

Genetic Conservation of the Grey Wolf

Ecological Genetics Research Paper

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In recent years there has been an increased interest in environmental preservation and restoration. Part of this includes ensuring that the ecosystems of concern are as healthy and functional as possible. An important part of the health of any ecosystem is the effect of apex predators. For most of North America this role was historically filled by the gray wolf (*Canis lupus*). Due to eradication programs and habitat destruction wolves were extirpated from almost all of the continental United States. In recent years wolves have been reintroduced in Yellowstone National Park and have spread to other areas as well. Due to the widespread ecological benefits the wolves have had on Yellowstone, interest in wolf reintroductions in other areas may increase in the future. Before we can successfully conserve the existing wolf populations or reintroduce new populations we must understand the role genetics will play in the success or failure of these wolf populations. Only after understanding the composition, structure and function of wolf genetic diversity and determining the effects human activity has had on this diversity can we form a well informed conservation plan to encourage the health of the American wolf population into the future.

Since the range of gray wolves has been so greatly reduced it is difficult to know the amount of genetic diversity that was once present in the species. It would be expected that a species that once ranged over such a large area and lived in so many different habitat types that there would be a great amount of genetic diversity with the wolf species. Since wolves can range over large areas, up to 1000 km on some occasions, many have assumed that there would be little genetic structuring among populations in close proximity. However, as described by Muñoz-Fuentes et al. (2009) differentiation can occur between wolves within this dispersal range between populations in different

habitat types. This difference between adjacent populations of wolves means that there could be structuring between among wolf populations that were previously thought to be one large population. This makes it challenging to determine how much genetic diversity should be present in populations that are now isolated. One example of the variation between wolf populations separated by large distances is the variation between the Canadian wolves (*Canis lupus lycaon*) and the Mexican gray wolves (*Canis lupus baileyi*). All of the remaining Mexican wolves, with the exception of a few recently released into the wild, are all contained in three separate captive populations, the Aragon, McBride and Ghost Ranch lineages. It was found for the major histocompatibility complex (MHC) genes that the alleles contained within the Mexican wolf populations were almost entirely different than the alleles of the Canadian wolf populations (Hedrick et al. 2000). Another documented variation between wolf populations within the geographic distance of dispersal is melanism differences between wolves that inhabit the boreal forests and those that inhabit the tundra. It was found that the K^B allele which codes for black coat color in wolves is more common within the wolves that inhabit the forests than the tundra (Anderson et al. 2009). These variations among between populations may help to explain how wolves were able to adapt to such a wide variety of habitats. Based on these studies environmental differences are more important than geographic distance in determining the structure of wolf populations.

Within breeding populations of wolves, migration plays a major role in maintaining genetic diversity and the health of future generations. Because of their breeding system in which only a few individuals are involved in mating, wolves tend to

have small effective population sizes (N_e) relative to the total population. This makes isolated small populations even more vulnerable to the effects of genetic drift. Since many of the remaining wolf populations are small we are beginning to see these effects. Aspi et al. (2009) found that the wolf populations of northwest Russia and Finland (*Canis lupus*) were diverging due to a lack of migrants between the regions. It appears that barriers to migration can lead to the halt of gene flow between wolves that are only separated by short distances. This isolation can lead to increased inbreeding and a loss of genetic diversity (Aspi et al. 2009). In another study deleterious effects of inbreeding were seen in the Scandinavian wolf (*Canis lupus*) populations. It was observed that the wolves of the region were undergoing inbreeding depression due to a lack of migrants. The effects of the inbreeding depression were observed as decreased litter size, and congenital malformations. It was concluded that the Scandinavian wolves may experience reduced fitness due to the exposure of deleterious alleles (Hagenblad et al. 2009). Even among the captive Mexican wolf populations there seems to be divergence. It was found that for the genes of the major histocompatibility complex that only one allele was shared between two of the lineages, while the other four alleles were found in only one lineage (Hedrick et al. 2000). Before beginning a breeding program to increase genetic diversity in the Mexican wolf population it is important that we understand the causes of these differences.

There are several mechanisms that have produced variation patterns among wolf populations. Selection, drift, environmental gradients and migration have played a major role in determining the distribution of genetic variation. In regard to the prevalence of black wolves in the boreal forest south of the tundra, one possible explanation is that

the K^B allele's introduction from domesticated dogs into wolves has provided a predatory advantage to wolves that live in the forests (Anderson et al. 2009). If this is the case then it would be expected that the wolves that once inhabited the other forests of America would have also received an advantage from the dark pigments. While it is hard to be certain of the causes of the differences between the Mexican wolves and their Canadian relatives due to the extirpation of the wolves that once inhabited the region between the two populations, the difference in the alleles of the major histocompatibility complex could also be due to selection. Since the MHC is believed to be a major component of canine resistance to pathogens (Hedrick et al. 2000) it is reasonable that the difference between the two populations could be due to selective pressures placed on wolves by the pathogens of the different environments.

