrid backcross, and the American chestnut before addressing how the proponents of the transgenics methods assert the superiority of the transgenic tree for restoration of the American chestnut. I hope to draw out in this comparison the logical frameworks that the transgenics proponents are appealing to in their outreach material and petition to the USDA: first, an appeal to naturalness—primarily in the context of the natural gene engineer and source for the O_xO gene; second, an appeal to minimal human intervention—both through the allowance of natural gene inheritance by avoiding the use of a gene drive but also by rejecting the use of the Chinese chestnut genetics which bear the mark

of thousands of years of human intentional breeding; third, an appeal to genetic purity through the desire to remain as true as possible to the original American chestnut genome by minimizing the *amount* of genetic introduction—in this case *where* the genes come from is immaterial, purity is a matter of percentages rather than relatedness in a phylogenetic tree; and lastly, the matter of genetic purity comes together with a racial and cultural lens in the context of the contrast with the Chinese chestnut cross—thus an appeal to a form of nativist purity also comes into play in some outreach content. By turning first to a material analysis of the Chinese/American backcross and American chestnut trees I hope to set the stage for my rhetorical analysis by establishing a clear understanding of where the backcross program presently stands regarding successes in morphological similarities to the American chestnut as well as blight tolerance—therefore we can read scientist arguments in favor of the transgenics approach in light of the status of the backcross program.

The Chinese/American Backcross Program

While I will interrogate a number of different objections that are brought against the Chinese/American hybrid crosses in a moment, a central question we can address immediately is the question of similarity of appearance—where does the tree fall materially? If we set aside problems of genetic relatedness, human intervention narratives, or other concerns, will we still have problems with a tree that just doesn't *look* like the American chestnut that we remember? The Chinese chestnut tree has been bred for thousands of years as an orchard tree—intended to grow in a shorter, more spreading habit so humans can more easily access the larger nuts. The American chestnut is often valued for its straight-grained timber and its tall growth habit—traits that also help the tree to compete in crowded forest conditions (shorter trees would be shaded out

and likely killed). As TACF notes, their key “ideotype” for their Chinese/American hybrid backcrossing project has a series of goals that go beyond just blight resistance:

- Main stem survives indefinitely with blight infection.
- Blight cankers superficial and extensively callused with minimal exposed wood.
- Trees grow as single-stemmed trees at rates and maximum heights more similar to American chestnut than Chinese chestnut.
- Leaf, twig, and nut characteristics similar if not indistinguishable from American chestnut.
- Trees compete and reproduce under competition in the eastern hardwood forests.
- Seedling recruitment is observed near parent trees.
- Populations adequately represent the diversity and adaptive capacity remaining in the post-blight *C. dentata* population.
- A subset of the population has tolerance to both *Cryphonectria parasitica* and *Phytophthora cinnamomi*. (qtd. in Wheeler et al. 2018, 11)

Central aspects here are “Leaf, twig, and nut characteristics” as well as the growth rate and height and growth habit as single-stemmed trees, rather than the multi-trunked habit common with Chinese chestnuts. The backcross program begins with a single cross of a Chinese chestnut to the American chestnut and then a series of three consecutive “backcrosses” to pure American chestnut trees to regain these desirable American phenotypic traits—at each stage selecting for blight resistance (see Figure 3.2, next page; The American Chestnut Foundation 2016).

At the final stage, intercrosses between these “BC₃” (third generation backcrossed) trees produce the BC₃F₃ trees (or, B₃F₃) that are presently deemed the best outcomes of the hybrid program—named “Restoration Chestnut 1.0” (French et al. 2017). A 2006 study of the backcrosses’ American chestnut characteristics looked at minute characteristic differences

THE AMERICAN CHESTNUT FOUNDATION'S BACKCROSS BREEDING PROGRAM

TACF's backcross breeding program begins by crossing an American chestnut and a Chinese chestnut. This is followed by three successive generations of crossing back to American chestnut trees to restore American characteristics. In between each breeding step, the trees are inoculated with blight fungus (*Cryphonectria parasitica*) and only those trees showing strong blight resistance and American characteristics are chosen to breed additional generations. For the final two generations, trees with proven blight resistance are intercrossed with each other to eliminate genes for susceptibility to blight introduced from the American parents.

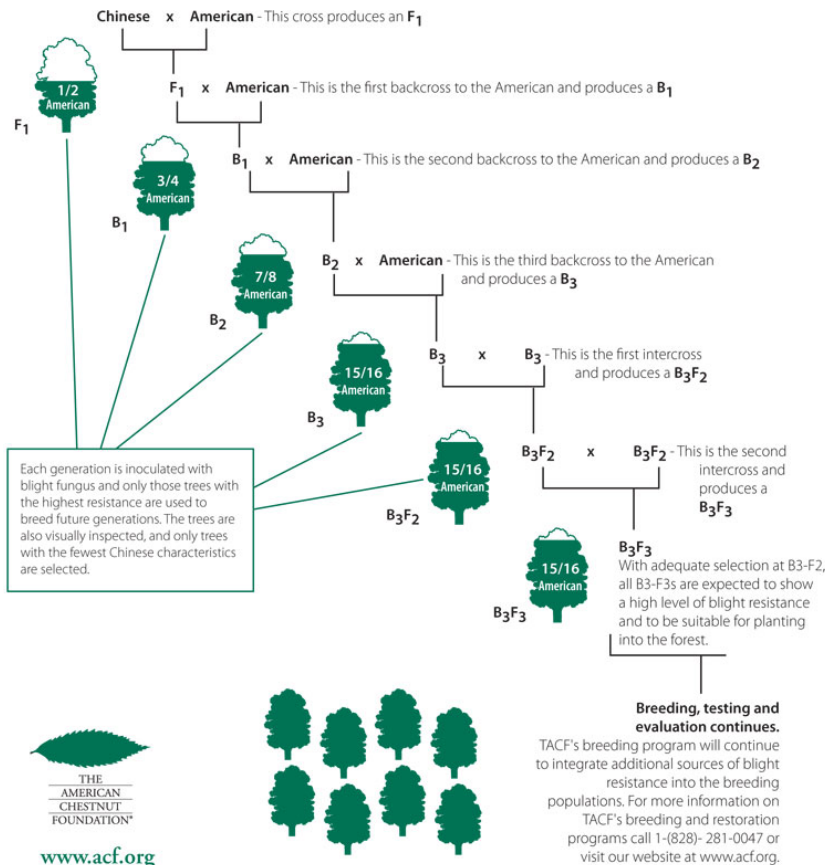


Figure 3.2: American Chestnut Foundation Chinese/American backcross program, The American Chestnut Foundation, 2016.

between the different trees, from the length and depth of the “teeth” on the leaves, angles and shapes of buds, to twig color and hair density (Diskin, Steiner, and Hebard 2006). The analysis supported that such American morphological traits *could* be recovered over the course of the successive three generation backcrosses to American chestnuts. They noted, however, “although certain individual American chestnut traits are not fully attained in the BC₃ as a whole, in each case the majority of individuals do resemble American chestnut for that characteristic”—they found 96% of BC₃ generations aggregate morphology falling within the American chestnut range (Diskin, Steiner, and Hebard 2006, 446). Of course, maximum height on the B₃F₃ trees won’t be

achieved for many years as these are long-lived trees, so it will take longer for the program to have a complete understanding of what traits have been passed down and what traits (like height) might not have made it into the generations of blight tolerant chestnuts presently in TACF’s trials.

However, the B₃F₃ “Restoration Chestnut 1.0” has already been used as a restoration planting in both mining reclamation projects as well as on Forest Service lands, which has offered some preliminary understanding of the tree’s ability to compete and grow in more “natural” conditions (Clark et al. 2014; French et al. 2017). Between 2009 and 2013 the USFS planted 20,775 seedlings and direct-seeded nuts on Forest Service lands from the Blue Ridge

(TN & NC) through the Allegheny (WV & PA) Mountain regions (Clark et al. 2014; see Figure 3.3). Compared to pure American chestnuts planted out at the same time, the B₃F₃ seedlings showed “slightly reduced growth,” but “similar blight resistance to the Chinese chestnut” in some cases (U.S. Forest Service, Southern Research Station, n.d.).³⁴ In the report on their study findings, the Forest Service team noted that the B₃F₃ didn’t express

significant difference in resistance to the

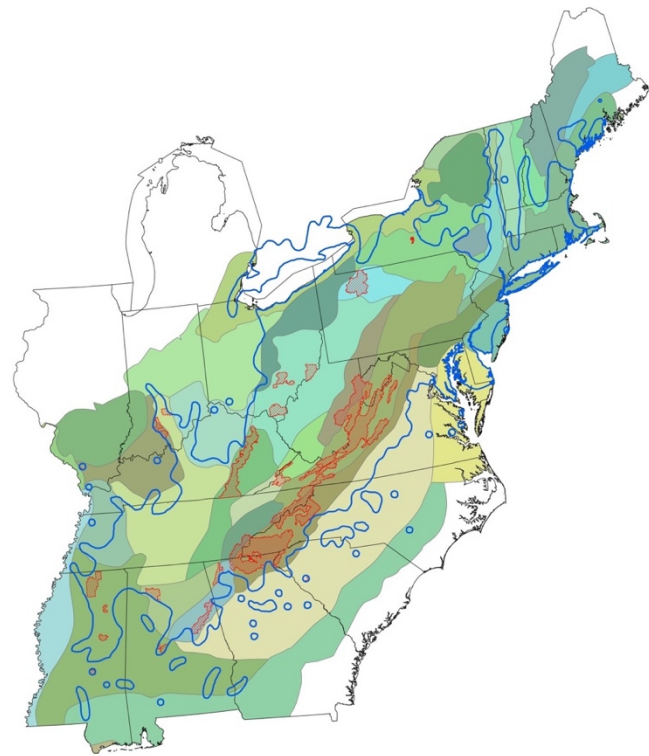


Figure 3.3: USFS Lands (in red) and American Chestnut range (blue line). Hybrid chestnuts have been planted in USFS lands from Tennessee to Pennsylvania, image from (Clark et al, 2014).

³⁴ A key concern for these plantings in the southern end of the American chestnut’s range is *Phytophthora cinnamomi*, a root pathogen that causes rot in wet conditions. Additional plantings of B₃F₃ in 2015 are testing a new root preparation method (a modified version of Forrest Keeling Nursery’s Root Production Method®) rather than traditional bare-root plantings to protect the vulnerable seedlings (U.S. Forest Service, Southern Research Station, n.d.).

Chinese chestnut during the fourth year of the planting when the “blight incidence was relatively low,” but after year 8 the blight incidence was much higher and the gap in performance was much more pronounced with the hybrid not showing the same level of resistance as the Chinese chestnut under those conditions (Clark et al. 2019). The overall resistance of B₃F₃ being somewhat intermediate between the Chinese and American led to hypotheses that blight resistance is passed on through more genetic loci than previously assumed, leading the principal team to begin more complex genetic testing of the hybrid trees to better understand Chinese chestnut resistance and patterns of inheritance (Steiner et al. 2017; J. W. Westbrook, Zhang, et al. 2020). The hybrid lines at TACF are principally built from work already begun by the USDA through their “Clapper” line (mentioned earlier) and the “Graves” line (initially developed in 1953), named for Arthur Graves of the Connecticut Agricultural Research Station (Mehlenbacher, Phillips, and van Buijtenen 1999, 9). Westbrook, Zhang, et al.’s research suggested that “The ‘Clapper’ and ‘Graves’ BC₁ sources of resistance may have inherited different portions of their Chinese chestnut grandparents’ genomes. Furthermore, the two different Chinese chestnut grandparents may have unique loci for blight resistance” (2020, 43). In addition, their study noted that the low heritability of blight resistance phenotypes indicated “that some alleles for blight resistance have been lost in some backcross generations and lines as a result of low-accuracy phenotypic selection”—the hope is that with higher accuracy selection using genomic prediction models, a better balance of American traits and blight resistance might be gained (Westbrook, Zhang, et al. 2020, 43). However, the study still asserts the need for full

genome mapping of both American and Chinese chestnuts as well as genotyping of the backcross individuals to fully track how blight inheritance operates (2020, 45).³⁵

Based on these results, it seems that so far TACF's backcrossing program has successfully regained the physical appearance of the American chestnut in their hybrid trees, but perhaps lost the full benefits of the cross with Chinese chestnuts and true blight tolerance in the process. The program is clearly weighing its tradeoffs between "Americanness" and "how much" Chinese genetics it will tolerate, though its current research now indicates perhaps more Chinese genes might be necessary to actually gain the full polygenic range of blight tolerance that the tree might impart. Of course, the continued precision of genetic science might produce identifiable genetic markers for each of these blight tolerance alleles in the Chinese chestnut genome—perhaps creating a highly precise breeding program. Nonetheless, breeding trees is a slow process and it will still be many years in the making to bring such a project into fruition. Part of the draw of synthetic biology applications such as transgenics, where we will now turn, is the ability to speed up this process and render the overall project of returning a blight tolerant American chestnut to the Eastern forests an *efficient* one. Of course, many people (including scientists) see traditional breeding methods as simply human-harnessed evolution—ultimately a natural harnessing of species that might have bred naturally—whereas synthetic biology applications go further to meddle too deeply and therefore produce too many uncertainties. The questions of "naturalness and novelty" are therefore fundamental to debates over which avenues to take: transgenics or backcrossing?

³⁵ The study does note, however, that these genome maps are forthcoming for the species in question—so this level of selection accuracy is perhaps not far off.

Naturalness & Novelty Appeal

Two central features of the transgenics program are regularly discussed as “natural” and therefore as not necessarily novel: the OxO gene and *Agrobacterium* itself—the tool for transferring the gene to its new home. While the bacterium has been somewhat transformed from its original form to better accommodate its new purposes, scientists working on the transgenic American Chestnut project continually stress that it is a *natural* genetic engineer, using this distinction to further establish Darling 58’s acceptability as a cultivar for planting in the wild. The OxO gene is described as a “natural defense” found in many plants and grains, described as “common” and “consumed daily by humans and livestock” (A. Newhouse et al. 2020, 3-4). While arguments over “naturalness” might once have been central to GMO debates, since the turn of the 21st century these concerns have been entertained less frequently. In our contemporary moment, over 30 years since Bill McKibben boisterously claimed we’d reached the “end of nature,” environmentalists have become increasingly comfortable with the term “Anthropocene” to describe our current epoch of human-dominated global systems, and it is no longer just in academic circles that conversations about the social construction of concepts like nature and wilderness are being had (McKibben 1989). Even GMOs in food systems which had caused such a stir in the 1980s and 90’s over their “unnaturalness” (when they were widely referred to as “Frankenfoods”) have become, if not globally accepted (some European nations being particular holdouts), are increasingly accommodated (Jasanoff 2005; Teferra 2021). Distinctions like natural and unnatural don’t seem to be central in these debates any longer and have now been replaced by concerns over the corporate control of life, agricultural monopolies, or threats to biodiversity rather than the former seemingly abstract concerns about “naturalness”(Shiva 2012; Millstein 2015). However, naturalness in the context of *novelty* is

nonetheless maintained as a key rhetorical framework for scientific support of the transgenic American chestnut—particularly at the regulatory stage.

William Powell as the representative of the transgenic American chestnut not only emphasized *Agrobacterium*'s naturalness at his public TEDx talk, where he stresses that they use a “natural genetic engineer” that “in the wild moves genes around in plants” but also in the technical document for Darling 58's USDA petition for non-regulation (TEDx Talks 2013, 8:40-8:50). In the petition it states: “The idea that this may be the *first transgenic organism in a natural setting is being challenged* by recent research suggesting that about 7% of all dicot species may have been *naturally transformed* in their evolutionary past with DNA from *Agrobacterium* (Matveeva and Otten, 2019)” (Newhouse et al. 2020, p. 184; my emphasis). As they observe, if transgenic organisms in wild ecosystems (or, in their words “a natural setting”) are *not*, in fact, a novelty, a primary argument against introduction of Darling 58 into the wild might fall away—potentially allowing for a clearer road to deregulation. Recent recognition of the widespread nature of gene sharing, particularly Horizontal Gene Transfer (HGT), or the transfer of genes between unrelated organisms through processes other than sexual reproduction, has led to biologist questions about whether these gene transfers have supported adaptive changes and suggestions that evolution is far more “weblike” than the traditional branching tree of the Darwinian imaginary (Jain et al. 2003; Chu, Sprouffske, and Wagner 2018; Supple and Shapiro 2018; vonHoldt et al. 2018). Newhouse et al. are harkening upon this massive outpouring of research in molecular biology that now understands bodies—particularly our genetics—to no longer be as discrete as we had formerly imagined. Therefore, to share genes is a mundane practice in the wider world of nature and could not be considered “novel.”

While “novelty” is not a central determining factor in United States deregulation, it has international significance in GMO regulatory circles with policies such as the 1997 European Novel Foods Regulation³⁶ (Jasanoff 2005) and informal significance for the general public as indicated by public surveys (Petit, Needham, and Howe 2022). This claim to naturalness in transgenics is therefore only important to Powell and other supporters of Darling 58 insofar as it establishes the lack of novelty in the case of the tree’s introduction into wild ecosystems. Because *Agrobacterium* is a natural engineer, and therefore genetic engineering “mimics natural phenomena,” they note that “a blight tolerant American chestnut will not be the first ‘GMO’ to enter the natural forest environment, just the first *developed intentionally* for restoration” (A. E. Newhouse and Powell 2021, 4; my emphasis). Note here the emphasis on *intent* is the only area they see their project has truly distinguishing itself from the ubiquity of gene sharing, and therefore transgenic organisms, in the wild.

The OxO gene’s naturalness is also deemed important in the context of regulatory concerns—particularly as it might pose potential risk. Its naturalness and therefore ubiquity in natural systems is regularly stressed in the petition, articles, and outreach materials on the topic in order to emphasize that humans and nonhumans not only interact with the gene regularly, they in fact *consume* the gene regularly in the form of foodstuffs such as grains, strawberries, tea, peanuts, apricots, bananas, etc. (The American Chestnut Foundation 2018; Powell, Newhouse, and Coffey 2019; A. Newhouse et al. 2020). As noted in the petition, “The variety of plants and other organisms in which OxO activity has been identified and published suggest that OxO activity is widespread in nature, and is likely found in many other foods and wild plants as well”

³⁶ “Novel Foods” referred to any food not consumed “to a significant degree...in the EU before 15 May 1997” when the policy went into effect. These included novel sources of vitamins or nutrients or production processes.

(A. Newhouse et al. 2020, 54). Part of the tree’s regularly process will include an inspection and approval by the Food and Drug Administration for consumption approval, so confirming its edibility (chestnuts are, of course, a popular foodstuff) is essential.

Kent H. Redford and William M. Adams also address the problem of novelty and naturalness in conservation in their book, *Strange Natures: Conservation in the Era of Synthetic Biology* (2021). As they stress, despite concerns over naturalness, “artificiality” has long been a tool of conservation efforts:

The question of whether it is natural to use a bulldozer to create a reedbed to attract wild cranes to converted carrot fields may seem a long way from the application of gene editing in conservation. But it is not. Both raise questions about the place of artificial methods and modern technologies in shaping the nature of nature. Both call attention to the tension between novelty and naturalness. (Redford and Adams 2021, 195)

Redford and Adams stress that when we alter ostensibly “natural” ecosystems with human technologies—whether or not these are for purposes intended to support wildlife survivance—there will always be a measure of “artificiality” to any conservation management action. This reality produces key questions for the conservationist:

...if we are happy with bulldozers and planted reedbeds, in what ways are they different from genetic technologies and human-transformed organisms? ... There is no doubt that the idea of using synthetic biology tools to deliberately alter the genomes of wild species is a tricky one for conservationists. But is novelty and weirdness a sufficient basis for rejecting such interventions? (Redford and Adams 2021, 195-196)

As Redford and Adams suggest here, novelty arguments are also aligned with assumptions that the “weird,” “abnormal,” or interventions that provoke feelings of disgust should be rejected. Extensive research into the moral place of disgust emerged throughout the 1990s-2010’s, some arguing for the moral relevance of repugnance in the context of even novel technologies like GMOs and other biotechnological advancements such as human cloning (Kass 1998). Other scholars, however, have suggested such feelings of disgust towards such technologies might also

just be a byproduct of the prior moral judgement itself rather than evidence of the technology's immorality (May 2016). And according to Leslie Paul Thiele, in our contemporary moment of the Anthropocene, disgust itself may be on the wane—no longer claiming sensory and moral relevance in a world increasingly secured from material threats (e.g. parasites, poisons, etc.) and, after the “end of nature,” now has little role in policing “boundaries... [that] secure, protect, and promote what was pure and natural” (Thiele 2019, 5).

Minimal Human Intervention Appeal

Even if transgenics is a naturally occurring process, objections might still be held over the place of humans as the drivers of the intervention—in this case the *Agrobacterium* is not acting alone to transform Darling 58 into a blight resistant tree. Proponents of the transgenic chestnut thus also appeal to an overall *minimalist* human intervention approach when compared to conservation interventions deploying Chinese chestnut genetics or gene drive technologies. I'll break down each of these comparisons separately as they are anchored in markedly different genetic technologies but are both ultimately anchored in a similar desire to minimize wherever possible the control of the human engineer and maximize the evolutionary agency of the American chestnut itself.

In the first case, comparisons to Chinese chestnut crosses stress the extensive human intervention into the chestnut over thousands of years of intentional breeding that produced the Chinese chestnut as it appears today. All of those minute changes are evident in the tree's present phenotypic traits as its ancestors were selected for such traits over time. These selected traits, of course, were also those that principally served humans by making the trees shorter, nuts larger, etc. and thereby the tree an overall more valuable orchard addition and the nut a valuable food-

crop. Any Chinese/American chestnut cross would therefore bear the mark of thousands of years of human intervention and genetic manipulation—even a 1/16th Chinese chestnut tree like the B3F3 cross. Assuming we wish to maximize the tree’s *evolutionary* naturalness and therefore minimize the overall human intervention in its genetic make-up—avoiding Chinese crosses would be a presumably preferable path.

Secondly, to further minimize overall human intervention into the American chestnut’s evolutionary trajectory engineers can also avoid the use of gene drives, or skewed inheritance measures, in their engineered trees. Gene drives are, if possible, even more controversial in synthetic biodiversity conservation due to their assurance that the desired gene will be inherited from one generation to the next. Bypassing traditional Mendelian inheritance, gene drives are sometimes used to skew sexes in populations of invasive or pathogen-carrying species—eventually causing the desired population to crash and disappearance of the offending species (e.g. rat or mosquito) (Piaggio et al. 2017). They can also be used to rapidly flood a natural population with an engineered gene with only a small number of released animals—making certain biotech interventions both more cost-effective and rapid (Piaggio et al. 2017; Hartley, Taitingfong, and Fidelman 2022). Critics of the technology fear, however, that gene drives could too easily get out of hand—if a sex-skewing gene jumped species for example it might wipe out a native species before scientists were able to rein it in (Civil Society Working Group on Gene Drives 2016). Of course, engineers have already proposed “daisy drives” that would remove the gene drive after a certain number of generations or other built-in safe-guards to assure such cascading effects wouldn’t have as large of an impact (Wintle et al. 2017).

