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Calculation of the generation interval in two different ways for Gyimesi Racka sheep

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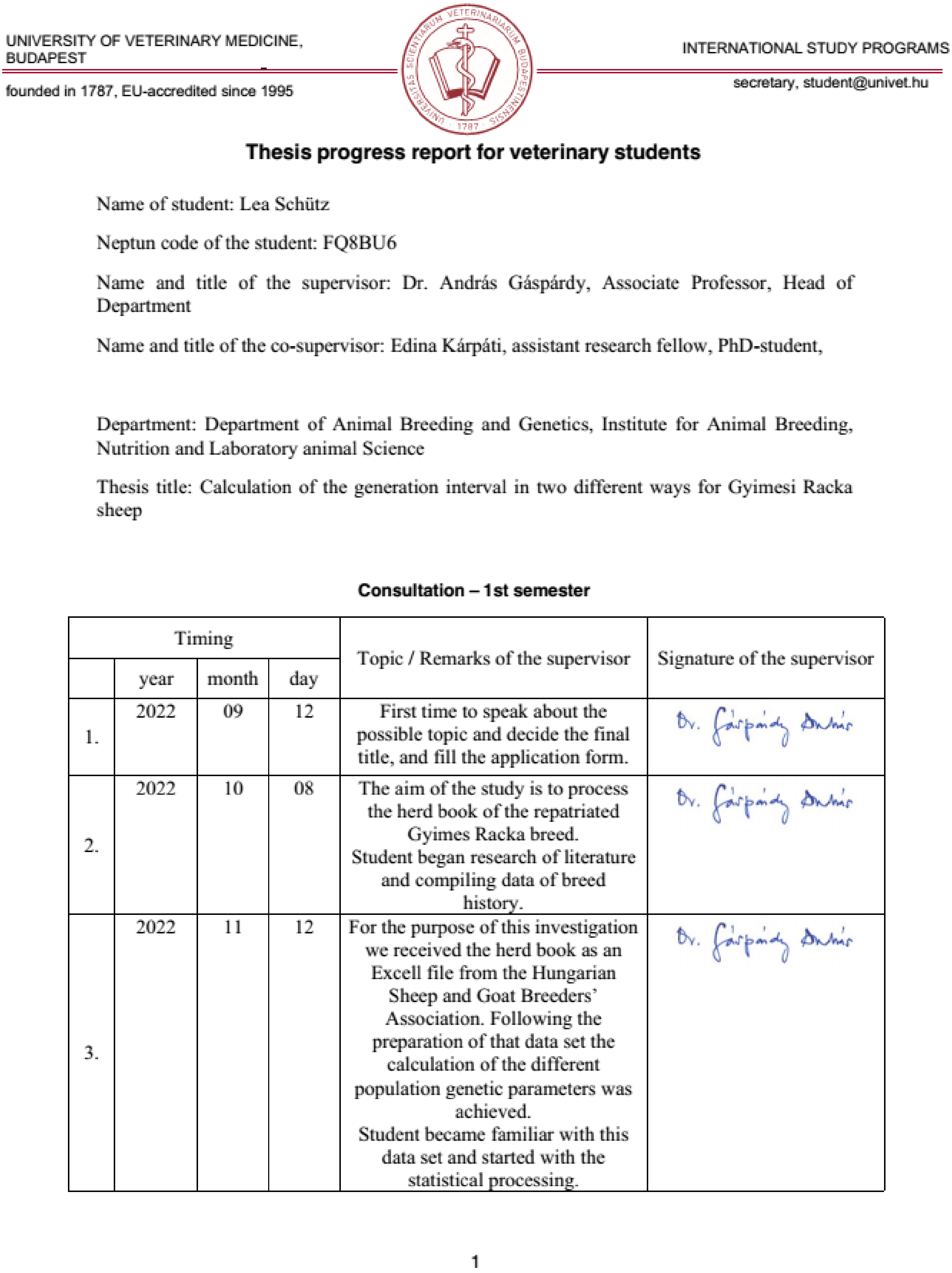

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Thesis progress report for veterinary students

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Thesis title: Calculation of the generation interval in two different ways for Gyimesi Racka sheep

Consultation – 1st semester

Timing				Topic / Remarks of the supervisor	Signature of the supervisor
	year	month	day		
1.	2022	09	12	First time to speak about the possible topic and decide the final title, and fill the application form.	Dr. Gáspárdy András
2.	2022	10	08	The aim of the study is to process the herd book of the repatriated Gyimes Racka breed. Student began research of literature and compiling data of breed history.	Dr. Gáspárdy András
3.	2022	11	12	For the purpose of this investigation we received the herd book as an Excell file from the Hungarian Sheep and Goat Breeders' Association. Following the preparation of that data set the calculation of the different population genetic parameters was achieved. Student became familiar with this data set and started with the statistical processing.	Dr. Gáspárdy András

