

Management of subdivided populations subject to conservation programs using genomic information

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Summary

The main objective in conservation programs is to maximize the global genetic diversity while restricting the levels of inbreeding. This can be achieved by using the Optimal Contribution method (OC). Most populations of endangered species or breeds are subdivided into different breeding groups. To cope with this, OC methodology was extended to optimally manage subdivided populations, originally using pedigree-based coancestries. This method determines the optimal contribution of each individual to the next generation to maximize the global genetic diversity while balancing the relative levels of coancestry between and within subpopulations. In the context of single population management, it has been proven that the use of marker-based coancestries could lead to a more efficient management. However, different molecular estimators have different effects on the genetic diversity maintained and in the evolution of the allelic frequencies. In this simulation study we tested the different outcomes from OC performed using different genomic coancestry matrices computed using over 50,000 SNPs. Two genomic matrices estimated were evaluated: i) the matrix describing the excess in the observed number of alleles shared by two individuals relative to the expected number under Hardy-Weinberg equilibrium ($\Theta_{L\&H}$); ii) the genomic relationship matrix obtained using method 2 described by VanRaden (Θ_{VR2}). Both $\Theta_{L\&H}$ and Θ_{VR2} depend on allele frequencies of the base population but in the case of a subdivided population, it is unclear which frequencies should be used. We compared two approaches: i) using initial frequencies in the global population; and ii) using the average initial frequencies of the subpopulations involved in the calculation of each particular coancestry. The consequences of using these coancestry matrices (as well as the pedigree-based coancestry matrix, Θ_{PED}) in the management of a subdivided population during ten discrete generations were evaluated in terms of the global levels of genetic diversity maintained (either expected heterozygosity or allelic diversity), its distribution within- and between-subpopulations, the trajectory of allele frequencies and the migration flow between subpopulations. Allelic diversity was measured as the percentage of loci that continued segregating at a given generation. The use of $\Theta_{L\&H}$, giving an appropriate weight to the coancestry within-subpopulation, led to the highest values of global and within-subpopulations expected heterozygosity, lower inbreeding levels and a similar allelic diversity than the use of Θ_{PED} or Θ_{VR2} . In general, computing the genomic coancestry matrices using subpopulations allele frequencies instead of the global frequencies led to lower values of global and within-subpopulations expected heterozygosity and higher inbreeding levels.

Keywords: optimal contribution, subdivided populations, genomic coancestry