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INBREEDING ASPECTS IN RABBIT BREEDING

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ABSTRACT

In the course of this study pedigree analysis of the Pannon White rabbit breed was performed for the period 1992-2014. The inbreeding level of the population was determined. Besides, effective population size characterizing the genetic variability of the population and the pedigree completeness were also calculated.

Key words: inbreeding, Pannon White, rabbit populations, genetic variability

INTRODUCTION

Genetic variability determines the ability to respond to environmental variations and changes in the breeding goal (De Rochambeau et al., 2000). In case of a successful breeding program, genetic variability of important traits is essential for the breeder's point of view (Groeneveld et al., 2010). Meuwissen (2009) summarized the most relevant problems in connection with genetic diversity and highlighted that, the greatest challenge is to feed the growing human population (9 billion people by 2050). He also mentioned, that only a few companies create new breeds which are highly productive. However, these breeds are able to create economic values and displace the well-adapted local breeds. This fact may sound risky, since breeds in intensive meat production usually have genetic problems such as higher mortality, lower fecundity, slower growth, developmental defects, reduced fitness and stress tolerance (Allendorf and Leary, 1986; Darwin, 1868; Falconer, 1989; Ledig, 1986; Lerner, 1954; Wright, 1977) -but with this perspective- other breeding alternatives will no longer be available. Kaposvár University is one of the rabbit breeding centers in the past 30 years in central Europe. Pannon White rabbit -bred by the university- Based on crossing experiments Pannon White breed had superior performance of Dressing Out percentage compared to other intensive rabbit hybrids (Matics et al. 2014).

The aim of the study was to examine the effects of intensive selection on the population structure and inbreeding in the Pannon White breed.

MATERIALS AND METHODS

Animals and experimental design

The analysis consisted of pedigree data of 8170 animals in the nucleus born between 1992 and 2014, 22 generations of selection by kindling batch were taken into account in the calculation- in Kaposvár University and the following parameters were calculated by ENDOG 4.8 (Gutierrez and Goyache, 2005):

- Pedigree completeness as the sum over all known ancestors of the terms computed as the sum of (1/2)n where n is the number of generations separating the individual to each known ancestor
- Wright's inbreeding coefficient (Wright, 1922)

$$Fx = \sum \left[\left(\frac{1}{2}\right)^{n_1 + n_2 + 1} (1 + F_A) \right]$$

Where F_x is the inbreeding coefficient of the animal in question; n_1 , n_2 represent the number of generations between the sire and dam respectively and their common ancestor; F_A is the inbreeding coefficient of the common ancestor.

• Wright's inbreeding coefficient based on 4 generations (F_4)

$$\Delta F = \frac{F_{t-1}F_{t-1}}{1 - F_{t-1}}$$

Where ΔF is the rate of inbreeding per generation; F_t and F_t -1 are the average inbreeding at the i^{th} generation.

• Effective population size (Ne)

$$Ne = \frac{1}{2\Delta F}$$

F_4 was calculated in order to detect inbreeding in recent generations.

RESULTS AND DISCUSSION

Inbreeding coefficients of bucks and does in the reference population born between 2010 and 2014 were summarized in Table 1. The realized effective population size (Gutiérrez et al., 2008, 2009) was constant in recent years (81, 75, 80, 76, 78). According to these results, genetic variance was preserved in the Pannon White breed.

| Year | F* | Ν | Mean | S.D. | Min | Max |
|------|-----|-----|------|------|------|------|
| 2010 | F | 195 | 8.55 | 3.25 | 3.12 | 31.1 |
| | F_4 | 195 | 2.26 | 4.13 | 0.00 | 25.6 |
| 2011 | F | 249 | 9.83 | 3.91 | 3.53 | 31.9 |
| | F_4 | 249 | 2.91 | 4.13 | 0.00 | 26.6 |
| 2012 | F | 255 | 9.91 | 2.00 | 5.71 | 21.9 |
| | F_4 | 255 | 2.23 | 1.96 | 0.00 | 14.1 |
| 2013 | F | 276 | 11.1 | 2.64 | 7.63 | 32.0 |
| | F_4 | 276 | 2.21 | 2.85 | 0.00 | 25.8 |
| 2014 | F | 253 | 11.5 | 1.72 | 8.58 | 18.9 |
| | F_4 | 253 | 1.75 | 1.79 | 0.00 | 9.57 |

