Action: Creating corridors to influence biodiversity-- Impact on Genetic Variation

Key Messages:

- Ten studies assessed the impacts of man-made habitat corridors on genetic variation.
- Six of the ten studies found that corridors increase gene flow and genetic variation between fragmented populations.
- Two of the ten studies found that corridors are effective for maintaining gene flow between fragmented populations and preventing genetic isolation.
- Two of the ten studies found that genetic analysis is not a sufficient way to assess corridor effectiveness because of a lack of data and excess of confounding factors.
- Four of the ten studies followed before-and-after designs and three of the four concluded that corridors increase gene flow and genetic variation between fragmented populations.

Background information

With the increase in human population and development worldwide, habitat fragmentation, the breaking apart of continuous patches of habitat, is on the rise (Liu, He, and Wu 2016). Habitat fragmentation has detrimental effects on biodiversity, decreasing measures such as species richness, population abundance and distribution, and genetic diversity and increasing likelihood of species extinctions (Fahrig 2003). Habitat corridors, strips of habitat or passable landscape connecting otherwise isolated habitat fragments, have been proposed and implemented worldwide as a means of reconnecting isolated habitat patches and hopefully mitigating these issues (Mann and Plummer 1995).

In particular, this review focuses on the impact of habitat corridors on genetic variation. Small populations in fragmented habitats lose genetic variation, since they have a smaller gene pool and are more prone to inbreeding (Lacy 1997). Populations with low genetic variation have lowered resistance to disease and parasites, reduced ability to cope with environmental changes, decreased mean fitness, and increased susceptibility to extinction (Lacy 1997). Thus, the goal of this review is to determine whether man-made habitat corridors are an effective means of ensuring or re-establishing genetic variation in populations isolated by habitat fragmentation.

Supporting Evidence From Individual Studies

1. A study conducted in 2006-2008 in Banff National Park in Alberta, Canada (Sawaya, Kalinowski, and Clevenger 2014) found that wildlife crossing structures allow for maintenance of genetic connectivity in grizzly (*Ursus arctos*) and black bear (*Ursus americanus*) populations. Researchers used bear traps, hair rubs, and DNA samples from bear management actions (capture, mortality, etc.) to generate genetic data and compared it to data collected from greater bear populations. Data indicated a genetic discontinuity at the highway for grizzly bears but not for black bears. Parentage tests showed that 47% of black bears and 27% of grizzly bears successfully bred across crossing structures. Gene flow was documented by showing migration, reproduction, and genetic admixture across the wildlife crossings. Thus, researchers determined that crossing structures allow sufficient gene flow to prevent genetic isolation of fragmented populations.
2. A review conducted in 2009 of the effectiveness of wildlife overpasses to provide connectivity and prevent genetic isolation in population patches isolated by road construction (Corlatti,

Hacklander, and Frey-Roos 2009) found that there is no evidence that overpasses do or do not effectively address genetic issues. This conclusion was based on the fact that a minimum number of individuals is required to assure gene flow and the need to consider demographic parameters of subpopulations, which are lacking in most studies.

3. A study conducted in 1997-2000 in Donaghy's Corridor in Queensland, Australia (Paetkau, Vazquez-Dominguez, Tucker and Mortiz 2009) used genetic analysis to verify long-distance movements across a planted corridor in the Cape York Rat (*Rattus leucopus*) and Bush Rat (*Rattus fuscipes*) populations. Genetic data was collected with ear clippings from mice captured in trapping grids. The first genetic samples were taken in the final year of corridor planting and compared to samples taken over the next 2 years to evaluate levels of population interchange. Because 16 long-distance movements were documented through the genetic analysis, researchers concluded that the planted corridor increased gene flow and genetic variation between the isolated rat populations.
4. A before-and-after study conducted in 2005-2013 in Victoria, Australia (Soanes et al. 2017) found that, while the Hume Freeway is not a complete genetic barrier, installation of crossing structures mitigated site-level gene flow disruptions in squirrel glider (*Petaurus norfolcensis*) populations. Researchers conducted trapping surveys to collect genetic material from squirrel gliders at 13 sites, including mitigated, unmitigated, vegetated median, and non-freeway areas, before and after crossing structures were installed. Using trapping and radiotracking techniques, the researchers identified first-generation migrants and parentage of trapped individuals. This data indicated unrestricted gene flow across the road at all sites except for one. At the impacted site, installation of the crossing structure increased gene flow and restored it to unimpaired levels within 5 years, suggesting that crossing structures may be an effective site-specific intervention to increase gene flow and genetic variation.
5. A study conducted in 2002 at Savannah River Site in South Carolina on Common Buckeye butterflies (*Junonia coenia*) (Wells et al. 2009) found that planted corridors likely increase gene flow and promote genetic variation in the population. Butterflies were collected from experimental patches, dissected to determine gender, and analyzed for genetic information at nine enzyme sites. Higher levels of genetic variation were observed in connected patches than unconnected patches, suggesting that increased dispersal between populations influences their genetic structure and that habitat connectivity established via corridors increases gene flow and genetic variation.
6. A study conducted in 2008-2009 in New York City, New York (Munshi-South 2012) found that white-footed mouse (*Peromyscus leucopus*) population migration and gene flow rates are associated with percentage of connectivity through tree canopy cover. Trapping surveys were conducted at 15 sites across NYC, and tail snips were collected for genetic analysis. All individuals were genotyped at 18 unlinked loci to examine genetic differentiation and migration between urban populations. Researchers concluded that connectivity based on percent tree canopy cover effectively predicted gene flow in the white-footed mice, indicating that more connected areas have more genetic variation.
7. A study conducted in 1998-2010 in the Huron-Erie Corridor (HEC) in the Great Lakes Region (Haponski and Stepien 2014) found that the HEC helped maintain connectivity and genetic

