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Progeny information about the Hungarian Furioso-North Star Horse population based on pedigree data

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Abstract

The general aim of animal conservation programmes is to maintain genetic diversity. The genetic structure of Furioso-North Star horse breed was studied based on pedigree records. The base pedigree information was given by the Furioso-North Star Horse Breeding Association. Herd book data of the active breeding population of registered Furioso-North Star horses in 2016 was analysed. The North Star VIII-13 (III. tm.) stallion had 95 registered foals. The Furioso VI-52 (XIII.tm.) horse had the most selected progenies with 50 offspring. Ékes broodmare had the most registered progenies with 13 offspring. Daimio I-10 Árverő and Ékes had the most selected progeny with 8-8 selected foals.

Keywords: pedigree analysis, Furioso-North Star horse, progeny

Introduction

The general aim goal of animal conservation programmes is to maintain genetic diversity. Complete pedigree information is considered very important in the animal breeding, especially in horse breeding. The Furioso-North Star breed is originated from Mezőhegyes Stud (founded in 1785) based on two stallions founder stallions, Furioso Senior and North Star Senior (EDWARDS and GEDDES, 1991). Four genealogical lines have been formed during the years, Furioso A, B and North Star A, B (GERGELY et al., 2016). This breed is an important gene resource.

The demand to get to know the genetic variability of livestock animals has been continuously increasing (WOOLLIAMS et al., 2002). In pedigree analysis, information about the animal's ancestors, relatives and progenies is used to carry out analyses to estimate parameters, which characterize the genetic structure and diversity of the populations (MAIGNEL et al., 1996). This analysis will suggest appropriate strategies to monitor mating and manage genetic variability to enlarge the selection basis useful for a selection program (VALERA et al, 2005). In recent years many publications have described the genetic variability of different breeds of horses based on pedigree analysis The complete or partial results of genetic diversity and population parameters were reported in the literature for various horse breeds, including Brazilian Sport Horse (MEDEIROS et al., 2014), Dutch harness horse (SCHURINK et al. 2012), Hanoverian (HAMANN and DISTL, 2008), Holstein (ROOS et al., 2015), English

Thoroughbred (BOKOR et al., 2013), Lusitano (DA SILVA FARIA et al., 2018b), Old Kladruber (VOSTRÁ-VYDROVÁ et al., 2016), and Quarter Horse (DA SILVA FARIA et al., 2018a) Shagya Arabian (PJONTEK et al., 2012) breeds.

Therefore, the aim of the research study was to analyse the pedigree information of the registered Hungarian Furioso-North Star population especially the progeny data.

Material and methods

The basis of the current study was the Hungarian breeding population of Furioso-North Star Horse breed in 2016. The active population (3208 horses) was chosen as reference when needed. The base pedigree information was given by the Furioso-North Star Horse Breeding Association. There were the pedigree data of 16746 animals in the developed database.

The population was described with number of progenies (for sires and mares) and number of selected progenies what were computed using POPREP (GROENEVELD et al., 2009) software.

Results and discussion

The genetic diversity is crucial part in the genetic conversation work. To maintain the genetic variability of the breed from generation to generation the number of selected progeny could be important information. In an ideal situation each animal has the chance to become parent to the next generation. This does not work in a real population because of the selection, financial problems etc., so the number of progenies per breeding animals are really heterogeneous. In the conservational point of view, the optimal solution is if every broodmare having selected 4 mare offspring, that way guaranteed keeping the broodmares genotype. This solution also not working in nowadays, because every breed having a lot of constraints.

Figure 1, shows 30 breeding stallions having the most registered progeny in the analysed whole database. There were almost 100 offspring within the pedigree of Furioso-North Star horses from two stallions, North Star VIII-13 (III. tm) from North Star line and Gyanu I (Furioso XXXVI. tm) from the Furioso line, respectively. There were 15 stallions in the whole population having more than 50 registered progenies. There was only one English Thoroughbred (Masetta) among the thirty stallions. The most stallion had just 1-2 offspring in the herd book, 106 horses had more than 10, and only 8 had more than 20 progenies.