Table 1: Descriptive statistics of the Pannon White rabbit's inbreeding coefficients

F*: Type of inbreeding coefficient; F: Wright's inbreeding coefficient; F_4: Wright's inbreeding coefficient based on 4 generations

As expected, pedigree completeness and Wright's inbreeding coefficient were strongly correlated and can be described with complete generation equivalent (CGE) (Leroy, 2011). Inbreeding coefficients for the total population were presented in Figure 1.



Figure 1: Inbreeding trend (F) according to pedigree completeness (CGE)

Animals with longer and more complete pedigree data had higher inbreeding coefficients than rabbits with short or incomplete pedigree. Nagy et al. (2010) summarised the results of horse, cattle, pig and rabbit populations and proved, that populations with higher pedigree completeness have increased inbreeding. In case of correcting the effects of pedigree in rabbit and pig breeds, animal models were completed with CGE. (Farkas et al., 2007; Nagy et al., 2013). Despite the reproductive characteristics of the rabbit (multiparous with short generation interval), it is an ideal specie for pedigree analysis. Many studies focused on the population structure of the rabbit consequently in Hungary however, there are only a few foreign studies available. Kerdiles and Rochambeau (2002) and Ragab et al. (2015) examined the population structure of French and Spanish hybrid lines, founded before the Pannon White. The longer period of selection in these lines than in the Pannon White breed, resulted in higher inbreeding in both lines, Inbreeding coefficient was 20-25% in French lines after 20 generations, but Spanish lines had higher values (25-31% after 36 and 41 generations of selection). In Pannon White, inbreeding rate after 20 generations was only 11.5%.

Differences with the Pannon White were also influenced by other factors. The nucleus population of the breed consists on 100 does and 60 bucks. French lines operate with fewer bucks (100 does with 28 bucks, 60 does with 17 bucks). Unfortunately, there is no information about the doe-buck ratio in Spanish lines. In French lines, effective population size was also described by the rate of inbreeding, and family-size variance (Hill, 1979). The two different method showed identical results and the effective population sizes were 37 and 50 (Kerdiles and Rochambeau, 2002). In Spanish lines, effective population size was calculated from the rate of inbreeding and by the number of male and female breeding animals (ranged between 53 and 60).

Martín et al. (2016) examined the population structure of a local breed from Ibiza, the ibicenco, where primary function of the breed was to serve the local market. The pedigree completeness of this rabbit breed is slight, it has only 3.4 complete generations. By comparison, rate of inbreeding is quite high (mean value: 10.8%) which could be explained with the excessively small population size (9.6). Martín et al. (2016) used a totally different calculation method for the effective population size, the authors took into account the different levels of pedigree completeness and standardised the consanguinity coefficients. This method is described in detail by Cervantes et al. (2014). Pannon white has larger effective population size compared to Spanish and French rabbit lines and the angora breed (varied between 37-91), however direct comparisons of them should be treated carefully due to the different calculation methods. Comparative studies for the effective population size were obtained on dog, sheep and cattle breeds (Leroy et al., 2013) where correlation coefficients between methods for computing Ne varied from negligible (0.09) to strong (0.74). Nagy et al. (2010) used methods based on family-size variance and inbreeding rate in order to determine effective population size. However, sometimes, calculations based on the rate of inbreeding gave no results (when inbreeding rate

decreases). In contrast, the realised effective population size showed great stability, since the breed has long and complete pedigree tracked back to many generations (Gutiérrez et al., 2009).

CONCLUSIONS

It can be concluded, that the effective population size exceeded the minimum recommended (FAO, 2012) population size (50-100), in order to maintain genetic variability.

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