



**An Investigation of Ecosystem Restoration through Facilitated Adaptation**  
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## 1. Abstract

In what scientists are calling the "sixth mass extinction," thousands of species have gone extinct starting from the early Pleistocene, and many more are at risk of extinction each year due to human impacts on the global ecosystem. One potential intervention to slow this process is facilitated adaptation—the use of various methods to change a species' gene pool to display stronger, more adaptable traits. Some of the methods characterized by facilitated adaptation include selective breeding, facilitated migration, and gene editing. This research analyzes a number of select case studies that exemplify when to use one form over another—a decision that is further investigated through the creation of a decision matrix. Each scenario that could potentially benefit from intervention has many variables including species' importance, lifespan, genetic diversity, and present alleles, emphasizing the careful consideration needed when choosing the most appropriate form. With these factors in mind, facilitated adaptation can be used to restore a habitat's species interactions, and stronger connections between species can lead to a more stable environment.

## 2. Key Words

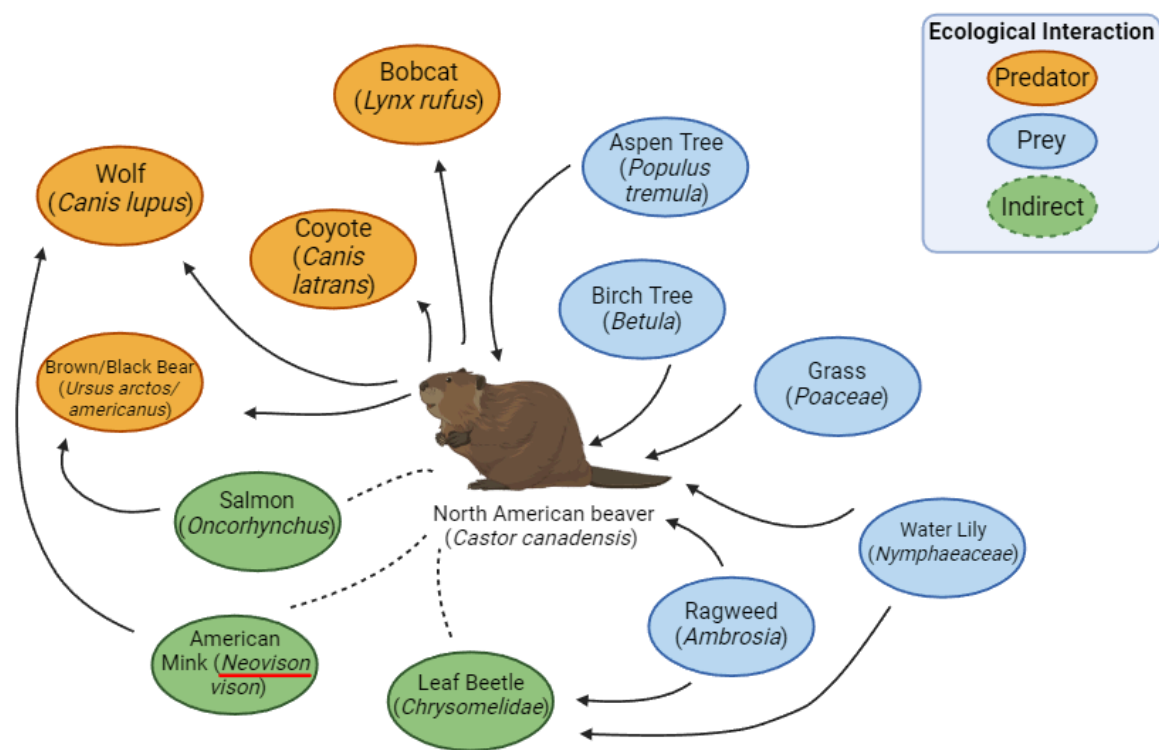
- 1) Facilitated adaptation
- 2) Biodiversity loss
- 3) Selective breeding
- 4) Assisted/facilitated migration
- 5) Gene editing
- 6) Conservation
- 7) Anthropocene