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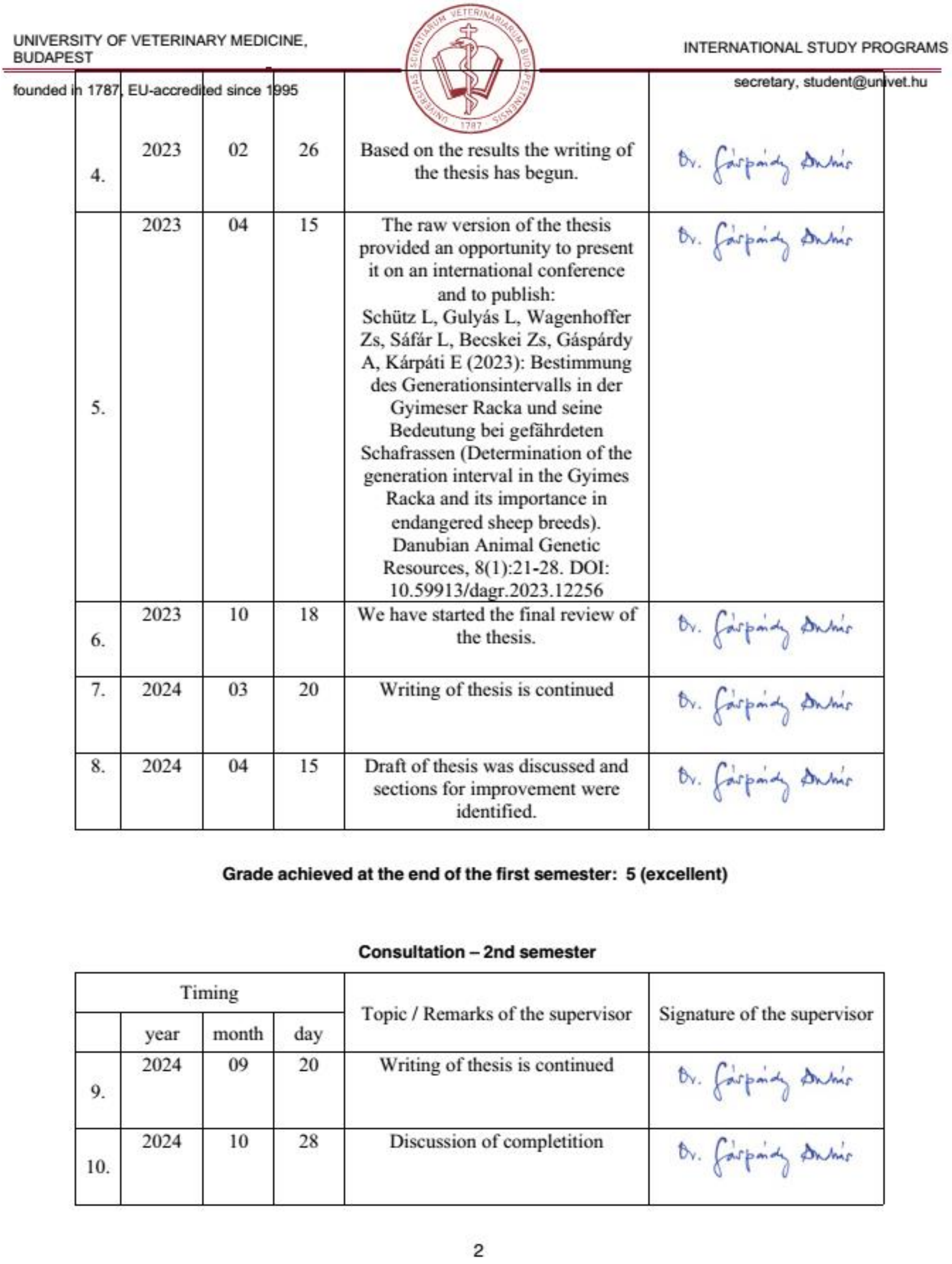

4.	2023	02	26	Based on the results the writing of the thesis has begun.	Dr. Gáspárdy András
5.	2023	04	15	The raw version of the thesis provided an opportunity to present it on an international conference and to publish: Schütz L, Gulyás L, Wagenhoffer Zs, Sáfár L, Becskei Zs, Gáspárdy A, Kárpáti E (2023): Bestimmung des Generationsintervalls in der Gyimeser Racka und seine Bedeutung bei gefährdeten Schafrassen (Determination of the generation interval in the Gyimes Racka and its importance in endangered sheep breeds). Danubian Animal Genetic Resources, 8(1):21-28. DOI: 10.59913/dagr.2023.12256	Dr. Gáspárdy András
6.	2023	10	18	We have started the final review of the thesis.	Dr. Gáspárdy András
7.	2024	03	20	Writing of thesis is continued	Dr. Gáspárdy András
8.	2024	04	15	Draft of thesis was discussed and sections for improvement were identified.	Dr. Gáspárdy András

Grade achieved at the end of the first semester: 5 (excellent)

Consultation – 2nd semester

Timing				Topic / Remarks of the supervisor	Signature of the supervisor
	year	month	day		
9.	2024	09	20	Writing of thesis is continued	Dr. Gáspárdy András
10.	2024	10	28	Discussion of completition	Dr. Gáspárdy András

11.	2024	11	28	Completition of thesis	Dr. Gáspárdy András

Grade achieved at the end of the second semester: 5 (excellent)

The thesis meets the requirements of the Study and Examination Rules of the University and the Guide to Thesis Writing.

I accept the thesis and found suitable to defence,

Dr. Gáspárdy András
signature of the supervisor

Signature of the student: ……………………………………………

Signature of the secretary of the department: ……………………..…………

Date of handing the thesis in………… ………………….....

Content

Abstract

In modern and profit-oriented production conditions, indigenous animals are increasingly forced out of breeding, which means not only a decrease in their number, but also their genetic narrowing. The groups of Racka sheep include the most important indigenous sheep breeds of the Central and South-East Asian region, which are characterized by pronounced genetic diversity. The preservation of genetic diversity is served by the appropriate application of population genetic parameters. The aim was to determine the length of the generation interval in the Gyimesi Racka based on the pedigree data using two calculation methods and to compare the obtained results with the corresponding results of other breeds, as well as to make suggestions to breeders of the breed for the appropriate breeding selection.

In the case of endangered domestic animals under genetic protection, it is favourable if the generation interval is long. As expected, there was a discrepancy during the application of the two calculation methods. It is also important to emphasize that different calculation approaches yield varying results.

After analysing the rest of the pedigree, the results will then provide a basis for further molecular genetic studies. According to it, the individuals with the most diverse alleles will be selected and recommendations will be made to breeders to select the most suitable individuals. With this knowledge, valuable alleles can be truly preserved for posterity through cryopreservation techniques.

Absztrakt

A modern és profitorientált termelési körülmények között az őshonos állatok egyre inkább kiszorulnak a tenyésztésből, ami nemcsak az egyedszámuk csökkenését, hanem a genetikai beszűkülésüket is jelenti. A racka juhok csoportjába tartoznak a közép- és délkelet-ázsiai régió legfontosabb őshonos juhfajtái, amelyeket kifejezett genetikai sokszínűség jellemez. A populációgenetikai paraméterek megfelelő alkalmazása a genetikai sokféleség megőrzésének szolgálatában áll. A szerzők célja az volt, hogy törzskönyvi adatok alapján kétféle számítási módszerrel meghatározzák a generáció intervallum hosszát a gyimesi racka juhoknál, és a kapott eredményeket összehasonlítsák más fajták megfelelő eredményeivel, valamint javaslatokat tegyenek a fajta tenyésztői számára a megfelelő tenyészkiválasztáshoz. A genetikai védelem alatt álló, veszélyeztetett háziállatok esetében kedvező, ha a generáció intervallum hosszú. A két számítási módszer alkalmazása során a várakozásoknak megfelelően eltérés mutatkozott. Fontos hangsúlyozni azt is, hogy a számítás eltérő módon történő megközelítése is befolyásolja a kapott eredményeket.

Eredményeik birtokában a szerzők a teljes törzskönyv elemzését kívánják elvégezni, amely később alapot ad további molekuláris genetikai vizsgálatokhoz. Mindezek alapján kiválasztásra kerülnek azok az egyedek, akik a legváltozatosabb allélokkal rendelkeznek, valamint ajánlások készülnek a tenyésztők számára a megfelelő egyedek kiválasztása érdekében. Ennek birtokában kriokonzerválási eljárásokkal valóban megőrizhetőek értékes allélok az utókor számára.

