

Pedigree based description of the Pannon White rabbit

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HIGHLIGHTS

- Pannon White rabbit has a deep and reliable pedigree.
- There was bottleneck effect during breed history.
- Most of alleles were already fixed during breed history.

ARTICLE INFO

Keywords:

Pannon White
Genealogical information
Genetic diversity

ABSTRACT

The aims of the current research were to evaluate the quality of the pedigree, generation interval, gene origin, inbreeding, and effective population size of the current Pannon White rabbit breeding population. The pedigree information was supplied by the experimental farm of the Hungarian University of Agriculture and Life Sciences, who is responsible for the maintenance of the Pannon White rabbit breed. The studbook data of the registered animals up to 2022 were analysed. The active population in 2022 was chosen as the reference population for the current study. The complete generation equivalent was 12.11 whereas the average maximum generations was 39.15 for the reference population. All animals of the breeding stock were inbred, the average Wright's inbreeding coefficient was 12.52 %. Kalinowski's decomposition of inbreeding showed that inbreeding is originated mainly from the past. The proportion of rabbits having more than 30 GCI was above 30.02 % for the total population, whereas it was above 36.45 % for the reference population.

1. Introduction

The main purpose in the Hungarian rabbit breeding, as in other European countries as well, is meat production. Besides the effective selection program, the breeding program also requires the maintenance of genetic variability, the prevention from over-use of some lines/animals during the mating program.

The pedigree analysis has become an important tool in recent years for the description of genetic variability of livestock breeds, especially for horses (e.g. Bokor et al., 2013; Klein et al., 2022), cattle (Baumung and Sölkner, 2002; Gutiérrez et al., 2003) and other species (Goyache et al., 2003; Krupa et al., 2015; Ács et al., 2019; Nguyen et al., 2023) were also studied. Surprisingly, only a few studies worked with rabbits. Sakthivel et al. (2018) gave information about genetic structure of a New-Zealand White population, whereas Rahim et al. (2023) reported about the genetic diversity of the German Angora rabbit. A similar

analysis was carried out for the Pannon White breed around 10 generations before (Nagy et al., 2010). The received information could be used not only for maintaining of genetic variance but could be basis of further analysis of inbreeding effect on performance traits (Curik et al., 2020).

The aims of the current research were to evaluate the quality of the pedigree, generation interval, gene origin, inbreeding, and effective population size of the current Pannon White rabbit breeding population.

2. Materials and methods

The pedigree information was supplied by the experimental farm of the Hungarian University of Agriculture and Life Sciences, who is responsible for the maintenance of the Pannon White rabbit breed. The studbook data of the registered animals up to 2022 were analysed. The genealogical information was traced back from present rabbits back to

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<https://doi.org/10.1016/j.livsci.2024.105460>

Received 10 January 2024; Received in revised form 29 February 2024; Accepted 27 March 2024

Available online 28 March 2024

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the founder animals. The following information was stored for each animal in the database: ID of the individual, ID of the sire and ID of the dam, birth date and sex. There were the pedigree data of 301,278 animals in the developed database. The active population contained bucks and does having progeny in the year of 2022 were chosen as reference population for Pannon White breed.

The pedigree analysis was carried out using Endog v4.8 software (Gutiérrez and Goyache, 2005). Before the analysis, the database was checked by the Pedigree Viewer v6.5 (Kinghorn, 1994). The distinct measurements for inbreeding were estimated using Grain v2.2 (Doekes et al., 2020) software.

The following parameters were used to describe the populations:

Equivalent complete generations (GenEqu) was computed 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. The number of complete generations (GenCom) was the furthest generation where all ancestors of the individual are known. The maximum number of generations (GenMax) was the number of generations separating the individual from its furthest ancestor (Maignel et al., 1996).

Generation Interval (GI) was computed as the average age of the parents at the birth of their offspring kept for reproduction (James, 1977). Generation intervals were estimated on four different pathways separately in this study: sire-to-daughter, sire-to-son, dam-to-daughter, and dam-to-son ways. The four pathways were compared pairwise for each using independent samples *t*-test.

Number of founders (Nf) was defined as the number of animals with unknown parents (Bokor et al., 2013). Number of ancestors (Na) was the minimum number of individuals in the pedigree, which explains the total genetic variability in the reference population (Bokor et al., 2013). Effective number of founders (fe) was calculated as the number of equally contributing founders that would be expected to produce the same genetic diversity as in the population under study (Boichard et al., 1997). Effective number of ancestors (fa) was the marginal contributions of ancestors that would be expected to produce the same genetic diversity as in the population under study (Boichard et al., 1997).