Because of the small size of many wolf populations genetic drift can play a major role in determining genetic structure for a region. A good example of this is the northwestern Russian and Finnish wolf populations. At one time these wolves would have been part of the larger Russian wolf population, but they have since become isolated. Aspi et al. (2009) found that these populations were beginning to differentiate from the larger wolf population due to the effects of genetic drift caused by population bottle necks. Like in America most of the wolves in this area have been eliminated in the past. The area has then been recolonized by a small number of wolves from the larger population. Due to barriers to the movement of the wolves the flow of genetic material between populations has slowed to the point where genetic drift can affect the gene pool. Because of the negative effects genetic drift and increased inbreeding can have on wolves, migration has played an important role in maintaining genetic diversity at a

high enough level to avoid inbreeding depression. The Scandinavian wolf population is an example of the “genetic rescue” that can be performed by even one migrant. Following the immigration of a single male wolf from the neighboring Russian population, the genetic variation was increased in the inbred Scandinavian population (Hagenblad et al. 2009).

Environmental gradients can also influence the genetic makeup of local wolf populations. In British Columbia it was determined that ecological factors were the most likely factor in differentiating inland wolf populations from their coastal neighbors. 56% of the variation between the wolves could be accounted for by vegetation cover alone (Muñoz-Fuentes et al. 2009). It was hypothesized by the authors that migratory wolves are more likely to migrate to habitats that are similar to the one they are familiar with. It would make sense for wolves to be more successful in a habitat like the one they had learned to survive in and that their ancestors had been successful in. Another factor Muñoz-Fuentes et al. considered is that the type of prey available in an environment could have a strong effect on the genetics of a population. It was determined that larger wolves received a net predatory advantage in subduing large animals like elk (*Cervus canadensis*). This comes with a tradeoff of decreased acceleration and maneuverability (MacNulty et al. 2009). Due to this trade off larger wolves could be more successful in areas with large prey animals such as moose (*Alces alces*), elk, and caribou (*Rangifer tarandus*), while smaller individuals could be favored in more densely forested areas where smaller prey animals such as whitetail deer (*Odocoileus virginianus*) make up more of the wolf diet. These environmental gradients could play an important role in

predicting the genetic changes of wolves adapting to changing environments and the success of those colonizing a new area.

Human activities have made major alterations to the natural environment. Wolves have been one of the species to have their existence altered the most by humans. These effects are caused mostly by the extermination of wolves from many parts of their natural range, the destruction of wolves' natural habitat, and the captive breeding programs of wolves.

The most obvious effect that humans have had on wolf populations in the United States is the elimination of wolves from most of their natural range. In the years after European colonization of America, an organized effort was made to kill the wolves that shared habitat with humans. The only wolves that survived these eradication programs were those who lived in areas so remote that few humans encountered them. By reducing the wolf populations, humans increased inbreeding, cutoff migration routes, and eliminated a large amount of genetic diversity. As seen in the Scandinavian wolf population these effects can have negative effects upon the fitness of wolf populations that extend beyond the killing of individual wolves (Hagenblad et al. 2009).

Along with killing wolves, humans have also altered the habitats that the wolves once occupied. This habitat destruction eliminates migration routes, reduces prey availability, and reduces the number of wolves that can inhabit an area. As stated earlier wolves are a widely dispersing species. The males can roam up to 1000 km to establish themselves in a new area. This migration is impeded by the construction of roads, fences and urban areas. Aspi et al. (2008) hypothesized that the reduced migration

between the Russian and Finnish populations was due to the construction of roads and barriers remaining from the Iron Curtain. By reducing migration we are creating the potential for genetic structuring where none would have naturally occurred. This can also increase the inbreeding within the isolated populations and lead to deleterious alleles becoming more common. Humans have also greatly reduced the populations of the animals that the wolves depend on for prey. The most striking example of this is the near eradication of the bison of the plains. With their prey reduced the wolves were forced to find new areas to hunt or to turn to predation on livestock which leads to further conflict with humans. The reduced amount of suitable habitat and prey abundance reduces the number of wolves that can inhabit an area. This reduced population increases inbreeding and increases the effects of genetic drift.

Another way in which humans have affected the genetic makeup of wolves is through captive breeding programs. These programs are designed to conserve wolves but without proper genetic understanding they can alter the allele frequencies of wild populations in undesirable ways. In the captive Mexican wolves crossbreeding between the lineages was being considered to increase their genetic diversity for the MHC genes (Hedrick et al. 2000). Before performing this type of cross it is important to understand how the structuring arose and if the low amount of variation is natural. If the alleles arose in different locations as a response to different pathogens, then crossing populations could result in wolves that are poorly adapted to local environments and have a reduced fitness. A study of the related species the red wolf (*Canis rufus*) indicated that captivity could also have an effect upon the gene expression of individuals (Kennerly et al. 2008). While captive breeding programs will likely play a role

in the conservation of the grey wolf in the future we must be cautious about the genetic consequences of our good intentions.