The 30 breeding stallions having the most selected progeny in the analysed whole database is presented in Figure 2. The Furioso VI-52 (XIII.tm.) horse had the most selected progenies with 50 offspring. There were 17 stallions in the whole population having more than 20 selected progenies. The 60% of stallions had just 1 selected in the herd book, another 16% had just two foals and 3% had more than ten selected progenies. Due to the breeding method of the Furioso-North Star, we found 8 English Thoroughbreds among stallions having most selected progenies.

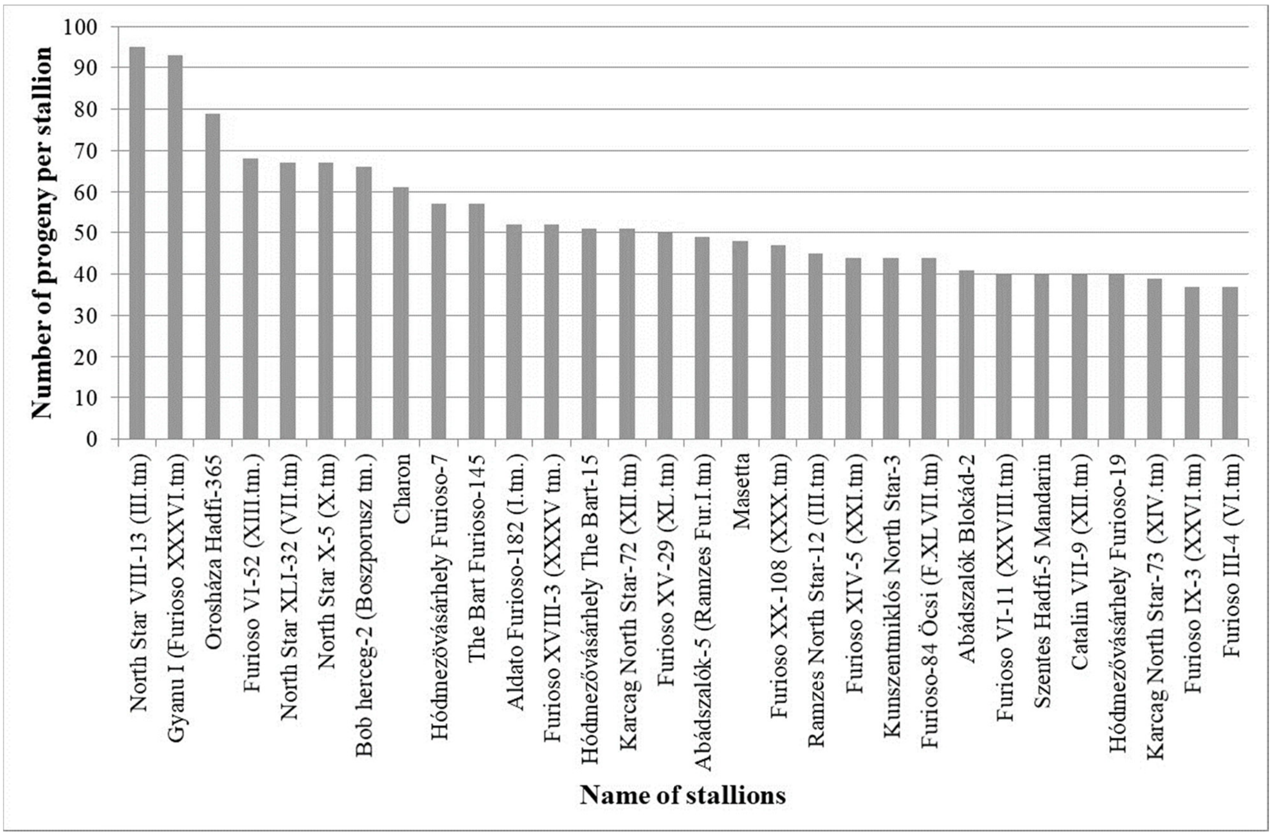

Figure 1. Stallions having the most registered progeny

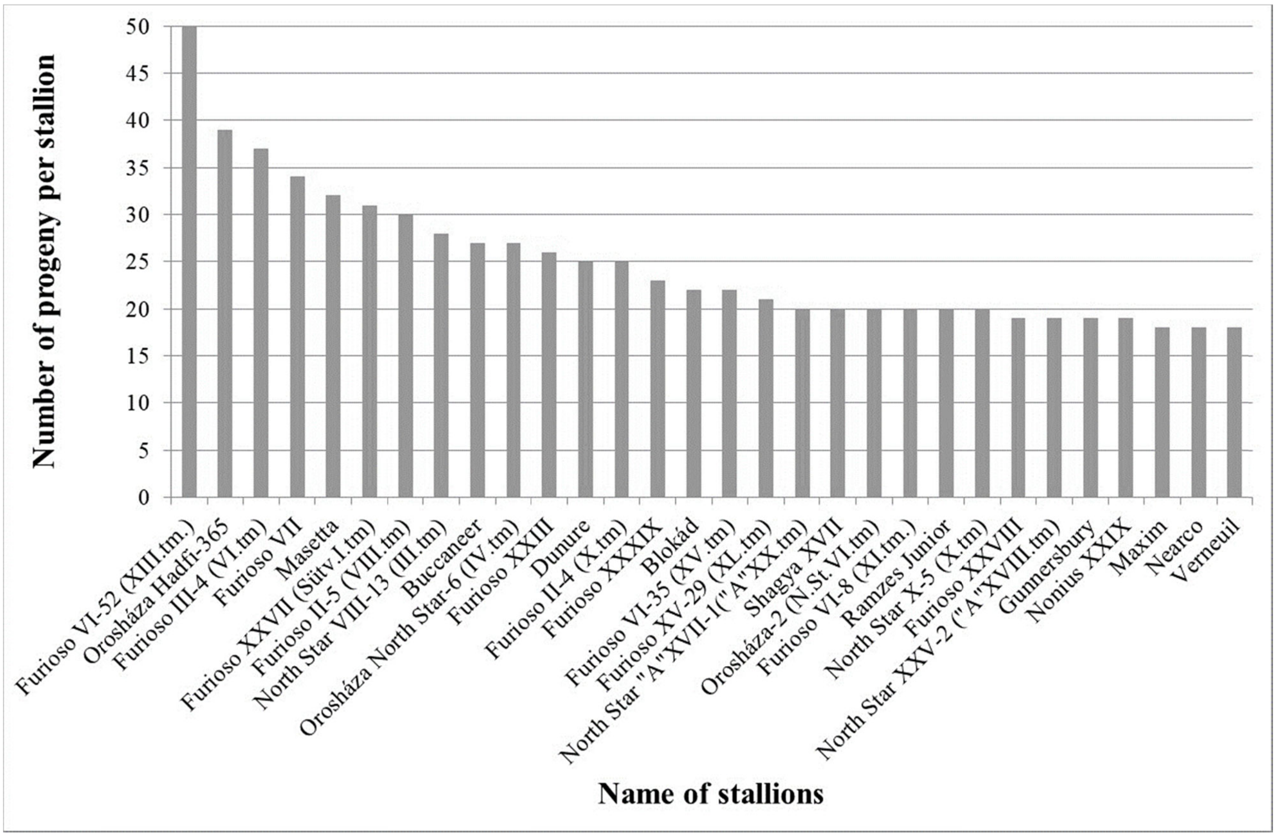

Figure 2. Stallions having the most selected progeny

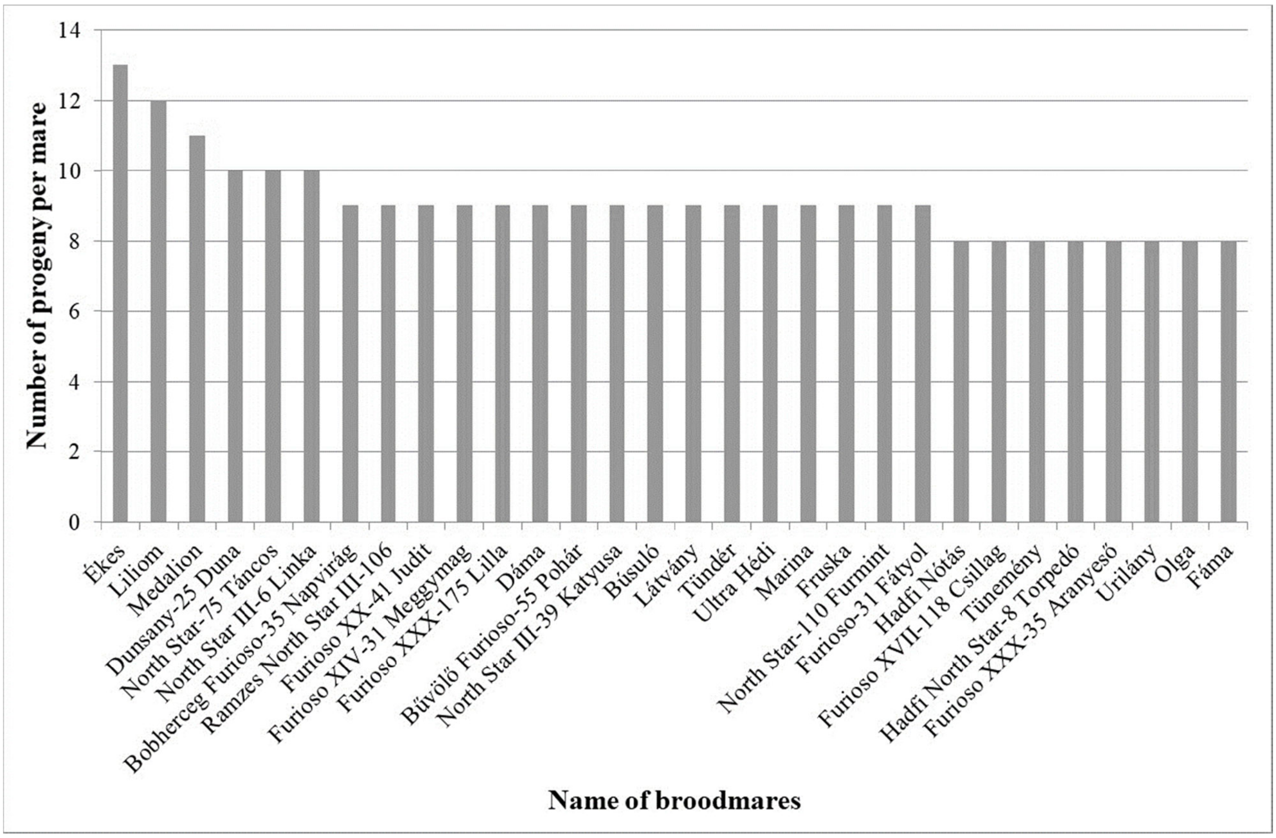

Figure 3. Broodmares having the most registered progeny