The inbreeding coefficient was calculated firstly using the Wright method (F_{Wright}), which means the probability that the two alleles at any locus in an individual are identical by descent (Wright, 1922). The probability that any allele in an individual has been homozygous in previous generations at least once was also computed (F_{Ballou}) (Ballou, 1997). The Kalinowski method represents that part of the genome where alleles are currently in identical by descent status and have also been identical by descent in an ancestor of the animal at least once. The inbreeding coefficient was split into two parts following the method of Kalinowski et al. (2000), whether identical alleles were inbred in the past (F_{Kal}) or became inbred in recent generations (F_{Kal_new}). Ancestral History Coefficient (AHC) quantifies the frequency that a randomly taken allele has undergone identical by descent status in the past (Baumung et al., 2015). Average relatedness was the probability that a randomly drawn allele from the population, belongs to a given individual (Colleau, 2002).

Effective population size (Ne) shows the number of breeding rabbits that would lead to the same increase in inbreeding, as observed in the population under study, if they would contribute equally to the next generation (Goyache et al., 2003). This parameter was calculated in several different ways: based on the individual increase in inbreeding (Ne_f), computed using the regression on equivalent generations (Ne_{reg}), and based on the log-regression on equivalent generations (Ne_{log}) (Colleau, 2002).

Genetic conservation index (GCI; Alderson, 1992) was also calculated for all the individuals in the pedigree. The index was computed from the genetic contributions of all the identified founders as $GCI = 1/\sum p_i^2$ where p_i is the proportion of genes of founder i in the pedigree of an animal. The Alderson's (1992) index is based on the assumption that the ideal individual would receive equal contributions from all the

founder ancestors in the population. Based on this assumption, the higher the GCI value the higher the values of an animal for conservation (Alderson, 1992).

3. Results

Fig. 1 represents the average pedigree completeness for the pedigree depth of 1 to 6 generations by birth year for the Pannon White breed. The values after 2015 are not reported as the pedigree is closed and they had reached 100 %. The average pedigree completeness for animals born within the last 10 years: from 1 to 6 generations deep = 100 %.

Table 1 shows the main indexes estimated for the total as well as the reference population. The more deep and complex pedigree information allows the precise results due to less unknown ancestors. This is important, as e.g. the estimation of inbreeding strongly depends on the pedigree quality (Farkas et al., 2007). The maximum number of generations was the highest (47 generations) for 21 animals. The mean number of complete generations was above 12 for the reference populations and it was 15 for 44 rabbits. Due to the long breeding history, the complete generations equivalent was high both for the total population and especial for the reference animals.

The genetic variability of the reference populations also presented in Table 1. Number of founders and number of ancestors were decreased from 850 to 177 and from 529 to 149, respectively. The fe and fa values were slightly decreased for the reference population whereas their ration was quite similar and shows that the population was affected by bottleneck effect.

The 10 most influential ancestors' contribution to the genetic variability can be seen in Table 1. These 10 ancestors accounted for nearly 41 % of the genetic diversity for the total population and approximately 45 % for the reference stock. Surprisingly, the most important and the 2nd ancestor covered the same amount of genetic diversity: 5.93 % within the total population and 7.56 % within the reference population.

The genetic variability of the total and the reference populations also shown in Table 1. The total population could be described with 529, whereas the active population with only 149 individuals. The covering of the genetic variability was quite similar for Na50, Na60 and Na70, respectively. The tendencies of these numbers are in agreement with the previously presented numbers in this table.

The estimated generation intervals are shown in Table 2. The four pathways were compared and were found to be significantly different ($P < 0.05$), using independent samples *t*-test. It was the longest for the buck-to-daughter pathway whereas it was the shortest for the doe-to-son pathway.

The current breeding populations were always quite small, so mating of related rabbits could not be avoidable during a long-time breeding history. Computation of ancestral inbreeding coefficients could provide information that alleles identical by descent for the first time or were already homozygous. Table 3 summarizes the inbreeding information of the breed.

The inbreeding was calculated in several various ways. Ancestral inbreeding coefficients were also estimated to determine if inbreeding was happening presently or in the past. The Wright inbreeding coefficient was below 8.00 % for the total population and around 12.5 % for the current breeding stock. The Ballou's ancestral inbreeding coefficient and the A_{HC} were higher than it is usual, especially the A_{HC}. The estimated F_{Kal_new} values were smaller than F_{Kal} for the total as well as for the reference populations, so inbreeding originated mostly from the past.

