

**Action:** Use Genetic Techniques to Monitor the Effectiveness of Wildlife Corridors

**Key Messages:**

- Genetic technologies allow for more non-invasive comprehensive analysis of corridors effectiveness.
- Genetic analysis provides conservationists with empirical data of wildlife using corridors while providing census information on the individuals crossing, reproductive success, and genetic admixture.
- Corridors facilitate reproductive success by increasing males' access to females.
- With genetic information, conservationists can better target areas in need of corridors to prevent inbreeding depression. Furthermore, genetics information reveals the change in genetic diversity of wildlife before corridors and after their introduction to monitor the effectiveness of the corridor.

**Background Information:** As human populations continue to grow, development expands into wild spaces which results in small, isolated patches of viable habitat. Small patches are unable to maintain large populations of wildlife and as animals attempt to migrate into new spaces, they encounter obstacles like major roadways. Many animals die attempting to cross these barriers and their deaths continue to lower the population size of species and the number of breeding adults. Additionally, decreased mobility and lowered carrying capacity cause populations to experience population decline. Without intervention, continually declining populations experience inbreeding and reduced gene flow which assists in population size reduction as well as causing populations to become more susceptible to catastrophic events that can cause extinction. This reinforcing cycle of population reduction and genetic diversity decline has been described as the extinction vortex which explains the importance of maintaining genetic diversity in animal populations (Frankham, 2005).

To ensure successful conservation practices, genetic diversity must be protected in wild populations. Genetic techniques can be used as a potential tool to monitor wildlife corridors to ensure genetic diversity is being maintained. Additionally, genetic tools can be applied to assist with monitoring the effectiveness of the corridor. Genetic analysis gives insight into information that cannot be gathered through standard observation methods, like what individuals are crossing and what is their reproductive success, which can be important information when studying the success of a corridor or when considering where to develop new corridors (Frankham, 2015).

**Supporting Evidence from Individual Studies**

1. A genetic analysis study conducted in 1999 looked at the genetic differentiation of the moor frog (*Rana arvalis*) throughout natural corridors established in the Drenthe and NoordBrabant provinces of the Netherlands (Arens, 2007). At the Drenthe study site, 232 samples were taken from two adjacent ponds while 208 samples were collected from the NoordBrabant pond sites. Through microsatellite analysis, researchers found that populations near corridors exhibited a higher level of polymorphism (11–61 alleles per locus compared to 5–12) and number of alleles per population was high given estimated population sizes. In addition to this finding, the study found that genetic differentiation

was small to moderate in the frog populations that had access to natural corridor spaces that allowed for gene flow. Even in cases with moderate gene flow, the frog populations contained high allele frequencies in comparison to their estimated population sizes.

2. A monitoring study conducted in four regions of the Swiss Plateau and northern Prealps of Switzerland used the genetic structure of the roe deer (*Capreolus capreolus*) populations to assess the ability of roe deer to use corridors of differing penetrability (Burkat, 2016). In the study, natural corridors were defined as elongated landscapes that bordered artificial spaces that could act as a barrier for wildlife movement and were classified in three groups: intact corridors that were highly permeable, impaired corridors which permitted minimal movement, or interrupted which were nearly impermeable and permitted the least movement. 1102 heart tissue samples from roe deer individuals obtained from hunters in the time between December 2004 and December 2005, Burkat et al identified that samples collected from areas near intact corridors had lowest  $F_{ST}$  values (mean  $F_{ST} = 0.008$ ), indicating high gene flow, while the least permeable corridor experienced low gene flow (mean  $F_{ST} = 0.022$ ,  $P \leq 0.05$ ). Although the study found low gene flow in impaired or interrupted corridors, the gene flow in these populations experienced less genetic differentiation than populations with no access to corridors.
3. A spatial study on the red-backed vole (*Clethrionomys gapperi*) and the deer mouse (*Peromyscus maniculatus*) in the Pend Oreille River drainage of northeastern Washington during 1985-1987 found that natural corridors enable the migration between populations of habitat specialists (Mech, 2001). The two species were chosen for this study because of their different dieting habits. While the deer mouse is considered a generalist, the red-backed vole is a specialist and the comparison of these two systems revealed information about how difference in foraging habits can influence corridor use. Blood samples were collected from 131 red-backed vole individuals and 76 deer mouse individuals. Genetic distance in the vole populations were highest in isolated populations ( $0.59 \pm 0.18$ ) and lowest in spaces connected by corridors ( $0.19 \pm 0.01$ ). Unlike the vole populations, deer mouse populations experienced a near zero genetic distance across all study areas. This comparison found that corridors have greater impact on diet specialists.
4. A randomized, controlled study in 2006-2008 in Banff National Park, Alberta, Canada found that grizzly (*Ursus arctos*) and black bears (*Ursus americanus*) along the Trans-Canada Highway use established overpass and underpass corridors to move through fragmented habitat and this movement has facilitated gene flow (Sawaya, 2014). DNA was collected from 1317 hair samples gathered from hair traps with an additional 6543 samples collected from bear tree rubs set up near, on, and around the corridors. Using 20 loci markers, 113 grizzly bears and 101 black bears were identified throughout the study with 15 grizzlies (eight males and seven females) and 17 black bears (nine males and eight females) were identified on the corridors. Through  $F_{ST}$  values revealed high gene flow in both bear populations that correlated with use of the underpasses and overpasses. Additionally, the study established that habitat fragmentation had little effect of genetic structure in grizzly bears but affected the population structure by gender as a result of sex-biased dispersal. Corridors mitigated this bias in dispersal which furthered reproductive success.