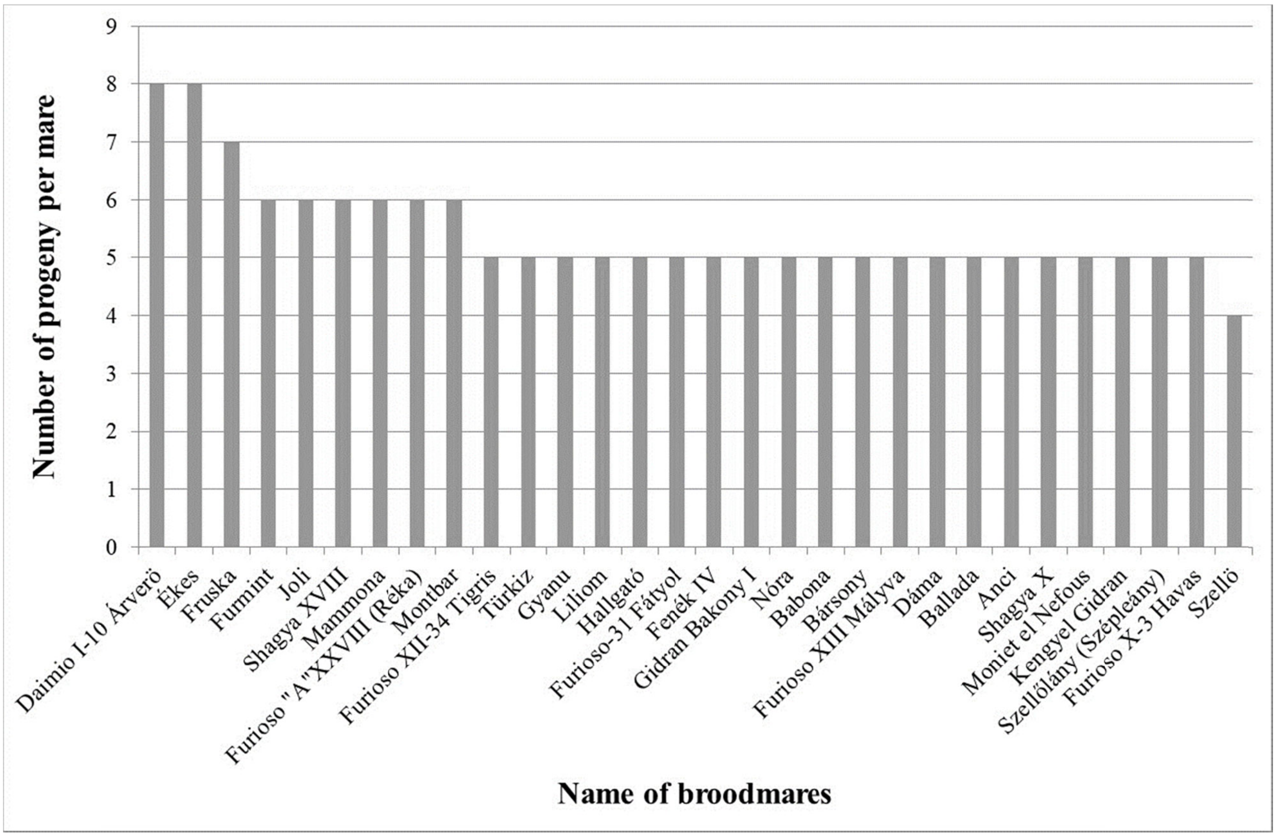

Figure 4. Broodmares having the most selected progeny

Figure 3. illustrates 30 breeding broodmares having the most registered progeny in the analysed whole database. This indicator is really informative about the selection of the breed. There were 6 broodmares in the whole population having more than 10 registered progenies. Every broodmare had at least 8 times foaling. Ékes had the most registered progenies with 13 offspring. In the whole database the 80% of broodmares had just one progeny and just 129 horses had five and more registered foals.

The top 30 breeding broodmares having the most selected progeny in the analysed whole database are shown in Figure 4. There were 6 broodmares in the whole population having more than 10 registered progenies. Every broodmare had at least 