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*Model calibration with empirical data*

*While all parameter values are selected to simulate natural populations, input values and parameters need to be adjusted and calibrated to accurately reflect real-life scenarios. With that in mind, we compared the simulations to two known populations: banner-tailed kangaroo rats restricted to a 1 km area in southeastern Arizona and moose on Isle Royale. These two wild populations were selected with a matched-pairs concept in mind, so that the two species are similar in several life history traits (restricted in area and access to limited corridors between populations; are diploid, sexually reproducing mammals; are herbivores; reach maturity at 1 year old; and are solitary animals) but vary in generation time. As such, simulations will be compared to empirical data to correctly calibrate simulation parameters, and values will be altered to maintain a more accurate representation of wild populations.*

*We expect that the results of migration on the population – fitness, inbreeding, lifetime reproductive success, heterozygosity and FST – will not necessarily change independently, but in tandem. For example, an increased frequency and intensity of migration will have a longer sustained benefit in population wide diversity as compared to little, irregular, or no migration events. We estimate that the average loss of genetic diversity occurs at a rate of 1/2N, in which N is the size of the diploid population, so that smaller populations have the greatest risk. In that same way, if one migrant is introduced into the population compared to five migrants in that same generation, the focal population with fewer migrants will have lower overall fitness benefits, higher inbreeding coefficients, and lower heterozygosity and allele frequencies.*

*We will also evaluate our model for insight into using migration as a predictive metric of population extirpation. We will specifically compare the predictive utility of migration of individuals with high and low fitness to examine population viability. We hope these analyses will add utility to on-going efforts to identify conservation need in wild populations and determining if translocation with selective migrants allows the population to maintain diversity for a longer duration.*

The heterozygosity of the focal population remained largely unchanged following the stochastic population decline in connected populations, however there was an approximately 20% decline in heterozygosity following the stochastic population decline in a population without immigration, with little further change as the population size increased (Figure 2). In populations where there was no population connectivity until habitat was restored, management intervention increased the genetic diversity in the focal population more than if there was no assisted gene flow (Figure 3). Adding 100 individuals into the population increased genetic diversity quickly, but steadily declined to below the ideal one migrant per generation level after the 350 year period (Figure 3A). Surprisingly, adding 25 individuals in four migration events did not have the same effect as adding the same number of individuals at once, with the overall heterozygosity slowly decreasing after translocation events (Figure 3B). When simulating adding a corridor so that one migrant per generation could enter the population, the population’s heterozygosity increased incrementally over time, suggesting additional adaptive potential in this population (Figure 3C).

The timing of translocation events resulted in a slightly higher increase in overall heterozygosity in the immediate years following translocations when introduced when the population size is small, with the long-term trajectory of such changes being largely the same (Figure 4).

When two populations have similarly high starting genetic diversity, the heterozygosity will remain high when the populations are connected (Figure 5A). When the focal population’s starting genetic diversity is low, the heterozygosity will increase with migration events, with a greater increase in heterozygosity when the source population’s starting diversity is high (Figure 5A). However, having unconnected populations with high starting genetic diversity will have approximately 40% greater heterozygosity over time than having two connected populations that have low starting genetic diversity. In the same situations, the focal and source populations will diverge slower in highly diverse populations whether connected or not than in a focal population with low genetic diversity; a lowly diverse focal population will have a 2-fold and 3-fold higher FST when the source population has a low and high starting genetic diversity, respectively (Figure 5B).

Adding migrants into the population resulted in increased proportion of migrant alleles, resulting in approximately 40% migrant ancestry in constantly connected populations, 30% migrant ancestry when introducing 100 individuals once, and 20-30% migrant ancestry when introducing 25 individuals four times and when restoring the habitat with a corridor (Figure 6). In all cases, random genetic drift resulted in increased FST of the focal population as compared to the founding initialized focal population in a similar rate among migration rates, but with a greater effect when the stochastic population decline is greater (Figure 7A). Divergence from the source population increased when there was no migration, but the populations became more similar, and FST decreased, when migration occurred. The FST compared to the source population increased by approximately 50% when populations were not connected and decreased by approximately 50% when connected with one migrant per generation, with assisted migrations resulting in measures between these two ranges of FST (Figure 7B).