Abbreviations

GI: Generational Interval
ss: sire-son (Father- son)
sd: sire-daughter (Father- daughter)
ds: dam-son (mother- son)
dd: dam-daughter (mother- daughter)
whole pop. – whole population
ref. pop. – reference population
GI – generation interval
AGE – mean age
Avg.: averages
nucl.: nucleus flock with other selection program
Br.: Brazilian

List of Figures and Tables

1. Introduction

In a modern and profit-driven production environment, indigenous animals are increasingly being driven out of breeding, which means not only a reduction in their numbers but also a loss of genetic diversity. Pedigree analysis is an effective method to determine several population genetic parameters, which is an excellent way to evaluate allele frequencies in animal populations. In most cases, the pedigree of our native breeds is closed and only offsprings of parents with pedigree are registered. In indigenous animal populations, where the preservation of genetic diversity is an important objective, it is particularly harmful to restrict breeding to a few favoured animals. The more inbred a population is, the greater the chance that valuable genes will be lost, and genetic variability will be reduced. This is often associated with a loss of vitality and adaptability. Indigenous breeds often carry genes for resistance (prion infection, parasitosis), are better adapted to climate change and can be expected to produce better in extensive environments. The latter makes them ideal for managing protected landscapes and can also be used for sustainability.

This thesis aims to determine the generation interval (GI) in the Gyimesi Racka using pedigree data and to compare the results with those of other breeds. Although the current research focuses only on the generation interval and thus only forms one part of a complete pedigree analysis, it is an important indicator closely related to genetic diversity. With the results obtained, a full pedigree analysis will be made, on which molecular genetic studies will be based on. Afterwards, the most allele-rich individuals will be selected, and recommendations will be made to breeders for appropriate breeding selection encouraging further breeding of individuals carrying valuable genes and initiating cryopreservation procedures.

2. Literature Review

2.1 The Racka sheep group

The Racka sheep group includes the most important indigenous sheep breeds of the Central and Southeast European region, the phylogenetic origin of which was described by Drăgănescu and Grosu[1]. This group is remarkable in terms of genetic diversity, which is explained by the different ecological niches and husbandry practices in different regions during their evolution. They are characterised by their 'island-like' breeding, as evidenced by the development of the Gyimesi Racka in Transylvania, an area inhabited by Hungarians [2]. The ancestors of the Gyimesi Racka were introduced from Asia Minor to the southern Carpathian Mountain ranges, and are nowadays bred in few pure-bred forms, except for the Ghimeș and Vrancea Mountains [3] (Munții Vrancei). In the early 1990s, it was reintroduced in small numbers into what is now Hungary. This population of the breed subsequently increased in the following years thanks to some major imports of breeding stock. The Hungarian herd book was opened in 2005 and the flock of Gyimesi Racka ewes living nowadays counts approximately 1000 individuals.

Figure 1. Group of Gyimesi Racka ewes
(Credit: Edina Kárpáti)

This breed is the largest variant of the Racka sheep group, with ewes weighing 45-50 kg on average and rams 80-90 kg [3]. It is characterized by a long horn-length, which is longer in rams [4], but hornless individuals are not rare among females.

The Gyimesi Racka is a true triple-purpose breed. Its mixed wool coat is dirty white, often interspersed with coloured patches. The head and leg ends are mostly black. The black patch around the eye is also a characteristic feature (Figure 1). On good pastures, 100-120l of milk can be milked from the ewes after weaning [5]. Its milk is rich in vitamins and minerals, and often used to make buttermilk. It also thrives well on cropper pastures and its meat can be the basis of succulent dishes [6].

Figure 2. Gyimesi Racka ewe in corridor at farm in Mátranovák
(Credit: Edina Kárpáti)

2.2 The Generational Interval in other breeds

According to Lush [7], the generation interval (GI) is the average age of parents when their offspring are born. However, the concept should be interpreted more narrowly, as the transmission of genes to the offspring generation is only valid for breeding animals involved in the formation of the next generation [8]. For indigenous sheep, the expected generation interval is 4 years.

After reviewing the literature, most authors give four paths in addition to the average generation interval (ss: sire-son, sd: sire-daughter, ds: dam-son, dd: dam-daughter), but some don’t specify the data in this way only giving the average of the populations [9]. Authors also differ in whether they give data for the whole population or only for the population intended for further breeding. Paiva et al.[10] in Brazilian Somali hair sheep also studied the breeding flock in addition to the total flock - Brazilian Somali hair sheep (breeding) ss: 2.47; sd: 3.12; ds: 4.69, dd: 4.76, averages: 3.91, Brazilian Somali hair sheep (all) ss: 3.36; sd: 3.29; ds: 4.71; dd: 4.64; averages: 4.00.

Venkataramanan et al. [11] examined data from the whole Nilagiri sheep flock in two time intervals from 1988 to 1991 and from 2008 to 2011 and found that the length of the generation interval on the paternal pathway increased in later years (ss: 2.58; sd: 2.54), but on the maternal side the values were closer to ideal in earlier years (ds: 4.34; dd: 4.28).

If we study population genetic parameters, it is worth examining the so-called reference population in addition to the whole population, which is the youngest members of the animal group, born in the last few years. This group is the best reflection of where the breeding is currently going and includes the last 4 years of the sheep, which corresponds to a generation interval. Oravcová and Krupa [12] also gave values for the reference population for the original Valachian sheep, which compares more favourably with the total flock as the generation interval increases in the former group (Valachian reference population: ss: 4. 96; sd: 2.69; ds: 6.94; dd: 6.84; averages: 4.94), compared to the whole population (ss: 3.52; sd: 2.64; ds: 4.70; dd: 5.36; averages: 4.07).

If we compare the different GIs of the different sheep breeds as it can be seen in Table 1, Texel has the lowest average (2.70 years) [13], while the former Valachian sheep reference population has the highest generation interval: 4.94 years [12]. Note that the Turcana sheep are brought to the Northern Carpathians with Vlach shepherds, where the breed is called Valachian (Walaska). The Romanov (INRA – National Institute for Agronomic Research, a French national performance recording system) has the lowest parameter on the sire-son pathway at 1.90 years [14], while 4.96 years is again the highest value in the reference population of former Valachian sheep [12]. For the sire-daughter relationship, the lowest value is again in Texel (2.00 years) [13], while the generation interval is highest for the Romanov sheep at 5.10 years [14]. For mother-son relationships, the Romanov INRA (2.00 years; [14]) and the reference population of the former Valachian sheep demonstrate the extreme values (6.94 years; [12]). In mother-daughter relationships, the lowest value is 2.49 years in Finnish sheep [15], while it is the longest in the former Valachian sheep reference population (6.84 years; [12]).

