Pedigree-based genetic diversity of Debrecen White rabbit

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Abstract: This research was carried out to evaluate the pedigree data of the Debrecen White rabbit breed. Pedigree information was supplied by the Debrecen White Rabbit Breeder Association. The final dataset contained all available information on animals registered by the breeding association up to 2023. The reference population was the active breeding stock in 2023. The estimated complete generation equivalent was 7.8, while the mean of maximum generations was 16.29 for the present stock. All individuals within the current population were inbred, with a 5.37% mean inbreeding coefficient. The division of the inbreeding coefficient showed that homozygosity is increasing in the current population. The genetic conservation index (GCI) was higher than 30 for 10.11% for the total population, and was above 38.69% for the current population.

Keywords: genetic variability; inbreeding; pedigree analysis

The Debrecen White rabbit, similar to other Hungarian rabbit breeds, is bred for meat production. This medium-sized breed can be used for production in intensive systems as well as backyard conditions. To avoid the mating of close relatives, a circular mating system is used during breeding, with five lines in the population. In addition to effective selection for meat production, the maintenance of genetic variability is also important. An understanding of genetic structure and information about genetic variability is important for commercial breeds as well as for breeds under gene conservation.

The avoidance of inbreeding and inbreeding load is crucial for commercial breeds due to the risk of the homozygosity of harmful genes due to strong selection (Nagy and Nguyen 2023).

Weigel (2001) suggests minimizing the genetic relationships between selected individuals to maintain long-term genetic diversity and to include optimal contribution theory in commercial breeding programs. Szoke et al. (2004) concluded that the rotational mating system preserves genetic variability. Sorensen et al. (2005) revealed that selection can result in the depletion of genetic diversity and decrease the effective population size in very large populations (e.g. Danish Holstein, Danish Jersey, and Danish Red). Rogic et al. (2022) also reported the importance of achieving a balance between genetic improvement and conservation in horse breeding. The authors suggest ensuring the optimal contribution of stallion lines and mare families as well as monitoring the level of inbreeding.

De la Rosa et al. (2016) recommend equivalent effective population size mating for genetic management based on their research on the Ibicenco rabbit breed. Sakhtivel et al. (2018) emphasised the monitoring of homozygosity when checking the inbreeding level and average relatedness (AR) coefficients to avoid possible fitness and production trait problems. Rahim et al. (2023), in their study of a German Angora rabbit population, concluded that increasing the inbreeding level and reducing the effective population size is expected to have a negative effect on population and genetic variability.

The objective of the current work was to analyse the pedigree data of the Debrecen White rabbit breed. We focused on the estimation of pedigree quality, inbreeding, and genetic variability. The results may be included in breeding programs and could be used for the long-term maintenance of the breed.

MATERIAL AND METHODS

Raw pedigree data were provided by the Debrecen White Rabbit Breeder Association. The final dataset contained the pedigree records of individuals registered by the breeding association up to 2023. The current breeding population is at one central farm for breeding and production and there are 50 smallholder stocks for production. The individual ID, sire, dam, birthdate, and sex data were stored for each rabbit in the database. The final database contained the pedigree data of 30 523 animals. The reference population was chosen as the active breeding stock (bucks and does) with progeny in the year of 2023.

The dataset was checked for duplicates and bisexual animals using the Pedigree Viewer v6.5 software (Armidale, Australia) (Kinghorn 1994) before the analysis. The evaluation of the pedigree was conducted using the Endog v4.8 software (Madrid, Spain) (Gutierrez and Goyache 2005). The various estimations of inbreeding level were calculated using Grain v2.2 software (Grain Intelligence Inc., Wien, Austria) (Doekes et al. 2020).

The population was described with the following parameters:

Equivalent complete generations (GenEqu), number of complete generations (GenCom) and maximum number of generations (GenMax) (Maignel et al. 1996).

Generation intervals (James 1977) were predicted for all parent–offspring pathways: sire-to-buck, sire-to-doe, dam-to-buck, and dam-to-doe. A pairwise comparison of the different pathways was carried out using the independent samples t-test.

Number of founders (Nf), number of ancestors (Na), effective number of founders (fe) and effective number of ancestors (fa) (Boichard et al. 1997).

The inbreeding of the population was characterized in various ways. In addition to the classical Wright method (F_{Wright}) (Wright 1922), ancestral inbreeding coefficients were calculated following Ballou (1997) (F_{Ballou}), Kalinowski et al. (2000) (F_{Kal} and $F_{\mathrm{Kal\_new}}$), and Baumung et al. (2015) (A_{HC}). AR was also computed (Colleau 2002).

Effective population size (Ne) (Goyache et al. 2003) was estimated using the individual increase in inbreeding (Ne_{f}), as well as based on the regression (Ne_{reg}) and log-regression (Ne_{log}) for equivalent generations (Colleau 2002).