## 3. Introduction

There is arguably no species that has had a greater impact on the state of the planet than that of the *Homo sapiens*. Even in the early Pleistocene, beginning around 2.58 million years ago, humans hunted various species to extinction as their hunting techniques advanced. Since the dawn of human civilization, between 73-80% of mammals have gone extinct in the Americas alone, including various large mammals such as the woolly mammoth ("The Present, Past and Future of Human-Caused Extinctions," 1989). This pattern has only accelerated in the past century with the growth of the human population. As the Industrial Revolution—which began in 1760 in Britain—progressed, issues regarding pollution in nature grew and anthropogenic climate change worsened. Human-caused carbon dioxide emissions have led to a global increase in temperature and natural disasters, rising sea levels, species loss, and much more (Albritton Jonsson, 2012). This epoch of time marked by intense human impact is known as the Anthropocene, during which there has been an incredibly high rate of extinction. In what scientists call the sixth mass extinction, biodiversity loss is not only extreme, but is occurring at a faster rate than the five extinctions prior. Around 1.2% of all bird species and 1.4% of mammals were determined either extinct or living solely in captivity by 2008 (Ceballos & Ehrlich, n.d.). This poses a threat not only to individual species but also to the other species they interact with and the habitats in which they live.

An ecosystem encompasses all the interactions between the species in a community and its abiotic environment. When one species is lost, the consequences are often far-reaching. The

interactions between trophic levels are necessary for the structure of an ecosystem, as the loss of a specific type of plant could have a chain reaction further up the food chain (Lagerstrom et al., 2022). There are some species—known as keystone species—that are so intertwined in the lives of various other species that, if lost, could threaten the functionality of entire ecosystems. For example, beavers create habitats through dam building that supports life for various other species (Figure 1). If beavers were to go extinct in an area, the freshwater lake may become a stream again, leaving many species homeless. In places where the North American beaver (*Castor canadensis*) lives, the micro-ecosystem they create sustains four to five amphibian species that otherwise would not have been able to survive in the same area if not for the beavers (Hossack et al., 2015). When such important species become endangered, as the beavers once were, a chain of events follows. Those that interact closely with the keystone species, such as amphibians that live in the lakes beavers create, will suffer. This is followed by more broken species interactions, eventually leading to the breakdown of an ecosystem. Many of these species and habitats in question are not only dependent on each other, but are also significant to human livelihood, bringing the problem back to its root cause.



**Figure 1.** Species interaction web highlights the importance of the American Beaver as a keystone species. Not only does the beaver have predator-prey relationships, but it also supports a host of aquatic pond life through dam building as indicated by the dashed lines. Without this species, there would be a lack of structure in this interaction.

As a response to the pressing issues brought forth by humans, species have three options: move, adapt, or die (Habary et al., 2017). In the case of tropical coral reef fish, many species have been documented moving toward the north or south poles in response to

increasing ocean temperatures. Alternatively, the fish could face selective pressure that results in evolution, leaving only those that can withstand the new, harsh conditions. Of course, the last option, or rather endpoint, is the death of those individuals that cannot survive. Species have a certain measure of adaptability, called phenotypic plasticity, which is the ability for a gene or genes to be differentially expressed, thus modifying an organism's phenotype. But, this characteristic only goes so far, which is why human intervention is often necessary for the conservation of many endangered species (Whitman & Agrawal, 2009).

Some may argue that prevention is better than a cure, but the high rate of species extinction calls for intervention at all levels while the core issues of climate change, deforestation, pollution, and more continue to be researched. Every day, the loss of species poses a threat to the stability of various habitats across the planet and, if left unaddressed, could leave permanent gaps in earth's tree of life (Ceballos & Ehrlich, 2023). One such intervention is the utilization of facilitated adaptation, a major method of which is to increase a population's genetic variation in order to assist evolution by endowing the population with adaptive capabilities. Just a few of many forms of facilitated adaptation include selective breeding, the artificial endowment of pre-existing alleles from one individual to the next generation; facilitated migration, the movement of alleles geographically; and gene editing, the modification of genes based on pre-existing alleles, or the construction of completely new ones.

This research discusses the potential effects of applying different forms of facilitated adaptation to threatened keystone species of an ecosystem that has been negatively affected by humans. The nuances of each form are analyzed, evaluating when and where it is best to use one form over the other. The effects, both positive and negative, of using facilitated adaptation on species within a particular environment are also discussed. The following three examples of facilitated adaptation have been selected for study: selective breeding, facilitated migration, and gene editing. These are a few of many forms, but were chosen due to their relevance and widespread use. They serve to highlight the real-world process and impact of facilitated adaptation and thus can be used to further develop and refine the tool.