In the case of the transgenic American chestnut, Darling 58, the SUNY-ESF/NY-TACF team has proposed a primarily “natural” method of inheritance for the added OxO-gene. By

leaving out gene drives this assures any future Darling 58 crosses with wild-type (WT) chestnuts will follow traditional Mendelian inheritance and still have young *without* the OxO gene. If the tree receives deregulated status from the U.S. Department of Agriculture—a designation the USDA has so far released a draft approval for in 2022—TACF will build up the genetic diversity of the Darling 58 founders by outcrossing them to WT chestnuts in controlled orchard plantings; it will be 20-35 years after deregulation before a sufficient diversified population of blight-tolerant trees are available for forest restoration (United States Department of Agriculture, APHIS 2022; J. W. Westbrook, Holliday, et al. 2020). TACF presently maintains 1,000 WT chestnuts in orchards for that eventual outcrossing and diversification project (The American Chestnut Foundation n.d.). Without the gene drive, some trees from these outcrossings will therefore still be susceptible to blight—assuring that some (relatively) “WT” chestnuts will always be present in the population (see Figure 3.4; The American Chestnut Foundation n.d.).



Figure 3.4: Blight cankers from first generation progeny Darling 58 x WT American chestnut. Tree on left inherited OxO gene and tree on right did not. The swollen canker on left indicates active response and new growth around canker; on right tissue around canker is sunken and dead and will eventually girdle the tree. Image from The American Chestnut Foundation.

Leaving out the gene drive can also be seen as a strategy allowing a measure of evolutionary agency to be maintained for the chestnut—even under engineered conditions.

While presumably the trees with the OxO gene will be evolutionarily more successful than those without (far more able to live to maturity and therefore reproduce), in the eventual wild plantings of trees containing the transgene near extant stands of WT trees and allowing natural patterns of outcrossing to occur rather than controlling the process, more agency is afforded the WT genome to “do what it will” with the new tool for survival that SUNY-ESF/NY-TACF has provided. Redford and Adams call this approach “rewilding the genome” where,

Like the release of a missing apex predator into an ecosystem, the edit would allow a cascade of biological processes to run.... [Rewilding the genome] allows genomes to continue to evolve as part of the wider evolution of diversity, rather than constraining them to reach any specific human-defined outcome. ... Such an evolving genome would be considered ‘self-willed’ in the sense that it would not be subject to ongoing human intervention. (Redford and Adams 2021, 207-208)

For a species like the American Chestnut which is functionally extinct, unable to exist beyond stump sprouts and tiny holdout copses of healthy adults throughout its range, the introduction of the OxO gene will effectively “put the tree on a level playing field again, allowing evolutionary processes to continue” (Brister and Newhouse 2020, 165). Where evolutionarily the tree is presently at a dead-end, effectively unable to reproduce without aid, the transgene could be a “jump start” that wouldn’t require ongoing assistance—giving the tree future evolutionary agency despite the human intervention in its genome. Philosopher Christopher J. Preston also sees the genome itself as a site of spontaneous agency, stating, “If agency is defined broadly in terms of the capacity for spontaneous and unpredictable action, then mutations will count as a form of agency and this agency clearly belongs to the genome itself” (Preston 2021, 505). And Preston even pushes this idea further and sees this spontaneous agency as one way synthetic or engineered organisms might even *resist* the intent of their creators through continued evolution.

“Rewilding” methods for overall ecological resilience are often taken up in other biotech conservation discourses around biotech-proxies of now extinct species: an acknowledgement that de-extinction projects can never bring back a complete original but only a surrogate species to play an ecological function. As Beth Shapiro explains in the context of proxy-mammoth de-extinction:

Once released into the wild, the hybrid elephant could stomp around, knocking down shrubs and consuming vast quantities of vegetation... This new hybrid animal could replicate the mammoth, without necessarily being a mammoth, with vast potential benefits to the arctic ecosystem... In my mind, it is this *ecological resurrection*, and not *species resurrection*, that is the real value of de-extinction. We should think of de-extinction not in terms of *which life-form* we will bring back, but *what ecological interactions* we would like to see restored. (Shapiro 2015, 130-131; italics original)

Returning the American Chestnut to Eastern forests is argued for in similar ways to a keystone species such as the mammoth because of the tree’s role as a “foundation species” due to its prior dominance in the forest ecosystems and consistency of its nut crop—both qualities that led many other species to rely upon it as a primary food source.³⁷ Restoring an engineered version of the tree to the forest will therefore be like a functional proxy—identical in every way to the original tree with an important change that allows for its survival where the original tree could not—and therefore will restore particular *ecological interactions* that have disappeared with its extirpation from most of its prior range. These ecological interactions mostly functioned without overt human intervention,³⁸ therefore once a foundation of Darling 58 have been outcrossed to WT trees and planted throughout their range the hope is that no future intensive human interventions would be necessary to maintain the populations. In addition, Darling 58 trees that are planted in

³⁷ While the tree is often colloquially in popular culture referenced to as a “keystone species,” to track with proper biological terminology it is actually a “foundation” species. Keystone species are predominantly ecosystem engineers or apex predators. Foundation species are typically the most abundant in an ecosystem, play a key role in providing and maintaining ecosystemic properties such as habitat structure, metabolic processes, flows of nutrients, etc. (Ellison 2019).

³⁸ However, there is research suggesting indigenous burning practices, planting, and settler logging all supported movement and opening of canopy that helped expand the range of the American chestnut in its past (Smith 1976; Russell 1987).

the wild will be able to freely cross with not only WT American Chestnut trees but also the genetically compatible native chinquapin (e.g. *C. pumila*)—crosses that could impart resistance on these other blight susceptible³⁹ genus *Castanea* relative species (A. Newhouse et al. 2020, 42).

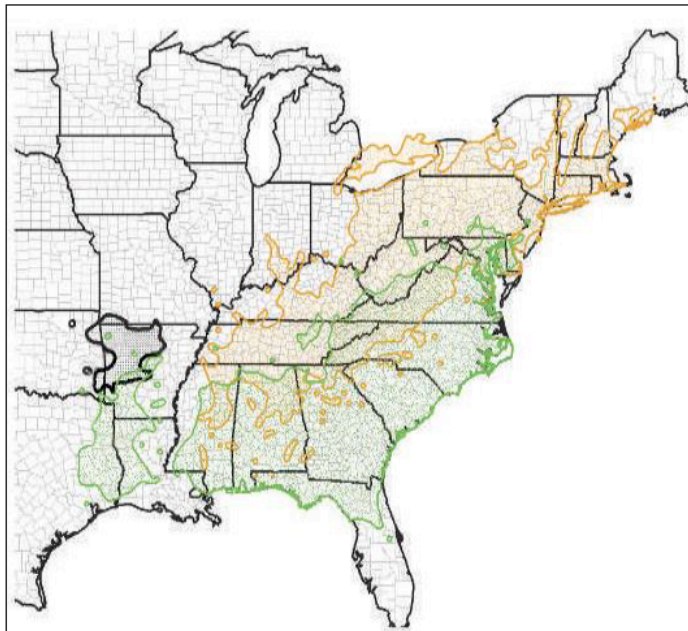


Figure 3.5: Ranges of North American *Castanea* species: *C. dentata* (orange), *C. pumila* (green) and *C. ozarkensis* (black stippled). Map based on Little (1977), reproduced from Shaw et al. (2012).

The American chestnut x Allegheny chinquapin is an already naturally occurring named hybrid tree *Castanea X neglecta* [*dentata x pumila*] that crops up along the crossover of *C. dentata*'s predominantly northern and *C. pumila*'s predominantly eastern and southeastern ranges (Shaw, Craddock, and Binkley 2012; Little 1977; see Figure 3.5). Naturally occurring crosses to

relatives in neighboring ranges is, as discussed earlier in this dissertation, a common occurrence, but it is more commonly an accepted occurrence in plant species as it is even more widely pervasive. One study of 282 families, 3,212 genera and $\approx 37,000$ species of vascular plants indicated interspecific hybrids occur in 40% of families and 16% of genera in the wild (Whitney et al. 2010). Despite these hybridization events, however, the American chestnut's western and northern populations maintained genetic distinctiveness from the Allegheny chinquapin (*C. pumila*), though the hybrid is reportedly difficult to separate from *C. pumila*. It might seem

³⁹ However, the chinquapin species have exhibited moderate blight resistance rather than complete susceptibility—therefore their populations have remained intact whereas the chestnuts were decimated by the blight.

somewhat surprising that hybridization events are common for the American chestnut, considering the rhetorical gymnastics dedicated to maintaining the species' optimal genetic purity with genetic engineering, however even the threat of *natural* hybridization dynamics can become added fuel to crisis discourses around maintaining species borders—where we will turn to next.

Percentages over Relatedness? The Genetic Integrity & Precision Appeal

Even without accepting the relative “naturalness” of the *Agrobacterium* transformation process and the minimalist intervention approach when compared to Chinese chestnut crosses, it might be impossible to deny the benefits the transgenic tree retains in *overall* genetic integrity and “purity” as an American chestnut specimen. As discussed earlier, recent scholarship on genetic markers for blight resistance in BC₃F₃ Chinese chestnut x American chestnuts has emphasized that the trait is far more polygenic than previously believed—meaning it is scattered across the Chinese chestnut genome rather than being expressed through one or two genes (J. W. Westbrook, Zhang, et al. 2020). This means successive backcross generations intended to remove more Chinese chestnut genes, and therefore enhance American chestnut phenotype, are even more likely to lose their blight resistance. In addition, Forest Service geneticist Nurul Islam-Faridi's chromosomal analysis of the Chinese and American chestnut uncovered key differences in the two trees' chromosome structures causing a mismatch when the trees are crossed (Hoyle 2008). Typically when reproduction occurs, chromosomes will line up precisely as pairs; because of the mismatch between the two chestnuts, some chromosomes meet only at the ends, creating a bulge at the center, others creating a cross shape—thereby the American and Chinese chestnuts can only pass down genes located on certain portions of their chromosomes.

Such chromosome abnormalities in the hybrid trees have provoked a couple of questions, 1) whether all blight resistant traits are able to be passed on (i.e. if some resistance alleles are located on mismatched chromosomes) and 2) if the alleles for resistance are on the “bulged” sections, thus in order to maintain blight resistance the hybrid trees might need to retain larger percentages of Chinese chestnut genes overall (as more Chinese chestnut genes would be passed down in such a scenario) (Hoyle 2008). By comparison, Darling 58 retains the entire American chestnut genome with only a couple new genes added to gain blight resistance—a final specimen that will more maximally maintain species genetic integrity and will avoid chromosomal mismatch problems altogether.

TACF describes Darling 58 x WT progeny (T_1) on their website as “essentially 100% American chestnut because none of the American chestnut genome has been removed or replaced” (The American Chestnut Foundation n.d.). They make an interesting rhetorical claim here, using the visual metaphor of percentages to illustrate the acceptability of T_1 genetics as proxies for the American chestnut. The trees are depicted as “essentially 100% American chestnut”—their “essence” derived by *retaining* their American chestnut genome rather than a loss through the *addition* of a small number of new genes. As explored in detail in chapter 1 of this dissertation, the genetic integrity appeal is a fundamentally normative approach to arguments concerning species genetic composition, using genetic “purity” and the rejection of “foreign” genes as undergirding premises for the norm (Rohwer and Marris 2015). And as the above TACF example demonstrates, the genetic integrity appeal also draws upon essentialist notions of species identity. Despite Darling 58 being a transgenic tree (therefore seemingly resisting essentialist notions of species identity if its offspring might be “essentially 100% American chestnut”), TACF’s insistence on the T_1 hybrid’s “100%” identity suggests it has maintained

genetic coherence and something authentic or fundamental about the species is still retained. While Redford and Adams question whether the addition of “genes from wheat ... [means] this [is] the restoration of the real American chestnut trees or something different and less authentic” (Redford and Adams 2021, 204), TACF clearly sees their creation as an authentic blight-resistant proxy to the original. *Where* the blight resistance comes from matters less than the retention of *all original* American chestnut genes and the overall minimizing of the *amount* of novel genetic material introduced. Percentages of the original genetic material become equated to authenticity in this figuration rather than some other measure—as long as there are no subtractions, the tree can still be considered authentic.

The biologists on the project further distinguish the transgenics project from the backcross project through *what* has been retained, noting that because the trees retain “all their wild-type genes and genome structure, with only blight tolerance added on” they are therefore “fully adapted to [their] native forest ecosystem” (A. E. Newhouse and Powell 2021, 2). Elsewhere the biologists stress it is a “much smaller change” and “Insertion of a small segment of DNA through GE [Genetic Engineering], without interrupting any existing genes, allows the offspring to retain all the alleles for height and other adaptations” (Powell, Newhouse, and Coffey 2019, 5). Consistently they stress that the change is *small* and all other genes that help the tree adapt itself to its environment are therefore retained. Indeed, because the trees are long lived, it is hard to know if backcross trees have inherited the desired alleles for height or other environmental adaptations—things you wouldn’t have to worry about in the precision edit approach that transgenics offers (Powell, Newhouse, and Coffey 2019). In addition, when we consider that the Chinese chestnut’s blight resistance is polygenic, when paired with its

chromosomal mismatch—transferring resistance between the two species might require significantly more genetic material from outside the American chestnut genome than desired.

While the genetic integrity appeal might seem “obvious,” I want to underscore why it actually stands out when compared against the other appeals scientists are making in support of the transgenic project. As noted earlier, the transgenics team is also simultaneously making “naturalness” claims based on our volumes of contemporary knowledge supporting HGT and the flow of genes across species borders—some of this flow supported by the same genetic engineer used in this project, *Agrobacterium*. This naturalness appeal is built on the foundation that transgenics, or the movement of genes from one unrelated species to another, is natural and therefore acceptable. The genetic integrity appeal assumes we desire a species to maintain its species borders whenever possible—the purer the species the more “valuable” it is to us in conservation terms. Like the chromosomes of the Chinese and American chestnuts—these appeals seem to have a mismatch. This is where the matter of “precision” and “percentages” become important to the overall connecting logic: transgenics might not be *perfect*, but it is still the *better* option to maintain overall optimal purity. As explored in chapter 1 of this dissertation in the context of the Florida panther—the American chestnut reached what I consider to be a conservation “tipping point,” where drastic measures involving genetic muddiness become acceptable due to the species being on the absolute brink of extinction. Almost like an unspoken arcing graph, biologists go from some acceptance of boundary crossers in species that are in the “safe zone,” to no acceptance of boundary crossers in those that are threatened, and then swing back again when a species appears to be near extinction. With no other options, what else is left but to accept some measure of hybridity? Biotechnology appears to offer a *more precise* way out of this conundrum.

And the SUNY-ESF research team, even while Darling 58 still waits its final approval for deregulated status, has already improved upon the tree with its new transgenic “DarWin” line (Neumann 2022). This new strain uses a “wound inducible” (“win”) promoter from poplar (*Populus deltoides*) that allows the tree to primarily⁴⁰ produce oxalate oxidase when wounded or infected by the pathogen—ultimately saving the tree vital energy for growth and reproduction. These kinds of edits indicate how scientists are adapting new and *even more precise* solutions to the problems the trees are facing. Rather than demanding energy from the trees all the time or altering behavior even when the pathogen isn’t present, the transgenic element of the tree is only triggered when needed. The developing team also notes that an inducible promoter might be overall more stable over the long period of time such a long-lived organism like the chestnut tree will need (Carlson et al. 2022). And the SUNY-ESF team doesn’t foresee very much holdup in deregulating DarWin after Darling 58 is approved—according to Powell, “the USDA will already be familiar with OxO expressing American chestnut trees, and therefore likely only go through step one of the review process. It is unlikely they would find a higher plant pest risk than Darling 58, since the ‘DarWin’ trees are producing less and more regulated OxO production”; Powell predicts DarWin can be approved 180 days after Darling 58 (qtd. in Neumann 2022, 5). While difficult to predict how the public will feel about the “DarWin” versus the “Darling 58” (and we can assume those fully against transgenic trees will remain unconvinced), perhaps a tree that only expresses its transgenic genes *in the presence of* the threats that are anthropogenic in origin (as the blight was brought to the United States by humans) might be a more compelling candidate for reintroduction into wild ecosystems.

⁴⁰ It still has “low level baseline expression” of the OxO gene even when not wounded or infected (Carlson et al. 2022).

While still not a perfect fix for species-level purity (though this is could be changing with intraspecies genetic editing), the level of precision that contemporary tools offer, particularly CRISPR-Cas9, provide opportunities for conservation biologists to maintain purist ideologies in more concrete ways by avoiding the hybridization methods they had previously resorted to. For example, a genetic rescue project reminiscent of the Florida panther efforts that instead used biotechnology is that of the black-footed ferret—a population made-up of ferrets from only 7 founding individuals. The USFWS recently partnered with Revive & Restore (nonprofit) and ViaGen Pets & Equine (for profit cloning company) to clone the cryogenically preserved cells of “Willa,” who died in the 1980s; the cloned ferret, “Elizabeth Ann,” will bring that lost genetic diversity back into a genetically depressed population and avoid any species outcrossing (Revive & Restore n.d.).⁴¹ In such a case, conservation biologists no longer need to resort to the same level of boundary crossing in order to protect the species they value and can therefore retain purist ideals that necessitate border policing and maintenance. Indeed, despite evidence that black footed ferrets exhibit impressive inbreeding avoidance (even when large numbers of closely related individuals are released together the males will travel considerable distances to avoid breeding with relatives), conservation biologists still carefully calculate and control ferret breeding programs—preventing ferret agency in mate selection and ultimately controlling ferret evolution (Wisely, McDonald, and Buskirk 2003; Cain, Livieri, and Swanson 2011). Based on the Darling 58 genetic integrity appeals, biotechnology—once accepted—will potentially offer *more* tools to shore up purist ideologies. The efficient precision edits that technology such as CRISPR-Cas9 and, to a lesser extent *Agrobacterium*, afford urgent conservation projects like

⁴¹ While Elizabeth Ann will retain the mitochondrial DNA (mDNA) of the domestic ferret whose denucleated cell was used for the cloning process, USFWS has planned their breeding program so only descent through her male line will be eligible for wild release, assuring no domestic ferret mDNA will enter wild populations (mDNA is only passed matrilineally) (Imbler 2021; Revive & Restore n.d.).

genetic rescue (e.g. black footed ferret) and adaptation (e.g. American chestnut) could become strategies to maintain stricter species boundaries (better tools for policing), rather than seized as opportunities to tear those walls down and rethink species altogether.

Racial & Cultural Politics: The Nativist Purity Appeal

And the purity negotiation is not just a matter of interspecies mixing, but because the backcross project involves lines of Asiatic origin, discourses rejecting those avenues take on racist and nativist aspects. The American Chestnut Cooperators' Foundation outreach formerly (as of site visit 4/4/2022) used words like “Oriental” or “foreign” in reference to the Chinese chestnut and the Chinese/American hybrids to flag why their “All-American Blight Resistant Chestnuts (non-GMO, no hybrid or foreign genes)” are the superior option (“Home - American Chestnut Cooperators Foundation” n.d.).⁴² Interestingly, however, similar casually racist and nativist overtones also seem to undergird reasoning for adopting the transgenic option for restoring the American chestnut—particularly when it is placed in contrast with the Chinese/American backcross as an alternative.

As part of the 2013 TEDx DeExtinction event (organized by Revive & Restore), William A. Powell, of the transgenic American chestnut project at SUNY-ESF, presented on his research efforts helping to restore the tree. In his talk, he first set up the loss of the tree (and therefore the need for its restoration) through not just its conservation value, but primarily through its cultural value as a feature of *American heritage*. His slide “Part of our Americana Heritage” featured “Chestnut” street signs and lyrics from the classic Christmas song written in 1945 by Robert

⁴² Their website was updated 11/6/2022 and no longer uses this terminology (e.g. “Oriental” or “foreign”), though their breeding program still emphasizes its trees as “all-American” (American Chestnut Cooperators' Foundation 2022).

Wells and Mel Tormé that begins “Chestnuts roasting on an open fire...” as well as the opening line of Henry Wadsworth Longfellow’s poem “The Village Blacksmith” which is introduced by a “spreading chestnut tree” (TEDx Talks 2013, 4:12; “The Christmas Song” 2023). Powell uses these cultural examples to emphasize that the American chestnut is “part of our natural heritage here in the United States” (TEDx Talks 2013, 4:12-15). After using historical photos and paintings to stress the tree’s regal size and *after* the emphasis on the tree’s role as a symbol of American heritage, Powell transitions into his explanation of the disappearance of the tree due to the human introduction of an “exotic pathogen from Asia” (5:03). Thus, while Powell does state human culpability in the introduction of the blight, the threat to American heritage is still framed as coming from a *foreign* source through its “exotic” origins in Asia. This sets up potential added resistance to any support for Chinese-related breeding programs, so the audience is well prepared for Powell’s arguments when he compares the two different approaches to developing blight resistance.

For Powell’s rhetorical comparison of the transgenics program and the Chinese/American backcross breeding program, he leans on the commonly used information metaphor for genomics to guide his audience in considering why even a 15/16 American, 1/16 Chinese hybrid chestnut is a significant fraction:

Let’s think of the chestnut and the chestnut genome as a book and let’s say that book is filled with words and the words represent the genes in the chestnut. We know about how many genes are in the chestnut and they would fill about a 180-page book. So if you’re 1/16th Chinese, what that means is about 11 pages or close to 3,000 words in that book are from Chinese--are in Chinese--. Now that might not be important because we have a lot of duplicate genes in the two but it might be important if this is a critical plot line or something like that. (TEDx Talks 2013, 7:19-7:54)

Powell goes on to stress that this becomes particularly significant because the Chinese chestnut has been bred for “thousands of years as an orchard tree”—therefore having many undesirable

traits we would need to later breed out of the wildtype American chestnut (emphasizing both the genetic integrity and human intervention appeals I've noted earlier). Powell's literary analogy allows him to easily boost up the benefits of transgenics by noting that they would only be moving 2-4 genes in their change—a massive difference from the nearly 3,000 words/genes of the hybrid example. To further illustrate this difference and bolster the cultural capital of the transgenic project, Powell uses a short passage from Henry David Thoreau's *Walden; or, Life in the Woods* (1854) to represent the small amounts of genetic material a transgenic program could bring in instead: "It was very exciting at that season to roam the then boundless Chestnut woods of Lincoln..." (8:34). Powell doesn't actually read the passage as part of his presentation, and, indeed, the passage might represent *more* novel words/genes than his actual transgenic tree will have introduced to its genome—so why include the example at all? Thoreau, and his key work *Walden*, are preeminent cultural symbols of white American environmentalism. Adding Thoreau's words as symbolic stand-ins for the transgenes imparting blight tolerance to the American chestnut provides a particular kind of cultural capital when placed in contrast to the Chinese/American chestnut backcross program: it marks this program subliminally as the more patriotic and fundamentally *culturally American* approach to a blight tolerant chestnut. It is more than a matter of scientific superiority, but also a matter of maintaining optimal cultural heritage and *Americanness* through the selection of the transgenic program over the Chinese/American backcross approach.