The effective population size is important during the maintenance of the breed. As the Pannon White rabbit breed has a closed studbook, there is the risk of the increasing of the average inbreeding year-by-year. Table 3 gives information about the Ne, which was estimated in three different ways. Due to the unequal contribution of the breeding individuals to the next generation, the effective population size is always smaller compared to the exact population size. The effective population

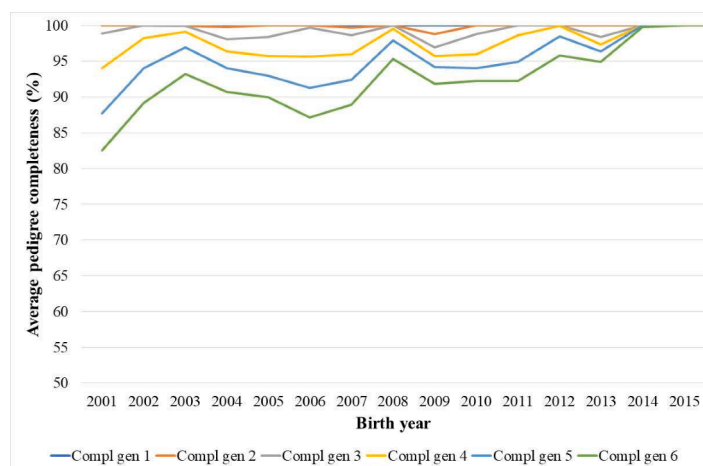


Fig. 1. Average pedigree completeness for 1 to 6 generations.

Table 1

Demographic parameters of the population.

	Total population	Reference population
N	301,278	952
GenEqu	13.01	21.56
GenCom	6.82	12.11
GenMax	24.49	39.15
Nf	850	177
Na	529	149
Na50	14	13
Na60	19	18
Na70	26	25
Na80	37	33
Na90	55	48
fe	50	44
fa	40	34
fa/fe	0.80	0.77
1st ancestor	5.93	7.56
2nd ancestor	5.93	7.56
3rd ancestor	4.60	5.84
first 10 ancestors	40.52	44.62

Nf: number of founders, Na: number of ancestors, Na50...Na90: number of ancestors contributing 50%...90 % of genetic variability in the population, fe: effective number of founders, fa: effective number of ancestors.

Table 2

Estimated generation intervals in years.

	N	Mean	Standard error of mean
Buck-to-son	3890	1.20 ^b	0.0099
Buck-to-daughter	11,432	1.25 ^a	0.0060
Doe-to-son	3914	0.95 ^d	0.0084
Doe-to-daughter	11,477	0.98 ^c	0.0048
Average	30,713	1.11	0.0034

Different superscript letters show significant difference ($P < 0.05$).

size based on inbreeding (N_e) was smaller for the total as well as for the reference populations, while other parameters were quite similar.

The distribution of the genetic conversation index (GCI) is shown in Table 4. The maximum GCI was 50.05 for the total population (9 animals) and 40.83 for the reference population (1 animal). The proportion of rabbits having more than 30 GCI was above 30.02 % for the total population, whereas it was above 36.45 % for the reference population.

4. Discussion

The pedigree completeness was more deep and complete in our case than it was reported for New Zealand White rabbit (Sakhtivel et al.,

Table 3

Inbreeding and effective population size in the population.

	Total population	Reference population
Inbred animals (%)	93.02	100.00
AR	5.51	6.70
F _{Wright}	7.98	12.52
F _{Ballou}	36.08	66.77
F _{Kal}	5.44	11.19
F _{Kal_new}	2.54	1.33
A _{HC}	59.78	140.17
N _{e_f}	98.31	78.72
N _{e_reg}	115.06	90.36
N _{e_log}	115.17	87.10

AR: average relatedness, F_{Wright}: inbreeding coefficient calculated using the Wright method, 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, A_{HC}: ancestral history coefficient, N_{e_f}: effective population size computed using individual increase in inbreeding, N_{e_reg}: effective population size computed using the regression on equivalent generations, (N_{e_reg}), N_{e_log}: effective population size computed based on the log-regression on equivalent generations.

Table 4

Frequency distribution of rabbits on their genetic conversation index (GCI).

GCI	Total population		Reference population	
	N	N%	N	N%
10.01 or less	89,081	29.57 %	332	34.87 %
10.01 to 20.00	65,998	21.91 %	0	0.00 %
20.01 to 30.00	55,739	18.50 %	273	28.68 %
30.01 to 40.00	53,155	17.64 %	48	5.04 %
40.01 or more	37,305	12.38 %	299	31.41 %

2018) and German Angora rabbit (Rahim et al., 2023). The deep pedigree allows reliable estimations of the further parameters.

Sakhtivel et al. (2018) and Rahim et al. (2023) reported smaller values for number of founders and ancestors as well as for fa and fe values. These differences might be also the result of the smaller initial breeding stocks. In our study, the fe/fa ratios were higher for the total as well as for the reference populations compared to their results. This could also strengthen that they had to pay more attention to the maintenance of genetic variability than it was necessary for the Pannon White breed.