5. A before and after study of the Hume Freeway in Victoria, Australia found proper placement of canopy bridges aid gene flow and genetic diversity in the squirrel glider (*Petaurus norfolcensis*) before 2005–2007 and eight years after installation. 13 sites were established along the freeway where 399 tissue samples were extracted. The before genetic analysis revealed that the highway did not act as a significant barrier for the squirrel glider. There was no significant genetic differentiation observed or reduced gene flow between populations on either side of the freeway except in one site. The site which experience these hinderances exhibited increased gene flow with the installation of a canopy bridge.

### **Conclusions and Recommendations**

Corridors play a crucial role in reducing the harm caused by human created barriers on wildlife fragmentation and inbreeding depression by permitting movement of animals to allow gene flow (Corlatti, 2009). To obtain a holistic view of how wildlife is interacting with corridors or how corridors reducing population decline, genetic tools should be applied to monitoring techniques. Genetic analysis gives more comprehensive information about the effectiveness of corridors that can not be obtained with other monitoring methods. With the use of genetic technologies, conservationists can determine the effect of corridors on sex dispersal, reproductive success, and genetic diversity of populations surround the corridor. As the organization continues to grow, Saving Nature should look into the benefits of genetic analysis and consider how these techniques can improve the understanding of the consequences of established corridors.

### **Supporting Studies**

- Arens, Paul, et al. "Genetic population differentiation and connectivity among fragmented Moor frog (*Rana arvalis*) populations in The Netherlands." *Landscape Ecology* 22.10 (2007): 1489-1500.
- Burkart, Stephanie, et al. "Evaluating the functionality of expert-assessed wildlife corridors with genetic data from roe deer." *Basic and applied ecology* 17.1 (2016): 52-60.
- Mech, Stephen G., and James G. Hallett. "Evaluating the effectiveness of corridors: a genetic approach." *Conservation Biology* 15.2 (2001): 467-474.
- Sawaya, Michael A., Steven T. Kalinowski, and Anthony P. Clevenger. "Genetic connectivity for two bear species at wildlife crossing structures in Banff National Park." *Proceedings of the Royal Society B: Biological Sciences* 281.1780 (2014): 20131705.
- Soanes, Kylie, et al. "Evaluating the success of wildlife crossing structures using genetic approaches and an experimental design: lessons from a gliding mammal." *Journal of Applied Ecology* 55.1 (2018): 129-138.

### **References**

Corlatti, Luca, Klaus Hacklaender, and F. R. E. D. Y. FREY-ROOS. "Ability of wildlife overpasses to provide connectivity and prevent genetic isolation." *Conservation Biology* 23.3 (2009): 548-556.

Frankham, Richard. "Genetics and extinction." *Biological Conservation* 126 (2005): 131-140.

Frankham, Richard. "Genetic rescue of small inbred populations: Meta-analysis reveals large and consistent benefits of gene flow." *Molecular ecology* 24.11 (2015): 2610-2618.