

Management of Populations under Biodiversity Aspects

Eildert Groeneveld*

The impact of breed extinction on biodiversity is all too obvious. Within breed loss of biodiversity is much less spectacular and does not get the attention it deserves. Therefore, also the management of small but also numerically large population needs to consider issues around genetic variability. A first step in managing populations efficiently is to have an up to date information on the population's status. This is particularly important in herdbook type situations, where individual herds and breeding decisions determine the population dynamics.

Thus, in breeding populations the following information should be readily available:

- structural information on the population like number of males and females used in the population, the number of matings they are involved in, the family sizes and the age classes of breeding animals.
- pedigree related information like level of inbreeding of various classes of animals, the rate of change of inbreeding, derived quantities like effective population sizes. On this same level additive genetic relationships could also be used which has certain advantages.
- all pedigree derived quantities rely heavily on their correctness. However, often parts of the pedigrees are not known. To be able to assess the value of the pedigree related information relies on knowing details about the completeness of the pedigree itself.

For most breeding programs, in particular of the cooperative kind, these information are not available. This makes efficient planning of sire usage and the effects on inbreeding unduly difficult.

What can and needs to be done? Firstly, all persons in charge of breeding programs need to be aware that they might have a problem here. They ought to know their sire usage, the contribution of individual sires to the next generation and the effect that this may have on inbreeding and thereby on the loss of genetic variability within the population. Knowing one's shortcomings is a first step to remedy the situation.

*Institute of Farm Animal Genetics, Mariensee, Germany

Secondly, research can address the issue by developing procedures of reporting these statistics for data collected in breeding programs. Furthermore, it will also be useful to develop management procedures which lead managers of populations through the process of specifying and analyzing an intended population structure (e.g. number of males and females and their usage in breeding) and its effect on expected rates of inbreeding.

One attempt to address the real time reporting issue has been developed by us through the Population and the Pedigree report. Both reports are designed as stand alone batch applications that run against an APIIS database picking up those breeds that are stored in the database. No preprocessing or data selection is required, i.e. the report generation is completely self contained and automatic.

The procedure falls into two parts. In the first step all numerical values are generated and, where required, stored in temporary tables in the database. This is done in Perl using standard SQL to query the database. In the second step, the final reports are type set using \LaTeX for high quality output. This step merges predefined explanatory text, outlining the problem and giving the computational procedures and formulae for each of the statistics and the final data. Furthermore, all data is also exported to comma separated files, so that they can be processed at liberty after the report has been generated by whatever the user chooses.

The reports are implemented using different software at different levels. Firstly, the actual values are computed using standard SQL scripts that run on the database itself

- textual high quality output
- output for further processing (database table, csv files)

These reports generate a large number of statistics that can be the basis for further and more detailed breeding work.

Alternatively or additionally, breeds can be managed by introducing a reporting infra structure that is used to generate the essential information for matings. Here, again the number of males used is of critical importance. Also, the representation of sires in the next generation should not be left to individual decisions of single breeders. This is not a popular decision to take, but nonetheless essential in effective genetic management.