Table 1. Generation intervals of different sheep breeds by parental pathways

	Parental pathways (in years)						
Breed	ss	sd	ds	dd	averages	Author(s)	Year
Dala	3.40	3.20	4.10	4.00	3.70	Joakimsen [16]	1969
Rygja	3.60	3.50	4.30	4.20	3.90	Joakimsen	1969
Cheviot	3.30	3.00	4.40	4.30	3.80	Joakimsen	1969
Steigar	3.70	3.70	4.40	4.10	4.00	Joakimsen	1969
Spælsau	3.40	3.80	4.70	4.30	4.10	Joakimsen	1969
Xalda sheep	2.67	2.86	3.23	3.11	2.97	Goyache et al.	2003
Zandi sheep	2.84	2.97	3.96	4.01	3.45	Ghafouri-Kesbi et al. [17]	2008
Finnsheep	2.96	3.15	2.65	2.49	2.85	Li et al.	2009
Bleu du Maine	2.90	4.00	3.00	3.60	3.40	Danchin-Burge et al.	2010
Charmoise	3.60	4.50	3.40	4.20	3.90	Danchin-Burge et al.	2010
Cotentin	2.80	3.80	2.70	4.00	3.30	Danchin-Burge et al.	2010
Romanov (on-Farm)	2.90	5.10	3.50	5.00	4.10	Danchin-Burge et al.	2010
Romanov (ex situ)	1.90	4.00	2.00	3.80	2.90	Danchin-Burge et al.	2010
Roussin de la Hague	3.20	3.90	3.00	3.90	3.50	Danchin-Burge et al.	2010
Solognote	3.10	4.20	3.10	4.00	3.60	Danchin-Burge et al.	2010
Former Valachian sheep (whole pop.)	3.52	2.64	4.70	5.36	4.07	Oravcová and Krupa	2011
Former Valachian sheep (ref. pop.)	4.96	2.69	6.94	6.84	4.94	Oravcová and Krupa	2011
Brazilian Somali hair sheep (all)	2.47	3.12	4.69	4.76	3.91	Paiva et al.	2011
Brazilian Somali hair sheep (breeding)	3.36	3.29	4.71	4.64	4.00	Paiva et al.	2011
Iranian Baluchi sheep	3.11	3.04	3.63	3.54	3.33	Tahmoorespur and Sheikhloo	2011
Kermani sheep	4.73	4.72	4.57	4.22	4.48	Mokhtari et al. [18]	2013
Nilagiri sheep (Overall)	2.49	2.64	4.16	4.12	3.36	Venkataramanan et al.	2013
Nilagiri sheep (2008-2011)	2.58	2.54	3.71	3.70	3.18	Venkataramanan et al.	2013
Nilagiri sheep (1988-1991)	2.24	2.24	4.34	4.28	3.29	Venkataramanan et al.	2013
Tsigai/Cigája	4.06	4.13	4.53	4.39	4.28	Arkenberg	2014

Table 1. Generation intervals of different sheep breeds by parental pathways (continued)

	Parental pathways (in years)						
Breed	ss	sd	ds	dd	averages	Author(s)	Year
Malpura sheep	2.85	2.72	4.13	3.97	3.37	Gowane et al.	2014
Moghani Sheep	4.51	4.05	4.94	4.43	4.48	Mokhtari et al. [19]	2015
Brazilian Somali sheep	3.52	3.51	3.43	3.57	3.53	Figueredo et al. [20]	2019
Dorper sheep	3.40	4.40	2.80	3.80	4.00	Kiya et al. [21]	2019
Brazilian Morada Nova sheep GI	3.20	3.60	3.50	3.70	3.60	McManus et al.	2019
Brazilian Morada Nova sheep AGE	3.50	3.50	3.70	3.70	3.60	McManus et al.	2019
Lori-Bakhtiari sheep	3.75	4.29	4.30	3.94	4.11	Vatankhah et al. [22]	2019
Lori-Bakhtiari sheep	4.68	4.54	4.12	4.05	4.35	Vatankhah et al.	2019
Cikta	3.80	3.90	4.20	4.10	4.00	Posta et al.	2019
Santa Inês sheep	3.46	3.33	3.40	3.28	3.34	Barbosa et al.[23]	2020
Bharat Merino sheep	3.57	3.40	4.95	4.93	4.19	Mallick et al.	2020
Belclare	2.20	2.20	3.30	3.20	2.73	Rafter et al.	2022
Charollais	2.90	2.90	3.70	3.70	3.30	Rafter et al.	2022
Galway	2.80	2.90	3.80	3.70	3.30	Rafter et al.	2022
Suffolk	2.40	2.40	3.60	3.70	3.03	Rafter et al.	2022
Texel	2.00	2.00	3.40	3.40	2.70	Rafter et al.	2022
	Parental pathways (in years)						
Breed	ss	sd	ds	dd	averages	Author(s)	Year
Vendeen	2.70	2.70	3.50	3.60	3.13	Rafter et al.	2022
Istrian sheep	3.40	3.50	4.00	4.30	3.80	Špehar et al. [24]	2022
Mecheri Sheep	3.02	3.03	3.59	3.45	3.27	Balasundaram et al. [25]	2023

Table 2 presents data from authors who reported generation intervals as averages.
The lowest value here is also 2 years in Mehra sheep between 1994 and 1999 [26]. Interestingly, the highest generation interval is for Texel in Germany (6.42 years; [9]), compared to 2.70 years reported in Table 1 for Texel bred in Ireland [13].

Table 2. Generation intervals by whole population averages

Breed	GI (year)	Author(s)	Year
Alpine Steinschaf	3.70	Justinski et al.	2023
Brown Mountain	4.06	Justinski et al.	2023
Berrichon du Cher	3.45	Justinski et al.	2023
Bentheim	3.76	Justinski et al.	2023
Carinthian	3.79	Justinski et al.	2023
Charollais	3.21	Justinski et al.	2023
Coburg	3.82	Justinski et al.	2023
Dorper	3.43	Justinski et al.	2023
Baraka	3.54	Justinski et al.	2023
German Grey Heath	3.92	Justinski et al.	2023
Ile-de-France	3.94	Justinski et al.	2023
Kamerun	3.99	Justinski et al.	2023
Krainer Steinschaf	3.87	Justinski et al.	2023
Lacaune	3.17	Justinski et al.	2023
Leine	3.83	Justinski et al.	2023
German Mutton Merino	4.07	Justinski et al.	2023
German Merino	4.02	Justinski et al.	2023
Merino Longwool	3.82	Justinski et al.	2023
Nolana	3.57	Justinski et al.	2023
East Friesian	3.08	Justinski et al.	2023
Ouessant	3.67	Justinski et al.	2023
Rhön	4.20	Justinski et al.	2023
Pomeranian Coarsewool	4.43	Justinski et al.	2023
Black Mountain	3.73	Justinski et al.	2023
German Blackhead Mutton	3.92	Justinski et al.	2023
Skudde	4.34	Justinski et al.	2023
Suffolk	3.54	Justinski et al.	2023