Feminist science studies scholar Banu Subramaniam, in her book *Ghost Stories for Darwin: The Science of Variation and the Politics of Diversity* (2014), explores the ways scientific study of variation and conservation efforts around invasive species have intersected with political narratives and historical traumas over race, immigration, eugenics, and in cases

such as these, “Rhetoric is never innocent. Histories of gender, race, and class politics are central to why certain ideas resonate and take hold.” (Subramaniam 2014, 117). The rhetorical frames of Powell’s TEDx talk build upon both cultural logics about American heritage as well as desires to maintain a nativist purity of that heritage through the relative genetic purity/integrity of the transgenic tree. As Subramaniam notes, “Anxieties abound about native and exotic species cross-breeding, thus ‘contaminating’ the native gene pool and gene purity. The rhetoric emphasizes purity by highlighting ‘leaking genes,’ ‘genetic pollution,’ and ‘contamination’” (151). She stresses this rhetoric mirrors discourses from anti-miscegenation policies, and the links between “the nationalization of nature and the naturalization of nation” have been widely marked as key components of fascist nationalism historically and today (148). Many contemporary scholars have noted this kind of connection between eco-fascist ideologies, nationalism, and the championing and protecting of native species as part of a nation’s identity and cultural heritage (Forchtner and Kølvråa 2015; Campion 2021; Rodrigues and García-Pereda 2021).

Not only does Powell emphasize the American chestnut’s cultural value in his TEDx talk—and notably this cultural narrative leaves out all indigenous use of the tree before or after colonization—he emphasizes this value even *over* its ecological values, including only a single slide about the tree’s ecological benefit whereas numerous slides tout its economic, agricultural, and cultural benefits to a distinctly Euro-American human population. And the slide on the tree’s ecological benefits itself is not devoid of European influence, as its evidence for the tree’s former dominance in Eastern forests is marked by a quote written in 1540 by Spanish explorer and conquistador, Hernando de Soto: “Where there be mountains, there be chestnuts.” This slide could have used scientific evidence or evidence from indigenous use of chestnuts to shore up its proof that the American chestnut was the primary canopy cover of the Northeast before the

blight, but Powell rather selects from a specific colonial history that marks early white-European dominance in North America. With this history, as Subramaniam would direct us to consider, comes a narrative that aligns white Euro-American identity with regional flora such as the American chestnut—a narrative of ownership and heritage that must therefore be protected as much as one might protect one’s own property from infiltration.

In a similar vein, the beginning of a contemporary cultural history book on the American chestnut by Susan Freinkel, *American Chestnut: The Life, Death, and Rebirth of a Perfect Tree*, that TACF recommends on the “Educational” page of their website frames the tree through an Appalachian claim to its *regional* value:

Many considered it the “perfect tree,” for chestnut had a value and versatility unmatched by any other hardwood. And nowhere were those qualities better appreciated than in southern Appalachia, where generations of impoverished mountain farmers had depended on the chestnut for food, lumber, and livelihood. “Chestnut defined the region,” says Charlotte Ross, folklorist at Appalachian State University in North Carolina. “If ever a region was associated with a tree, then the chestnut was *our* tree.” (Freinkel 2007, 1-2; italics original)

While undoubtedly true the tree *was* valued by poor Appalachian farmers, the assertion that such farmers *best* appreciated the tree’s value is an interesting claim, considering extensive native use of the tree as a key food source—chestnut shells and even chestnut wood burned for fires have been found at archaeological sites in Tennessee and Kentucky dating back to 10,500 BCE (Chapman et al. 1982; Delcourt et al. 1986; 1998). The narrative Freinkel begins her book with, as supported by regional folklorists, presents the American chestnut as distinctly Euro-American cultural heritage. The tree may belong to the symbolic “everyman” of American Appalachia, but this “everyman” has lived *generationally* as a farmer in the region alongside the chestnut. Therefore, we can presume, whether or not they have accrued considerable wealth over that time, this population is predominately white. A more contemporary cultural and natural history of the

American chestnut by Donald Edward Davis (*The American Chestnut: An Environmental History*, 2021) does an extremely thorough job documenting the history of indigenous use of the chestnut but, notably, TACF does not presently list Davis's book as an educational source on their website. TACF's "History of the American Chestnut Tree" page never once mentions indigenous use of the chestnut and casually mentions colonization by stating "In Colonial times, chestnut was preferred for log cabin foundations, fence posts, flooring, and caskets. Later, railroad ties and both telephone and telegraph poles were made from chestnut..." suggesting the ways the tree was in fact repurposed to forward colonial aims by supporting settler establishment on native lands through the construction of homes and the building of railroads (The American Chestnut Foundation n.d.). Truly "American" in this case must certainly also mean Settler Colonial, as the cultural heritage deemed of value and the ways the tree can be seen as valued (therefore why settlers valued it "best") were through Euro-American cultural values and economies.

The overall stressed importance of the American chestnut as a symbol of "Americana heritage"—and particularly as part of disappearing Appalachian rural lifeways—makes returning the tree with a distinct *American* genetic identity take on new meaning. In referencing Powell's literary analogy—what kinds of "critical plot points" of American cultural heritage are lost or replaced with something perhaps "distinctly Chinese" in a 15/16th American, 1/16th Chinese chestnut? Whether or not the tree ultimately *looks* the part is perhaps important (and the regular contrasts between the American's regal height and the Chinese's short stature should not go unnoticed), but the symbolic nature of the 1/16th Chinese tree—when placed in the context of the American chestnut's regularly asserted value to "American heritage"—can become its own sticking point for public acceptance. As one study (Petit, Needham, and Howe 2022) found, the

public is more accepting of the GE interventions in the American chestnut restoration project over the breeding projects with “Asian” species of chestnut, seeing more potential environmental benefits, even though they still see these GE avenues as potentially slightly “riskier.” While the study was a quantitative survey, therefore did not obtain enough follow-up data to fully understand why respondents ultimately rejected the breeding option, the authors suggested that, based on other literature, concerns over the Asian species being nonnative and less familiar than the wheat origins of the GE genes might be contributing factors. Particularly interesting, however, was that the authors also speculated about whether the administering of the survey in 2015 “when frequent anti-Asia (e.g., China) messaging and rhetoric started being disseminated by the American presidential election campaigns (Skonieczny 2018)” might have produced “familiarity” in the respondents and therefore “impacted some respondent answers to questions about breeding the AC [American chestnut] with nonnative chestnut trees from Asia” (481).

Anti-Asian, and specifically Anti-China, rhetoric in the U.S. has certainly not abated since the administering of the survey—rather we can point to a marked increase leading to anti-Asian hate crimes over the course of the COVID-19 pandemic. If Petit, Needham, & Howe’s speculations on the connections between public rejection for the Chinese/American breeding program and anti-Asian rhetoric are accurate (which more studies would be needed to prove), we can also assume these feelings will only continue to rise rather than decrease. American-Chinese relations are steadily deteriorating over time, as demonstrated by the recent media spectacle over the Chinese “spy balloon” the US military eventually shot down off the coast of South Carolina in early February, 2023. That many people in the general public were able to see the balloon with the naked eye and record images of it with their phones merely enhanced overall *public* panic about the object, adding further tension to contemporary on-the-ground racial relations in an

already racially divided country. How these events might impact future support for the Chinese/American backcross program would require further study, but any event producing renewed perception of “threats” from the “outside” will likely increase support for projects that enhance American cultural heritage and “nativist” values.

Discussion & Conclusions: What does the Prospect of Transgenics Conservation Reveal?

Darling 58’s Public Support & Regulatory Path

It is essential to note that, while Darling 58 has received quite a bit of support from both the scientific community as well as segments of the public, it does not have overwhelming support. 4,320 public comments were received by the USDA APHIS (from here on just APHIS) for the 2020 petition to deregulate Darling 58 (during a 60-day comment period, 8/19/2020-10/19/2020), of which APHIS reported 1,619 as in opposition, 2,698 in favor and 3 out of scope. They note in their Environmental Impact Statement, comments in opposition

...were in regard to environmental impacts of the unconfined release of [Darling 58], impacts to native communities, human health and safety impacts of using a wheat gene, the need for long term studies, the potential for chestnut to be more susceptible to chestnut blight as well as other diseases, the potential for impacts to organic producers, impacts to trade, and general anti-biotech sentiments. (Animal and Plant Health Inspection Service, USDA 2022b, iii)

In addition, APHIS notes that during the 30-day public comment period (8/6/2021-9/7/2021) for their Notice of Intent to prepare the Environmental Impact Statement, they received comments from “individuals, academic researchers, and non-governmental organizations,” of which the “majority of comments submitted were opposed to a determination of nonregulated status for darling 58 American chestnut” (iii). They did not specify the number of comments received, nor their exact substance, and the comments in opposition did not change APHIS’ ultimate draft decision for deregulation of Darling 58. In June 2022 they released their draft Plant Pest Risk

assessment and in July 2022 their draft Environmental Impact Statement, both steps asserting the transgenic tree does not pose a significant pest risk nor environmental or economic impact (Animal and Plant Health Inspection Service, USDA 2022a; 2022b). Even once APHIS releases its final versions of its approvals, Darling 58 still has two more steps before it has finalized all its regulatory approvals. It still awaits assessment from the Environmental Protection Agency, the regulatory body for all pesticides, due to the OxO gene serving as a “plant incorporated protectant” as well as the Food and Drug Administration, which assesses any GMO intended for human consumption for food safety. While the tree is certainly undergoing a range of regulatory steps before gaining approval for wild planting, there is still a gap between what these systems are intended to measure and what the public (and our ethical and value systems or instincts) might feel they should. For instance, APHIS aims to identify whether Darling 58 poses a *plant pest risk*, not whether it presents some other moral or ethical challenge that should prevent its introduction to natural systems. There isn’t a debate in these materials over matters of native sovereignty or public input; to fully incorporate diverse stakeholder interests and values, we must be considering “whose intentions” alongside “what consequences” (Barnhill-Dilling and Delborne 2021).

Barnhill-Dilling & Delborne (2021) emphasize that a Responsible Research and Innovation (RRI) framework for biotech conservation applications will consider 4 dimensions: anticipation, reflexivity, inclusion, and responsiveness (4). Anticipation orients us to consider “*whose intentions* are being anticipated as desirable consequences”:

In the field of conservation, it may appear so obvious what the intentions are for a given project that we forget that conservation initiatives are always shaped by values and interests. We work harder to save some species than others; we cherish some types of habitat in some places more than others; and different stakeholders envision tradeoffs between competing values differently ... In RRI frameworks, anticipation typically takes place through deliberative ... activities [that] introduce stakeholders, including technical

experts, to new perspectives and new ways to interrogate a potential innovation or intervention. (5)

Barnhill-Dilling & Delborne led such a stakeholder activity workshop for deliberation over the transgenic American chestnut, “Biotechnology, the American Chestnut, and Public Engagement,” that brought together developers of Darling 58, chestnut growers, environmental NGOs, an indigenous environmental organization (Haudenosaunee Environmental Task Force), federal agency representatives, and scholars in the field. Concerns over undermining of tribal sovereignty (a self-propagating tree might move onto tribal lands without their say), commercial chestnut contamination, and threat to health and “naturalness” of forests were all aired in the discussions. They note that “The combination of stakeholders not only expanded what we might anticipate about the chestnut project, but it also interrogated important assumptions about *whose intentions* have and should inform decisions regarding the release, governance, and management of the GE chestnut” (5). One direct result of such public outreach was the transgenic team deciding against patenting Darling 58, accordingly “responding to concerns expressed about the GE chestnut following in the footsteps of commercial agricultural biotechnologies” (Barnhill-Dilling and Delborne 2021, 6). However, I think it is important for us to consider that there might, ultimately, be very few other ways we can see public input manifesting in the eventual final result of Darling 58’s destiny. As discussed in chapter 1 of this dissertation, the power of the scientist-expert in the regulatory process as *respondent* to the public comments submitted does ultimately dictate final decisions, even on what we might consider fundamentally ethical matters. And since our regulatory system for biotechnology is concerned with clearly tangible threats to economies, likelihoods an organism will become a pest, etc. it is harder to see ways more abstract values or concerns voiced in comment periods might be addressed. Additionally,

the American chestnut is *not* a federally listed threatened or endangered tree in the U.S., thus making its regulatory path a bit clearer.

The appearance of T&E species in the Environmental Impact Statement (EIS) are thus only those that might be impacted by plant pest risk of the GMO. As required by the ESA, APHIS must clearly review “the biology, taxonomy, and weediness potential of the crop plant and its sexually compatible relatives” and therefore analyze “if the transgenic plant is sexually compatible with any T&E species of plants or a host of any T&E species” (Animal and Plant Health Inspection Service, USDA 2022b, 4-48). APHIS’s regulatory capabilities for GMOs like Darling 58 only exist “as long as APHIS believes they may pose a plant pest risk. APHIS has no regulatory jurisdiction over any other risks associated with [GMOS]” (4-48). APHIS assessed Darling 58’s “potential differences” to conventional American chestnut and the impacts it might have on T&E plants and animals as well as critical habitat. They particularly considered the potential for gene flow between the transgenic tree and T&E species, “including its potential to hybridize”—but no sexually compatible species are presently federally listed or proposed as T&E (4-50). They further considered Darling 58’s potential to drive other competing tree species toward extinction, but found it was not different enough from the American chestnut to pose such a threat to the plants the chestnut had formerly shared the forest with. Notably, however, concerns over HGT or the behavior of “third party” actors such as microbes as potential players in the movement of engineered genes into nontarget populations were not a point of discussion in the EIS.

Complications and Contradictions?

While I have focused primarily here on how scientists are arguing *for* the acceptance of genetically modified organisms and other biotech in conservation, it is also important to point out (as I suggest above) the ways in which HGT can just as easily be used to demonstrate why biotech should be kept *out* of natural systems. If genes are shared so readily, how can we trust any engineer’s promises that an engineered gene will be kept out of non-target populations? The daisy-chain drives I discussed earlier are one example of halting the introgression of a gene into a population using traditional means of inheritance: sexual reproduction— but what happens when we are thinking about horizontal means of inheritance? How do we halt the wildly unpredictable behaviors of the microbes in our stomachs, or on our skin? How are they potentially creating porous interfaces between our genetic makeups and other species’? There are many unknowns when it comes to how to answer these questions, or even how the expression of engineered genes might change over time or as they are passed on from one generation to the next. The intent of the engineer might be thwarted in ways we cannot always predict—even if the gene itself is one we plucked from another “natural” system. Presently, these concerns are not discussed in the APHIS EIS, as they narrow their concerns over “gene flow” to the movement of pollen, seeds, and whole burs. The initial petition from SUNY-ESF *does* discuss this as “theoretically possible” but “horizontal transfer of oxalate oxidase is already possible via the many other endogenous⁴³ sources of this gene ...so Darling 58 would not be a unique source of this gene in the environment” (A. Newhouse et al. 2020, 145). Again, they turn to their “naturalness and novelty” appeal here to reject OxO HGT as a concern.

⁴³ Endogenous refers to something that originates from within an organism—therefore referencing OxO genes that are naturally originating in certain organisms.

Perhaps these scientists will get more than they bargained for, using HGT and *Agrobacterium*'s “naturalness” as rhetorical strategies to bolster Darling 58—as truly opening up an understanding of the porousness of our species (and individual) borders in the public eye might provoke more questions than answers for biotech in conservation. It is possible, however, that such discussions might also reignite interest in the US Forest Service (USFS) and other branches of TACF's continuing work on the Chinese/American B₃F₃ cross. Indeed, it is also important (and perhaps rather perplexing) to note, that despite much of the rhetorical maneuvering that distinguishes the O_xO transgenic strategy from the Chinese/American hybrid breeding program, TACF's 2015-2025 10-year plan includes integrating the two programs. They propose that, if their transgenic tree achieves deregulated status (as it seems poised to do), they would not only outcross the tree to pure WT American chestnuts, but also some of their Clapper and Graves lines of resistances to better shore up the tree's range of blight tolerance (J. Westbrook 2018, 18). I believe however, this seeming hypocrisy in messaging and practice comes from a couple places.

On the one hand, there is the diversity of scientific viewpoints that need to be considered in the context of TACF and TACF's different regional chapters. Considerable division exists over the adoption of transgenics in general for some TACF members, and certain regions are more fully behind the hybrid program than the transgenics approach—some members even left the organization altogether in protest (Kelly 2020). The NY-TACF chapter has, of course, been the principal hub of the transgenics project, whereas the other chapters have been more fully involved in the backcross work. Thus, despite the fact the projects might be integrated in the future, language and rhetoric from the SUNY-ESF/NY-TACF team that seems to make extreme claims about “minimal” human intervention, genetic purity, and even nativist claims aren't

surprising as they seek to establish their project as both morally acceptable and justifiable in the face of conflict and division. Indeed, scientists are (just like any other pair of humans) liable to disagree, even when considering what percentages constitute “acceptable” amounts of nonnative material for backcross projects. As one TACF scientific advisor observed, “Fred [Hebard, chief breeder for TACF 1989-2015] hears 10 percent [Chinese genetics] and thinks, ‘Oh my God, that’s almost completely American chestnut, ‘I hear 10 percent and think, ‘Oh my God, that’s a huge amount of exotic material,’” (qtd in, Curry 2014, 232). But hypocrisy in the context of rhetoric versus practice for the transgenic/hybrid breeding programs has other dimensions aside from potential scientific differences of opinion: the need for public support often means the need for a simplified narrative.

Integrating transgenics with the hybrid/backcross project in the public discourse would complicate the overall message of the transgenics project—if the overall project still supports the hybrid efforts, why exactly do we need the transgenics track (particularly as it is so controversial)? Scientific communities consistently seek to simplify their messaging to hopefully better reach their constituents—sometimes to their own detriment as the public no longer understands the underlying problem (are we talking about weather or climate? Why do masking mandates keep changing? etc.). The SUNY-ESF/NY-TACF strategy to gain support for Darling 58 follows this same avenue for simplification as all of the strategies I have outlined in this chapter orient the public to perceive the transgenic tree as more natural, less interventionist, more pure, even more *native* (and culturally relevant) than other potential alternatives. All of these orientations seek to make the tree seem more *familiar* and therefore “simple” than such a technologically advanced solution might otherwise seem. This approach at its finest is a 2018 animated video produced by The American Chestnut Foundation describing the transgenic

project as a “simple solution”
“discovered” by scientists. The video
integrates highly stylized art that is
almost childlike in its simplicity,
making the science seem even more
basic. The technical process of
transgenics is merely described as
“transferring an oxalate oxidase gene

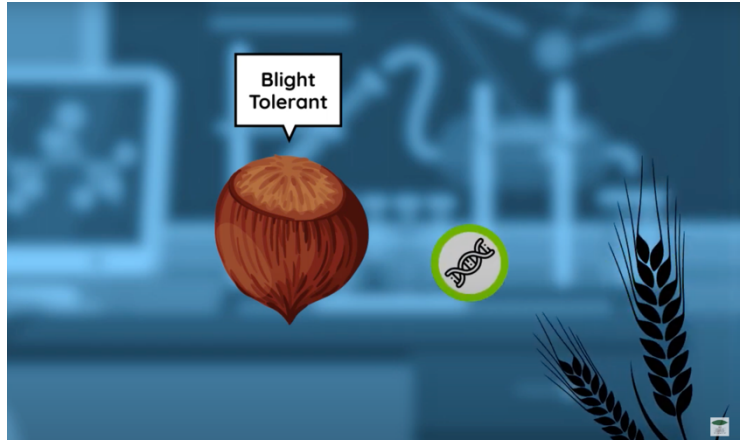


Figure 3.6: OxO gene leaps from wheat to chestnut. Screenshot from “American Chestnut Research” video, The American Chestnut Foundation (2018)

from wheat into the chestnut’s genome” (The American Chestnut Foundation 2018). In their
visual depiction, a little green encircled double-helix representing the OxO gene leaps from an
image of wheat grain to a single chestnut seed—a framing that downplays the complexity of the
actual process (see Figure 3.6). The video also emphasizes the happiness the return of the tree
will produce by including cheery people planting their transgenic chestnuts and an overall upbeat
tone throughout—making the process feel not only simple in scientific terms, but also less
controversial (see Figure 3.7). Presenting a unified and uncontroversial front with this



Figure 3.7: Happy people tend their transgenic chestnuts. Screenshot from “American Chestnut Research” video, The American Chestnut Foundation (2018)

educational video, TACF can ultimately shore up their overarching rhetorical campaign for the transgenic chestnut and simultaneously assure the public how “easy” even a seemingly complicated technologically and regulatory problem like this one can be.

Overlaps and Slippages: Purist Conservationists in Biotech Clothing?

Considering the rhetorical approaches proponents of the SUNY-ESF/NY-TACF Darling 58 approach to blight tolerance for the American chestnut taken together, what kind of slippages in understandings of species are apparent in these scientist and conservationist arguments in support of biotech conservation interventions? The genetic revolution and windfall in understanding of genomic information has had a particularly stark impact on biologist understanding of species-being, knowledge that has not only been put into practice to support biotech interventions, but also has supported a more thorough understanding of the porousness of species boundaries not only vertically through species hybridization but also horizontally through horizontal gene transfer. Biologist recognition of the evolutionary influence of hybridization and HGT and the role of natural transgenic engineers such as *Agrobacterium* provide an interesting new “naturalness” platform from which to argue for transgenic biotech interventions. Species aren’t as discrete or essential as formerly imagined—but despite this knowledge scientists nonetheless combine their “naturalness” argument with a “purity” track derived from the precision techniques afforded by the technology. When compared to older breeding methods, biotechnology enables the movement of only a couple necessary genes, allowing purist biologists and conservationists to continue their same nativist and purist rhetoric in new clothing. Interestingly, they also attest to “minimal” human interventionist appeals despite using genetic engineering methods by applying rewilding logics, natural patterns of

introgression (in some cases), and for Darling 58, intentional rejection of gene drives. The “minimal” human intervention appeal also aligns with purist and nativist narratives in the case of the transgenics versus Chinese/American backcross approach as the latter involves incorporating genetics that bear the mark of thousands of years of intentional human orchard breeding—which also produced an undesirable short stature. While the short stature was discussed as negative for the tree’s ability to thrive in the forest context, we can also place this against the cultural value of the regal stature of the soaring American chestnut’s height and see further racial coding in the way the trees are compared. That content intended for the general public such as the TEDx talk particularly traded on racially charged nativist rhetoric—first firing up a cultural fervor over the tree before making a sharp contrast between the overwhelming amount of “Chinese” left over in the breeding program—points to the way scientists see this as an avenue to reach a broader cultural “logic” of both species essentialism and racism. As the 2015 survey found (study published in 2022, Petit, Needham, & Howe)—it was actually the general public rather than forestry interest groups that were more commonly against the Chinese/American breeding program and favored the transgenics option. Why, they asked? Was this racism? A knowledge gap? Without more evidence, they couldn’t do more than speculate. In all, the range of rhetorical approaches ultimately have allowed conservationists to use the precision techniques afforded by contemporary biotechnology to continue supporting purist species ideals and practice policing conservationist methods.

