

Effective population size when applying optimal contributions based on genomic coancestry matrices

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Abstract

Effective population size (N_e) is a key parameter in conservation genetics. In population management, there is a consensus that the Optimal Contribution (OC) method maximizes N_e and minimizes the loss of genetic variability. This method optimizes the contribution of parents to the next generation by minimizing the global coancestry between potential parents weighted by their contributions. Thus, the coancestry matrix is a key element in OC. Given the current availability of genomic resources such as high-density single nucleotide polymorphism (SNP) arrays, genomic coancestry matrices have replaced the pedigree-based coancestry in OC. However, different genomic coancestry matrices have been proposed, and the consequences of using them in OC on the N_e achieved is unknown. The objective of this study was to evaluate, through stochastic simulations, the N_e obtained when optimizing contributions using different genomic coancestry matrices across 10 generations. The coancestry matrices compared included those described by Li and Horvitz (θ_{LH1} , θ_{LH2}), VanRaden (θ_{VR1} , θ_{VR2}) and Yang and colleagues (θ_{YA1} , θ_{YA2}). Population N_e was obtained from rates of true Identity-By-Descent (IBD) coancestry (N_{e_f}) and inbreeding (N_{e_F}). True IBD values for coancestry and inbreeding were obtained by simulating 10,000 multiallelic loci with unique alleles for each individual in the base population. Across replicates, coefficients of variation were lower for N_{e_f} than for N_{e_F} . Also N_{e_F} was very erratic across generations indicating that is advisable to compute N_e from the rate of coancestry. The optimization of contributions resulted in different N_{e_f} values depending on the genomic coancestry matrix employed. At generation 10, the highest N_{e_f} was achieved when using θ_{YA2} , followed closely by θ_{VR2} . The lowest N_{e_f} was achieved when using θ_{LH2} . With this matrix, N_{e_f} was about a quarter of that obtained when using θ_{YA2} . Thus, this study highlights the importance of choosing appropriate genomic coancestry measures when managing conservation programs.

Keywords: effective population size; optimal contributions; genomic coancestry, genomic inbreeding.