## 4. Case Studies

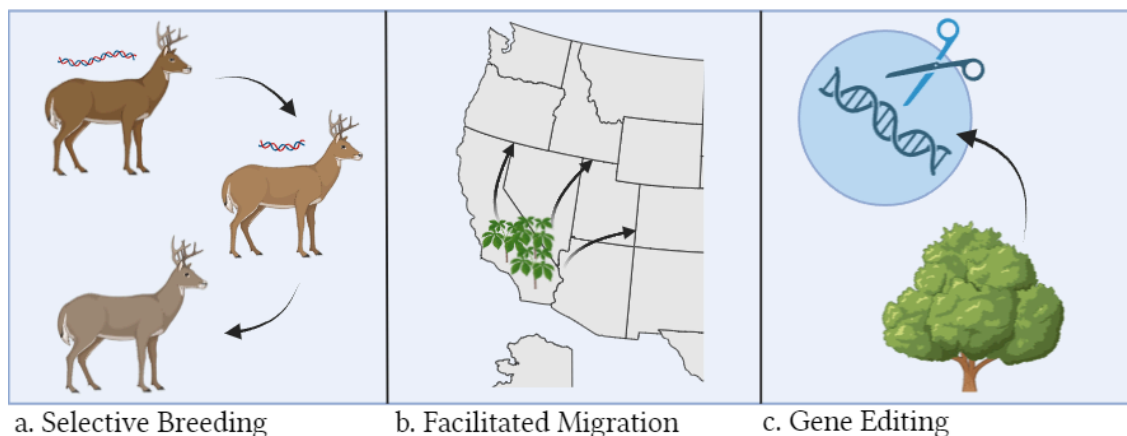
### ***Selective Breeding***

Selective breeding for desired traits is the most commonly understood method among the general public (Figure 2a). In a process similar to the domestication of canines or livestock, selective breeding targets specific traits already present in an individual or population and increases its frequency by artificially selecting for it. This process can endow an organism with traits that are better suited for its altered habitat. This method is arguably the most cost-efficient form of facilitated adaptation as well, making it well-suited for species with short to mid-length lifespans. The following examples showcase the versatility of selective breeding and situations where it has been effectively and ineffectively used.

Selective breeding targets a specific desired trait to artificially amplify its occurrence in a population by crossing individuals carrying that trait, ultimately leading to increased fitness of a population. For example, chronic wasting disease (CWD)—a fatal disease with no known cure—affects deer, elk, reindeer, sika deer, and moose, but genetic variation in these populations results in varying susceptibility. CWD is a prion disease, meaning it results from the misfolding of proteins, and is encoded by the prion protein gene, PRNP. Selective breeding has been utilized to help reduce the frequency of the disease spread from wild to farmed populations

of deer and elk. The PRNP gene that increases susceptibility to the disease was targeted on three controlled hunting grounds over four years by releasing whitetail deer with different PRNP genes into the wild populations. After the trial, through selective breeding, there was a 12% decrease in the PRNP gene, resulting in a decreased rate of CWD. This success shows the future potential for disease management in other large mammal species via selective breeding (Haley et al., 2021).

An example of a selective breeding case that would not be sustainable in the conservation of endangered species can be seen in the example of the Przewalski's Horse (*Equus przewalskii*). In 1995, a research team simulated the effects of breeding the horse by using mathematical calculations on pedigrees. At the time of the project, there were only 485 of these horses left, all of which were descendants of the same 13 horses. A horse that was the most genetically distant from the rest of the population based on its founder was selected as the "high-priority breeder." By focusing all attention on one horse with rare alleles for breeding, genetic diversity can be sustained. But, if a specific allele is targeted, it could have the opposite effect. Increasing the frequency of an allele (even a helpful one) could be harmful, as it leads to reduced genetic diversity. In cases with small population sizes, such as the Przewalski's Horse, there is little that selective breeding can do for the conservation of the species unless there is constant monitoring of the individual's pedigree (Miller, 1995).



**Figure 2.** Three major forms of facilitated adaptation include a) selective breeding, b) facilitated migration, and c) gene editing

### ***Facilitated Migration***

Climate change has been the driving force behind the creation and adoption of facilitated migration techniques (Figure 2b). Diverse habitats—ranging from tropical rainforests to deep-sea hydrothermal vents—have been experiencing more extreme weather, droughts, increased ocean temperature, and even the destruction of entire ecosystems. The intentional, human-facilitated movement of species away from their original habitats to more suitable locations as a response to the rapidly changing climate is known as facilitated migration. Some species have already begun to self-migrate to track their desired climate type, but there are many that are unable to move so easily, making them prime targets for facilitated migration (Hewitt et al., 2011).

