

Correlation Analysis among the Various Inbreeding Coefficients of Pannon Ka Rabbits

István Nagy^{1,*} , Árpád Bokor¹ , János Farkas¹, Anh Thi Nguyen¹ , János Posta²  and György Kövér¹

¹ Institute of Animal Sciences, Hungarian University of Agriculture and Life Sciences (MATE), Guba Sándor Str. 40, 7400 Kaposvár, Hungary; bokor.arpad@uni-mate.hu (Á.B.); farkas.janos.51@gmail.com (J.F.); nguyen.thi.anh@phd.uni-mate.hu (A.T.N.); kover.gyorgy@uni-mate.hu (G.K.)

² Institute of Animal Science, Biotechnology and Nature Conservation, University of Debrecen, Böszörményi Str. 138, 4032 Debrecen, Hungary; postaj@agr.unideb.hu

* Correspondence: nagy.istvan.prof@uni-mate.hu

Abstract: In a closed population with a limited population size, mating of related animals is unavoidable. In this study, the genealogy data of a synthetic maternal rabbit breed called Pannon Ka were used to calculate different inbreeding coefficients. The evaluated animals were born between 1995 and 2020, and the pedigree consisted of 5819 animals that originated from 4205 rabbit does and from 1314 rabbit bucks. The pedigree was further extended with 16,013 dummy progeny records in order to calculate litter inbreeding coefficients. Besides the conventional Wright inbreeding coefficients, the so-called ancestral and new inbreeding coefficients were also calculated using the gene dropping method. By the end of the evaluated period, the litter inbreeding increased to almost 11 and 60% for Wright and Ballou inbreeding, while the Kalinowski and the Kalinowski new inbreeding coefficients were 9.25 and 16.67%, respectively. Correlation coefficients were calculated for the does and for the litters. Finally, the effects of pedigree length and completeness were also taken into account using the complete generation equivalents in a partial correlation analysis. Based on the results, it could be seen that the different ancestral inbreeding coefficients had high correlation. Similarly, the conventional Wright inbreeding coefficients showed strong correlation with the new inbreeding coefficients. On the contrary, the correlation between ancestral and new inbreeding coefficients was low. Taking the complete generation equivalent into account did not give unambiguous results. It could be concluded that the different inbreeding coefficients are based on different concepts, and they are clearly different population parameters.

Keywords: Pannon Ka rabbits; ancestral inbreeding; new inbreeding; conventional inbreeding; correlation analysis



Citation: Nagy, I.; Bokor, Á.; Farkas, J.; Nguyen, A.T.; Posta, J.; Kövér, G. Correlation Analysis among the Various Inbreeding Coefficients of Pannon Ka Rabbits. *Diversity* **2024**, *16*, 524. <https://doi.org/10.3390/d16090524>

Academic Editors: Michael Wink and Simone Ceccobelli

Received: 15 May 2024

Revised: 16 July 2024

Accepted: 26 August 2024

Published: 31 August 2024



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1. Introduction

In the framework of the so-called Pannon Rabbit Breeding Program, the development of rabbit breeds started in the late 1980s by reciprocally crossing the New Zealand White and Californian White rabbits. Then, their progenies were mated among each other, applying a strong selection for average daily gain and dressing out percentage. The created breed (Pannon White) was recognized in 1992 and maintained ever since. The selection criteria were changed several times; at present, the breed is selected for litter weight at weaning and thigh muscle volume (measured with computer tomography). Later, in the mid-1990s, a new prolific breed was formed using the sperm of some Hungarian and foreign breeds to inseminate Pannon White does, and the born progeny was the basis of a new prolific breed. The selection objective was to improve the number of kits born alive, and the new maternal breed was recognized in 2003. Finally, from 2004, a terminal sire breed was developed using some Hungarian and foreign rabbit breeds showing high average daily gain. These rabbits were crossed with the Pannon white rabbits, and the progeny was the basis of the

new sire breed selected for average daily gain and thigh muscle volume (using computer tomography). The created breed was called Pannon Large, and it was recognized in 2013. Further details for the Pannon Breeding Program are provided in [1]. Since their foundation, all of these rabbit breeds have been kept as a closed population with a limited population size (cca 240 breeding animals per breed), which means that mating of related animals is unavoidable. The inbreeding characteristics of Pannon White and Pannon Large rabbits have been reported in several studies [2–6], but so far, the inbreeding level of the Pannon Ka breed has not yet been investigated.