Table 2. Generation intervals by whole population averages (continued)

Breed	GI (year)	Author(s)	Year
Swifter	3.03	Justinski et al.	2023
Texel	6.42	Justinski et al.	2023
Wald	4.96	Justinski et al.	2023
White Mountain	3.77	Justinski et al.	2023
German White Heath	3.74	Justinski et al.	2023
White Polled Heath	3.85	Justinski et al.	2023
German Whitehead Mutton	3.60	Justinski et al.	2023
Zwartbles	3.01	Justinski et al.	2023
Santa Inês	3.70	Pedrosa et al.	2010
Guilan sheep	2.385	Eteqadi et al.	2014
Guilan sheep (1994–1999)	3.455	Eteqadi et al.	2014
Guilan sheep (2000–2005)	2.315	Eteqadi et al.	2014
Guilan sheep (2006–2011)	2.015	Eteqadi et al.	2014
Mehraban sheep	2.15	Yavarifard et al.	2014
Mehraban sheep (1994-1999)	2	Yavarifard et al.	2014
Mehraban sheep (2000-2005)	2.18	Yavarifard et al.	2014
Mehraban sheep (2006-2011)	2.27	Yavarifard et al.	2014
Segureña sheep	3.79	Barros [27]	2017
Gute sheep (males)	3.7	Rochus and Johansson [28]	2017
Gute sheep (females)	3.5	Rochus and Johansson	2017
Shall sheep	3.755	Hashemi and Hossein-Zadeh [29]	2020

3. Material and Methods

3.1. Pedigree file

The basis of the research was the Excel database from the Hungarian Sheep and Goat Breeders Association (MJKSZ), which covers the whole country and contains the pedigree data of the Hungarian Gyimesi Racka population. Maternal generations were coded in Excel and the Pedigree file was controlled by Pedigree Viewer [30] (Figure3). The parameters used were calculated using Endog software [31], but pedigree completeness by birth year and generation was calculated using Poprep software [32] and TIBCO Statistica [33], respectively.

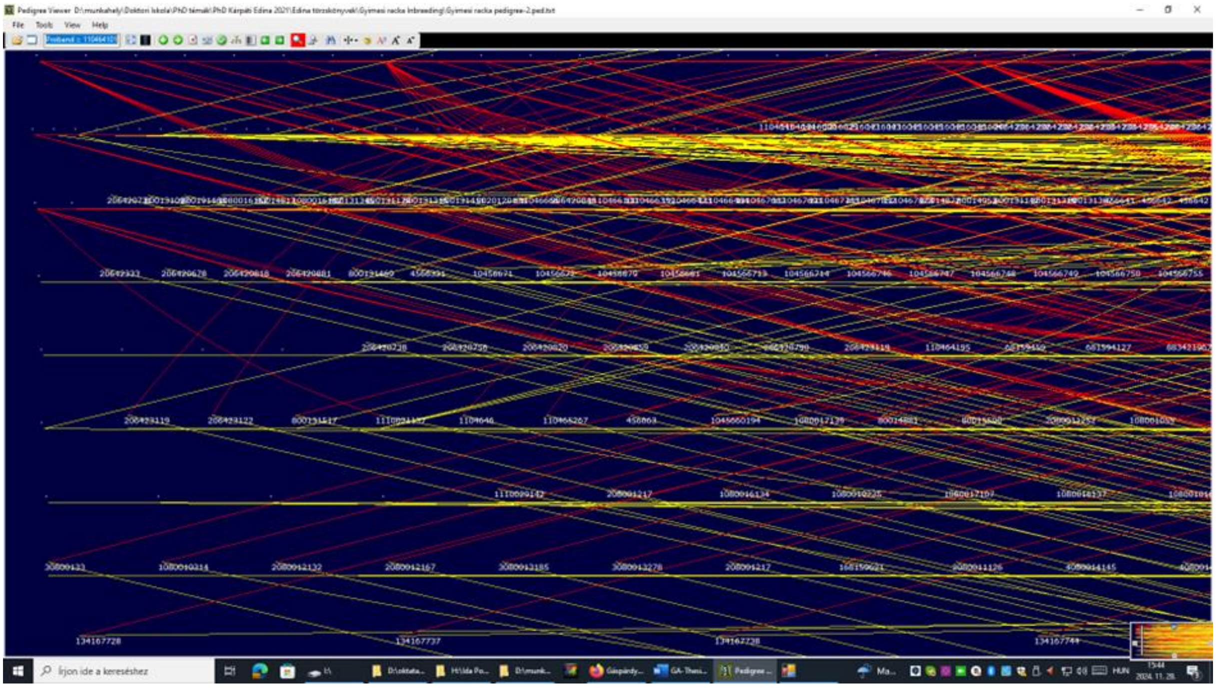

Figure 3. A fragment of the Gyimesi Racka pedigree

To determine the generation interval of the Gyimesi Racka, the Excel database of the Hungarian Sheep and Goat Breeders Association (Magyar Juh- és Kecsketenyésztők Szövetsége, MJKSZ) was processed. The study period was from 2005 to 2020. Data preparation included coding of maternal generations and creation of a pedigree file. The pedigree file itself is a data table with the first column containing all the individuals recorded in the pedigree and the second and third columns containing their parents (father, mother) with their identification numbers. The parentage of the founding individuals is unknown, so in these rows the parents are marked with a 0.

Table 3. Herd book summary

Population size	16947
Total number of founders	3838
Number of female founders	2255
Number of male founders	1583

3.2. Normality test of the used data

At the beginning of the processing, we checked if the data used for the generation interval is normally distributed using Kolmogorov-Smirnov one-sample test for a sample population and Lilliefors test on the whole population, illustrated in Figures 1 and 2. If the values are significant the hypothesis of normal distribution is thrown out.