Targets for facilitated migration may be large organisms with longer life spans, as it would be hard to breed or genetically modify them within a reasonable time frame. Trees, which have no way of moving during their lifespan, would not be uprooted and transported, but rather seeds would be planted in new areas to expand the population's range. One such species for which this has been trialed is the Joshua Tree (*Yucca brevifolia*), native to the Mojave Desert. Due to rising temperatures, the species is predicted to lose 90% of its natural range within the next 75 years (Cole et al., 2011). Its loss would also be detrimental to the species that have formed evolutionary bonds with the Joshua Tree, like the Yucca moth (*Tegeticula yuccasella*), which lays its eggs exclusively within the plant (Lagerstrom et al., 2022). Results from a simulation that included variables such as climate and range maps showed that the Joshua Tree's suitable range will expand past the desert at a rate of 22 to 33 m/year. In response, facilitated migration of the tree could intervene, as its natural movement rate is only around 2 m/year, thus there is no natural way for the Joshua tree to spread to a new location fast enough to track the changing climate. If protected, the species will be able to live within boundaries that do not force it to adapt or die as a result of climate change for some time (Cole et al., 2011).

One unintended byproduct of facilitated migration could be the species that may (or may not) move along with the target species. In an experiment to understand the effects on dependent species of hosts moved by facilitated adaptation, 39 Duvaucel's Geckos (*Hoplodactylus duvaucelii*) were moved through the islands of New Zealand along with dependent mites (*Geckobia naultina*) who eventually occupied the new islands as invasive species. Throughout the following year, the mites remained with the gecko hosts, even in their new habitat, raising questions about their potential impact on the new habitat (Moir et al., 2012). On the topic of interspecies relationships, it is unclear if the Yucca moths that have a mutualistic relationship would move with the Joshua tree if it were the focus of a facilitated migration project. This poses the question of the success of a species in a new location if it loses the interspecies relationships it depends upon (Lagerstrom et al., 2022).

### **Gene Editing**

In the case of gene editing (Figure 2c), genetic variation can be increased within a population by endowing it with completely new adaptive alleles. CRISPR-Cas9 is just one of many gene editing technologies capable of editing an organism's genome. By combining the functions of a guide ribonucleic acid (RNA) and the protein Cas9, the CRISPR technology is able to locate specific regions on a genome and delete, add, or modify sections of DNA (Jiang & Doudna, 2017). In terms of conservation, gene editing and CRISPR can be used to supply struggling populations with new variations of genes, or alleles, essentially amplifying the organism's phenotypic plasticity artificially. But, at this point in time, there have been few successful attempts at gene editing for conservation, making it a generally untested tool in the field (Fogel, 2011).

An application for gene editing is strengthening the resilience of a species by addressing the diseases that affect it. The American chestnut (*Castanea dentata*), once spanning the east coast of the United States, was an integral species of the temperate deciduous forest biome. Supplying canopy cover, nuts, and nutritious bark, the tree played an essential role in its ecosystem until the introduction of a fatal pathogen (Tibbetts, 2022). The chestnut blight fungus (*Cryphonectria parasitica*) killed around four billion American chestnuts, decimating the population ("Darling 58 /54," n.d.). In 2015, the American Chestnut Research and Restoration Project utilized gene editing of the oxalate oxidase (OxO) gene to increase blight tolerance. The

OxO gene was taken from wheat and added to the DNA of the American chestnut, making Darling 58, a synthetic tree. The OxO gene detoxifies oxalate, a chemical compound that aids the blight in killing the tree. Adding the gene to the American chestnut would decrease blight activity, thus increasing its tolerance to the pathogen (Steiner et al., 2017). The project is still ongoing in its efforts to introduce Darling 58 to the wild but, if successful, the modified tree has the potential to support forest ecosystems as it once did in the past (Tibbetts, 2022).

The possibilities of gene editing are partially held back by public opinion due to its relatively new use. In the case of the American chestnut, Darling 58 needs to be approved by the Environmental Protection Agency, US Department of Agriculture, and Food and Drug Administration in order to continue research in the wild (Tibbetts, 2022). A survey conducted by YouGov showed that 70% of adults believe that gene editing in wildlife can “easily [be] used for the wrong purposes” (Kohl et al., 2019). This hesitation both ensures that only the best version of gene editing is applied in the wild and also that progress is slow, making gene editing a tool of which many are wary.

### ***Additional Forms***

These case studies investigate only three forms of facilitated adaptation, but with many different species in very different scenarios, there is a need for alternative solutions.