Returning to the questions from Ronald Sandler I introduced at the beginning of this chapter, “Should restoration involve greater forward-looking design and creativity? ... Or, should recoveries involve less human design and control, and provide more space for ecological systems to reconfigure on their own...?” (Sandler 2020, 382), we can see the way that biologists

in charge of the Darling 58 project have *attempted* to follow the second trajectory—giving the tree as much overall agency as possible and only introducing a single gene supportive of its blight tolerance. Nevertheless the ideals that have ultimately undergirded the project are purist and nativist in nature (future species-directed evolution may be supported, but only a purist future). While the specific case study of Darling 58 offered less opportunities to explore the Sandler’s former idea of “creativity,” many conservationists are nonetheless also presently pointing to the ways that biotech tools can increase forward-thinking and future-oriented approaches to conservation (Piaggio et al. 2017). For species of cultural value and heritage like the chestnut, as they face danger from future and ongoing threats such as climate change, we can predict considerable funds and efforts expended toward long-view conservation efforts that might adapt these species for future conditions. Current efforts abound to support culturally and environmentally valuable global coral reefs and endemic bird species in Hawaii (Samuel et al. 2020; van de Water et al. 2022). These applications represent both responses to present crises as well as adaptations to future threats and thinking critically about new ways humans can engage with species’ evolutionary processes to support life’s future. And new *adaptive* approaches to conservation certainly must come bearing values and perceptions of species-being, particularly ideals about which evolutionary paths are seen as desirable and which are not. This work expands beyond just practical applications, however, and into creative visualizations of life’s future—which is where we will turn in the next chapter.

SPECULATIVE FIELD NOTES ENTRY II:
THE MIGHTY ASH

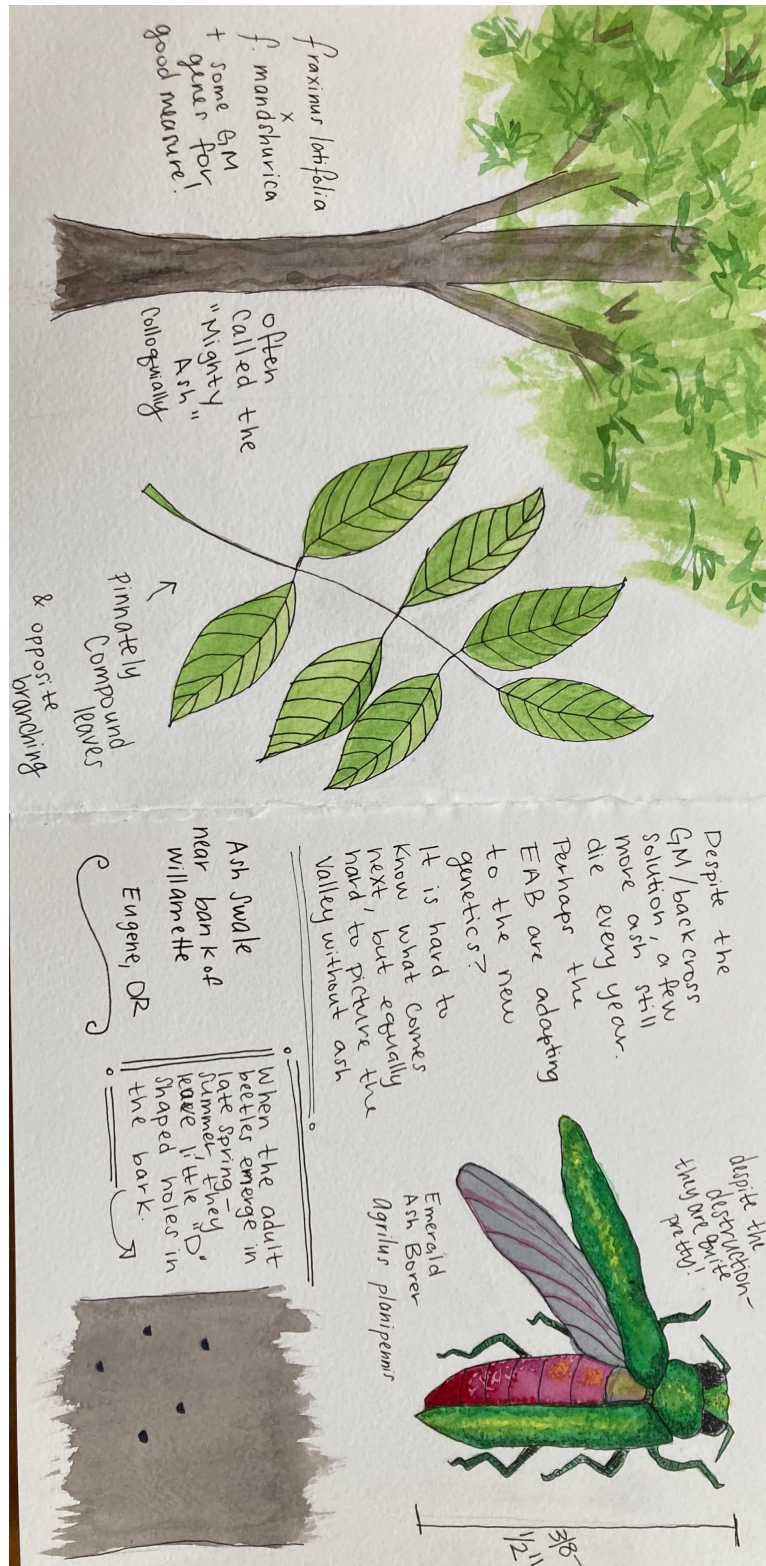


Figure SFN 2: Mighty
Ash & Emerald Ash
Borer Speculative Field
Notes Entry, Katrina
Maggiulli 2023



Figure SFN 3: Ash Swale over time
 Speculative Field Notes Entry, Katrina Maggiulli 2023

CHAPTER IV.
SPECULATIVE EVOLUTION & THE FUTURE OF LIFE

“Whether or not [forms of life] are evolutionarily successful, their justification is not that they are the most worthy, the best designed, the most tested, but simply that they live; they continue an arbitrary trajectory in the best ways they can.”

—Elizabeth Grosz, *The Nick of Time: Politics, Evolution, and the Untimely* (Grosz 2004, 251)

Introduction

As the discussion in chapter 3 indicates, conservation work is entering a new era in which the tensions within the current goals of conservation are becoming harder to ignore. Where contemporary conservation work has so frequently looked to the past for baselines and directives to guide restoration efforts, many concerned scientists and citizens are concerned that this past orientation will fail to keep up with the massive changes that rapid anthropogenic change will cause in an increasingly nearer future. It is becoming clearer that the current tools at our disposal are either failing or are just not enough to stem the tide of catastrophic biodiversity loss: the Endangered Species Act (ESA) has teeth but we are still losing species; traditional restoration methods fight internally over Edenic ideals and can't keep up with rates of habitat destruction (particularly on private lands); the necessity of drastic human intervention seems to paralyze settler conservation models predicated on values like wilderness—where humans visit, but do not interfere in “natural” processes. There seems to be no doubt that something must change—but what? How might we do conservation differently? Do we need to rethink the future we hope to bring into being and reorient our goals accordingly? While no robust dialogue is yet in place to substantively grapple with these questions in the conservation science or policy sectors, a

broader public is experimenting with creative, speculative endeavors that seek to engage with and reimagine our collective species futures.

Much like the history of conservation itself, these species imaginaries must be understood in the context of narratives of apocalyptic loss. In a contemporary moment that is characterized in part by massive scale anthropogenic extinctions, fear and uncertainty is increasingly voiced over “the future of life.” Do humans⁴⁴ truly have the ability to wipe the earth of billions of years of evolutionary history? Might the Anthropocene herald a death knell not just for life as we know it, but life full stop? The Cold War and arms race first spurred these concerns in the mid-late twentieth century—but the threat of nuclear annihilation was only the first of many human-driven threats to weigh on the global consciousness. Today, nuclear fallout has been all but replaced by apocalyptic climate change, biotech fiddling with species genomes, and the cycling of anthropogenic toxins and waste through the remotest corners of the earth. Numerous contemporary texts in popular science writing have explored these pending threats: from mid-late 20th century works including Rachel Carson’s *Silent Spring* (1962), Paul R. Ehrlich’s *The Population Bomb* (1968), and Bill McKibben’s *The End of Nature* (1989), to more recent installations in the field such as Elizabeth Kolbert’s *The Sixth Extinction: An Unnatural History* (2014). These texts brought fears of toxicity, famine, and biodiversity loss (dangers already experienced by BIPOC communities) to wealthy, white settler audiences, instilling the imminent risk of anthropogenic apocalyptic damage to life on Earth as a present concern for the privileged layperson. Alongside the designation of a new epoch, the Anthropocene, these alarm calls of

⁴⁴ Throughout this chapter I will use the general term “human.” I do this with the acknowledgement that the humans truly being discussed are white settler colonial and capitalist powers that drive environmental destruction, and not all humans. A critical treatment of “human” and its accompanying concept the Anthropocene is, unfortunately, beyond the scope of this project. I use the general term primarily due to its ubiquity across the literature I will address here and not out of a desire to implicate all humans in environmental degradation.

destruction are also universalized as caused by *all* humanity, rather than results of ongoing colonial and capitalist power. In E.O. Wilson's book *The Future of Life* (2002), he even goes so far as to refer to "humans" as "the planetary killer" (79). However, scholars such as Audra Mitchell and Aadita Chaudhury stress that these clarion calls frequently emphasize protecting a significantly narrower than "universal" community:

Over the last several decades, a popular and increasingly influential literature on 'human extinction', 'global catastrophic risks', and eco-apocalypse has emerged in the social sciences and popular culture. ... Their central aim is to diagnose the gravest global threats and to offer strategies to protect the future of what they regard as 'humanity'. Yet, despite their claims to universality, we argue that these 'end of the world' discourses are more specifically concerned about protecting the future of *whiteness*. (Mitchell & Chaudhury 2020, 310)

Just as the future of whiteness and particular human communities are emphasized in these narratives of destruction, we can also consider how speculations on the future of life broadly writ is ultimately concerned with particular aspects of that life over others.

In Rosemary-Claire Collard, Jessica Dempsey and Juanita Sundberg's (2015) piece "A Manifesto for Abundant Futures," they respond to both narratives of destruction *and* the contemporary neoliberal postnatural conservation movement which rejects traditional preservationist Edenic Nature⁴⁵ and instead aims to embrace novel ecosystems and views of nature as a "garden" whose good should be maximized equitably for all humans. Their manifesto cautions against a full embrace of this new conservation mode, as they note it is tempting to see abandoning "Nature" as a value as allowing conservation organizations to slough their imperial foundations (and therefore continuing interpellation). They stress that this transition to a new mode of conservation can all too easily become "another future-oriented invocation of *terra*

⁴⁵ Nature with a capital "N" is used by Collard, Dempsey, and Sundberg and others to signify the concept of an untouched and pristine Nature.

nullius, a blank slate” from which histories (and presents) of violence can be “erased”—at least, for white settlers that is (325). Imagining conservation futures, then, must reject temptations of erasure, whether the Edenic model of traditional conservation or the Anthropogenic, human-molded model of a postnatural conservation. For Collard, Dempsey, and Sundberg, the future they choose to envision is one of abundance:

In the face of ruination, we offer a manifesto for abundant futures, by which we mean futures with more diverse and autonomous forms of life and ways of living together. In the spirit of creativity and solidarity, we leave the definition of abundance open while taking inspiration from decolonizing frameworks, politics, and ethics... (323)

In addition to reckoning with ruination brought on by colonial-capitalist power and working pluriversally to support differential ontologies or worlding practices of different peoples, their manifesto calls for a recognition of animal autonomy: “by autonomy, we mean the fullest expression of animal life, including capacity for movement, for social and familial association, and for work and play” (328). Collard, Dempsey, and Sundberg’s manifesto not only helps us to see the ways in which concern for human well-being as well as well-being for other species can be addressed side-by-side without being driven by neoliberal ideals but they also help underscore the need for speculative endeavors that rethink potential futures—futures that venture beyond broad categories of good or bad (desirable or undesirable) and into murkier and less certain realms of possibility.

In addition to the ongoing practice of indigenous communities and thinkers, the field of multispecies studies has been some of the most active in the speculative and dynamic consideration of what it means to be part of multispecies relations on a damaged planet.⁴⁶ In

⁴⁶ See: Thom van Dooren’s *Flight Ways: Life and Loss at the Edge of Extinction* (2014) and *The Wake of Crows: Living and Dying in Shared Worlds* (2019); Anna Lowenhaupt Tsing’s *The Mushroom at the End of the World: On the Possibility of Life in Capitalist Ruins* (2015); Deborah Bird Rose’s *Wild Dog Dreaming: Love and Extinction* (2011); Donna Haraway’s *When Species Meet* (2008) and *Staying with the Trouble: Making Kin in the Chthulucene* (2016); the collections *Arts*

Eben Kirksey's *Emergent Ecologies* (2015), he rejects apocalyptic thinking and refocuses attention on “grounding hopes in shared futures” where varied species communities deal with circumstances where things have gone wrong—ecosystems and relations damaged by capitalism and militarism—and yet they chart new paths together, building new relationships predicated on “chance encounters” and “emergent opportunities” (6; 1). For Thom van Dooren, telling the stories of these relations is a key part of constructing a multispecies ethics: “however modest their effects, the stories that we tell play a role in the imagining and shaping of possibilities,” a process of “ethics as worlding” (van Dooren 2019, 14). Storytelling, whether present or speculative, thus serves an important role in working through ethical relations with other species. In van Dooren's exploration of human-crow relations, his work was interested in an emergent ethics:

How do these specific entanglements give rise to possibilities for life and death, and for whom? How do diverse ways of knowing and valuing (human and not) create particular relationships and accountabilities? Here, ethics emerges out of detailed engagements with the specificity of actual worlds in the making. This is an *emergent* ethics, not an *applied* one. (10)

World making itself, then, is a practice of emergent ethics—ethics produced through active entanglements and negotiations with other species. Finding an ethical pathway is therefore far more complex than the cookie-cutter approach of “applying” a predetermined ethical framework to a specific real-world context—an ethical way forward can only be forged through practice itself.

World building, however, not only happens in the present, but can also be a speculative practice as we look into the future to envision what worlds we either foresee or hope to bring into

of Living on a Damaged Planet: Ghosts and Monsters of the Anthropocene (A. Tsing et al. 2017) and *The Multispecies Salon* (Kirksey 2014).

being. As Donna Haraway as emphasized throughout her work, there is a deep need for what she calls speculative fabulations and other “SFs,”⁴⁷ storytelling practices which she describes as “a mode of attention, a theory of history, and a practice of worlding” (Haraway 2016, 213). These are speculative modes of storytelling that offer a “method of tracing, of following a thread in the dark, in a dangerous true tale of adventure, where who lives and who dies and how might become clearer for the cultivating of multispecies justice” (3). Speculative evolution imaginaries, or the speculative construction of future species, are just one such mode of speculative fabulation. In this chapter we explore a variety of speculative evolutionary works that seek to imagine possible futures for life on Earth. I address the different ways these speculative futures idealize or deprecate particular forms of life, envision human relationships with the evolution of other species, and consider the evolutionary agency of the organisms themselves. In navigating the interplay between hopes and fears for the future, these speculative evolutionary imaginaries all ultimately reveal differential ethics. What possibilities do these imaginaries see for life’s future? For the future of particular species? How do they interpret species-being (mutable? essentialist?)? Does human engagement in other species life, and the protection of this other life, feature in these imaginaries? By tracing the threads of these questions throughout different speculative evolution imaginaries (or speculative fabulations), one can tease out different modes of “ongoingness”—of worlds not ending but continuing—and consider how these different configurations might speak to potential futures that foster agency, abundance, and an emergent ethic of multispecies justice.

⁴⁷ Haraway includes science fiction, speculative feminism, science fact, string figures and others apart from but related to speculative fabulations in her understanding of “SF” (Haraway 2016, 2).

In the first section, I will address the fantasies of human extinction in the “new Eden” of Dougal Dixon’s *After Man: A Zoology of the Future* (1981/2018), where the wondrous (and wondrously familiar) future of life on Earth seems to depend on the removal of humans altogether. The second section turns decidedly away from such human death fantasies to consider two future imaginaries where humans never go extinct: Peter Ward’s *Future Evolution: An Illuminated History of Life to Come* (2001, illustrated by Alexis Rockman) and Shawn Sheehy’s *Beyond the Sixth Extinction: A Post-Apocalyptic Pop-up* (2018, illustrated by Jordi Solano). These “Anthropocene” imaginaries seem particularly interested in the interplay between desirable and undesirable worlds, deploying (in two very different ways) affects of disgust and revulsion as they explore their future bestiaries. The third section moves away from the book-bound forms of the prior two sections by analyzing a boardgame, *Evolution*, developed by Dominic Crapuchettes, Dimitri Knorre, and Sergey Machin with art by Catherine Hamilton, and Pinar Yoldas’s 2014 art installation *An Ecosystem of Excess*, to address organismal evolutionary agency—or imaginaries where organism agency takes a central role in their future evolution. In this final section I argue that these speculative endeavors offer insight not only into what potential future worlds might look like, but also the agential role nonhuman organisms will play in potentially bringing them into being. Ultimately, I see speculative evolution imaginaries as both useful practical tools for envisioning future interspecies relationships⁴⁸ as well as theoretical undertakings that depict and promote differential normative configurations for the human relationship with other species. In this vein, then, I argue that speculative evolution imaginaries must therefore always be analyzed with a critical eye towards the environmental values and ethical frameworks that undergird them, lest an overenthusiasm for the future potential of life

⁴⁸ Therefore, why I use this tool myself in the course of this dissertation through my speculative field notes.

allows the viewer to forget the essential evolutionary truth of extinction (anthropogenic or otherwise) that creates the necessary foundation for future species.

Speculative Evolution Imaginaries

After Man: *The Human-less Eden*

“Uncannily believable. ... some of [the species are] beautiful enough to live...”

—The New York Times Book Review, from back cover of Dougal Dixon’s *After Man: A Zoology of the Future*

Dougal Dixon’s *After Man: A Zoology of the Future* (1981/2018) is arguably the earliest book-length exploration of what the evolutionary future of life might look like and is centrally framed through an apocalyptic narrative, but a redemptive one as it tells a story of Nature/Eden regained. The cultural context of its publication in the early 1980’s is particularly important for us to consider as we delve into its contents, as we can also consider traditional preservationist conservation methods have a central role in environmentalism during this period. *After Man* is a self-proclaimed scientifically rooted account of future evolution, featuring dozens of species descended from present-day organisms. The bestiary is staged 50 million years after *Homo sapiens* follows innumerable species into extinction, and it is this key extinction that Dixon says creates the “vacuum [that stimulated]” the evolution of the new species (33). Following the introduction to evolutionary processes and a brief history of life, Dixon’s zoology separates its species by the habitats and climates in which they live. Notably, these climatic zones and plant communities are generally the same as those we would see in the present day, Dixon having kept them this way to avoid “alienating” his readers⁴⁹ (6). The difference is, these “familiar”

⁴⁹ Therefore, Dixon left out climate change as an actant on his future world. In his 2015 introduction he playfully notes that the “climate change envisioned in the late 1970s was not global warming, but the coming ice age” and would thus, if included, have resulted in a far different prediction (6).

ecosystems are versions completely recovered from human disturbance, having “[reverted] to their natural state ... long after man’s disappearance” (37). From the start, then, Dixon’s “future” looks remarkably like an Edenic version of the past: a time outside of time where nature exists unfettered by human contact. In fact, if it weren’t for the time-traveling nature with which the bestiary is narrated (the only intrusion of humans in this new world), it might be easy to forget it follows one of the most devastating mass extinctions of Earth’s history—indeed, it might be hard to tell time had passed at all.

Because the bestiary features life “after man,” the narration of each species is thus framed through the eyes of an imagined time-traveler who, with “knowledge of today’s animal life,” is able to “describe things with reference to the types of animals that will be familiar to the reader” (9). Because of this knowledge, the majority of the species are described in conjunction with their present-day ancestors and the ecosystem niches the new animals fill in the absence of their prior occupants. For example, the first species group featured in the text are the rabbucks of the temperate regions, descendants of modern-day rabbits who replaced the niches currently occupied by ungulates. The narrator matter-of-factly describes the extinctions of domestic (e.g. horses and cattle; dead due to their dependence on man) and wild ungulates (e.g. deer, elk and moose; disappeared when their habitats were destroyed) not to offer space for mourning or reflection, but rather to underscore the opportunity their extinctions provided: “A whole ecological niche was vacant with nothing to exploit it. Which creature was best placed to take the initiative?” (39). For Dixon, these opportunists are those we failed to kill, and not just incidentally, they are those we tried and failed to control or do away with: modern-day pests.

In this case, the pesky rabbit is what “[took] the initiative” to replace ungulates. The narrator observes that “the rabbit was so seriously destructive of man’s crops, that man made

numerous attempts to control it and even attempted to exterminate it. Yet no matter what actions he took he never succeeded in getting rid of it completely” (39). In other words, despite a past riddled with individual deaths, the rabbit-as-species “escaped” human control to achieve a boundless and abundant evolutionary future. In Banu Subramaniam’s book *Ghost Stories for Darwin* (2014), she remarks that the “seemingly innocuous history of genetic variation holds within it the countless bodies of the dead, the mutilated, the tortured, the irredeemable, the unwanted...” (7). From large scales such as the nation-wide extermination attempts of European rabbits in Australia⁵⁰ to small-scale rabbit “problems” such as the ongoing community polarization over feral rabbits in Cannon Beach, Oregon (Foden-Vencil 2018), rabbits have withstood extensive persecution over the years. The rabbucks of *After Man* are thus haunted by the innumerable deaths that preceded their present “success”— success that led them to diversify into numerous species, hopping varieties more reminiscent of their origins and the even more successful running varieties with deer-like hooves that spread globally. However, unlike contemporary conservation narratives of invasive species homogenization, the 50-million-year span has given the rabbucks plenty of time to geographically speciate over and over again. Thus, a future “overrun” by rabbits is nonetheless a biodiverse and species-rich future.

⁵⁰ Since the 1950s, extensive use of poison (sodium fluoroacetate and the use of carbon monoxide and phosphine to fumigate warrens) as well as biocontrol measures including releasing rabbits with myxoma virus or fly vectors with Rabbit Hemorrhagic Disease Virus (National Geographic Society 2020).