diversity in walleye fish (*Sander vitreus*) populations. Walleye fin clips were collected from seven HEC spawning groups and genotyped at nine unlinked loci to compare genetic diversity and gene flow. Genetic diversity among samples across the HEC was relatively similar, suggesting that, despite habitat degradation and pollution, HEC serves as an effective corridor connecting walleye subpopulations.

8. A before-and-after study conducted in 2011-2014 in Monongahela National Forest in West Virginia (Wood, Welsh, and Petty 2018) found that culvert restoration efforts increased migration and genetic variation of Brook Trout (*Salvelinus fontinalis*) populations. Brook Trout were collected at 14 locations in the Shavers Fork watershed via backpack electrofishing and taken for tissue sampling. Genetic diversity at impassable sites was first compared to genetic diversity at passable sites and later compared to diversity at the same impassable sites after restoration. Researchers found that there was not a significant loss of genetic diversity at impassable sites, which may be due to large enough population size on either side to prevent genetic drift. However, researchers also concluded that restored culverts were sites of increased numbers of first generation migrants, indicating their effectiveness in facilitating gene flow between isolated populations.
9. A before-and-after study conducted in 2008-2011 in the Lolo Creek Watershed in western Montana (Neville and Peterson 2014) found that genetic tools were not a reliable measure of detecting movement of cutthroat trout (*Oncorhynchus clarkii*) in restored culverts. Researchers identified sample sites that were initially barriers for trout passage and gathered tissue samples from trout before and after restoring or replacing the impaired culverts. After comparing the results from various types of genetic analyses, researchers found many factors like family structure, presence of siblings and hybrids, and low sample size that complicated use of genetic tools for making these kinds of assessments. Thus, researchers concluded that using genetic tools to evaluate corridor effectiveness is too complex and co-dependent to be reliable.
10. A before-and-after experimental study conducted in 1993-1994 in Valdres, Norway (Aars and Rolf 1999) found that constructed corridors facilitated transfer of root voles (*Microtus oeconomus*) between experimentally fragmented habitat patches. Researchers constructed six 50m-long corridors connecting six pairs of fragmented habitat and compared their results to that of six other control pairs of fragmented habitat not connected by a corridor. The rate of transfer of individuals between patches and the resultant degree of heterozygosity was monitored with capture-recapture methodology and genotyping via toe clippings. While male transfer between patches was high in populations with and without corridors, corridor populations saw a significant increase in female transfer. Increasing female transfer led to increased heterozygosity and genetic variation in connected versus unconnected populations.

Conclusions and Recommendations

Conclusions from the above papers overwhelmingly suggest that habitat corridors are an effective means of maintaining or increasing gene flow and genetic variation between fragmented populations. While two studies concluded that genetic analysis is not an effective means of assessing corridor success overall, they were hindered by inadequate population sizes to provide statistical significance or an abundance of confounding factors. However, three controlled before-and-after studies showed that corridors caused a statistically significant increase in gene flow and genetic variation. These before-and-after studies were supported by three others indicating that corridors increase genetic variation and two others indicating that corridors effectively maintain gene flow and genetic variation. All but one of the studies supporting the use of corridors analyzed their use by mammals, suggesting that corridors may be most useful in facilitating gene flow for mammalian species. Overall, this review indicates that the use of man-made habitat corridors is effective for maintaining or increasing gene flow and genetic variation between fragmented populations.

Supporting Studies

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