Ther concentration of the genetic variability slightly decreased compared to Nagy et al. (2010). The contribution of the 10 main ancestors to the genetic variability also decreased since Nagy et al. (2010)

study, so maintenance of genetic variability seems to be successful during the selection of the Pannon White rabbit in the last few years. The tendency from fa50 up to fa90 were similar for the total and reference populations, the difference was found for fa100 which was more than three times higher for the total population.

As it was expected, the buck pathways were longer than doe pathways. The buck pathways are smaller, whereas the doe pathways are slightly longer than it was previously reported by Nagy et al. (2010) for the same breed. Surprisingly, Sakhtivel et al. (2018) and Rahim et al. (2023) reported longer generation intervals than it was found in our research. The reason might be their smaller populations. For small populations, longer generation intervals might help to reduce annual increase of inbreeding, though the response to selection might also decrease. The average generation interval also shortened compared to Nagy et al. (2010), which might result higher genetic progress in the current population.

The low amount of inbreeding is very important to maintain the genetic variability. Higher inbreeding was found for the total population than it was reported by Nagy et al. (2010). The inbreeding of the reference population was much higher, its average is equal to the volume of half-siblings' matings to each other. The average inbreeding of the total population was in agreement with that of reported for German Angora rabbit (Rahim et al., 2023) whereas the inbreeding of the reference population was higher. Sakhtivel et al. (2018) reported higher inbreeding for New-Zealand White rabbit compared to our results. The AR value was much higher than half of the Wright coefficient, for the total population, so there was mating of related individuals. This ratio differed for the reference population, so it seems, mating of close relatives were less frequent in the present breeding stock. The Kalinowski decomposition of inbreeding suggest inbreeding mostly originated from the past, current fixation of alleles is lower, especially for the reference population. The F_{Ballou} value was much higher for the reference population and was quite similar to Ács et al. (2019) findings for dogs, but exceeded the values reported by Ballou (1997) for 25 different mammalian populations and Klein et al. (2022) for horses.

The effective population size estimated from the inbreeding, was smaller than those of estimated based on the (log-)regression on equivalent complete generations. All numbers were higher than 50, so maintenance of genetic diversity seems to be solved in the current Pannon White rabbit breeding stock. However, these numbers were below 100, the risk of decrease in fitness traits might arise. Our estimations were higher than those of reported by Rahim et al. (2023) and Sakhtivel et al. (2018) for German Angora and New-Zealand White rabbit, respectively. Our estimations for the reference population were in agreement with findings for horses (Klein et al., 2022) and similar or higher than it was reported for several pig populations (Krupa et al., 2015; Nguyen et al., 2023). Interestingly, Ács et al. (2019) reported reasonably higher numbers for dogs compared to our findings.

The GCI is mainly important for genetic conservation programs, to keep as much alleles in the population as it is possible. It might be also interesting for a commercial breed to maintain the genetic variability. The higher GCI value indicates the importance of an animal from conservation point of view, so taking into account this number during the selection work might be suggested to keep the variability of the breed. The computed values were higher than it was reported by Rahim et al. (2023) and Sakhtivel et al. (2018). The reason of our higher values might be due to the longer pedigree and the selection work carried out during the breeding history.

5. Conclusions

The average value of equivalent complete generations allows the estimation of reliable pedigree-based population genetic parameters for the Pannon White rabbit population. The breed had a bottleneck effect. Most of the current inbreeding coefficient was the result of previously fixed alleles for the recent breeding stock. The present study wants to

make an emphasis on the importance of pedigree analysis and maintain genetic variability not only for breeds for genetic conservation but also for commercial livestock populations. The calculated inbreeding coefficients might be included in the breeding value estimation system of the Pannon White breed to improve phenotypic merit of the breed. To understand the real inbreeding of the population, application of SNP-chip and comparison to our recent results might be favourable.

CRedit authorship contribution statement

János Posta: Methodology, Formal analysis, Conceptualization, Writing – original draft. **Zs. Matics:** Conceptualization, Data curation, Writing – original draft. **Zs. Gerencsér:** Conceptualization, Data curation, Writing – original draft.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

Janos Posta reports financial support was provided by Hungarian Academy of Sciences. Janos Posta reports financial support was provided by The Ministry for Culture and Innovation. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgement

This paper was supported by the János Bolyai Research Scholarship of the Hungarian Academy of Sciences. Supported by the ÚNKP-23-5-DE-473 New National Excellence Program of The Ministry for Culture and Innovation from the source of the national research, development and innovation fund.

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