4 selected offspring. Daimio I-10 Árverő and Ékes had the most selected progeny with 8-8 selected foals. The most broodmares (85%) had just 1 selected progeny. Just a few (1.2%) of broodmares had 3 and more selected offspring.

Conclusions and recommendations

There were two stallions almost 100 registered offspring North Star VIII-13 (III. tm.) and Gyanu I (Furioso XXXVI. tm.). The Furioso VI-52 (XIII.tm.) stallion had the most selected progenies within the Furioso-North Star pedigree. The Daimio I-10 Árverő and Ékes broodmares had the most selected foals in the population. Ékes had the most registered 13 foals from this 8 was selected.

Acknowledgement

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Challenges in conservation of Tyrolean Grey Cattle

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Abstract

The paper is concerned with the Tyrolean Grey Cattle breed, an autochthon, dual purpose, alpine mountain cattle breed. The objective of the paper is to describe the typical characterisation of the breed and reveal the possible changes of body measurements, type and maturity by time.

For the analysis body measurements of 59 animals were recorded in 2014, and with the collaboration of the "Südtiroler Rinderzuchtverband" herd book society body measurements data of 46 individuals (from 1946 until 1957) were collected. Adjustments for 3 years of age were achieved for each *body measurement* and *body index* by quadratic regression, then analysis of variance was performed according to time era. For control of the difference in *age at first calving* between the past and present cattle Gehan's Wilcoxon Test and Log-Rank Test were carried out.