It is this very species and organismal abundance that most clearly characterizes the bestiary's aesthetic. The illustrations vividly depict the various organisms in all their competitive and striving vibrance: the reader can sense the panic in the wide-eye of the dappled rabbuck as it is harried on both sides by a ferocious pair of falanx (carnivores descended from rats, see Figure 4.1); or feel the gentle scrabble of tiny tick bird claws along the hide of an indolent cleft-back antelope (41; 107). Each two-page ecosystem spread throughout the book features a full-page scene (often drawn over with additional specimen studies) in addition to a page of text that is

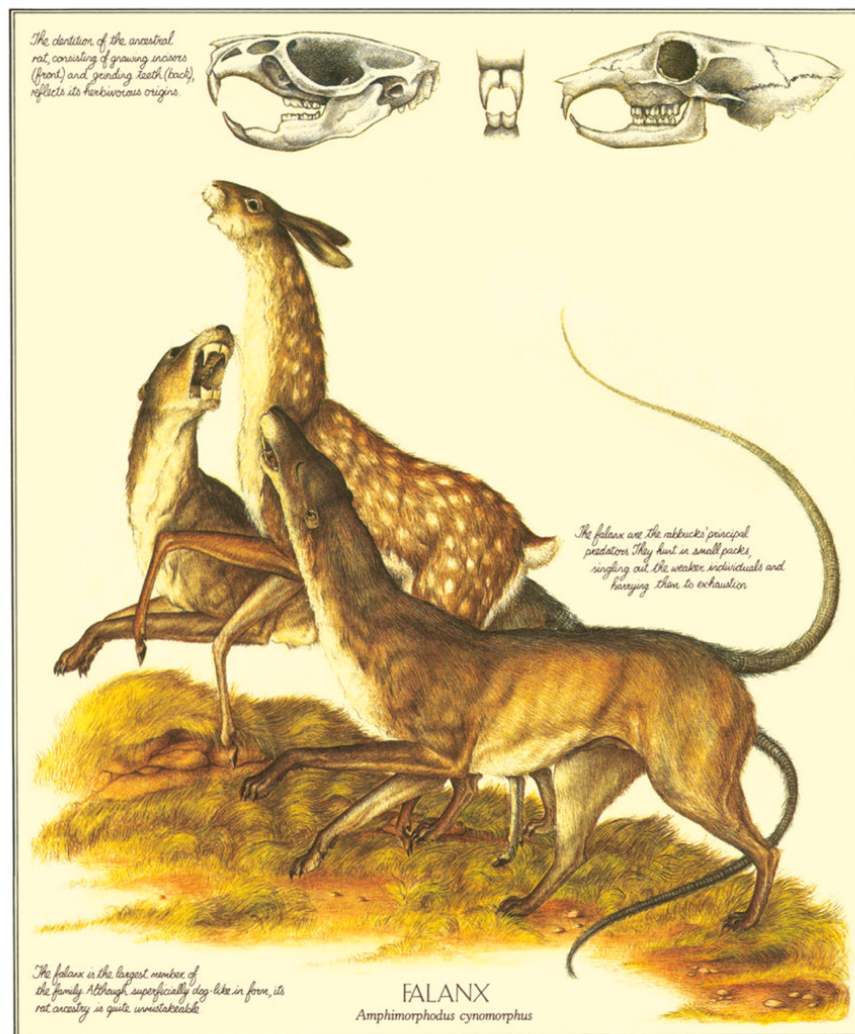


Figure 4.1: Falanx hunt Common Rabbuck, from Dougal Dixon's *After Man: A Zoology of the Future* (1981/2018), illustration by Diz Wallis

bordered with numerous additional images. Some of these spreads feature upwards of twelve individual animals: creatures running, jumping, feeding, inching along branches, lunging towards prey, beaks stabbing soil, or mouths stretched wide in a silent alarm call. Every page is bursting with life—often it seems there is barely the room to contain it, such that these miraculous creatures might creep their way out of the book entirely. The sheer number of bodies on each page, let alone the diversity among their forms, seems to cry out an abundance of life (see Figure 4.2). Despite existing in the after days of one of Earth’s most devastating extinction events, it is clear that life has not only survived, it has flourished.



Figure 4.2: Aquatic mammals of the tropical forests, illustrations by John Butler; from *After Man: A Zoology of the Future*, Dougal Dixon

Thus, despite the narrator's framing of these species through anthropogenic extinctions and attempted exterminations, the aesthetic of abundance refuses prolonged reflection on these checkered interspecies histories, seemingly offering the new biodiversity as a form of redemption. That the newly evolved rabbucks resemble so closely the deer they have replaced makes ignoring extinction all the easier: rabbits becoming deer; rats becoming wolves; the world is rendered different, but the same. It is no wonder the reviewer quoted in the epigraph to this section remarked that some of Dixon's species were "beautiful enough to live," indeed, they are so familiar it seems as though they live already. The emphasis on this morphological similarity for occupants of the same niche, even across millennia, is essential to the guilt-free success of Dixon's bestiary. For without the comfort drawn from this familiarity, the reader must grapple with their complicity (and complacency) in the extinctions occurring as they read. If *After Man* offers hope for the contemporary reader, then, it is the assurance that "nature" will replenish itself, picking up where it had left off before the pesky too-smart *Homo sapiens* intervened. In Dixon's words, "With the removal of this [human] interference I was able to let nature get back to work, just like it did after the dinosaurs were wiped out" (6).

In *Counting Species: Biodiversity in Global Environmental Politics* (2015), Rafi Youatt critiques this "comfortable story of nature restoring itself... [as it] is misleading in the time frames that matter for human beings. Each of these previous [speciation] buildups took millions of years..." (7). He goes on to stress that, "[if] another species-extinction event is under way, it means a long period of interaction with an ecologically impoverished and fundamentally different kind of nature than we have ever known" (7). Because *After Man* gleefully leaps across this zone of "ecological impoverishment," it allows for the period of extinction and loss to pass unseen with only fossil records remaining to indicate the dark origins of the new abundance.

Perhaps even Dixon's hypothetical humans were spared experiencing this loss due to their own, conveniently timed, extinction. While diversity and abundance characterize the future of life in *After Man*, this abundance is only rendered possible by both mass extinction and, specifically, human extinction—experiences the readers are spared, which ultimately serves to reassure the reader of the possibility of restoration without action. Without any depiction of multispecies thriving that includes humans, or even visually evident architectural or material reflections of their presence, *After Man* does little critical work that might gesture towards better contemporary practice, suggesting instead that the future of life may in fact depend on the extinction of humans altogether.

In *After Man*, the future of evolution is ultimately a fantasy of human extinction. This fantasy chooses finitude over the hard labor of overhauling social structures to rectify mistakes. Rather than even attempting to imagine what humans might do next to help other species, and, ultimately, recognize that the “human” at blame is the white settler subject, not humans full-stop, these fantasies prefer the simplicity of wiping away humans entirely. According to Hamish Dalley (2018), these extinction fantasies allow settlers to flirt with the idea of radical decolonial change and reparations but ultimately work to reassert settler futurity and make the settler “moves to innocence” described by Eve Tuck and K. Wayne Yang (Tuck & Yang 2012, 3). By envisioning human extinction, salvation (the ultimate way one can be rendered innocent) is reached as the ills and harms are washed away by the passage of time and made as if they had never been. In Mark S. Jendrysik's piece “Back to the Garden: New Visions of Posthuman Futures” (2011), he describes a recent trend in television series that imagine just such a human-devoid utopia:

In the face of ecological disaster, these works ask us to consider a world without people and take solace in the presumed resilience of nature. Instead of a human future of utopian

technological miracles or dystopian technological destruction, they imagine a nonhuman future in which the natural world flourishes. They combine speculation about the end of days with a desire to contemplate nature in its pristine state. These works project a new Garden of Eden blossoming on an Earth freed of the malign influence of human beings. (35)

One such show that Jendrysik critiques is the BBC series (rebroadcast on Animal Planet in the United States) *The Future is Wild* (2001), for which Dougal Dixon served as a consultant. Nearly exactly mirroring the premise of Dixon's *After Man*, *The Future is Wild* depicts a human-free Earth five million, one hundred million, and two hundred million years into the future. According to Jendrysik, "*The Future is Wild* is most satisfying as a sort of fantasy.... [W]e are told nature cannot die. We are not destroying the planet. Nature will flourish despite whatever we do. Our paltry efforts at reshaping animals and plants to our needs will fail" (48). Such a fantasy merely absolves humans of damage done by first asserting that there is nothing nature cannot fix in time and second by stressing that the only "right" relationship between humans and the natural world is one where humans cease to exist within it. This vision hauntingly reflects the logical conclusion of the most alarmist of overpopulation discourse: suicide as environmentalism.

Apocalyptic imaginaries that see human extinction as the "way out" for the natural world, are ultimately anchored in the imprecise fear of the end of life altogether. As Craig Childs questions in *Apocalyptic Planet: Field Guide to the Future of the Earth* (2012), "We fret about whether we will survive the next major change. But who are we talking about being the ones to survive? Humans ..., familiar ecosystems, or the simple presence of life itself?" (xvi). We might add to this list things like familiar *species*, perhaps even emphasizing the particularly charismatic species that find themselves as mascots for environmental organizations like the polar bear or

panda.⁵¹ How is our fear for the future of particular species couched in the universalizing fear for the future of life itself? Most reasonable environmentalists looking deep into the future are unlikely to see the polar bear or panda still thriving, though would likely also agree that it is highly unlikely *all* life might be so easily obliterated—so are the apocalyptic ideas of the snuffing of “all life” on earth ultimately rooted in a fear for megafauna and other aristocratic wildlife? A key aspect of this apocalyptic imaginary, as Dalley’s critique of settler extinction narratives indicates and Childs’s book queries, is the question of exactly *whose* future we are concerned for. Or, to put it in Audra Mitchell and Aadita Chaudhury’s words: “We often hear that the ‘end of the world’ is approaching – but *whose* world, exactly, is expected to end?” (310). Mitchell and Chaudhury assert that global narratives of eco-apocalypse and human extinction are not deployed to support action that protects all humans, but rather they aim to protect whiteness. I seek to extend their critique of the eco-apocalypse to move beyond just a concern for certain human communities to include an additional concern for certain *types* of non-human life—fear for the future of the most aristocratic of species, namely megafauna. As suggested even in chapter 2 of this dissertation, racist and nativist discourses can undergird the desire to protect species seen as “regal” or imbued with cultural heritage markers such as the American chestnut. These same ideals appeared in the way Eugenics discourses undergirded much early conservation work, particularly in the desire to protect the “aristocratic” wildlife such as the buffalo, elk, and other large mammals, and this desire to protect *certain* life is a longing that is not left behind even in 21st-century envisionings of distant futures. Peter Ward’s book, *Future Evolution: An Illuminated History of Life to Come* (2001, illustrated by Alexis Rockman), in

⁵¹ For a discussion of the polar bear symbol in climate change messaging, see Ursula K. Heise (2016), *Imagining Extinction: The Cultural Meanings of Endangered Species*.

particular illustrates these concerns through its lament for the loss of megafauna alongside a marked distaste for the “weedy” species that will replace them.

The Desirable and the Undesirable: Battling Disgust in the Age of Weeds

Through discourses such as remorse for loss of the noble or regal native species and disgust or a need to “learn acceptance” (or use) for the incoming “age of weeds,” the works in this section are both conversing with “end of nature” narratives that see a turn in their contemporary place in conservation—though in different ways. In the trajectory of conservation’s transition into a more neoliberal post-Natural mode (as Collard, Dempsey, & Sundberg have suggested), we can track this primary transition through Peter Ward’s *Future Evolution* (2001) in its remorse over leaving behind what came before, disgust for what comes next, and the relentless practicality for the misery of it all (overall a rather sobering work). And Shawn Sheehy’s *Beyond the Sixth Extinction: A Post-Apocalyptic Pop-Up* instead places us firmly within the post-Natural by *accepting* the “ugliness” of the creatures and considering instead the ways they can be specifically *useful*—a particularly neoliberal view on the species that also sees them as potentially redemptive figures for a distant, brighter future. This post-Natural “Age of Weeds” begins in longing and remorse, and finishes in seeking satisfaction in finding *use* in what we might previously have deemed *useless*: the weedy and pest species of our contemporary moment.

Peter Ward’s *Future Evolution* (2001), while primarily a text-based work with accompanying images by Alexis Rockman, is nonetheless conceptually a similar mental exercise as Dixon’s *After Man*: each offers historically framed descriptions and explanations for the possible future evolution of life on Earth (a global rather than local view). The two books,

however, diverge very quickly from one another around a single point: the continued existence of humans. Dixon imagines human extinction, while Ward sees humans as virtually “extinction proof” and will ultimately be on Earth until the planet is consumed by our sun’s final demise. Rather than seeing the future as an Edenic return, then, Ward sees the future of Earth as an unending period of “ecological impoverishment” (Youatt 2015). Where Dixon’s sweeping look at the future of Earth might be encouraging or comforting, Ward’s is haunting and hostile. Ward even playfully reflects on his own book in contrast to Dixon and the BBC show *The Future is Wild* in the preface: “This book might be far more entertaining if I took the road of the BBC, or of a visionary named Dougal Dixon, and portrayed an interesting bestiary evolving in a new Eden following the fall of humanity. But I do not think those paths are anything but fantasy” (xv). Even the foreword by paleontologist Niles Eldredge contrasts the work with Dixon, remarking that Dixon “produced a whimsical work of great charm with his imaginary ‘sand sharks’ and other beasts of the future” (xi). In this way, despite the fact that Ward’s text, much like Dixon’s, can only speculate on possible futures without claims of certainty, *Future Evolution* is framed as a “harsh but true” series of facts—a vision of the biologically diminished world we have created and will not be able to prevent from coming into being.

The mood, then, of *Future Evolution* is markedly darker than *After Man*—it focuses more on species the reader will know well, either through contemporary conservation efforts or recent extinction. Rather than wiping away the ghosts of innumerable deaths, as *After Man* does, *Future Evolution* instead lingers in mourning in both text and image on these deaths, framing the potentiality of future evolution as always haunted by these specters. This mood is made especially evident through the illustrations by Alexis Rockman. Instead of serving as a clear and instructive natural history guide like the illustrations of *After Man*, Rockman’s images are unsettling, ominous, and often either dimly lit or intentionally less clear on certain details. In one image, the meeting of a Norway rat and a rail in Polynesia (circa 1767) is saturated in the blood-red light from a sun just hovering over the horizon (46; see Figure 4.3). The figures of the rail and rat are backlit and therefore the details on their bodies are darkened and the viewer must look carefully to see the striped pattern of the rail’s feathers. Further darkening the scene is a



Figure 4.3: "First Encounter" watercolor and ink on paper, 26.25 x 38.25 inches by Alexis Rockman

black cloud lifting up and across the sun from the ship anchored in the bay. Rockman draws on the same deep sunset palette multiple times throughout the text, in one a victorious human figure stands on a vague shape of the continents in blood-red, the scene is only lit by the lingering gold tones of a sun already below the horizon (154). In another, the figure of a thylacine blurs into the background of a fiery sunset with distinct wooden posts and barbed wire partially blocking it from view—the thylacine almost appears to be a mirage caught in the last rays of sunlight, about to disappear entirely with the night (118; see Figure 4.4). Rockman’s images seem to emphasize



Figure 4.4: "Thylacine," 1997, watercolor and ink on paper, 26.25 x 38.25 inches, by Alexis Rockman

again and again that we are in the twilight years—that the sun is setting on many species and the hope of a new sunrise is less and less likely. The darkened rail; the blurred thylacine; the global battlefield bloodied by the human’s mastery: all of these images reject scientific clarity in favor of an affect of violence and loss. And even in Rockman’s clear and brilliantly lit images, he still maintains an unsettling quality. For instance, his image entitled simply (hauntingly), “The Farm” features a farmland populated with the genetic pursuits of man: a bulbous pig sporting human



Figure 4.5: "The Farm," 2000, oil and acrylic on wood, 96 x 120 inches, by Alexis Rockman

organs, a Chinese crested dog with a blue ribbon, rectangular watermelons, a naked chicken with 6 wings, and, nearly hidden next to a basket of square tomatoes, the Vacanti mouse sprouting a human ear from its back (xviii, see Figure 4.5). There is nothing comforting about Rockman's vision of the fate of farm life, even with the cheery and vibrant greens, reds, golds and the cloudless robin's egg blue sky. The aesthetic difference between *After Man* and *Future Evolution* is important in its ethical implications: whereas *After Man*'s illustrations are brilliant and clear—instructive reassurances of nature's eventual recovery through human extinction, the images of *Future Evolution* keep readers guilty and uncomfortable. In fact, it is somewhat remarkable how

depressing *Future Evolution* manages to make an otherwise wondrous premise: how new life forms might emerge in the future.

With Rockman's illustrations deepening the somber mood of *Future Evolution*, Ward's words develop a different kind of melancholic remorse—one that is matter-of-fact but nonetheless carries with it the tone of loss: the oncoming “dyspeptic” age of weeds (135). Ward sets up his “potential winners of the future” through contrast with a whimsical speculation of the evolution of the “Zeppelinoids,” jelly-fish like creatures evolved from toads that float in the air aided by gasbag gullets. The reader is at first entranced by his charismatic and mysterious “Zeps” to whom the only threats are lightning strikes as they “prowl the air, floating serenely above the treetops, filling the skies with their numbers, their shadows dominating the landscape” (121), but Ward quickly follows this rumination with a resounding rejection of such a possibility:

But is the fundamental assumption underlying this scenario—a long period of extinction followed by the emergence of a new class of evolutionary dominants—at all likely? No. For just as humanity has changed the “rules” of evolution that have operated on this planet for hundreds of millions of years, so too has the usual sequence of events following mass extinction been modified. (121)

The incoming winners of the “weedy” species are thus set-up through a rhetoric of loss and rejection. The mere possibility of novelty is met with a resounding “No.” Similarly, Ward further sets up his prediction for the future of Earth through an additional rejection of possibility: that large animals—“megamammals”—will not only go completely extinct, but they will also not reappear in our evolutionary future. According to Ward, the large habitat areas needed for these species to speciate and survive paired with the booms in human population will ultimately result in their *forever* disappearance (114). This fact is one he claims “that conservationists refuse to accept: the Age of Megamammals is over” and will never come again (128).

The series of rejections—of both future megamammals and the fictitious and playful “Zeppelinoids”—both set up the turn to the “winners” of the recovery fauna—those that “possess weedy qualities”:

Chief among these will be those species best preadapted for dealing with humanity: flies, rats, racoons, house cats, coyotes, fleas, ticks, crows, pigeons, starlings, English sparrows, and intestinal parasites, among others. These and our domesticated vassals will dominate the recovery fauna. Among plants, the equivalents will be the weeds. (116)

Ward adds as well that these species are all not only currently preadapted to take advantage of human spaces, but they are also the “champion ‘evolver[s],’” or those able to most quickly adapt and evolve in response to new contexts, a circumstance that assures these species will not only dominate the next 10 million years but also that their descendants will dominate the millions of years that follow (124). In some ways this message is similar to Dixon’s: the future will be populated by the evolutionary descendants of our contemporary human adapted species like rats and rabbits, however, whereas Dixon’s emphasis is on the future wondrous species, Ward’s is instead on the contemporary rats and weeds that produce future species. This reorientation connects the weedy future species with loss and remorse rather than the abundance that characterizes their futures in *After Man*.

The category of “weeds” has gained particular attention in rhetorical analyses of conservation work, particularly in the context of invasive species management (Kendal et al., 2017) as well as other fields such as disability studies where the term comes to stand in analogously for unwanted groups. In Gerald O’Brien’s article “Anchors on the Ship of Progress and Weeds in the Human Garden: Objectivist Rhetoric in American Eugenic Writings” (2011), he remarks on the particular use of a horticultural metaphor for describing the aims of Eugenics where “unfit” persons were regularly referred to as “‘human weeds’ (Hardt 1912, 180) who threatened to choke out—primarily through their rapid growth—the good crops (Huntington &

Whitney 1927)” (13). Weeds, at their most basic level, are merely “plants in the wrong spot”—a plant that happens to be in a location where it is not wanted or is a threat (or perceived threat) to what *is* wanted. Ultimately, then, to label something (or someone) a weed (i.e. unwanted) is to make a judgment of value. As Ward himself remarks, “[w]eeds have many definitions, which are often colored by human values” (111). In the edited collection *Trash Animals: How We Live with Nature’s Filthy, Feral, Invasive, and Unwanted Species* (2013), editors Kelsi Nagy and Phillip David Johnson II discuss the fauna equivalent of the “weedy” or unwanted species—the “trash animal”:

Worthless, threatening, dangerous, destructive, and ugly. Varmints, vermin, pests, scavengers, nuisances, and exotics or invasive alien species.... These terms make us think of animals like snakes, coyotes, carp, starlings, pigeons, prairie dogs, rats, mice, cockroaches, and locusts, to name just a few, and there are many, many others. It is common to think of these animals as harmful, filthy, despicable, or useless. We take it for granted that these and other animals are perceived as having little or no value. These “worthless” species are often associated with, treated like, and called “trash.” (Nagy & Johnson II 2013, 1)

“Trash animals” and “weeds” are boundary-crossing species—they thrive in “native” ecosystems, non-native ecosystems, and human spaces alike and are frequently distinguished by the key characteristic of being either adamantly unwanted or having no perceived value. For Ward, “weedy species” will be Earth’s “recovery fauna,” with us for millions of years as we edge towards a new evolutionary age (116). If the evolutionary future of Earth, then, is framed as an age of weeds we must ultimately see it as an age of the unwanted or valueless—the age of trash.

And the world Ward imagines 10 million years into the future is undoubtedly a world of trash (135): his imagined time traveler lands in a massive garbage dump where he meets dozens of new species evolved from rats, snakes, pigs, and crows. While he barely considers plant-life (except to remark on a small copse of trees harboring hungry crow-descendants), all of the

animal life he sees is notable for its successful use of the human-produced space of the landfill. There are varieties of rat specialized with narrowed heads, needlelike claws, and “thin ribbonlike tongues” that helped them to seek out food more dexterously in cans and piled refuse and a pig descendant had evolved a “small trunk instead of a nose, which allowed it to root efficiently through the piles of rotting offal” (137). The pig in particular catches the time traveler’s attention as it is not only the biggest animal he sees, but it also sports an array of rat-like creatures dangling—parasitic—from its sides “like remoras clinging to a shark”: “he thought at first that they might be babies, but they were clearly parasites of some sort, looking like hairy lampreys with greedy sucking mouths. Or perhaps vampires would be a better description” (137). The time traveler’s disgust at these creatures is evident in his contrast between the imagined remoras or babies and the actual parasitic “hairy lampreys,” the assertion that their mouths were “greedy,” and that the mythical category of the homicidal vampires seemed like a better comparator than even a parasitic lamprey. At every turn, the evolved now parasitic rats drew from the time traveler a deep distaste, at which point “[h]e *shuddered in revulsion* at this bestiary. All seemed exquisitely adapted to these piles of garbage; in fact, all seem adapted exclusively for life in this setting” (137, my emphasis). With Ward’s time traveler “shudder[ing] in revulsion,” the reader cannot mistake the emotion they are expected to have in response to these landfill-adapted creatures: disgust. Indeed, it is particularly instructive that the revulsion is immediately followed up by the note that these species are “exquisitely adapted to [the garbage dump]”—it seems that even the fact that these “weedy” species are able to live in and adapt to a human-produced apocalyptic wasteland must count against them. The time traveler’s visit also seems to end untimely, as the speculative segment concludes with the time traveler fleeing a massive flock of colorful crows sporting a “knifelike” talon on each foot, birds he at first didn’t waste a second

glance on. The segment ends with his final reflection: “the lions of the world now had wings” (137). It seems the time traveler couldn’t help but conclude even his life without a remorseful reflection on the loss of charismatic megafauna and their replacement with much smaller organisms—those he blatantly ignored before they marked him out as prey.