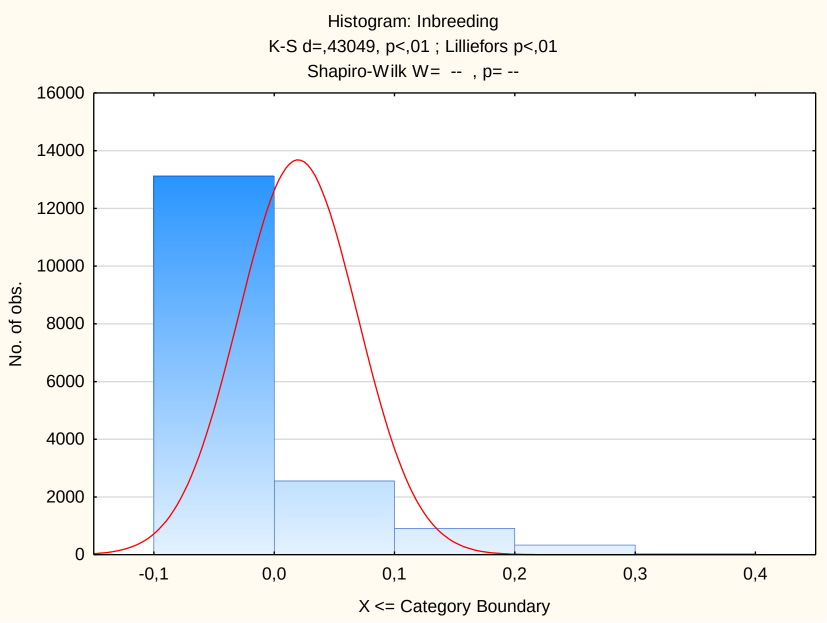

Figure 4. Course of generation interval and normality test in the entire population

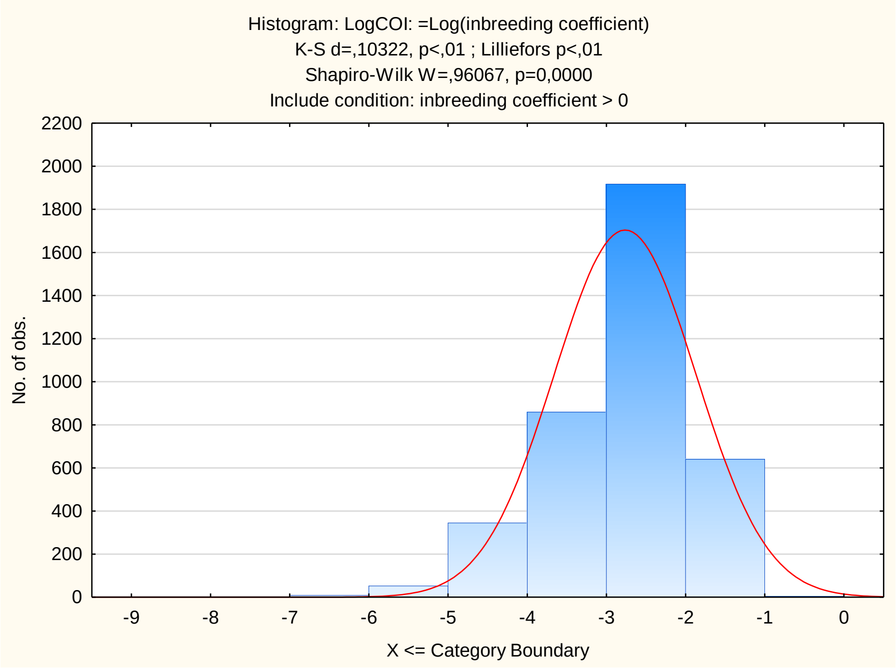

Figure 2. Course of logGI and test of normality in the inbred subpopulation

The tests did not confirm a normal distribution therefore to normalise the data, a natural log transformation was performed. An example of the application of the natural logarithm transformation in pedigree analysis is given by Kárpáti et al. [34], who calculated Wright's inbreeding coefficients[35] of Gyimesi Racka in two different ways.

3.3. The generational interval

Again, according to Lush [7], the generation interval (GI) is the average age of parents when their offspring are born. In indiginous sheep breeds that interval is expected to be around 4 years.

This parameter is used in animal breeding practice to estimate the success and progress of selection. In cases where production efficiency and the production of a marketable product are the main considerations, animals are subject to much greater selection pressure. At this time, the success of selection is negatively affected by the extension of the generation interval, and some authors even advocate its reduction [36]. The generation interval can be reduced primarily by lowering the age of the parents at the birth of the first lambs, but the intervals between lambings can be reduced as well. Nowadays, modern biotechnological methods are also of great importance, as they can significantly increase the number of offspring born per unit time. For example, ewe lambs can be super ovulated, and the generation interval can be reduced to as little as one year [37].

The opposite is true for our native endangered species, which have survived in smaller numbers. In their case, the lengthening of the generation interval is of great importance, since a longer generation interval also has a positive effect on the evolution of genetic diversity [38].

In our present research, the generation interval has been defined in both a narrower and a broader sense. In the former case, we are talking about relationships between parents and their offspring, in which case the offspring will themselves be breeding animals. And in the latter case, relations between parents and non-breeding offspring were considered. We have identified the following pathways:

- parent - all offspring
    - sire - breeding offspring
    - sire - non-breeding offspring
    - dam - breeding offspring
    - dam - non-breeding offspring
- parent - breeding offspring
    - sire - sire
    - sire - dam
    - dam - sire
    - dam – dam

The generation interval lengths were determined by pathways using one-factor analysis of variance. Confirmed differences between means were analysed using Tukey's HSD test (significant difference) for unequal N (see the number of individuals in chapter Result and discussion).

4. Results and discussion

4.1. Results

Table 4 shows the evolution of the generation interval of the Gyimesi Racka without natural logarithm transformation (raw data), both in a broader and narrower interpretation. In the category of all parents and all offspring relationships, we identified 15308 breeding records with an average generation interval of 4.04 years (Table 4). However, if we only talk about the breeding individuals, the number of relations between them and their parents was significantly lower (2089) and the generation interval was also less favourable in their case (3.66 years). The shortest progeny pathway was between rams and breeding progeny (3.14 years), with only 99 progeny paths, and the longest was between dams and non-breeding progeny (4.63 years). None of the categories of paternal paths reached the 4 years normally used for sheep.

Table 4. Results of generation intervals of the Gyimesi Racka according to the paths of broad and narrow interpretation (without natural logarithm transformation)

Category (paths)	**Number of connections**	**Arithmetic mean**	**-95% lower CI[1]**	**+95% upper CI[1]**
Parent – all offspring	15308	4.04	4.01	4.07
Sire – breeding offspring	1168	3.28[a]	3.20	3.36
Sire – non-breeding offspring	7410	3.69[b]	3.65	3.73
Dam – breeding offspring	921	4.13[c]	4.00	4.26
Dam – non-breeding offspring	5809	4.63[d]	4.57	4.69
Parent – breeding offspring	2089	3.66	3.58	3.73
Sire – sire	99	3,14[a]	2.88	3.40
Sire – dam	1069	3.29[a]	3.20	3.38
Dam – sire	80	4.00[b]	3.59	4.41
Dam – dam	841	4.14[b]	4.01	4.28

[1] lower and upper 95% bounds of confidence interval
[a, b, c, d] – $p < 0.001$, Tukey HSD (honest significant difference) for unequal number of individuals per paths

Using the natural logarithm transformation (Table 5), there were remarkable changes in the generation interval, which affected all categories of the examined pathways. After the transformation overall lower and therefore more unfavourable values were obtained. The generation interval for the whole herd book -all parents and all offspring born- was only 3.61 years, while the generation interval for the breeding individuals was 3.29 years. The paternal progeny pathways were also shorter in this case, and the generation interval between breeding rams and their prospective breeding ram lambs was below 3 years (2.92 years). The longest (4.13 years) was again only between dams and non-breeding offspring, which is 0.5 years lower than in the non-transformed data.