Quantifying inbreeding in a population involves measuring the extent to which individuals are related to each other, typically carried out using inbreeding coefficients. The inbreeding coefficient ($F_{(x)}$) was first developed and introduced by Wright [7], measuring the probability that an individual has inherited two alleles at a locus from a common ancestor. The limitation of this approach is that it only accounts for the inbreeding occurring in the immediate individual and does not account for the degree of inbreeding in the individual's ancestors, which can lead to an incomplete understanding of the inbreeding effects, especially when considering the long-term implications. To address this limitation, ancestral inbreeding coefficients, which incorporated the inbreeding levels of the ancestors into the calculation, were developed [8,9]. Ballou's ancestral inbreeding coefficient ($F_{\text{Bal}(x)}$) can be understood as the probability that an individual inherits an allele that has experienced inbreeding at least once in the past. This coefficient was then derived using the gene dropping method [10]. While employing gene dropping to estimate ancestral inbreeding, Kalinowski et al. [9] did not define the ancestral inbreeding coefficient as Ballou did. Instead, they estimated the proportion of an animal's genome that is currently identical by descent (IBD) and had been IBD in one of its ancestors ($F_{\text{Kal}(x)}$). They divided the standard inbreeding coefficient into two components: alleles that had previously undergone inbreeding and alleles that became identical by descent (IBD) for the first time [9]. The probability of the latter was defined as Kalinowski's "new" inbreeding coefficient. New inbreeding is anticipated to be more detrimental than ancient inbreeding. Consequently, recent studies on cattle [11–17], horses [18–20], sheep [21,22], pigs [23,24], rabbits [2,5,25], dogs [26,27], and some wild animals [28,29] have estimated the new inbreeding coefficient alongside other inbreeding coefficients. Since the number of different inbreeding coefficients being defined and analysed is growing, the correlation between these inbreeding coefficients have been examined [5,18,22–24,30]. However, the correlation between different inbreeding coefficients differs across studies and requires more research.

The objective of this study was twofold. Our first aim was to calculate the various inbreeding coefficients of the Pannon Ka rabbit breeds (based on genealogy information). The second objective was to perform a correlation analysis on these inbreeding coefficients.

2. Materials and Methods

This study was not carried out on live animals, so Animal Care and Use Committee approval was not obtained.

2.1. Pedigree Data and Pedigree Completeness

The data analysed in this study were provided by the University of Kaposvár, the legal predecessor of the Hungarian University of Agricultural and Life Sciences. The present study was conducted on Pannon Ka (maternal line). The pedigree records of the given breed covered 16,013 kindling records, which originated from 4205 rabbit does and from 1314 rabbit bucks. The total number of animals in the pedigree file was 5819; data were collected between 1995 and 2020. Further, the pedigree was extended with 16,013 dummy progeny records in order to calculate litter inbreeding coefficients.

The completeness of the pedigree was assessed using the following metrics: (1) the number of full generations traced (PorC), which is the number of generations separating the offspring from the most distant generation with known ancestors; (2) the maximum number of generations traced (PorG), defined as the number of generations between the individual

and its most distant ancestor; and (3) the complete generation equivalent (CGE) for each animal in the pedigree records, calculated by summing $(1/2)^n$ for all known ancestors, where n represents the number of generations between the individual and each known ancestor [31]. The CGE was computed using the ENDOG 4.8 software [32] and for the does and for the litters.

2.2. Inbreeding Coefficients

The conventional inbreeding coefficient ($F_{(x)}$) was calculated based on the concept of [7], while the ancestral inbreeding coefficients were derived from the concepts of Ballou ($F_{Bal(x)}$) [8] and Kalinowski ($F_{Kal(x)}$) [9]. The Kalinowski “new” inbreeding coefficient was calculated by subtracting Kalinowski’s inbreeding coefficient from the conventional inbreeding coefficient: $F_{New(x)} = F_{W(x)} - F_{Kal(x)}$.

All inbreeding coefficients were computed separately for the does and for the litters using the Grain 2.2 software [33].

2.3. Correlation Analysis

The Pearson correlation and partial correlation (taking into account the effect of CGE) between the inbreeding coefficients, estimated using different methods, was calculated using [34], both for the does and for the litters.

3. Results and Discussion

The mean complete generation equivalent of the dams and of the litters and the mean dam and litter inbreeding for the whole period and the litter inbreeding for the kindling year of 2020 are presented in Table 1.

Table 1. Mean dam and litter pedigree parameters of the Pannon Ka rabbit breed.

	Litter	Litter (2020)	Dam
Inbred animals (%)	92.61	100	88.97
F_Wright (%)	7.19	10.92	6.61
F_Ballou (%)	28.42	58.60	24.40
F_Kalinowski (%)	4.05	9.25	3.45
F_Kalinowski_new (%)	3.14	1.67	3.16
CGE	9.06	15.47	8.34

CGE: complete generation equivalent.