The genetic conservation index (GCI) was estimated following Alderson's (1992) formula to check the assumption as to whether the ideal individual would receive equal contributions from all founder ancestors in the population.

RESULTS AND DISCUSSION

The basic indexes calculated for the total and the active population can be seen in Table 1. The highest value for the maximum number of generations was 20, and 51 animals belonged to this class. The average complete generations for the current breeding stock was close to four, and it was six for six rabbits. The complete generation

Table 1. Pedigree completeness for Debrecen White breed

Parameter	Total population	Reference population
N	30 523	641
GenEqu	3.81	7.80
GenCom	2.08	3.92
GenMax	7.65	16.29

GenCom = number of complete generations; GenEqu = equivalent complete generations; GenMax = maximum number of generations; N = number of rabbits

equivalent was almost two times greater for the total population, as well as in the case of the active breeding animals compared to the number of complete generations. The number of complete generations and the complete generation equivalent was lower than reported for the total populations of German Angora (Rahim et al. 2023) and New Zealand white rabbits (Sakhtivel et al. 2018).

The number of ancestors and number of founders were changed from 2 211 to 58 and from 2 194 to 204 (Table 2). The *fe* and *fa* values were much lower for the present breeding stock, whilst their ratios were quite similar and reported a huge bottleneck effect in the population during the breeding history. Our estimated fe value for the reference population exceeded the values reported by Sakhtivel et al. (2018) and Rahim et al. (2023), while the estimated fa value was quite close to their estimations. Because of this, the bottleneck effect affected the Debrecen White population more intensively than their breeding populations. This also emphasizes the fact that more attention needs to be paid to maintaining genetic variability during the selection process for this breed.

Table 2 shows the estimated genetic variability for the total and the active breeding populations. Here, 2 211 ancestors covered the variability

Table 2. Contribution to genetic variability for Debrecen White breed

Parameter	Total population	Reference population
Nf	2 194	204
Na	2 211	58
fe	169	50
fa	77	15
fa/fe	0.46	0.30

fa = effective number of ancestors; *fe* = effective number of founders; *Na* = number of ancestors; *Nf* = number of founders

of the total population, but only 58 for the active population. The concentration of genetic variability is very significant in case of the reference population (Table 3).

The 10 most important ancestors in terms of their contribution to genetic diversity are shown in Table 4. These 10 ancestors covered almost 30% of the genetic variability in the case of the total population, and around 71% for the present breeding stock. Astonishingly, the most important second and third ancestors contributed almost the same percentage of genetic variability (4.4%) for the total population, whilst the influence per individual of the first three ancestors was above 10% for the reference population.

The generation intervals are presented in Table 5. The independent samples *t*-test was used to make a pairwise comparison of the four different pathways. The sire-to-offspring pathways were found to be the longest compared to the dam-to-offspring pathways. The ages of the sires at the birth of their progenies were almost double those calculated for dams. Our values for sire pathways were longer than those estimated by Sakhtivel et al. (2018), whereas our estimations for dam-to-buck and dam-to-doe pathways were longer compared to their results. Longer generation intervals were reported by Rahim et al. (2023) for dam-to-offspring pathways than our findings.

Table 3. Concentration of genetic variability for Debrecen White breed

Parameter	Total population	Reference population
fa_{50}	39	6
fa_{60}	65	7
fa_{70}	104	10
fa_{80}	187	14
fa_{90}	444	21
fa_{100}	2 211	58

$fa_{50...100}$ = number of ancestors contributing 50%...100% of genetic variability in the population

Table 4. Ancestral contribution to the gene pool for Debrecen White breed (%)

Ancestor	Total population	Reference population
1st	5.04	12.06
2nd	4.42	10.61
3rd	4.40	10.00
First 10	29.61	71.23

Table 5. Estimated generation intervals from various parent-offspring pathways (years)

Parent – offspring pathways	N	Mean	Standard error
Sire-to-buck	348	1.65[a]	0.053
Sire-to-doe	3 898	1.69[a]	0.016
Dam-to-buck	362	0.88[b]	0.024
Dam-to-doe	4 006	0.87[b]	0.007
Average	8 616	1.27	0.009

[a,b]Different superscripts show significant difference ($P < 0.05$); N = number of rabbits

