Genetic Diversity in Dutch Cattle Breeds (MRY and FH)

Student: Myrthe van Eijndhoven (840123218090)
Supervisors: Ir. P. Oliehoek (WUR) and Ir. S.J. Hiemstra (CGN)

Introduction
In the second half of the last century genetic progress and extreme emphasis on high production led to big changes in the structure of the Dutch cattle population. Intensive use of a relatively small group of highly selected sires and dams became possible with use of Artificial Insemination (AI) and Embryo Transfer (ET). Another remarkable aspect was the introgression of the Holstein-Friesian (HF) breed, imported from USA and Canada into the Dutch dairy cattle population in the early 1970’s (Braake et al., 1994). Consequently, these developments in cattle farming had a negative influence on the development of population size, composition and genetic diversity of local breeds, such as the Meuse- Rhine- and Yssel (MRY) and Dutch Frisian (FH) cattle (Oldenbroek, 1999). For both conservation of breeds and development of sustainable livestock production, maintenance of genetic diversity is an essential aspect.

In the present study, changes in population demographics and genetic diversity from 1970 until 2005 are analyzed for both MRY- and FH- cattle breed populations. Furthermore, tools for the analysis of genetic diversity are used to optimise the cryoconservation of genetic FH-founder material from the current population.

Material and methods
In total 4,446,561 MRY- and 7,318,522 FH- purebred and crossbred animals were registered till 2006. In order to analyse trends in numbers of purebreds and crossbreds over the years, a demographic analysis is performed including animals born from 1970 until 2005. Within this analysis various subpopulations are distinguished specified respectively by the percentage of MRY- or FH-genes in the individual animals.

The amount of genetic diversity within the MRY- and FH- breeds is analysed by estimating the average coefficient of inbreeding (\( \overline{F} \)), the average coancestry (\( \overline{mk} \)), and the founder genome equivalence (\( f_g \)) for the animals in the study populations (Balou and Lacy, 1995; Falconer and Mackay, 1996). To exclude the genetic diversity contributed by other sources than the actual MRY- or FH- populations only information from purebred animals is used. The modified algorithm of Colleau is used to compute the \( \overline{F} \) and \( \overline{mk} \) for each reference population (defined as animals born within each year from 1970 till 2005) (Sargolzaei el al., 2005; CFC, 2006). The \( f_g \) then could be obtained by \( f_g = 1/2 \overline{mk} \) (Caballero and Toro, 2000).

To optimise the cryoconservation of FH founders, genetically important individuals are selected from the population by minimizing the average coancestry using two different methods within the GENCONT program (Meuwissen, 2002). The first method assessed the optimal genetic contribution of all potential candidates (i.e. % of offspring per candidate), while in the second approach the number of animals to be selected was fixed with an expected equal number of offspring.

Results
The trends in number of MRY- and FH- offspring born are shown in graphs 1 (MRY) and 2 (FH) for various subpopulations. These graphs clearly show a decrease in number of animals born over the last one (crossbreds) to two (purebreds) decades. Within both breeds a relatively sharp increase in the number of crossbred animals is recognized from the late seventies. Only 899 FH- and 3454 MRY-purebred calves were registered in 2005 which is a reduction of almost 100% since 1980.
Graph 1 and Graph 2 show the total number of registered animals born per breed per year from 1970 to 2005, specified for the percentage of MRY- or FH-genes respectively.

We found that the estimated $\overline{F}$ of animals born in 2005 is 0.027 for MRY and 0.049 for FH, while the $\overline{mk}$ of animals born in 2005 is estimated at 0.034 for MRY and 0.027 for FH. This corresponds with a $f_g$ for the FH population (18.6) is estimated higher then the $f_g$ for the MRY population (13.6) born in 2005, while generally the $f_g$ has decreased over the years (Graph 3). The estimated $f_g$ of the current FH-population, also including the animals within the current genebank collection, is 19.1. The $f_g$ of the next FH-generation could theoretically be maximised to 84.2 by following the results of the optimal genetic contribution method in which 125 males and 157 females were selected from the current population including genebank material.

**Discussion and conclusion**

Generally it can be concluded that both populations have decreased in size, as well as in genetic diversity (variation). However, the calculated potential $f_g$ illustrates that this variation in the FH-population can be increased in the next generation by proper utilisation of available genetic material through aimed selection and mating.

Note that the pedigrees of both breeds contain gaps, qualifying animals with unknown parents as founders. Therefore, the $\overline{F}$ and $\overline{mk}$ could be underestimated and the $f_g$ overestimated. On the other hand, unregistered animals which were not included in this study could contain unique genetic material.


Oldenbroek, J.K., 1999 *Genebanks and the Conservation of Farm Animal Genetic Resources*. DLO Institute for Animal Science and Health, Lelystad, The Netherlands