ASSESSMENT OF EFFECTIVE POPULATION SIZE USING MOLECULAR MARKERS

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Effective population size (*e N*) is a parameter of central importance in population genetics. *e N* of an actual population is defined as the size of an ideal (Wright-Fisher) population having the same rate of inbreeding as the actual population. Although *e N* plays a predominant role in many applications of population genetics, it is 'notoriously difficult to estimate' (Wang, 2005). Approaches for the estimation of *e N* can be classified as follows:
1 Retrospective pedigree-based approaches;
2 Approaches based on demographic population parameters;
3 Molecular approaches;
3.1 Single-locus – multiple generation approaches based on variability of allele frequencies;
3.2 Multi-locus – single generation approaches based on linkage disequilibrium;
After a short review of some methodological issues we will present results comparing different markerbased approaches to estimate current and past effective population size. Results are based on microsatellite genotypes in a limited number of chromosome segments and on whole genome SNP genotypes, respectively. It will be demonstrated that a substantial amount of genomic information is required to receive a sufficiently reliable estimate of *e N* . The SNP-based estimation of *e N* was studied in two experimental strains. It worked well in a New Hampshire population where sufficient genetic variability was maintained, while the same approach failed in a White Leghorn strain with significantly reduced genetic variability and extended linkage disequilibrium blocks. Based on these findings, general recommendations on the usefulness of marker-based approaches to the estimation of effective population size are made.