The particular frame of attentiveness and emotive response of Ward’s time traveler ultimately structures the intended, indeed, expected, response readers should have to the age of weeds bestiary: disgust at what life has become, and lingering remorse at what it once was. The time traveler meets his end at the deadly talons of carnivorous pack-hunting crows and can only seem to think of the nobler lion he might once have fallen prey to. His inquisitive exploration into the future of life only results in revulsion at its garbage-adapted ways. The paired nostalgic remorse for a lost nobility alongside the disgust for contemporary degenerate life places Ward’s vision of the future of life in a Eugenics-inflected mode. As explored by disability studies scholars, the issue of disgust was particularly essential to the United States’ eugenicist “ugly laws” that “barred people with 'unsightly or disgusting' disabilities from public spaces on the grounds that their appearance was offensive and a legal liability” (Wheeler 2017, 382). Stephanie Wheeler (2017) notes that these laws were a “eugenicist intervention into language” that guided meaning, just as eugenicists guided life, “by discouraging the production of those meanings that would be deemed undesirable: diseased, maimed, mutilated, deformed, disgusting bodies cannot ever be healthy, beautiful, appealing, or useful” (383). In this logic, those persons or creatures framed as “disgusting” cannot simultaneously be “appealing or useful.” In Susan Schweik’s book *The Ugly Laws: Disability in Public* (Schweik 2009), she describes the laws as “legalized disgust”: “The law seems to have its own kind of raw shuddering body: law as gag reflex, a law with guts. Disgusting adds a biological force to the ordinance, framing it as the legal concomitant

of nausea” (94). Schweik’s take on disgust as adding “biological force” to the law is particularly resonant with Ward’s time traveler. His “shuddering body” is a gut-deep revulsion to an undesirable future for biological life—one that, when considered alongside the trustworthy factual nature of the accompanying full text of *Future Evolution*, carries a sense of gut-truth: ultimately, some species and some evolutionary futures are better than others.

While Ward seems to have made up his mind about the desirability of a world populated by human-waste adapted creatures, other imaginaries take a different approach. Even in the foreword to *Future Evolution*, paleontologist Niles Eldredge remarks that the book’s artist, “Alexis Rockman, whose often brightly colored canvasses just as often project dark themes, has in the course of his career created a vision of life on earth totally informed by the presence of humanities—tin cans and discarded tires forming the substrate of an exuberant, ongoing life” (xii). Disgust doesn’t seem to appear in this consideration of future life based in human refuse—the future seems to be nonetheless “exuberant” and “ongoing.” And in other artistic and academic conversations, species that thrive under human contexts are celebrated. For instance there is Anna Lowenhaupt Tsing’s (2015) multispecies ethnography of the matsutake mushroom that thrives in “human-disturbed forests” and other blasted landscapes: “When Hiroshima was destroyed by an atomic bomb in 1945, it is said, the first living thing to emerge from the blasted landscape was a matsutake mushroom” (p3). Or there is also the artist Mona Caron, whose massive weed murals have sprung up around the world, some towering dozens of stories into the air, celebrating what she calls the “rebellious resilience of weeds” (Caron n.d., see her website: monacaron.com/weeds). Drawing on scientific conversations debating the conservation value of invasive or non-native species and “novel ecosystems,” popular science writers and environmental journalists such as Emma Marris (*Rambunctious Garden: Saving Nature in a*

Post-Wild World 2011) and Fred Pearce (*The New Wild: Why Invasive Species will be Nature's Salvation* 2015) have similarly sought to reclaim ecosystems and species that traditional conservation would have targeted for destruction. In Shawn Sheehy's speculative pop-up bestiary, *Beyond the Sixth Extinction: A Post-Apocalyptic Pop-up* (illustrated by Jordi Solano, 2018), the tensions between disgust and the unwantedness of "weedy" species and their resilient and redeeming qualities are played out in the most playful of forms: the pop-up book.

Just as Ward's future imaginary dwells within the messy and psychologically deleterious confines of the evolutionary "recovery" period after the sixth mass extinction, Sheehy's "post-apocalyptic pop-up" also chooses to set its stage in the twilight age of "ecological impoverishment" that *After Man* had skipped over. However, differing from Ward, Sheehy seems to *see* the species of this era themselves more clearly, but for a decidedly services-oriented reason. *Beyond the Sixth Extinction: A Post-Apocalyptic Pop-up* (illustrated by Jordi Solano, 2018) depicts the shadowy world of the 4800's District of Cago (what was once Chicago)—a region long assumed devoid of life. The pop-up is framed as a report by the fictional "Willek Muriday, Chief Scientist and Regional Director" to the Regional Survey Team Members, entitled "A Field Guide to Creatures of the Cagoan District," dated 7 May 4847, and labelled for immediate distribution (1). The prefatory material written by Muriday asserts that his team are the follow-up expedition to

A landmark survey executed in the region fifty years ago by evolutionary biologist Natalio Milius ("Accelerated Speciation in the Cagoan District: A Preliminary Survey," *Biostatistics Review*, 7 February 4797, pp. 7A5-7B7) [that] revealed that various highly adaptable species were filling evacuated niches and showing signs of rapid evolution. (1)

The field guide, or primer, framing of the text is reminiscent in form (if not the species themselves) to Dixon's *After Man*. But even with the playful nature of the pop-up form, the book is markedly darker than *After Man* and even *Future Evolution*; the sparseness of life, the dreary color-palette, and even the bodies and natures of the species themselves set this vision apart.

Where wonder and abundance framed *After Man* and mourning took the foreground in emotional framing for *Future Evolution, Beyond the Sixth Extinction* is instead unsettling, leaving behind a reader who, even if inclined to be hopeful, is ultimately disturbed rather than soothed by the future of life depicted. Sheehy's evolutionary visions for the future of pigeons, cockroaches, mice, and dandelions (to name a few) are all not only changed by their evolutionary adaptations, but they are specifically framed as *mutated* through radiation induced "mutagenesis"—they are rendered haunting by pairing familiar qualities of their ancestral species with alien qualities that wouldn't be out of place in a horror film.

While "mutation" in a scientific community will merely gesture towards the material process of DNA mutations that help propel evolutionary change, Sheehy's bestiary is operating at a genre-bending place that gives the terminology of mutation the same sinister sense it carries in the popular subgenre of "body horror" where bodies are rendered diseased, deformed, parasitized, or (as in zombie films) are actually consumed. In the sub-genre realm where visceral discomfort of the "gross-out" reigns, the concept of "mutation" draws on imagery like the nuclear-mutated cannibalistic hillbillies of *The Hills Have Eyes* (Aja 2006) or the toxic-run-off mutated isopods that begin parasitizing and killing citizens of a small Maryland town in *The Bay* (Levinson 2012). According to Ronald Allan Lopez Cruz in his article "Mutations and Metamorphoses: Body Horror is Biological Horror" (Cruz 2012), body horror's "powers of repulsion" are in its disregard for "what is considered normal anatomy and function in biological species (not limited to human)," thus making the genre ultimately a genre of *biological horror* (p. 161):

Biological horror throws all of that [biological patterns and norms] out the window, giving us the natural horrors of mutants, hybrids, transforming creatures, and walking corpses. Ultimately, it relishes the destruction of the organic form to the point of unnatural evolutionary insignificance. (Cruz, 2012, p. 167-8)

In body, or biological, horror, mutations render the body or creature monstrous, thereby crossing the body over boundaries of accepted norms. As Jeffrey Jerome Cohen states in his seminal essay “Monster Culture (Seven Theses)” (1996), the monster “polices the borders of the possible, interdicting through its grotesque body some behaviors and actions, envaluing others” (p. 13); the monster toys with the illicit and directs our attention to the boundaries of the possible, the acceptable, instructing us on where not to tread by itself doing so. The species and aesthetic of Sheehy’s imaginary are thus not just mutated in a scientific and evolutionary sense, but also in a psychological sense—their forms disrupt commonsense “rules” of nature and thereby produce the same guttural upset that an encounter with the mutant human-fly hybrid, “Brundlefly,” from David Cronenberg’s classic *The Fly* (1986) might do. But where Sheehy departs from biological horror as defined by Cruz is in its very evolutionary *significance*—the sense of the “unnatural” in Sheehy is nonetheless significant to an overall evolutionary trajectory in the species he depicts.

The first signature marker of Sheehy’s “biological horror” aesthetic in *Beyond the Sixth Extinction* is the post-apocalyptic color palette that blends dull mud with an oil slick. An oversized cockroach, called the rex roach, flaunts oily-green elytra, vast purple-black orbs for eyes, and a massive pinkish and veined abdomen that suggests throbbing, quivering animacy. Each species revealed is more disturbing than the last as even superficially familiar creatures like the pill-bug-like peteybug are shown to vomit *E. coli* that break down polycarbonates or the pigeon-descendants are depicted harboring hungry, beady-eyed young tucked in brood pouches evolved from wings. The species’ habitats are no better: distant views are impossible due to air fogged with pollution—even the sole photosynthesizing species is rendered in a pinkish haze rather than anything resembling full sun. The entire effect of Sheehy’s chosen color-palette, the repulsive qualities of his species-monsters, and the barren toxicity of their setting is nausea-

inducing. The pop-up versions of the species offer a slight reprieve from the haze, featuring warmer and brighter tones in their paper bodies. A reader might linger there, with the book laid open to fully lift the bodies from the page, reading their field guide-oriented traits tucked under a flap. These traits lack explanation, however, and since the pop-up models precede the full explanatory pages and illustrations, these traits often unsettle rather than clarify. The rotrap (*Ingurgia fixus*), for example, has listed under the category “Mutagenesis” the following: “root-like tail; limbs encircling mouth; bidirectional digestive tract; heightened radioresistance” (Sheehy, 2018, 34). What is the purpose of the rotrap’s “root-like tail,” or, indeed, what *is* a root-like tail? The rotrap pop-up features barnacle-like protrusions from a brick wall, each with spiky mouths and four appendages surrounding them (see Figure 4.6). This 3-D version is eye-less and lacks detail and thus gestures towards the form of the rotrap rather than offering the identification-oriented clarity one might expect from a “field guide”. The three-dimensional

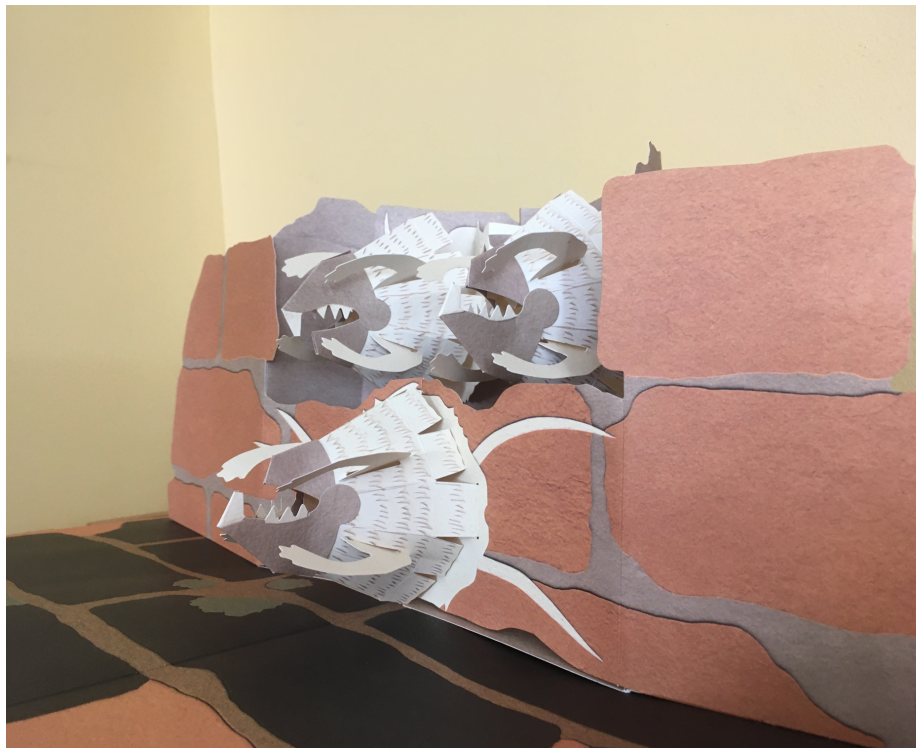


Figure 4.6: Rotrap paper pop-up in *Beyond the Sixth Extinction* (2018), paper art by Shawn Sheehy, photo taken by author

nature of the pop-ups, however, demand our attention even if they are vague on details. The rotraps reach out from the page, grasping at the human holding the book, demanding physical space. The reader must alternate between leaning forward to read the text and jerking their head back to make way for the next creature literally unfolding before them. The very physicality of the pop-up confronts the reader, refusing the easy and idle engagement with which a 2-dimensional book can be browsed as even to open the book fully the reader must give it ample space. And while the illustrations lack this physical demand, they confront in their own particular way. With a flip of the page, the obscurity of the pop-up rotrape is replaced by a haunting rat-like creature protruding from a wall, tiny limbs grasping, mouth gaping, and numerous naked tails radiating along the wall behind it—anchoring it in place (see Figure 4.7). The illustration might not demand physical space like the pop-up, but psychological space is snatched as, once seen, it is impossible to un-see this being that has made a twenty-sixth-century defunct nuclear reactor its



Figure 4.7: Rotrape description page, illustrations by Jordi Solano, *Beyond the Sixth Extinction* (2018)

home. Much like the operation of on-screen body, or biological, horror, the mere vision of the rotrap (let alone the idea of sharing space with it) leads the viewer to shiver with disgust. The rotrap seems to buck biological norms by blending the anchored motility of sessile organisms such as the barnacle with plant-like roots derived from a multiplicity of rat tails. The disruption of assumptions that movement, or motility, is typically a beneficial evolutionary trait (and therefore one that is unlikely to be shed through adaptive process) also upsets the sense of biological patterns and norms. The range of illustrations of the rotrap on its two-page spread deepen the feeling of guttural upset while still pairing its unnaturalness with biological patterns that are sufficiently familiar as to prevent the reader from rejecting the rotrap out of hand as “impossible.”

Jordi Solano’s illustrations of the creature include its full form—lit eerily from below by a ghostly blue light, as well as small grayish-brown monochromatic snapshots of parts of the rotrap that help tell the natural history of its connections with the rex roach life cycle. In one, we see the rotrap’s spiky maw consuming a roach nymph, in another we see the rotrap’s furry back covered with leech-like roach larvae sucking its blood, and in a third, there is the vague form of the rotrap protruding helplessly from the side of the image—its short, flailing limbs unable to stop the massive roach abdomen from laying small eggs on the rotrap’s back. The overall effect of these windows into rotrap and rex roach lives is unsettling to say the least. The rotrap’s impotence in preventing the rex roach’s visceral birthing and blood-sucking life stages is barely offset by the rotrap’s eventual consumption of roach nymphs, as even the rotrap’s consumption of creatures raised on its own blood carries with it a twisted sense of the ouroboros—the snake who eats its own tail. The fictional scientist, Willek Muriday, that Sheehy frames as the author of

the report adds further detail, and another layer of self-consumption, to the rex roach-rottrap relationship in the accompanying text:

I. fixus shares a strange interdependence with the rex roach. The roach lays its eggs on the rottrap so that newly hatched larvae can suck the rottrap's blood—a meal that enables the roaches' development to the nymph stage. Fortunately for *I. fixus*, the smell of rot within its gullet attracts various crawling insects—including some newly molted roaches—who then enter the rottrap's mouth and are consumed. When a rottrap dies, roach nymphs eat the decomposing remains until the body comes loose from the wall and falls into the water below. (36)

The final leg of the rottrap-roach relationship ends with the roach nymphs' final consumption of the decomposing corpse of a rottrap that was likely fueled in life by the roach's own brethren.

The cycle, then, of the roach and rottrap bears a sense of squeamish disgust at the bodily reality of their world paired with a redemptive suggestion that there is a cycle of birth, death, and renewal even within the confines of the most toxic of human environments: the nuclear reactor.

It is without a doubt that the upset and disgust the reader might feel at the sight of the rottrap is intended to be a reflexive one—an opportunity for self-reflection. Muriday's preface to the field guide asserted two components that have fueled the rapid pace of evolution in the Cagoan district that resulted in such remarkably strange adaptations: "steady tropical temperatures" that allow for year-round procreation (this can be assuredly attributed to the advanced effects of climate change) and "high levels of background radiation" that boost the likelihood of "random cell mutations ... [which] increases the potential for gene mutation and novelty in the offspring" (1). This latter process of rapid evolution caused by radiation-induced mutations is referred to throughout the text as "mutagenesis." The bizarre adaptations of creatures like the rottrap, then, are framed as nuclear-derived—an approach that forces the reader to confront their own complicity in the rottrap's existence. Similarly, each species features a different bioremediation trait that renders anthropogenic toxic waste benign, in some cases even

converting it into usable nutrients. The horror felt at the sight of the rotrap, then, must be a self-reflexive horror as it makes clear that humans all but brought these haunting creatures into existence, forcing the “hand” of evolution to respond to toxic wastes of all kinds—the new ecological niches available to Anthropocene life. Indeed, even Peter Ward in *Future Evolution* discussed this very likelihood:

Animals inhabiting cities, and especially those living in areas with high concentrations of toxins, such as sewers, groundwater systems, and at the base of landfills, might undergo adaptation to withstand high levels of otherwise lethal chemicals, high acid or base concentrations, and even the elevated temperatures found in smoldering landfills. (85)

The framing of human culpability in producing the haunting species of a future Chicago-wasteland allows the tiny pop-up figures like the rotrap to continue grasping at the minds of readers long after they have shut the book. Rejection of our connection with these future creatures is denied by the creatures’ adaptations themselves and we are left viscerally unsettled by the unanswered question of whether their world can be at all desirable—and if not, is there any way we can stray from the path that leads towards them?

Rather than imagining life’s future as beyond the touch of human hands and beyond the “ecological impoverishment” of the post-sixth extinction period, *Beyond the Sixth Extinction* rejects the temporal leap and thus physical and psychological distancing of *After Man* but it also rejects the similarly present-oriented nostalgia of *Future Evolution*. Sheehy instead attempts a reconciliation with the life that is less beautiful, perhaps, but more immediate and, as he says in the author’s note, more vital: “Ultimately, creatures like these could serve as bioremediators, transforming toxic sites into robust ecosystems. Though strange and chilling, such creatures might prove to be essential to the future of life on the planet” (40). While suggesting we must learn to live with these creatures, a commendable pursuit as the species are undoubtedly brought into being by human action, his editorial emphasis on the creatures “[*serv*ing] as bioremediators”

implies that they have a dirty job to do, at which point other less “chilling” species might return and replace them. This reorients attention away from the present “ecological impoverishment” of the 49th century he depicts and towards a distant redemptive future. The ugliness of beings like the rotrap is thus only a temporary setback: they will be the workhorses to fix the planet, at which point their descendants will be free to flourish in the diversified forms like *After Man* that are “beautiful enough to live.” Where Sheehy’s species seem to tell one story, then, his authorial note and imaginative inclination perhaps suggests something different.

Redeeming unwanted or undesirable species through their “workhorse” skills, however, is not just a component of Sheehy’s future imaginary, but is also prevalent in contemporary scientific literature interested in bioremediation practice and adapting to a climate-changed world. In M.N.V Prasad’s piece “Exploitation of Weeds and Ornamentals for Bioremediation of Metalliferous Substrates in the Era of Climate Change” (2011), he details the grasses (e.g. ryegrass, switchgrass, velvet mesquite) that can be used for phytostabilization (i.e. plant-based reduction of heavy metal mobility in soil), the ornamentals (e.g. lemon-scented geraniums, Portulacaceae) that can assist in remediating mine tailings of heavy metals, and the wide range of aquatic plants (many of which are regarded as highly invasive) that can phytoaccumulate heavy metals to remove them from waterways and waste water. Citing a 2005 Elless et al. study, Prasad stresses how phytoremediation can be directly beneficial to humans: “Arsenic hyperaccumulating fern, *Pteris vittate* (an important foliage ornamental), was used in the pilot-scale demonstration phytofiltration project to produce drinking quality water from arsenic contaminated ground water in New Mexico, a classic example of service to mankind” (Prasad 2012, 500). Prasad’s emphasis on the fern’s “service to mankind” makes it clear that he is inviting readers to be moved by this impressive example and thus be similarly encouraged to

deploy ornamental plants in remediating human-poisoned landscapes for human benefit. In a similar vein, biologists Zoë A. Doubleday and Sean D. Connell (2018) suggest humans “[make] the most of weedy futures” by taking advantage of the species that will thrive in Anthropocene oceans—namely cephalopods, jellyfish, and algae—by globally adopting them into the human diet (Doubleday & Connell 2018, 603). The relationality Doubleday and Connell imagine for the Anthropocene-future is made abundantly clear by the title of their article: “Weedy futures: can we benefit from the species that thrive in the marine Anthropocene?” (2018). Ironically, they identify the issue of overcoming disgust as a key market challenge for transitioning to species that might seem unappetizing to Western eaters and they cite insights from the insect-eating (entomophagy) movement as instructive: “entomophagy advocates suggest that education is key to reducing the ‘disgust factor’ and boosting public awareness of insects as a nutritious and sustainable food source (van Huis et al. 2013)” (603). Overcoming “disgust” or, in Sheehy’s words, the “chilling” nature of weedy species are thus not viewed as strategies for promoting relationships with these species, but rather as necessary for fully taking advantage of their benefits to humans.⁵²

Weedy, invasive, pest, or “trash” species have undoubtedly gotten a bad rap and are widely victim to elaborate, expensive, and frequently toxic, plots for their removal from regions where they are deemed unwanted. Engagement with these species for the average human is always framed by fear, disgust, and the resulting strategies of death: mouse traps, ant “bait,” rat poison, Roundup. Even when the “wanted” species (even humans) are violently affected by these morbid methods (the hand in the mouse trap; the dog eats the rat poison; the toxic reek of

⁵² While consumption of other species can undoubtedly lead to deeper relationality with those organisms, my focus here is on the initial *justification* for connecting with these other species rather than how that justification might develop different relationships in the future. In this example, the emphasis on *using* and *benefiting* from the other species becomes the primary, even sole, justification for engagement with them.

herbicide drifts in the window...), the fault never seems to fall on the human hand that administers them, but rather the unwanted species that “necessitated” the action. The unwanted species are thus framed as abject, other, wholly foreign and monstrous to the human space. This framing is abundantly clear in campaigns like the U.S. Department of Agriculture Animal and Plant Health and Inspection Service’s (APHIS) pest education campaign, “Hungry Pests,” whose mascot is “Vin Vasive”—a mutant humanoid constructed by the creepy-crawly bodies of thousands of insects that are barely contained by his dapper sport-coat (U.S. Department of Agriculture n.d.). Or, in a less obviously monstrous but no less chilling framing, is the genre-bending documentary *Rats* (Spurlock 2016) that deploys horror genre tropes throughout the film (jump scares, ominous music, enhanced sounds like scratching or squeaking, visceral body-horror etc.) that ultimately frame rats as horror-monsters that infiltrate the inviolable sanctuary of our homes, our bathrooms, our baby’s crib... In light of the cultural treatment weed and pest species receive in the contemporary moment, it is not very surprising that speculative endeavors such as *Beyond the Sixth Extinction* (2018) or *Future Evolution* (2001) struggle with orientations of disgust. That *Beyond the Sixth Extinction* attempts to find the redemptive or redeeming qualities of these species to underscore is commendable, but the framing of the species as ultimately just bioremediators that are plowing the way for life’s future actually prevents the book from clearly confronting the reader’s relationality with these weedy species. Despite the lively depictions of the complex webs of relationships between the different species of the District of Cago, the species cannot be valued in themselves and must be seen as tools—we must “make the most” of what these weedy futures can do for us as humans.