Table 6 gives an overview of the homozygosity of the Debrecen White rabbit. The inbreeding coefficients were estimated in several different ways. The classical Wright inbreeding coefficient was lower than 2.0% for the total population, and was estimated to be approximately 5.4% in the case of the active breeding stock. The estimated ancestral inbreeding coefficients will help to answer the question as to whether inbreeding occurred in the past or is currently happening. The recent inbreeding (F_{Kal_new}) result was higher than that of ancestral inbreeding (F_{Kal}) for the total and also for the active breeding stocks; thus, it can be concluded that the observed homozygosity did not originate from the past, but has occurred more recently. This may be the reason for the huge bottleneck effect that influenced the breed in the 2010s and also the loss of pedigree information for several breeding animals from this period. Low inbreeding values are important to maintain genetic variability. Though the present results may have been affected by the pedigree quality, they do seem to be acceptable at the current level. The average level of inbreeding in the active breeding population was higher than was estimated for the total population. Both the current and the total population had lower average inbreeding levels than those estimated by Sakhtivel et al. (2018) for New Zealand White and Rahim et al. (2023) for German Angora rabbits. The average AR value was greater than the classical inbreeding (Wright) coefficient in the case of the total population, so it could be concluded that the mating of related individuals occurred in this population. This tendency was the same for the reference population, although the ratio was smaller. Due to rotational mating, closely related rabbits are not mated to each other, but the mating of distantly related individuals also seems to be quite frequent in the current breeding population. The risks associated with increased

Table 6. Homozygosity of Debrecen White breed

Parameter	Total population	Reference population
Inbred animals (%)	59.7	100.0
AR	1.91	4.39
F_{Wright}	1.73	5.37
F_{Ballou}	2.95	11.17
F_{Kal}	0.42	1.66
F_{Kal_new}	1.31	3.71
A_{HC}	3.19	12.19
Ne_f	61.1	53.4
Ne_{reg}	1 490.1	156.5
Ne_{log}	1 467.8	168.5

A_{HC} = ancestral history coefficient; AR = average relatedness; F_{Ballou} = the probability that any allele in an individual has been homozygous in previous generations at least once; F_{Kal} = identical alleles were inbred in the past; F_{Kal_new} = identical alleles were inbred in recent generations; F_{Wright} = inbreeding coefficient calculated using the Wright method; Ne_f = effective population size computed using individual increase in inbreeding; Ne_{log} = effective population size computed based on the log-regression on equivalent generations; Ne_{reg} = effective population size computed using the regression on equivalent generations

Table 7. Distribution of individuals based on the genetic conversation index

GCI	Total population		Reference population	
	N	*N* (%)	*N*	*N* (%)
10.00 or less	19 549	64.05	8	1.25
10.01 to 20.00	3 971	13.01	174	27.15
20.01 to 30.00	3 918	12.84	211	32.92
30.01 to 40.00	2 335	7.65	181	28.24
40.01 or more	750	2.46	67	10.45
Average	30 523	11.23	641	26.87

GCI = genetic conversation index; *N* = number of rabbits

inbreeding may become apparent in subsequent generations. The separation of the classical inbreeding coefficient, following Kalinowski decomposition, suggests an increase in inbreeding in the current population, and the current fixation of alleles is becoming more frequent. Based on our results, applying the mating and selection strategy used for small populations (selecting more males than it is usual for commercial breeds) might help to keep inbreeding low.

In addition to inbreeding, an effective population size is also an important parameter in the long-term monitoring of a population. Table 6 presents the predicted *Ne* values, which were estimated in several ways. Debrecen White is a conventional breed for meat production, so the contribution of possible breeding candidates to the creation of the next generation is not equal. This will result in a smaller effective population size than the real size of the population. The effective population size estimated using inbreeding (Ne_f) was quite small both for the total and the reference populations. There were huge differences for other parameters between the total population and the reference breeding stock. All numbers were greater than 50, so the genetic variability of the active Debrecen White rabbit stock might be enough for the maintenance of the breed. Our numbers showed more favorable genetic variability within the breed compared to German Angora (Rahim et al. 2023) and New Zealand White rabbits (Sakhtivel et al. 2018), but were lower compared to Posta et al.'s (2024) findings for the Pannon White rabbit breed.

The maximum GCI was 49.67 for the total population. There were five animals in the total population, whereas only a single rabbit was found with this value in the active population (Table 7). The GCI was higher than 30 for more than 10% for the total population, whilst it was close to 40% for the reference population. The estimated average GCI for the total population was 11.23, which is lower than that predicted by Rahim et al. (2023). The estimated GCI was 26.87 for the current breeding population.

CONCLUSION

This study showed that the Debrecen White breed has experienced reasonable genetic loss. The current level of classical inbreeding could be the result of the present fixation of alleles in the active breeding stock and not because of fixation in the past. The estimated inbreeding coefficients should be taken into account during the selection of Debrecen White rabbits. Nevertheless, in order to understand the real homozygosity of the breeding stock, evaluations based on single nucleotide polymorphism (SNP)-chip analysis may also be recommended.

Conflict of interest

The authors declare no conflict of interest.

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