Table 5. Results of back-transformed generation interval (GI_{back}) of the Gyimesi Racka according to the paths of broad and narrow interpretation

Category (paths)	**Number of connections**	**GI_{back} geometric mean**	**-95% lower CI[1]**	**+95% upper CI[1]**
Parent – all offspring	15308	3.61	3.58	3.64
Sire – breeding offspring	1168	3.01[a]	2.94	3.08
Sire – non-breeding offspring	7410	3.33[b]	3.30	3.37
Dam – breeding offspring	921	3.69[c]	3.58	3.81
Dam – non-breeding offspring	5809	4.13[d]	4.08	4.19
Parent – breeding offspring	2089	3.29	3.23	3.36
Sire – sire	99	2.92[a]	2.72	3.15
Sire – dam	1069	3.02[a]	2.95	3.09
Dam – sire	80	3.62[b]	3.28	4.00
Dam – dam	841	3.70[b]	3.58	3.82

[1] lower and upper 95% bounds of confidence interval

[a, b, c, d] – $p < 0.001$, Tukey HSD (honest significant difference) for unequal number of individuals per paths

4.2. Discussion

Based on our results, we can establish the following: regardless of the farm management of the offspring (breeding or non-breeding), generally the generation interval was always shorter in paternal relationships. Yet between dams and offspring it is only slightly longer which is a statistically proven relationship reflecting the traditional mating method and the extensive husbandry. However, this difference is not so large (about 0.5 – 1 year) that the contribution of the two parent sides to the next generation's abilities could become excessively disproportionate, assuming similar, less than average, genetic abilities of the parents.

In this case, there is a significant difference in the evolution of the generation interval according to the sex of the parents, but this is of course not the case for the sex of the offspring ($p > 0.05$). For ram producing mothers this value is 4.00 years, interestingly for mothers contributing to reproduction with female offspring this value is not much higher (4.14 years, $p > 0.05$).

Prod'homme and Lauvergne [39] described a generation interval of 2.2 to 4.1 years on the paternal side and 3.9 to 5.6 years on the maternal side for a Merino Rambouillet flock with a closed pedigree.

Goyache et al. [40] reported generation intervals of 2.67-2.87 years on the paternal side and 3.11-3.23 years on the maternal side for Xalda sheep, which are also endangered, and which are extant in small numbers, only 562 individuals and 26 flocks were recorded during their study.

In Finnsheep, very low generation intervals were obtained for all possible pedigrees (father-son 2.96 years, father-daughter 3.15 years, mother-son 2.65 years, mother-daughter 2.49 years [15].

Studying the French sheep breeds in small numbers, wider intervals were observed, with average generation intervals ranging from 2.90 to 4.10 years. In particular, in a Romanov nucleus population (Romanov INRA - Romanov ex situ in vivo), significant differences in the length of generation intervals by sex of offspring were found (father-son: 1.90 years, father-daughter: 4.00 years, mother-son: 2.00 years and mother-daughter: 3. 80 years). The same study also showed that if artificial insemination with frozen semen was less frequently used, genetic variability was highly dependent on the matched dam and ram. The less the ratio was skewed in favour of one sex or the other, the more favourable it became. In addition, the number of ewe lambs intended for further breeding is a factor and similarity of maternal and paternal pathways a major advantage in maintaining a rare or endangered breed [14].

Pedrosa et al.[41] in their study on the Santa Inês sheep had an average generation interval of 3.70 years. In addition, they highlighted the importance of monitoring genetic variance in breeding work and the priority to prevent genetic narrowing. The usage of managed mating plans was suggested as one of the possibilities to achieve this.

Oravcová and Krupa[12]studied the former Valachian sheep in the total flock at 2.64-3.52 years on the paternal side and 4.70-5.36 years on the maternal side, while in the reference population the total was 2.69-4.96 years (paternal side) and 6.84-6.94 years (maternal side). Unfortunately, other population genetic parameters of the former Valachian sheep also showed that the genetic variability of the breed is low, which may be related to the deterioration of condition and production indicators.

In the nucleus population of closed Baluchi sheep, where the mean GI was 3.33 years, the paternal side was shorter (3.11; 3.04) than the maternal pathway (3.63; 3.54). Data were collected from about 30 years of records [42].

Venkataramanan et al. [11] also examined the data for the whole flock of the fine wool and meat-type Nilagiri sheep divided into two time intervals between 1988 - 1991 and 2008 - 2011. They found for the GI of this also endangered breed (less than 1000 individuals during the study period) that the parameter increased on the paternal line (ss: 2.58; sd: 2.54), but the value on the maternal side was close to ideal in the earlier years (ds: 4.34; dd: 4.28).

Arkenberg [43] characterised the population genetic parameters of an old Hungarian sheep breed, Tsigai (Cigája), where the average GI of all lineages was 4.28 years, of which the paternal side was slightly shorter (4.10 years) and the maternal side longer (4.46 years). In addition to the mean values, their studies also gave median values, which were more reliable data: parent-offspring: 4.04, mother-offspring: 4.02, father-offspring: 3.93, father-son: 3.92, father-daughter: 3.93, mother-son: 4.04, mother-daughter: 4.01 years.

In the reference population of Gowane et al. [44], the rams producing dams had the lowest generational interval (2.72 years) whereas the dams producing rams (4.13 years) were the highest.

Eteqadt et al. [45] calculated an average generation interval of 2.38 years and divided this into several periods in the reference population, which was highest between 1994-1999 (3.455 years) and then started to decrease rapidly (2000-2002: 2.315 years; 2006-2011: 2.015 years).

In India, Bharat Merino is a synthetic fine-wool sheep breed. Mallick et al. [46] studied a total of 5,511 animals with a mean generation interval of 4.19 years, the pathways as follows: sire-son (n: 528) 3.57; sire-daughter (n: 2216) 3.40; dam-son (n: 529) 4.95; dam-daughter (n: 2238) 4.93.

