

Marker-based estimation of effective population size from one-generation population samples

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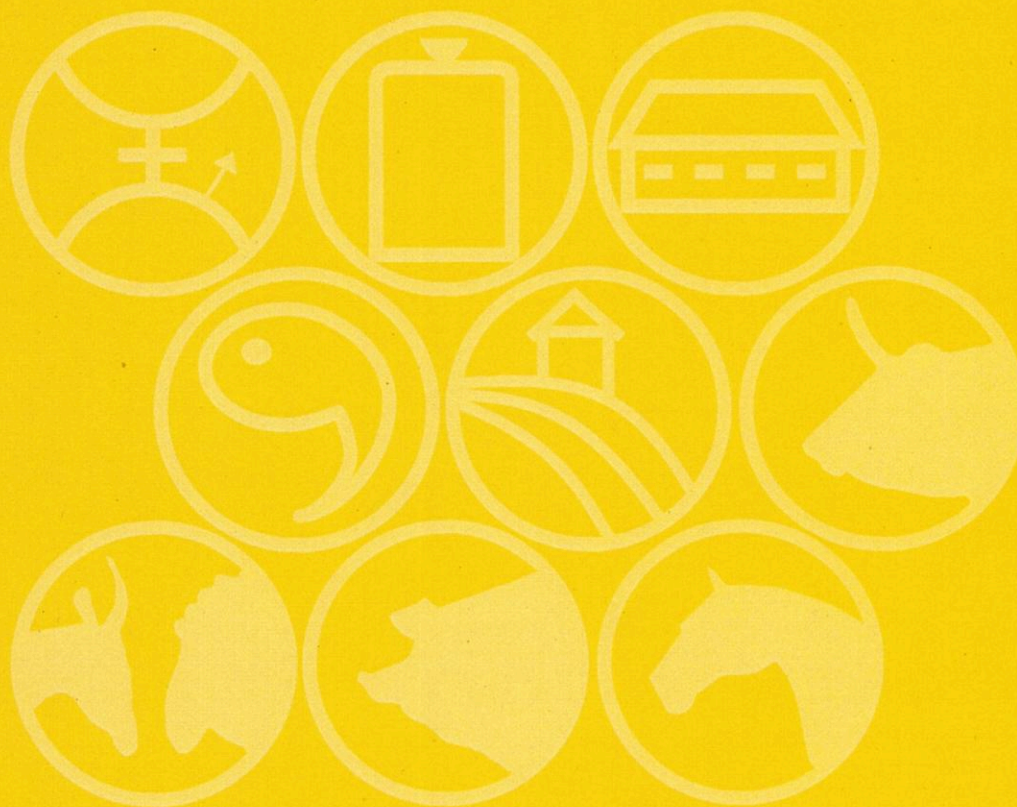
Effective population size N_e is a parameter of central importance in decision-making for and design of conservation strategies. However, N_e is notoriously difficult to estimate and both pedigree-based and demographic approaches lack robustness. Estimation of N_e from chromosome segment homozygosity (CSH) based on marker genotypes in one generation population samples was applied to 2 commercial and 3 experimental chicken strains, in which 75 individuals were genotyped for 30 microsatellites in 6 segments. Marker-based estimates of N_e are substantially lower than the pedigree-based values (7 to 10 generations). This is due to a substantial excess of observed over expected CSH. It is argued, that historic events (e.g. bottlenecks) may have a sustaining effect on the genetic constitution of the lines, which may not be detectable from recent pedigree information. Based on the empirical results we derive the amount of molecular information required for a sufficient statistical resolution. Approximately 7500 SNPs are necessary to discriminate between two populations differing in N_e by 20%, (5% error probability, 90% power, 2-sided test). Since molecular tools providing this amount of information are within reach, the marker-based assessment of effective population size will be a useful option in the near future.

Design and implementation of an information system for national genebanks management

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A long-term storage of genetic materials is essential in each country. In order to manage a large number of samples from different species in animal agriculture, a general data model must be considered and implemented. This paper presents an approach for the development of a sample management information system at the country level. Designed as client/server architecture, our information system is a platform independent web application based on open source software packages. As a result, the developed information system provides for information management of national genebanks. It allows users to record the origin of genetic material, keep track of samples along with the storage places, and make analyses reports. The software is freely available under the Open Source GNU public license.

**Book of Abstracts of the 59th
Annual Meeting of the European
Association for Animal Production**



**Book of abstracts No. 14 (2008)
Vilnius, Lithuania
24-27 August 2008**