For both Peter Ward and Shawn Sheehy, the tensions between futures desirable and undesirable are clearly played out through an engagement with the visceral human response to

creatures who thrive off of our own trash or the most unnatural and undesirable of ecosystems: urban space. The disgust that we may feel at these creatures is ultimately self-disgust. To be repulsed by human trash or genetic mutations caused by nuclear fallout is to be repulsed by the human too-muchness of the Anthropocene. However, in processing and reconciling these potential futures, the disgust is turned from humans themselves and towards the pest and weed species that most closely accompany us in human-molded space. Just as contemporary pest and weed species are viewed with distaste, so too are future species evolved through adaptation to anthropogenic toxins. Indeed, even contemporary conservation biologists debate how we should ethically view rapid microevolutionary changes in species responding to anthropogenic activity: "Philosophically, [conservation biologists] must also grapple with the issue of whether the evolution of adaptations to disturbance and degraded habitats is sometimes beneficial or something to be rigorously avoided" (Ashley et al., 2003, 115). But if we were to reject frameworks of disgust for animals that feed on trash, might relationships between humans, their waste, and other species instead offer new forms of flourishing—not as a means, but an end in itself? In her project *An Ecosystem of Excess* (Yoldas 2014), artist Pinar Yoldas offers her own version of what an ecosystem rooted in anthropogenic wastes might look like. The species and traits that respond to oceanic plastic pollution in her work are both sublime and uncanny, disrupting reassuring visions of nature “righting” human wrongs in a distant future and reorienting and re-imbedding the viewer in a tangled present.

Building New Life Through Death: Agency & Speculative Evolutionary Process

Central to Yoldas’s inspiration for *An Ecosystem of Excess* was the scientific discovery of pelagic microorganisms and insects thriving in the plastics of the Great Pacific Garbage Patch.

The insects found new reproductive success through the added materials on which to lay their eggs and some of the microorganisms were found to in fact *eat* the plastics themselves. *An Ecosystem of Excess* inquires: “If life started today in our plastic debris filled oceans, what kinds of life forms would emerge out of this contemporary primordial ooze?” (Yoldas, 2014). While the species she creates are not real (yet), the foundation Yoldas builds off—plastic-eating microbes—*do* actually exist in the wild. Her work, alongside the boardgame *Evolution* which I will also discuss in this section, offer productive ways to interrogate central ideas of agency that can be downplayed in speculative evolution imaginaries too oriented around apocalypse. These two works instead seek to engage with a sense of what I term *ongoingness*, of worlds not ending but continuing—even in-spite-of hostile circumstances. There is not a sense of normativity coloring pasts or futures in these stories of evolution as in some of our previous imaginaries, such as *Future Evolution*, just *different ways of doing things*, ways of adapting, making do.

Taking up contemporary research on microbes and plastics, Pinar Yoldas playfully envisions different aspects of life that might be altered due to plastics entering the food chain: birds now have Pantone feathers dyed through consumption of certain plastics; balloon-eating turtles eventually gain elastomer shells which allow them to float; and a pelagic reptile lays transchromatic eggs that change color to blend in with the white plastic nurdles that have replaced beach sand. At the center of the installation are, perhaps, what are biologically most key about these new creatures: the very organs adapted to processing plastics, all bubbling in individual glass jars. The beakers containing the organs are lit from below and glow eerily, drawing the eye to their shocking array of plasticine and vibrant alien forms. The stomaximus, or digestive organ of the plastivore, drifts in its glass jar (see Figure 4.8, next page). It features a



Figure 4.8: "Stomaximus" from *An Ecosystem of Excess* by Pinar Yoldas (2014)

jungle of small nodules along its rhizome-like form that host colonies of microorganisms specialized to different forms of plastic across the poly-spectrum. The bulbous yet reminiscently floral form of the E-plasticeptor draws in ocean water to examine it for polyethylene—the food source of the unidentified creature it might call home—before pumping the water back out in a stream of bubbles. The petronephros, or plastivore kidney, pulsates oddly—its form shrinking and then expanding outward as it filters out toxic additives that even plastivores can't withstand. Even in their disembodied state, the floating organs of *An Ecosystem of Excess* are bizarrely functional. The disturbing yet wondrous presentation of the plastisphere organs presents them

with a sublime aspect—the alien nature of the often brilliantly colored organs keeps the viewer from forgetting their purpose is to help process the most indigestible of substances: plastic. This same framing helps resist the viewer inclination to see the eggs as just *normal* eggs, or the tiny turtle as just a different colored turtle. The alienness of the organs, and even the uncanny resemblance of the plastic nurdles to tiny pebbles, reinforces that this is not some Edenic world regained as in *After Man*, but rather an anthropogenic ecosystem that even in its human-derived nature can still instill wonder and care. Those who encounter *Ecosystem of Excess* are thus encountering not merely a comforting reassurance of life’s future, but a confrontation as well: a mixture of wonder and unsettling guilt at the evidence of the impacts (“good” and “bad”) of human “excess.” For, the irreverence these new species have for the toxicity of plastics cannot fully eclipse the innumerable deaths this ecosystem is built on: those creatures whose bodies, not adapted to plastics, rot on ocean shores, corpses stuffed with multicolored polymers.

Because the central figures of *An Ecosystem of Excess* are the very internal organs of the plastivores themselves, the importance of present-day deaths cannot be overlooked. Images of sea life that has met its death through interaction with plastics are all too familiar to the contemporary environmentalist. Young cormorant or albatross bodies rotted to reveal the brightly colored plastics that bloated their bodies and ended their lives; turtles who, while young, swam into a soda can ring and were never able to swim out—the list goes on and on and likely flashes before your eyes even now, so familiar are these images. The move of *An Ecosystem of Excess* to move *inward*, then, is particularly significant to the visual politics of the installation. If plastic-filled corpses are so familiar, the internal organs of plastivores takes on an expanded meaning: it is these very organs that protect these plastivore bodies from the belly-bursting deaths of their ancestors and therefore the significance of their innards could not be clearer. This

framing is markedly different from the other evolutionary relationships with death and extinction that many other speculative evolutionary narratives employ. In *After Man*, particularly, we are not encouraged to linger on the histories not just littered in bodies—but practically piled mountains high. Dixon discusses the inheritors of the future Earth in the context of their success despite the best efforts of humans to exterminate them. Rats, rabbits, and starlings all feature important ancestral roles for the vibrant ecosystems of the future but because of this future success the reader is not encouraged to linger on or consider the disturbing futility of all that death. *After Man*'s perspective seems to encourage the view that life will always rebound from humans—that our impact will not be forever. In *An Ecosystem of Excess* it is clear that human excesses will not be so easily left behind.

An Ecosystem of Excess thus asks the viewer to dwell within the eerie space of a kind of ghost story. What is viscerally haunting about organs suspended in jars helps anchor the exhibit in the similarly haunting nature of carcasses lacking organs—innards rotted away from avian skeletons for a ghastly reveal: bottle caps and lighters where organs should be. In Banu Subramaniam's book *Ghost Stories for Darwin: The Science of Variation and the Politics of Diversity* (2014), she frames her engagement with the study of variation in evolutionary biology through seeing ghosts:

At first, I did not see the ghosts, not at all. Now I cannot believe that I ever missed them! Today they stand out in the landscapes around me. The many ghostly figures among the morning glories, the apparitions among the changing landscapes, and the luminous figures rendered invisible by the histories of science. I now see the hauntings, the ghostly apparitions, the shadowy silhouettes of our past appearing all around me, staring at me, insisting on being seen. (6)

In *An Ecosystem of Excess*, even with the hopefulness of its framing as life stemming fully from what is generally seen as wholly unamenable to life, is nonetheless suffused with ghosts. For every individual organism in the plastisphere there are innumerable corpses stretching back into

obscurity—all of those ghosts haunting the present successes of the plastivores. In some installations of *An Ecosystem of Excess*, facts drift alongside plastic particles in a wall projection baldly stating that “1,000,000 sea birds die each year due to plastic pollution” (Yoldas 2014). These words, even drifting amongst plastics, cannot fully illustrate the horrors of these deaths, but they nonetheless mark the presence of their ghostly hauntings amid the liveliness of the plastisphere species. But, importantly, these deaths are not futile in the way the rabbits of *After Man* so plainly are, they represent a kind of organismal agency that is not afforded to the dead of *After Man*, *Future Evolution*, or even *Beyond the Sixth Extinction*.

An Ecosystem of Excess's creatures are not genetically modified organisms; they have not benefitted from direct human aid to adapt to their anthropogenic ecosystem. Their organs, while technicolor, are not created through mutations from radiation, so they also did not have the benefit of anthropogenic sources in driving (and speeding) their evolutionary changes as the organisms of *Beyond the Sixth Extinction* did. Nonetheless, despite the obstacle of excruciatingly slow evolutionary time, these species have found a way to not only *use* human-based ecosystems (like the species of *Future Evolution*), but actually *consume* its toxic wastes—drawing nourishment from what once could only be seen as deadly substance. While certainly we cannot imagine the species from *Beyond the Sixth Extinction* as coming into being without the failed attempts of many organisms and species, what sets *Ecosystems of Excess* species apart is the long, hard road (suffocating in the dead) of its species' extended timeline that eventually got them to the point of meaningfully drawing up energy from plastics rather than succumbing through death to their weight. What is thus particularly extraordinary about these plastivore creatures is that they have, ultimately, taken survival in the Anthropocene into their own mouths:

they have brought their plastivore-nature into being through the very act of consuming plastics themselves.

There can be no doubt that the organisms from which the *An Ecosystem of Excess* organs have been “extracted” came to evolve these parts through the process of eating. A central

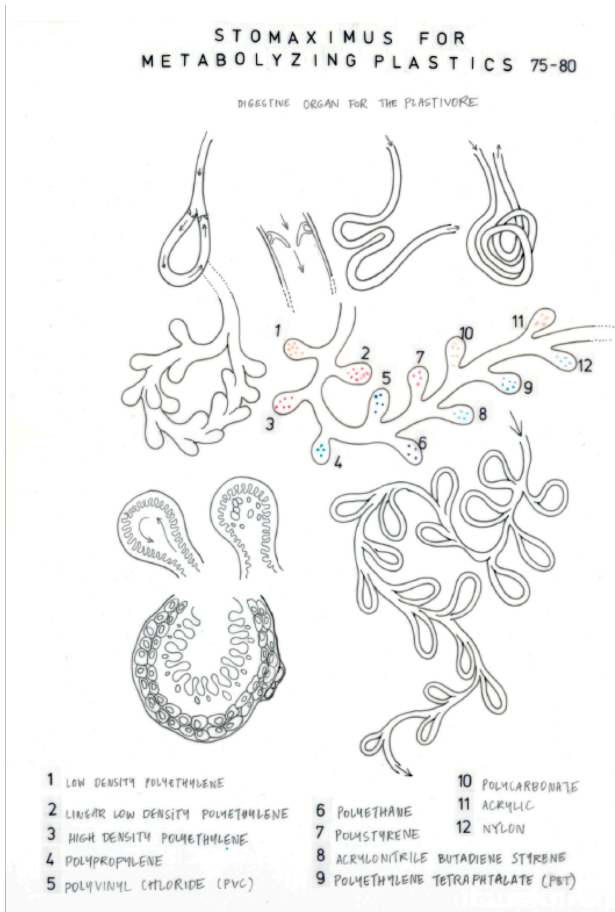


Figure 4.9: Stomaximus diagram, Pinar Yoldas, from *An Ecosystem of Excess* (2014)

inspiration for Yoldas’s work was the discovery of microorganisms presently feeding on ocean-borne plastics, thus, the stomaximus (digestive system) of the plastivore is home to an array of microorganisms specialized to different plastic types (aksioma 2014, see Figure 4.9). Without these plastic-munching microorganisms, the more complex vertebrate plastivores could not exist. The importance of microbial life to the plastivore digestive system should be no surprise as even humans rely on a similar system. While our gut-biomes might not be home to microbes that break down plastics, they are nonetheless populated by hundreds of different species of

bacteria who each bring their own genetic aptitudes to the digestive party. Vast amounts of literature exist exploring the benefits and importance of these microbes to human (and other species) health currently exists, some of which is particularly interested in the evolutionary relationship between the microbiome and host evolution ([Sekirov et al., 2010](#); [Rosenberg & Zilber-Rosenberg, 2016](#)). Shifts in diet undoubtedly plays an important role in the evolution of

organisms: the morphology of an animal's head must match up with the size and form of the foods it consumes; the physical capacity for speed or agility are similarly essential for predator species in catching their prey. In the same way, the digestive capacity of an organism must be in line with the foods it consumes. The 4-chambered stomach of ruminant animals, for example, is one highly complex recent evolutionary breakthrough that perfected drawing nutrients from the kinds of roughage that other mammals could not (Ley et al., 2008). What has recently become clearer, however, is the role that the microbiome and coevolutionary forces have played in the relationship between species evolution and diet (for example, see Ren et al., 2019).

In particular, studies comparing gut microbes of herbivores, omnivores, and carnivores (bearing in mind that ancestral mammals are carnivores) indicate that “gut bacterial communities required to live largely on a plant-based diet were likely acquired independently from the environment” and were not passed down through hereditary means (Ley et al., 2008, p. 1650). One study by Huang, et al. (2021) identified convergent gut microbiomes of the giant and red pandas to be driven by their exclusive bamboo-diets rather than genetic relatedness, as the two pandas belong to distinct phylogenetic families in the order Carnivora. That diet itself directs the development and evolution of an organism's gut microbial communities should be no surprise and is even corroborated in research on different human communities and diet, most notably in the case of a seaweed-digesting enzyme in the intestinal microbiomes of Japanese people specifically. Studies have shown that the ability to produce the enzyme, which aids in the digestion of seaweeds and uptake of their nutrients, was obtained by gut microbes through contact and horizontal gene transfer with extrinsic microbes—specifically those brought into the human digestive system through the consumption of seaweed (Hehemann et al. 2012). In other words, *eating* seaweed allowed certain humans to better digest it, just as eating bamboo helped

pandas digest bamboo or eating grass evolutionarily altered ruminant mammals. We can infer this same process might then have taken place in the evolution of Yoldas's plastisphere species (while imaginary)—they have *eaten* their way into the form and abilities that they now have.

Evolution, or adaptation, in this sense is fundamentally (at least in part) driven by the organisms themselves through their choice of diet. Just as we take in and add to our own microbiomes through the process of eating food—a process that in turn continues to help us digest our food—these pelagic plastisphere species have taken up the tiny microorganisms feasting on water-borne plastics and have evolved the ability to draw on the labors of those new micro “friends” to glean nutrients from their tiny endeavors. And much like the famous flamingo pink, the sea birds of these plastiverse seas have also taken on the colors of their foods and bear feathers of technicolor brilliance. “You are what you eat” is an adage that seems particularly true of these gyre-prowling species as they take on not only hues but also, in some cases, plasticine buoyancy (like the Pacific balloon turtle)—an affinity to balloons derived from their Great Pacific Garbage Patch gleanings. What is particularly catching about this vision, is that there can be no doubt the organisms have, *through their own actions*, become members of the newly formed plastivore class. Through in-taking plastics these organisms have slowly but surely eked their way from the bloated and battered corpses lining the shores to rot and thereby reveal their deadly cargo, to the plastics consuming species of their “contemporary” moment. In Stefan Helmreich's (2018) article inspired by *Ghost Stories for Darwin*, he remarks on Darwin's early consideration that the tree of life (in his 1837 notebooks) perhaps would be better termed as a “coral of life” as the bases of the branches are all dead and the living species, much like living coral, all accrete on top of the bodies of the dead. The living bodies of the plastivores should be seen through this “coral of life” where their present lives depend entirely on those past

innumerable corpses littering ocean shores—those organisms that chose, whether in confusion or not, to feast on the vibrant plastics drifting in the open seas and thereby began to open up a different evolutionary future for their descendants.

While operating in a vastly different context than *An Ecosystem of Excess*, the critically acclaimed boardgame *Evolution* developed by Dominic Crapuchettes, Dimitri Knorre, and Sergey Machin with art by Catherine Hamilton, also manages to bring organismal agency to the foreground of evolutionary process. In addition, it does so in a way that brings choice and adaptive process as close as possible to the everyday human. Where *An Ecosystem of Excess* exists either bound by the space of the art museum (or the depths of the internet), *Evolution* enters the home, making itself the matter of intimate family and friend interactive space. The *Evolution* boardgame lets humans try their hand at actively engaging in the evolution of different species by “adapting” their species using trait-cards that improve their species’ abilities to get food (either as herbivores, carnivores, or through scavenging) and protect themselves from predators (through physical attributes like horns or social or sheltering traits like defensive herding or burrowing; see Figure 4.10, next page). At first glance this game might not appear to fit within the purview of speculative evolution; it is devoid of any concrete bestiary of future species and the “species” developed in the course of the game would likely be seen by biologists as an evolutionary tree of different forms evolved from a single ancestral beginning rather than an individual species of their own. However, the Player Aid Cards have a “Scientific Names”



Figure 4.10: General gameplay of Evolution, image by Florence Sullivan, game illustrations by Catherine Hamilton

section that gives players a strategy to name their species at the end of the game. The player selects what two traits were most important or valuable to their species, and then using a chart with categories for “Genus” and “Species” they can select the words that correlate with the chosen traits. For example, the first time I played the game my most successful species had the two highly valuable traits of “Burrowing” and “Intelligence,” so I named it *Intellectus fossor*. This naming strategy makes the species developed concrete by creating a solid “end point” for their adaptation: the end of the game. The species developed in the course of the game are thus just as clearly products of speculative evolution as the creatures from Dixon’s *After Man* bestiary are.

Game play of *Evolution* is made up of a tenuous balance between the amount of food available and the species traits that either enhance access to food or protect the species’ populations from outside attack. To “succeed” in this paperboard ecosystem, players must always be attentive to the changes in their fellow players’ species populations, sizes, and traits in order to respond in the next “round” with evolutionary adaptations of their own. To focus on a

single species and ignore the dynamics of the others in the game is to resign your species to extinction. If you aren't tracking the body size and population of a neighboring carnivore, your own herbivore (intent on food gathering traits such as "foraging" or "long neck") might leave itself open to attack. Conversely, in my own experience playing the game, when it became clear that carnivores would not be able to survive in our particular ecosystem (and the body size of all the other species were beyond what any new carnivores would be able to handle), I began replacing defensive traits with others such as foraging or cooperation, or other population expanding traits. This strategy made for a clear lesson on why species introductions (particularly carnivorous or omnivorous species) onto islands were so devastating: without a need for defense, why would defensive traits remain? There are so many other ways of living and being in the world.

In the Amazon customer reviews, a buyer named "Joe" remarked on a similar experience he had while playing *Oceans*—the nautical rendition of the original *Evolution* game:

What we quickly realized within the games we played, you are only successful if your species live in unison with the other fish in the game. For example, in my last game I had a predictor [sic, predator] and two shark feeders who lived off of my shark successfully eating. For that to work, I had to eat my wife's whales each turn to stay alive. Throughout the game I had to make decisions on my turn to keep my wife's fish [sic] alive just so that I could continue living off of them. (2020)

Joe's experience illustrates the collaborative nature of real ecosystems: species don't evolve on their own, they always evolve in relation to those around them. A dynamic interplay develops between the different species in an ecosystem where the fates of some become intertwined. For Joe, the fates of not only his shark, but also the two species of shark feeders who fed off of the shark all relied on the survival of the whales and fish that his wife had evolved. For all three of Joe's species, in order to survive, he had to play in a way that assured a continued supply of whales and fish—a dynamic that certainly required keeping his own shark population below that

of the whale and fish populations. Ultimately, this active process of selecting particular traits, discarding others, and maintaining a balance with other species all helps underscore the idea of organismal agency in evolutionary processes.

Every species developed throughout the course of a single game of *Evolution* is one developed with intention and in relation to other species. While we can of course point to the human game player as the source of this intention, the process of navigating your own species' traits in relation to the others in the game is suggestive of the importance of organism action in the context of their species' evolution. While many might balk at the suggestion that creatures beyond humans make conscious decisions for their own evolution, it cannot be doubted that the choices of organisms ultimately has an impact on the evolutionary trajectory of their species. D. M. Walsh (Walsh 2015) has argued compellingly in his book *Organisms, Agency, and Evolution* for a new approach to evolutionary theory beyond the Modern Synthesis that takes organismal agency into account, what he terms "Situated Darwinism." For Walsh, Situated Darwinism frames evolution as a "fundamentally ecological phenomenon" rather than molecular as it is seen according to the Modern Synthesis. By ecological, he claims "that evolution arises out of the engagement of purposive entities—organisms—with their affordances" (163). Rather than adaptation driven by environment, adaptation in this sense is driven by affordances: a joint property of organisms and their environment that provides either opportunities or impediments to the agents (organisms) in question and which alters as changes occur in both the environment and organisms—in a sense, then, affordances are coevolved properties. Agency, in this framework, is the ability for organisms to "experience its conditions [e.g. environment] as affordances" and their capacity to then implement adaptive responses to those affordances (163-164). In other words, the organism must be able to respond to fortuitous circumstances by

exploiting them and respond to unfavorable conditions by attempting to better them in some way and thereby adapt to those circumstances. As Walsh notes, “The adaptive plasticity of development is a manifestation of organisms’ ability to enlist their phenotypic repertoires in response to, and in alteration of, their affordances” (164). For Walsh, then:

The organism isn’t just a middleman, caught between the machinations of the inner computational realm and the vicissitudes of the external environment. It is a participant in evolution. Organisms are actively involved in creating and constituting the conditions of their existence. (173)

In this view, organisms are not merely convenient carrying bags for genetic material where the real work of evolution is happening—they are active, agential beings whose lives and actions can have long term affects.