Regarding the body measurements and body indices the results showed increased body parts and altered body proportions, caused by selection for larger frame and dairy type, respectively, during that time (in most of case $p<0.05$). It was also determined that there is a significant difference in age at first calving ($p<0.001$) between the past (cca. 40 months) and present (cca. 34 months) Tyrolean Grey Cattle populations.

The conclusion of the investigation is that the Tyrolean Grey Cattle breed is still today a robust cattle and related to the aboriginal form despite of some discernible modification proven.

Keywords: Tyrolean Grey Cattle, body indices, age at first calving

Introduction

This study shall carry out a recent evaluation and a review about the differences between the present and former Tyrolean Grey Cattle. It should contribute successfully the preservation of that breed, which is still considered as an endangered livestock breed of Alpine region. At the beginning of the investigation, the South Tyrolean Grey Alpine Cattle Association ("Südtiroler Rinderzuchtverband") was contacted to receive information.

The Tyrolean Grey Cattle breed or Grey Alpine (in German called „Tiroler Grauvieh", in Italian „Razza Grigio Alpina Tirolese") is an autochthonous, dual purpose, mountain cattle breed. The majority of the Austrian population which consists of about 18,000 cattle is situated in county Tirol (ZAR, 2015). In Italy the Grey Alpine cattle is distributed primarily in the Province of Bolzano (South Tyrol) and in valleys of the Dolomites in the Provinces of Trentino and Belluno; total population in Italy counts approximately 14,000 heads (Südtiroler Rinderzuchtverband, 2017). It is expected that aboriginal peoples brought the so called „Torf breed“ along from Asia Minor/Middle East to the Alpine regions. This breed was a small short horned cattle. Later, this original” Short Horn” cattle was crossed with the larger „Allemannen-breed“ and „Kelten-breed“, and so resulted the progenitor of the Tyrolean Grey Cattle (BREM et al., 1990). The presence of the Tyrolean Grey Cattle is documented since 800 A.D. Roman authors, like Plinius and Strabo, reported about the Grey Alpine breed and lauded the high milk yield. Nineteen Seven were made the first uniform standards for the Tyrolean Grey Cattle containing the compilation of the physical characteristics, behavioural traits and performances of all these little different livestock, creating one standardized breed (INNERHOFER, 2002).

According to the breed standard the animals are of medium size (height at withers is 126/133 cm, cows and bulls) and weight (body weight is 575/950 kg, cows and bulls) and have a robust constitution, a correct fundament, very hard claws and hardiness. They are rustic, frugal, have a strong instinct for finding their own food and are able to convert even coarse vegetation efficiently. This mountain pasture competence is also really important for pastures and meadows, because the Grey Alpine is grazing in a sparing way. The colour of the coat is determined in a greyscale. Characteristics are also the dark, nearly black muzzles and claws. On the back there is often a dorsal stripe of lighter shade. The horns are varnish-black or dark-grey and at their end mostly brighter.

The investigation was realized in three fields: 1.) Herd book data evaluation to receive information about the connection among the individual cows of this breed. The distinction of the genetically related animals is very crucial for the mating on the course of the maintenance of the genetic diversity. 2.) Evaluation of the conformation by taking the body measurements with respect of the age of the animals and period of time. 3.) Analysis of age at first calving as measure of maturity. These later evaluations are important to determine the breed characteristics, as well as to compare the results got 80 years ago and today in order to reveal any possible changes.

Material and method

Pedigree-based inbreeding coefficients and body measurements adjusted for 3 years of age were computed. Besides taking body measurements, the identification number of cow, the identification number of her parents, the date of her birth and the date of her first calving were also recorded.

For the calculation of the coefficient of inbreeding, a genealogical research was implemented. The genealogical research is composed of the pedigree collection until 5th generation of all 62 investigated cattle. The pedigree information was placed at the disposal from the “Südtiroler Rinderzuchtverband”. The identification numbers of all cows with the ancestors were digitised in computer. The genealogical tree from mother side and father side were compared for control of relation of identical ancestors and then inbreeding coefficient was calculated.