One such alternative is hybridization, a variation of selective breeding, which breeds two different species or two individuals of the same species that are genetically distant. In terms of conservation, hybridization can create new genetic combinations, endowing a population with new alleles. This tool is best suited for small populations with little genetic diversity, and a major potential risk is over-breeding the parent species and losing them to the resulting hybrid (Chan et al., 2019).

Another, more controversial form of facilitated adaptation is cloning, or the creation of a genetically identical individual from a parent individual. Cloning can help species that are on the brink of extinction since its purpose is to create more individuals, often as a last resort when two fertile individuals of opposite sex do not exist. The obvious downside to this method is the lack of increase of alleles as cloning is akin to asexual reproduction (Holt et al., 2004).

Finally, the study of epigenetics—variations in gene expression that do not physically alter the genetic code—is another tool that can be utilized for conservation. One application of epigenetics is DNA methylation which can be used for gene suppression. This can be important for species that have a potentially beneficial phenotype that could help them adjust to their changing environment but are unable to make use of it without aid. This tool would best be used for species with the potential for phenotypic plasticity as they would express changes made above the gene (Rey et al., 2020).

## **5. Discussion**

### ***Investigation of Case Studies***

Each of the examples explained above has certain criteria for why it was chosen to be researched, or why it should not be chosen in the future. Due to the expensive and time-consuming nature of facilitated adaptation projects, it is imperative for those that are undertaken to be beneficial in the long term.

First, it is important to choose a species to focus on that has the potential for a significant impact on the surrounding species or environment; ideally, it should be a keystone species.

While the goal of facilitated adaptation is to help one particular species, choosing a keystone species can have positive knock-on effects that should be considered. If a species were to be rehabilitated to fit into its niche, not only would it help that one species, but it could benefit the species that it interacts with as well—take the American beaver for example. For this reason, if there are certain species that have pre-existing relationships with numerous other species, it would be in the best interest of both the research team and the ecosystem to focus on adapting that particular population. Other species to consider would be those that act as model organisms for experimentation, such as certain types of coral.

Moreover, it is crucial to consider the success of species conservation with the different forms of facilitated adaptation. For each of the various types of facilitated adaptation, there are certain characteristics exhibited by species that would make the best use of the tool. For example, facilitated migration would work best for species that are long-lived due to the effort it takes to physically move an entire population; it makes the most sense for larger animals or trees, which have very long lives, to use this particular style.

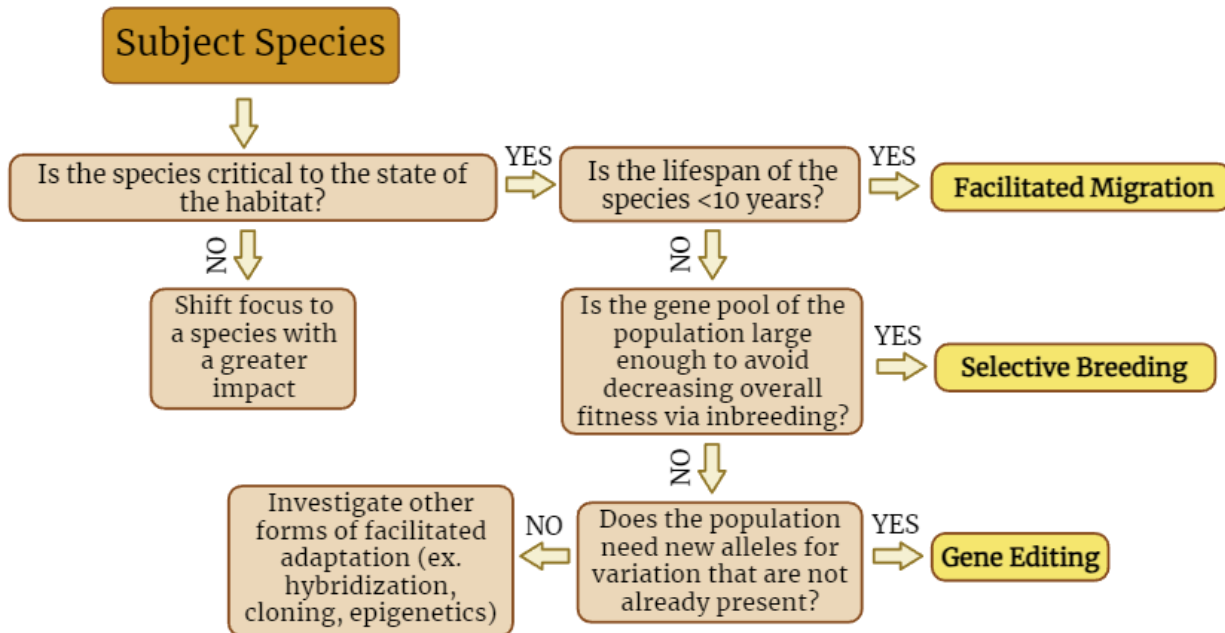
On the other hand, selective breeding would not make sense for these species because their long lives would make breeding and raising offspring a very long process, meaning results would not be visible for many generations. In the case of selective breeding, it makes sense to use animals that have shorter lifespans. For example, the lifespan of a deer (around 6 years) is much shorter than that of a Joshua tree (around 150 years). Although 6 years or more is still a substantial amount of time, selective breeding is not as expensive or complicated as other projects, such as gene editing, which makes it a better choice for certain restoration efforts.