If we look at the species of Pinar Yoldas’s *An Ecosystem of Excess* from a Situated Darwinist perspective, we can see how her organisms can be viewed as responding to shifting “affordances” in their pelagic context. The contemporary (real-world) studies charting increased reproductive success of particular pelagic insects due to using plastics as egg-laying material is particularly suggestive of organisms taking advantage of novel affordances (Goldstein, Rosenberg, and Cheng 2012). Opportunities both close and open up with the addition of massive amounts of very slowly degrading material to the ocean surface—opportunities that organisms don’t hesitate to take advantage of and, if successfully exploited, will contribute to the increase and adaptive direction of those species. Similarly, the widespread consumption of plastics by pelagic birds like the albatross is another example of organisms attempting to take advantage of a novel food source. While this is certainly, in the short term, an example of a negative affordance that results in the deaths of billions of birds, *An Ecosystem of Excess* suggests how a continued consumption of these plastics might nonetheless allow the organisms to turn what were once negative affordances to positive ones—opening up an entirely new adaptive lineage through their

eating habits. Just as *An Ecosystem of Excess* offers us examples of how organismal agency can operate in the long term—allowing shifting feeding behaviors to direct their adaptive capabilities and morphology, *Evolution* the game gives insight to the *process* of evolution and the importance of organismal *action* to building the evolutionary trajectory of life. Shifts in diet, range, behaviors, etc. all have the potential to create cascading effects across geological time and can also even have large impacts in the short-term.

For *An Ecosystem of Excess* and *Evolution*, organismal agency is foregrounded as an essential part of evolutionary process, but they also do not shrink away from the complex ethical space of human involvement in this same process. Both speculative imaginaries clearly envision humans in their ecosystemic space, and as more than temporary surveyors or time-travelers. For *Evolution*, the human player has a clear hand in how evolution unfolds, and in *An Ecosystem of Excess*, the scientists might not be visible in the exhibition, but they nonetheless linger in the shadows, their material engagement with their specimens nowhere clearer than the depth of touch evident in the floating organs. While suggestive of an invasive intrusion into the interior of these creatures' bodies, there can be no doubt that there is material engagement between the humans of *An Ecosystem of Excess* and its novel organisms. This world does not imagine itself as beyond the hand of humans nor as a necessary, if ugly, step towards remediation. It rejects the simple erasure of uncertainty and harm, instead asking: what if we can never erase these toxic harms? How then do we live? How do we reconcile the deaths wrought by our excesses and the new life evolved in its wake? And how too do we acknowledge the agency of these organisms even while confronting human action as an indirect hand in molding their evolutionary trajectory? These species are self-made through their adaptive responses and are therefore agents in their own evolutionary paths. Recognizing these organisms' own agency helps reject the

inclination evident in imaginaries such as *Future Evolution* toward seeing species adapted to anthropogenic environments as a fun house mirror of humanity that triggers repulsion rather than care. Taking organismal agency seriously will similarly refuse framing species like the plastivores of *Ecosystem of Excess* as “bioremediators” or workhorses for a cleaner future Earth. Despite their toxin-consuming ways, these are just creatures, in Elizabeth Grosz’s words, “[continuing] in the best ways they can” (2004, 251).

Conclusion

In an age of catastrophic biodiversity loss paired with a pop culture penchant for apocalypse, imagining the future of life on Earth can be a daunting prospect. However, the creative endeavors broadly termed “speculative evolution” that I explored here are one innovative entry point into envisioning what these future worlds—beyond apocalypse—might look like. Speculative evolution imaginaries allow us to consider materially what the Anthropocene as a geologic epoch might mean for organismal life thousands, if not millions, of years from now. I see these imaginaries as instructive about different environmental values as the worlds they create frame what futures are deemed desirable or undesirable and what role is considered acceptable for humans to play in the production of these futures. These speculative evolution texts also operate affectively, generating longing, remorse, and revulsion as they navigate potential species futures (both wondrous and haunting) in relation to the divergent roles they envision for humanity.

In the idyllic visions of a future Eden depicted in *After Man: a Zoology of the Future* (1981) by Dougal Dixon, the future of life is tied to eventual extinction of humans. In Peter Ward and Alexis Rockman’s *Future Evolution: An Illuminated History of Life to Come* (2001),

humans remain but Eden is replaced by trash animals, weeds, and their descendants evolutionarily specialized to life among human refuse—a vision that is framed as “dyspeptic” and revolting (Ward, 2001, 135, 137). Shawn Sheehy’s (2018) take on future organisms adapted to human waste takes an optimistic remediating perspective that plays off the human disgust for creatures so disturbingly adapted to toxic ecosystems but nonetheless promises an eventual renewal and Edenic return once these species have rendered environmental toxins benign. The imaginaries of the first two sections of this chapter thus trades on the apocalyptic-utopian binary, seeing apocalypse as either inevitable or as a necessary step towards a future utopia. Their environmental ethics lie in either assuring us that inevitable apocalypse might have a deep future pay off or settling the heavy weight of remorse on our shoulders—the only hope lying in the highly unlikely possibility that “humans” can turn from their present course.

In the third section the sense of apocalypse or utopia is absent as the central foci are not the human emotions tied to the future organisms but rather the organisms themselves. In Pinar Yoldas’s *An Ecosystem of Excess* (2014) we see futures constructed by the very creatures most damaged by present day human waste. Yoldas’s plastivore organisms create their own potential futures through consuming plastics—building new life from a long history of death. Whether there is hope in their futures it is not a hope that is dependent on human action or inaction—it is merely about organisms making do with what is available to them. This agential approach to the evolution of species is also underscored in the boardgame *Evolution*, where gameplay depicts organisms (and players) selecting and discarding traits to better suit themselves to their present circumstances. Whatever those circumstances might be, judgement of their value is aside the point as the central focus is the organism or species response—their agency—rather than the conditions they are evolving under. These imaginaries thus offer a different view on evolutionary

processes and futures, one that is divorced from species with “purpose” or better or worse overall outcomes—the focus is rather on *making do*, on *ongoingness*, on *living on in spite of* present circumstances.

These speculative imaginaries don’t exist in a vacuum—their authors are driven by different motivations for sharing them and these motivations reveal different views on how we *should* act to perhaps bring or avoid bringing these species into existence, or, conversely, suggest ways that human value judgements are, perhaps, beside the point when it comes to speculative future species. Analyzing speculative evolution imaginaries thus allows us to critically assess varied ethical frameworks into the future. They allow us to consider what the valuation of different kinds of “damaged” or “pristine” ecosystems might mean for our relations with future creatures and perhaps compel us to consider instead what these relations might look like if we focus less on what *we* think “should” be and more on what “might” be—including who *we* might be in relation to that new future. For no matter what new organisms we find ourselves sharing space with in the future, “their justification is ... that they live” (Grosz, 251). And as Collard, Dempsey and Sundberg stress, the futures we should most strive for are those characterized by the abundance, agency and autonomy, or “wildness,” of life—thus reorienting our attention to the possibilities *other* species might bring into being, rather than our own intentions. Speculative evolution imaginaries can offer us a tool for rethinking and engaging with what these future worlds, and future relationships, might look like.

CHAPTER V.

CONCLUSION:

NURTURING LIFE'S FUTURE

“SF is practice and process; it is becoming-with each other in surprising relays; it is a figure for ongoingness”
—Donna J. Haraway 2016, 3

Conservation as Worldmaking

Conservation is ultimately a creative endeavor. Human values are inherent in the management that supports future life—the decisions that foster particular species futures while rendering others impossible. Just like the biotech conversations that so readily frame themselves as a design problem, but also cleverly question—haven't we been “designing” ecosystems all along? Where are the boundaries of creativity in conservation practice? Where are the limits of values and valuation? These ideas flow into “objective” scientific practice in the context of conservation—the borders just as porous as those of species. This is not an argument to claim all nature is therefore a human construct, but rather to recognize ourselves as cocreators alongside other species. To be realistic about this fact would be a powerful step in acknowledging the work we do in conservation as not *inherently* value-positive for the species/populations we seek to protect and therefore deeply complicated ethically. For what would it look like if the golden-winged—blue-winged studies I discussed in chapter 1 had concluded the hybridization *was* in fact anthropogenically caused? Would warbler management include lethal removal of blue-winged warblers from hybrid zones to protect vulnerable golden-winged genetics? Would Brewster's and Lawrence's hybrids be viewed as threats like the hybrid red wolves and coyotes? How do the future possibilities for species swiftly become otherwise with scientific discovery?

What is deemed permissible and *worthy* fluctuates with scientific opinion, and scientific opinion itself is not fixed but constantly evolves—adapting to new data and new methods over time.

Therefore, by expanding our view into speculative visions of the future—creative imaginaries that blend scientific knowledge with values, hopes, and fears—I hope to draw out some of the ways our conservation management practice *already* brings into being species we value and prevents the creation of assemblages that we have deemed less worthy of our protection. By sterilizing coyotes and hybrid red wolves on the perimeters of red wolf populations, we *actively bring into being* a “pure” red wolf that *would not exist otherwise*. We have deemed valuable the purity of red wolf genetics over any potential value the red wolf might seek to gain from coyote introgression. The ultimate value call over the potential loss of the species resulting from complete genetic combination with coyotes is one we have made *for* the red wolves. While it is undoubtedly true that, when mates are in plenty, red wolves select other red wolves over coyotes, it is hard for me to justify the idea that the kind of genetic continuance individual red wolves might gain through reproduction with a coyote is somehow less satisfying than that with a red wolf (they are still reproducing, having young, etc.). Is the “idea” of red wolves as a species meaningful to the red wolf? Or only to humans? If the red wolf still passes on its genetics before dying itself, even if it was the last of its species, would such “species *genetic* extinction” be meaningful to the wolf? If we are to take nonhuman agency seriously, these are meaningful questions to ask, for if we are only keeping a species intact under tight human controls with extreme reliance on conservation management funds—how functional is the species really? And are we perhaps holding the red wolf back from valuable adaptive capabilities it could glean from coyote genetics due to their excellent adaptation to human-modified ecosystems? These are complex ethical questions with no clear answers. I hope, however,

through such questions (and the case studies I explored in this dissertation) a clearer sense has emerged of the potential for managing *alongside* agential and evolving beings that are also actors and partners in the management process. What could conservation management look like that supports true species diversity—the kind that abhors strict species boundaries, flouts rules, and twists its lineages in webs like braided rivers through time?

Looking Forward for Conservation

Where might conservation go from here to resolve some of problems I have documented so far and to nurture life's future? As explored briefly in chapter 1, there are already scholars calling for clear policy that would recognize the conservation value of hybrid individuals as one way forward. Jackiw, Mandil, and Hager (2015) see both ethical and ecological ground on which such hybrids could be included in conservation efforts, though they distinguish between anthropogenic (unintentional) and natural hybrids while nevertheless finding potential value in anthropogenic hybrids if they provide potential adaptability or utility without any adverse effects. Other scholars stress such anthropogenic-natural distinctions are unnecessary and uphold harmful stereotypes which promote Western views on nature over other approaches—thus “moving on from [this] dualist thinking ... [will] allow pluralist approaches to conservation, in which non-Western perspectives will find more space” (Donfrancesco and Luque-Lora 2022, 2). There is certainly a clear need to engage with indigenous conservation practices more substantively in USFWS work—particularly in developing more collaborative approaches that engage tribes in decision making processes from the *beginning*. Barnhill-Dilling and Delborne (2019) sought to bring such practices into the work on the transgenic American chestnut planning process, planning meetings with Haudenosaunee leaders and Nation members to gain

feedback on the project. Nation members were mixed over the transgenic tree, some elders were worried the transgenic tree wouldn't respond to traditional names for use in medicines (the tree wouldn't be able to hear when spoken to in ceremony the way a non-transgenic chestnut would), others, such as a traditional woodworker, were excited by the idea of being able to work with the wood and eat the nuts they had been unable to experience personally—thus “re-indigenizing diet...and re-establishing relationships with the chestnut” (4). Whyte, Brewer, and Johnson (2016) have emphasized the importance of recognizing the distinction between the current view on scientist privileged knowledge and Indigenous scientist “protocols”:

Different from seeing scientists as having privileged knowledge of how to circulate resources, some Indigenous scientists express protocols that often represent humans as respectful partners or younger siblings in relationships of reciprocal responsibilities within interconnected communities of relatives inclusive of humans, non-human beings (i.e., plants, animals, etc.), entities (i.e., sacred and spiritual places, etc.) and collectives (i.e., prairies, watersheds, etc.). (2)

The frame of *responsibilities* to these communities of relatives emphasizes openness to learning from these kinship relations in support of caretaking and stewardship of the collective future.

Guernsey, Keeler, and Julius (2021) suggest policy such as the Endangered Species Act could be updated and “indigenized” to better reflect indigenous conservation values by “including kinship as a central conservation value” (279).

As indigenous views of kinship suggest, expanding beyond dichotomies of natural-anthropogenic will also better allow for encompassing nonhuman agency in conservation practice. As Donfrancesco and Luque-Lora (2022) stress, “to say that particular wolves (*Canis lupus*) are anthropogenic simply because they contain genes inherited from hybridization events with domestic dogs (*C. l. familiaris*) (Stronen & Paquet, 2013) is to ignore the independent agency of those wolves (and dogs) to mate, reproduce, and live on” (2). As they emphasize, designating such hybrids as anthropogenic ultimately “silences” the agency of the wolves and

dogs themselves. To designate hybridization events as anthropogenic, and therefore unnatural, also creates logical inconsistencies for conservation as well—as Rohwer and Marris (2015) note, such arguments would ultimately imply that *all* anthropogenic change to species genetically (whether intentional or not) is bad—an ultimately difficult concept to stomach under the conditions of the Anthropocene. Indeed, take the example of the Florida soapberry bug (*Jadera haematiloma*). The bug evolved feeding on the native balloon vine (*Cardiospermum corundum*), but the phylogenetically related Asian flamegold tree (*Koelreuteria elegans*) was introduced as an ornamental in the 1950s, rapidly becoming an invasive plant species in the region: “from the bugs’ standpoint, their seeds are an abundant new resource” (Carroll and Fox 2008, 247). In an amazingly short period (100 or fewer generations), the bugs matured 25% faster, were 20% more likely to survive their juvenile period, and their mouthparts evolved from an average of 9.3 mm shrinking to 6.9 mm due to the smaller fruit size of their new food source—overall, their “lifetime fecundity has nearly doubled” (247). A similar process is happening as the balloon vine from the Americas now spreads invasively in Australia and native soapberry bugs on that continent are rapidly evolving larger mouthparts to respond, damaging the new invasive plant at twice the rate of their previous, native food source: however, “whether that control will be strong enough to select for counteradaptation in the invader is yet to be determined” (248). Such fascinating examples of rapid evolution in response to *anthropogenic* species introductions would, in a model of “anthropogenic change is bad” thus be identified as inherently bad changes. Considering the uphill battle many land managers face over certain invasive plant species that undermine the overall function of native ecosystems, seeing the adaptation of native species to newcomers should be an encouraging sign, rather than one to lament. Examples such as these help us recognize the ways native species are not passive victims to invasive attack, as they are

so often framed in “invasion” rhetorical frameworks, but rather agential beings themselves that are *partners* in conservation efforts to adapt and respond to these changes to ecosystem communities.

To incorporate these kinds of adaptive considerations into conservation practice, many scholars in the past couple decades have been calling for “evolutionarily enlightened conservation”—a processual approach that would better capture the constantly shifting materiality of adapting and evolving *real* populations of nonhuman animals and plants through time (Moritz 2002; Ashley et al. 2003; Mace and Purvis 2008; Hoffmann and Sgrò 2011; A. Robert et al. 2017). Such approaches might deviate greatly from contemporary approaches which have often emphasized “irreplaceability and viability” which doesn’t necessarily capture processes of adaptation (Mace and Purvis 2008, 13). However, some scholars still suggest measures such as “phylogenetic distance” or using a combination of the Phylogenetic Species Concept and measuring the genetic distance or branch length on a phylogenetic tree to capture character disparity—a wider net of species difference across the diversity of life (14). Such measures might not be able to capture the way hybridization can have a role to play in evolutionary processes over time as hybrid lineages would *merge* branches before later diversifying. As a suggested remedy to the present single-species focused approach, and one that would capture hybrid lineages, Ennos et al. (2012) have developed a Process-Based Species Action Plan that could accommodate diversity that develops from hybridization and complex evolutionary processes (Ennos et al. 2012). They differentiate their model from the present approach as follows: “the conventional Species Action Plan (SAP) seeks to prevent the extinction of an individual, pre-existing, named taxon. ... The Process-Based SAP attempts to safeguard the evolutionary processes generating novel lineages, such that the potential for the

creation of novel biodiversity is conserved” (195; see Figure 5.1). Such a model would work quite well, in fact, for the evolving complex of *Vermivora* wood warblers, as it allows for the flux across species boundaries and seeks to support diversity overall through management of habitat rather than maintaining strict species purity. A third model, developed by Cowling and

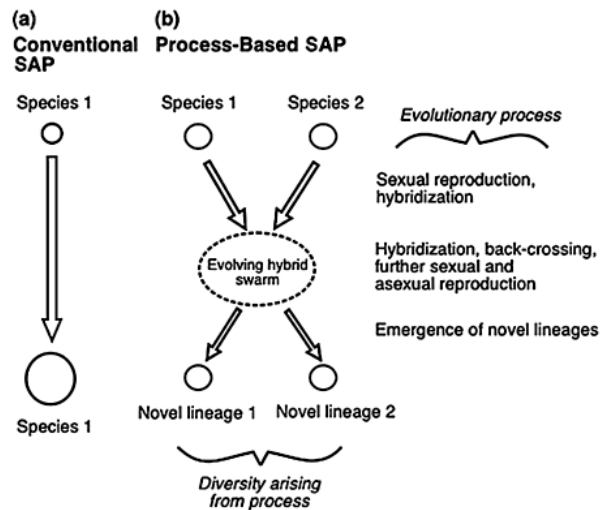


Figure 5.1: Diagrams of Conventional Species Action Plan (SAP) & Process-Based SAP, figure from Ennos et al. 2012

Pressey (2001), suggests a spatial approach to evolutionary conservation in which managers consider the spatial requirements for preserving irreplaceable evolutionary processes and evolutionary drivers. For their case study, they considered aspects such as sufficient space for sand movement corridors, whole riverine corridors, whole-patch fires, the maintenance of plant and insect biodiversity

and plant-insect pollinator relations, etc. Many considerations were made about disturbance regimes that were necessary drivers for evolutionary processes as well as the co-evolutionary processes between species, for instance plants and their pollinators (Cowling and Pressey 2001).

One 2018 study sought to address current manager and scientist perspectives on incorporating evolutionarily enlightened conservation management, finding that, overall, there was interest in incorporating such concepts, but a range of barriers were identified as preventing their ready implementation on the ground (Cook and Sgrò 2018). A stronger grasp of the science was one barrier, as well as an overall lack of resources and cooperation between managers and researchers. In addition, the ability to represent the *benefits* of the changes to management were deemed a potential problem, particularly due to evolution operating at potentially long

timescales, whereas many management processes expect short-term focuses for management outcomes. In all, the study stressed that “most managers strongly support the view that evolutionary biology is important for conservation management ... but demonstrate there is a long way to go to achieve routine integration of these concepts into management practices” (1281). As I have demonstrated in my dissertation, there is a further two-fold problem that develops through the operation of policy that prevents the adoption of these more innovative approaches to species. First, there is the broader public belief in species boundaries as fixed, a belief that is reinforced by the *legal need* of the ESA to clearly delineate between species and thus identify the targets for conservation protections. Conservationists recognize that delisting petitions (ever at the ready by private and corporate interests eager to free up land-use) are something that must be avoided as much as possible—these processes bog down already strapped agency resources as biologists take the time to go over petitions. This is ultimately an internal structural limitation of the policy-reliant system of protections: if species uncertainty is allowed, the species’ protections will become vulnerable. Therefore, encouraging a static, essentialist view on species works (almost counterintuitively) in conservationists’ favor. Second, the ESA’s “best available science” mandate, particularly when paired with limited USFWS funding, often encourages biologists on the ground to operate with high levels of personal discretion in decision making. While this doesn’t mean the science is *wrong*, per se, it often means biologists will lean on prior precedent instead of trying new things. What have we done before? What does older literature say? There is a “wait and see” approach when it comes to newer scientific literature (for the most part), particularly if it overturns long standing precedent in the Service. Trying a completely new approach to managing species that accounts for evolutionary processes, blurring across species borders, and overall species uncertainty is not

something that is presently supported under the current restrictive policy framework for T&E conservation. In addition, as Mace and Purvis (2008) note, the emphasis of policy such as the ESA on individual species rather than “the interactions between [species], [and] their interactions with the biotic or abiotic environment” (13) limits the policy’s ability to capture the evolutionary processes that actually *generate diversity*. Capturing evolving lineages in T&E conservation seems unlikely to adhere anytime soon, unless conservationists and policymakers take a substantive look at the content of the ESA itself—a process that gives many environmentalists the chills, as fears of opening the “books” on the only environmental policy with “teeth” provokes fears that the policy will only be weakened, rather than improved.

Evolution as a Story Without End

At the conclusion of *The Mushroom at the End of the World*, Anna Tsing reflects on Ursula K. Le Guin’s “Carrier Bag Theory of Fiction” in which, “like a forager rather than a hunter,” the “storyteller might pick up diverse things of meaning and value and gather them together”: “in this kind of storytelling, stories should never end, but rather lead to further stories” (Tsing 2015, 287). The hunter desires the kill—a conclusion—the forager seeks continuance, ongoingness. I see an evolutionary view as our forager: gathering adaptations endlessly but never really finishing the story, as there is no conclusion to the story of evolution—it is an ever-flowing river through time that changes as it encounters new obstacles. The essentialist view on species is the hunter hoping for a bounded, *conclusive* understanding of species: an ending to the story, a closing of the book. To embrace evolutionarily enlightened conservation is to embrace stories that never end—species that are constantly *rewriting themselves* and therefore to which we must be attentive, responsive, and *responsible*. No ending is predetermined, for there is no

“end,” only a multitude of pathways: narratives that branch, merge, and branch again as they braid through time. The future I wish for conservation is one that embraces such ongoingness—stories without end—and acknowledges the profound responsibility that comes with helping *write* those stories ourselves. As conservationists we are also storytellers, we are also makers of worlds, and we write those futures into being alongside the other species we share those worlds with. Nurturing life is respecting its agency as a fellow storyteller—attending to its material configurations, the choices species make in relation to and in resistance of our own efforts. To nurture life it to *listen* to the stories it is trying to share with us in return.

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