5. Conclusion

Based on the data provided by the Hungarian Sheep and Goat Breeders Association, we identified 15308 pathways for the Gyimesi Racka in all parents and all offspring categories where the birth dates were known. If we only look at the relationship of individuals for further breeding, this number is considerably less (2089). Based on this data, we have examined the generation interval in two different ways. In the first approach, based on the original raw data and then using a natural logarithm transformation to normalize the data.

As expected, we found a difference between the two calculation methods.

An example for the application of the natural logarithm transformation in pedigree analysis and its differences in results is provided by Kárpáti et al. [34], who calculated Wright's inbreeding coefficients of individuals in the Gyimesi Racka in two different ways. They found that, in contrast to untransformed data, the results obtained using transformed data more accurately reflect changes within the population. For example, using the transformed data, it was possible to detect an increase in the inbreeding coefficient of the inbred subpopulation per maternal generation (last five: from 5.69% to 9.54%) more quickly, whereas using the untransformed data, the inbreeding coefficient in the same category was virtually stagnant between 8 and 10%.

Here following pedigree relationships were determined: parent – all offspring, sire – breeding offspring, sire – non-breeding offspring, dam – breeding offspring, dam – non-breeding offspring, parent – breeding offspring, sire – sire, sire – dam, dam – sire, dam – dam.

The average generation interval calculated without transformation is about 4.04 years. The detailed parent-offspring lineages show remarkable differences in the length of generation intervals depending on the sex of parents and the use of offspring. They are shorter for the sire-offspring path than for the dam-offspring one and they are significantly shorter for the connection between parents and offspring for breeding than between parents and offspring only. The longest generation interval was found in the relationship between mother and breeder (4.63 years). The shortest interval between successive generations was found between breeders and their lambs for breeding (3.28 years). However, the trends change when looking at the relationship between parents and their offspring that are used for further breeding. In this case, there is a significant difference in the evolution of the generation interval according to the sex of the parents, but this is of course not the case for the sex of the offspring ($p > 0.05$). For ram producing mothers this value is 4.00 years, interestingly for mothers contributing to reproduction with female offspring this value is not much higher (4.14 years, $p > 0.05$). For the relationship between fathers and their lambs for breeding this value was even lower (3.14 years).

The natural logarithm transformation was applied to all categories of pathways studied. In all cases, the transformation resulted in lower, i.e. less favourable, values. The generation interval for the whole flock, i.e. all parents and all offspring born, was only 3.61 years, while for the breeding individuals a generation interval of 3.29 years was obtained. The paternal pathways are also shorter in this case, but here the generation interval between rams and their prospective breeding rams was already below 3 years (2.92 years). The longest was 4.13 years, again only between dams and non-breeding offspring, but this was 0.5 years lower than in the non-transformed data.

The lower values on the sire side were obtained because rams were replaced more often and remained in breeding for a shorter time, while dams remained in breeding for one year longer on average ($p < 0.05$). Thus, the statistically proven difference between the sex of the parents reflects the traditional mating method and the extensive husbandry. However, the difference is not so large (about 0.5 – 1) that the contribution of the two parentage sides to the next generation's abilities could become excessively disproportionate, given similar average genetic abilities of the parents, which are the least different from the average.

All these pedigree-based studies offer opportunities for further research. If we can get a picture of genetic variability, we can select the individuals that carry the most diverse alleles. The biological samples collected from them form then the basis for molecular genetic studies. These can be used to describe the genetic make-up of an animal breed and to compare the individuals in its population with the genetic material of other breeds (GenBank sequences, Gáspárdy, 2021). This is intended to shed light on the relationships between different breeds and to clarify their origin. In addition, the spatial changes of sheep breeds (dispersal from the domestication centre, movements during colonisation activities, etc.) will be traced. The mapping of genetic diversity and the practical application of this knowledge is an important interest of breeders. Especially in the case of rare animal breeds, the aim is to learn about the breed- and flock-specific allelic variants. It is a cardinal future task to protect individuals carrying rare allelic variants and to keep them in breeding, even if the appearance and production characteristics of the given individual do not justify this at first glance. Representing the maternal lines of indigenous breeds, these female representatives reliably characterize genetic diversity.

Unfortunately, however, the number of founding families is decreasing from generation to generation, so it is necessary to strive for a representative individual to survive from each family. The indispensable basis for gene preservation as precisely as possible is the processing of correctly maintained pedigree data, during which we can get to know the founding female individuals and identify the ancestral families that can be derived from them -Founder Sampling Method. In order to get a complete picture of genetic diversity, we must select descendants who are still living representatives of the oldest families for DNA sample collection [47, 48]. The more generations the family has lived, the better, but in general it can be said that the animals for statistical processing must be selected from individuals representing families that have lived through at least 7-9 generations. Based on genetic research, Annus et al. [49] showed that Tsigai sheep share a common origin with European breeds.

In many cases the origin of the breed varieties is disputed. Especially if they are phenotypically similar and bred in neighbouring countries under different names. Analysis of mitochondrial DNA has shown that the Gyimesi Racka breed in Hungary and the Turcana breed in Romania are very closely related [50].

These few examples above illustrate that population genetics studies can be combined with molecular methods to great effect. All this helps us to recognise the alleles of our endangered species, which is an important aspect of gene conservation.

Summary

The thesis focuses on the Gyimesi Racka sheep, a breed that is considered endangered. The primary objective of this part of the study is to determine the generation interval of this breed and to understand its significance in the context of conservation efforts for endangered sheep breeds.

It is of high importance to study the generation intervals in livestock, particularly for breeds at risk of extinction. In the literature review the breed Gyimesi Racka is described and a short overview of its history is given. Then a comprehensive overview of existing research of various sheep breeds, their generation intervals and therein their differences is given.

In the methodology section the data collection process is described, which involved creating a pedigree file of the data from 2005 – 2020 and conducting normality tests on the data to ensure its reliability, which was not given but due to the source of the data accepted as such. The study then employs two different methods to calculate the generation interval, first without normalization and then with natural log transformation.

The results were that the generation interval in both calculations were under 4 years which is the time that should be standard for an endangered species. The generational interval of the raw data looked more favorable and closer to the 4 years.

The generation interval that was log transformed before showed worse numbers, the GI from sire- sire even being under 3 years. Overall in both calculations the paternal pathways showed shorter GIs compared to the maternal pathways.

All this shows that there is still work to be done to preserve the Gyimesi Racka sheep breed as such and with this to keep genetic material to vanish.

The generation interval is the just the start for a bigger research area of the genetic outline of this breed, their founding animals, the genes already lost and different suggestions to the farmers to save an endangered sheep breed and preserve as many genetic traits as possible.

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