When considering a conservation plan to preserve the genetic variation of the grey wolf the two main considerations are to ensure that migration can occur and that there is enough suitable habitat to maintain wolf populations at a level that limits inbreeding. Also reintroductions will most likely play a role in the future of the wolf in America. When determining the strategy for accomplishing this it is imperative to consider what we know about the genetic structure of wolves and to learn as much as possible to fill any gaps in our knowledge.

Migration is critical for the proper flow of genetic material in wild wolf populations. To prevent the effects of inbreeding it is important that there are migration routes between wolf populations. This means that in some areas wildlife bridges may need to be constructed over highways and other manmade obstacles to the movement of wolves. In extreme cases assisted migration may be necessary to move wolves past large areas of intense human activity. When planning the migration routes it is important to remember the effects of environmental conditions. Muñoz-Fuentes et al. (2009) and other researchers observed that ecological factors seemed to have a greater impact upon the genetic structure of wolf populations than did geographic distance. Because of this the migration routes planned out should link wolf populations that live in similar habitats rather than simply linking the closest populations. Likewise assisted migrations should seek to move wolves to a habitat similar to the one they were captured in.

Since wolves require large amounts of territory it is important to ensure that wolves have areas with large amounts of appropriate habitat to support the population. If the populations are maintained at a high enough level it will reduce inbreeding and the loss of alleles due to drift. Like when planning migration we must consider the effects of the environment upon the wolves when planning the areas to be used as habitat. If an area is inhabited by wolves who are adapted a forest habitat it would not be logical to set aside a large amount of land that is mostly open tundra with only a small amount of forest.

If it is considered advisable to reintroduce wolves to areas from which they have been eliminated, then we must take genetic factors into account to ensure the greatest chance of success. This too will depend largely upon the genetic structuring due to ecological conditions. When considering capturing wolves to be introduced to an area it is important to capture wolves from an area as similar to the intended release site as possible, even if this population is further away than one from a dissimilar environment.

As we go into the future the conservation of the grey wolf will continue to receive a lot of attention. The ecological benefits that wolves provide to an ecosystem will encourage some to preserve the current range and seek to expand it. Others will oppose the conservation efforts due to the wolf's predatory nature and the long held fear and hatred humans have had for the wolf. To truly conserve the species we must use all of our genetic and ecological knowledge, as well as educate people as to the wolf's role in the world.

Works Cited

- Anderson, T.M., vonHoldt, B.M., Candille, S.I., Musiani, M., Greco, C., Stahler, D.R., Smith, D.W., Padhukasahasram, B., Randi, E., Leonard, J.A., Bustamante, C.D., Ostrander, E.A., Tang, H., Wayne, R.K., Barsh, G.S. (2009) Molecular and Evolutionary History of Melanism in North American Gray Wolves. *Science* 323: 1339- 1343.
- Aspi, J., Roininen, E., Kiiskilä, J., Ruokonen, M. Kojola, I., Blijudnik, L. Danilov, P., Heikkinen, S., Pulliainen, E. (2009) Genetic Structure of the Northwestern Russian Wolf Populations and Gene Flow Between Russia and Finland. *Conservation Genetics* 10: 815-826.
- Hagenblad, J., Olsson, M., Parker, H.G., Ostrand, E.A., Ellegren, H. (2009) Population genomics of the inbred Scandinavian wolf. *Molecular Ecology* 18: 1341-1351.
- Hedrick, P. W., Lee, R. N., and Parker K. M. Major Histocompatibility Complex (MHC) Variation in the Endangered Mexican Wolf and Related Canids. *The Genetical Society of Great Britain* 85: 617-624.
- Kennerly, E., Ballmann, A., Martin, S., Wolfinger, S., Gregory, S., Stoskopf, M., Gibson, G. (2008) A gene expression signature of confinement in peripheral blood of red wolves (*Canis rufus*). *Molecular Ecology* 17: 2782- 2791.

MacNulty, R.D., Smith, D.W., Mech, D.L., and Eberly L.E. (2009) Body size and predatory performance in wolves: is bigger better? *Journal of Animal Ecology* 78: 532-539.

Muñoz-Fuentes, Darimont, C.T., Wayne, R.K., Paquet, P.C., and Leonard, J.A. (2009) Ecological factors drive differentiation in wolves from British Columbia. *Journal of Biogeography* 36: 1516-1531.

Post, E., Peterson, R.O., Stenseth, N.C., McLaren, B.E., (1999) Ecosystem consequences of wolf behavioral response to climate. *Nature* 401: 905-907.