Due to its expensive and unverified nature, gene editing would be best used in scenarios where certain genes are not available for breeding or when there is a very specific habitat a species must live in to survive (or to combat specific diseases). This works best for the American chestnut because the gene needed for blight resistance is not present in its population; it is found in a different species, so there needs to be genetic intervention to endow individual chestnuts with the gene. Even though its lifespan is long, facilitated migration would not work since the disease that affects the tree would likely spread with it.

It is also important to take note of past failures in facilitated adaptation research to avoid repeating the same mistakes. For example, in the case of Przewalski's Horse, selective breeding was not a good choice because there were very few genes available to increase genetic diversity in the population. If not carefully considered, the population could become inbred, which would actually decrease the population's overall fitness. Gene editing would have been a better option because it has the potential to introduce new alleles to the population, increasing diversity and more likely, overall fitness. Similarly, the pests moving along with the Duvaucel's Geckos are important to consider. Although geckos are an important species to the health of the environment in New Zealand, issues with invasive species are an undesirable expense of facilitating migration projects.

Considering the restrictive qualities of the various facilitated adaptation applications, it is imperative to choose the option best suited for the scenario. Figure 3 outlines a clear guide to choose the best form of facilitated adaptation through a decision tree. Following each of the steps ensures the best choice for rehabilitating the population in question.





**Figure 3.** A guided decision tree for proper application of facilitated adaptation. Beginning from the subject species, the first question directly under the arrow determines if the species in question is a valid test subject. If not, the focus should be shifted to either entirely another species or a species that fulfills a similar role to the endangered species. The next question determines if facilitated migration is the correct choice by eliminating options that have a lifespan of ten years or less. The following question focuses on selective breeding by highlighting the importance of a healthy gene pool to avoid problems in later generations. The last question suggests gene editing as an option if the population in question would benefit from a new allele introduced to it. The final step suggests alternative methods if the criteria above are not met fully. Some examples include hybridization which combines the genetic information of different species or epigenetics which investigates how the environment affects the individual.

### **Consideration for Future Conservation Efforts**

Throughout the process of deciding which method of facilitated adaptation to use, there should be careful consideration of measures taken to decrease overall harm. While facilitated adaptation has the potential for positive outcomes, there are still clear downsides if not handled properly.

Even before a project is started, the correct facilitated adaptation form should be chosen using the decision matrix (Figure 3). An incorrect choice could lead to unnecessary loss of resources and, more importantly, further disruption of an ecosystem beyond the initial problem. During the project, the state of the environment should be closely monitored for any major negative changes. If there are unintended consequences, there should be efforts to restore the habitat. After the main project is done, there should still be periodic checks to maintain a healthy ecosystem and observe any changes. Variables that succeeded and failed should be taken note of to properly make adjustments for future facilitated adaptation projects.



The success of a project can be measured through the strength of interspecies bonds. For example, successful reintroduction of the American beaver should lead to a stable relationship between beaver and lynx populations. The two species should have a dependent relationship where one is affected by the other's population changes. This dependency indicates that the facilitated adaptation project restored not only the frequency of the target animal but also that its surrounding environment is recovering. As species begin to interact with each other again, the food chains that lie within the habitat will strengthen and reform; when species interactions are strong, both biotic and abiotic components of the habitat are able to develop once more. By the end of the restoration effort, the habitat should be in much better condition; with its interspecies bonds connected once more, the habitat should be similar in strength to its state before anthropogenic change indicating a shift to a more stable environment.

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