These values were lower compared to that of the same inbreeding coefficients of the Pannon White rabbits [5], which can be explained by the longer breeding history of the latter breed. The estimated correlation and partial correlation coefficients among the various inbreeding coefficients of the does and of the litters are presented in Tables 2 and 3. All of the calculated correlation coefficients were highly significant ($p < 0.0001$).

Table 2. Correlation and partial correlation coefficients among the different inbreeding coefficients of the does.

	Correlation Coefficients				Partial Correlation			
	$F_{(x)}$	$F_{Bal(x)}$	$F_{Kal(x)}$	$F_{New(x)}$	$F_{(x)}$	$F_{Bal(x)}$	$F_{Kal(x)}$	$F_{New(x)}$
$F_{(x)}$	1	0.67	0.81	0.65	1	0.25	0.67	0.88
$F_{Bal(x)}$		1	0.94	−0.09		1	0.69	−0.11
$F_{Kal(x)}$			1	0.07			1	0.25
$F_{New(x)}$				1				1

$F_{(x)}$: Wright inbreeding coefficient; $F_{Bal(x)}$: Ballou inbreeding coefficient; $F_{Kal(x)}$: Kalinowski inbreeding coefficient; $F_{New(x)}$: Kalinowski new inbreeding coefficient.

Table 3. Correlation and partial correlation coefficients among the different inbreeding coefficients of the litters.

	Correlation				Partial Correlation			
	$F_{(x)}$	$F_{Bal(x)}$	$F_{Kal(x)}$	$F_{New(x)}$	$F_{(x)}$	$F_{Bal(x)}$	$F_{Kal(x)}$	$F_{New(x)}$
$F_{(x)}$	1	0.64	0.82	0.61	1	0.33	0.78	0.91
$F_{Bal(x)}$		1	0.93	−0.06		1	0.61	0.08
$F_{Kal(x)}$			1	0.05			1	0.46
$F_{New(x)}$				1				1

$F_{(x)}$: Wright inbreeding coefficient; $F_{Bal(x)}$: Ballou inbreeding coefficient; $F_{Kal(x)}$: Kalinowski inbreeding coefficient; $F_{New(x)}$: Kalinowski new inbreeding coefficient.

Looking at the results in Tables 2 and 3, it can be seen that the two ancestral inbreeding coefficients showed very similar correlation coefficients, while the conventional and Kalinowski new inbreeding coefficients were moderately strong. On the contrary, the estimated correlation coefficients between the ancestral and new inbreeding coefficients were weak and sometimes even negative. Taking into account the effect of the complete generation equivalent on the correlation coefficients, the values were partly increased and decreased. The number of similar studies in rabbit breeding is low, according to our knowledge; it was only evaluated in [5,25,30]. The results for other species were summarized by Nagy and Nguyen [35]. These studies all reported partly similar results, namely that high correlation coefficients were reported between the Ballou and Kalinowski ancestral inbreeding coefficients in both studies. Moreover, the authors of [5] reported similar values, although the calculated correlation coefficients between ancestral and new inbreeding were higher compared to those reported here. On the contrary, the authors of [25] found zero correlation coefficients between the new and ancestral inbreeding. Nevertheless, it has to be noted that the authors of [25] did not use the concept of [9] for the new inbreeding calculation but used a different concept [36].

4. Conclusions

By means of correlation coefficients among the various (conventional, ancestral, and new) inbreeding coefficients, our study clearly demonstrated that the various inbreeding coefficients measure different concepts and that they represent different population parameters, especially the ancestral and new correlation coefficients, which are practically uncorrelated. Taking the pedigree length and completeness into account did change the correlation coefficients, and therefore, it can be concluded that their inclusion into analyses is necessary.

Author Contributions: Conceptualization, I.N.; methodology, I.N., Á.B., A.T.N., G.K. and J.P.; software, G.K., J.F. and J.P.; validation, G.K., J.F. and J.P.; formal analysis, Á.B.; investigation, I.N.; resources, I.N.; data curation, Á.B. and J.F.; writing—original draft preparation, I.N.; writing—review and editing, I.N., Á.B., A.T.N., G.K. and J.F.; visualization, I.N.; supervision, I.N.; project administration, I.N.; funding acquisition, I.N. All authors have read and agreed to the published version of the manuscript.

Funding: The financial help from the “MATE Kutatási Kiválóság 2024 projekt of the Hungarian University of Agriculture and Life Sciences” is gratefully acknowledged.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data used in this analysis constitute a business secret and thus are not available.

Conflicts of Interest: The authors declare no conflicts of interest.

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