The average lifetime and relative reproductive success of the population was similar (LRS = 1.4) when the population size was stable but decreased as the population decreased and then increased when the population increased. As the population goes through a greater decrease in population size, the lifetime reproductive success of the individuals in the population must be greater to result in a population with the same carrying capacity (i.e., the maximum LRS = 2 in a vulnerable population but maximum LRS = 2.5 in an endangered population with the population is increasing; Figure 8).

*Additional things that my model can do that I didn’t do here (can implement in epiABM if desired):  
Preferentially choose migrants as mates – put in SI of this paper maybe?  
Parents have a higher chance of breeding with higher combined heterozygosity (natural selection)  
Enact higher fitness consequences when population density is low  
Have conserved (coding) SNPs in both populations that if get a mutation, can be lethal  
Instead of random migrants, select migrants based on heterozygosity [or something else]*

*SI FIGURES/RESULTS TO MAKE  
All the same figs, but in the other IUCN categories  
Ne vs Nc measures?  
migrant vs nonmig LRS – need to figure out how to define how many generations removed from a migrant parent is considered a “migrant” or “native” for this calculation*

For example, it is possible that immigrants provide a temporary boost in genetic diversity to small, inbred populations but that many of these new alleles, which may not be beneficial in the local environment, are lost from the population in a few generations. Alternatively, the influx of new alleles may persist in the new populations, particularly when small populations grow quickly, providing a lasting pool of genetic variants.

REMOVED FIGURES

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Figure 2. Change in population demography measures with one migrant entering the population per generation in populations of various conservation rankings over time. (A) Proportion of alleles with migrant ancestry. (B) Observed heterozygosity of putatively neutral SNPs. (C) Fst as compared to the initialized focal population. (D) Fst as compared to the initialized source population.

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Figure 3. Change in population demography measures in the absence of population connectivity with populations of various conservation rankings over time. (A) Population size. (B) Observed heterozygosity of putatively neutral SNPs. (C) Fst as compared to the initialized focal population. (D) Fst as compared to the initialized source population.

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Figure 1. Population size over time. Total number of individuals when a population goes through vulnerable (red), threatened (blue), and endangered (green) stochastic population declines.

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Figure 2. Best and worst case scenarios of genetic diversity during population subdivision. Heterozygosity over time when populations are connected via one migrant per generation (teal) and when populations are not connected (burnt red).

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Figure 3. Increase in genetic diversity with assisted migration strategies. (A) Heterozygosity when adding 100 indv after habitat quality is restored (y = 151). (B) Heterozygosity when adding 25 indv four times after habitat quality is restored (y = 151, 165, 181, 195). (C) Heterozygosity when restoring the habitat via a corridor so that one migrant per generation can enter the population from year 151 on. (D) Averages of all 5 runs of the different migration rates depicted in panels A-C following habitat restoration.

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Figure 4. Average change in genetic diversity with varying migration rates and implementation times. Purple and pink lines depict the same migration rates (adding 100 indv once and 25 indv four times, respectively) during habitat restoration at the low population size (bright colors) and following restoration so that the population is permitted to grow (pastel colors).

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Figure 5. Change in population demographics over time with different staring allele frequencies (0.05 ≤ p ≤ 0.15 or 0.40 ≤ p ≤ 0.50) in both populations when there is one migrant per generation. (A) Heterozygosity over time with varying starting allele frequencies. (B) FST over time with varying starting allele frequencies. Black lines depict average change over time with no migrants.

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Figure 6. Average proportion of migrant introduced SNPs following assisted migration events.

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Figure 7. FST over time following assisted migration events. (A) Divergence of the focal population from the founding, initialized population over time. (B) Divergence of the focal and source populations following various translocation events.

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Figure 8. Average lifetime reproductive success over time.

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SI Figure 1. The effect of having migrants preferentially chosen during sexual selection with zero migrants, one migrant per generation, and one migrant per generation following corridor construction. (A) Heterozygosity. (B) FST as compared to the initialized focal population. (C) FST as compared to the source population. (D) Proportion of migrant SNPs in the population. (E) Sex ratio. (F) FIS. (G) Average lifetime reproductive success. (H) points for LRS (to show that there is one indv that is skewing the RRS). (I) Relative lifetime reproductive success where the denominator is the individual with the greatest LRS in that run.