All present data (61 cows) were recorded in South Tyrol in the surroundings of Bozen/Bolzano in the summer 2014. The former data (48 cows) of the Grey Alpine Cattle from were collected from the first existing herd book of the South Tyrolean Grey Cattle Association covering a ten-year-long period (from 1940 until 1957; Herdbuch “Südtiroler Grauviehzuchtverband”, 1949).

The body measurements were checked in scatterplots by age (Table 1 and Table 2). Four outliers (two animals over 6 years in the 40´s and 50´s period and two ones above an age of 10 years in 2014) were deleted from the statistical evaluation, because these greatly affected the fit of the regression curve.

Table 1. Quadratic equations of age dependent body measurements in time period 1946-1957

Height at withers	100.0802+6.3876*x-0.6203*x^2
Chest depth	51.4964+4.3124*x-0.4199*x^2
Chest circumference	136.289+14.1627*x-1.4395*x^2
Coxal distance	30.8594+5.2111*x-0.5459*x^2

Table 2. Quadratic equations of age dependent body measurements in 2014

Height at withers	125.6178+1.364*x-0.0881*x^2
Chest depth	70.8517+1.0239*x-0.0247*x^2
Chest circumference	185.7699+1.6825*x-0.0684*x^2
Coxal distance	47.8723-0.521*x+0.0464*x^2

Adjustments for 3 years of age were achieved for each body measurement by quadratic regression, then analysis of variance was performed according to time era. For example the new value for the coxal distance of Grey Alpine cattle 1946-1957 is calculated by the following equation:
coxal distance adjusted for 3 years of age = 30.8594+(current coxal distance-30.8594)+(5.2111*(3-current age))-((0.5459)*((3-current age)^2)).

From the body measurements were calculated the body indices (Table 3). The larger the index value, the more pronounced is the index property at the animal.

Table 3. Calculation of body indices

Index of compactness	100* chest circumference / height at withers
Index of narrowness	100 * height at withers / coxal distance
Index of leg length	100* height at withers / chest depth
Index of strength	100 * chest circumference / chest depth

Then like before for body measurements, qudratic equations were determined for body indices (Table 4 and Table 5).

Table 4. Quadratic equations of age dependent body indices in time period 1946-1957

Index of compactness	85.0311+43.6224*x-7.5091*x^2
Index of narrowness	417.013-93.9716*x+14.8665*x^2
Index of leg length	97.698-20.7971*x+3.5804*x^2
Index of strength	206.3627+49.0656*x-8.6092*x^2

Table 5. Quadratic equations of age dependent body indices in 2014

Index of compactness	144.0396+1.4283*x-0.1207*x^2
Index of narrowness	254.6761+8.7285*x-0.6426*x^2
Index of leg length	69.4121-0.6111*x+0.0498*x^2
Index of strength	251.1413+3.6698*x-0.5165*x^2

In case of body indices too the adjustments were achieved for 3 years of age, individually. For example the equation for index of compactness 2014:
index of compactness = 144.0396+(current index of compactness-144.0396)+(1.4283*(3-current age))-((0.1207)*((3-current age)^2)).

The average age of the cows at the taking of body measurements was slightly over 3 years (with a range of 1.6–12.7 years of age, and a median of 3.72 years). This was the reason that body measurements and the body indices were adjusted for 3 years of age.

Additionally, we were interested to know the age at first calving in the Grey Cattle population and to carry out a comparison which will reveal its possible change by time.
First, from the date of birth and date of first calving the age at first calving was calculated. Later on, the age at first calving was evaluated by survival analysis (two-sample comparison). The difference between the past (cattle born between 1946 and 1957) and present (cattle born between 2001 and 2012) values the Gehan's Wilcoxon Test and Log-Rank Test were carried out. This statistical evaluation was done by the Statistica (Statsoft Inc., 2013) data analysing software.

Results and discussion

The average of inbreeding coefficient as a measure of homozygosity was as low as 1.13% (max. 2.73 and min. 0.20%).

Regarding the body measurements the results showed increased body parts, caused by selection for larger frame and dairy type, during that time (Table 6).

Table 6. Results on body measurements adjusted for 3 years of age according to the time era (in cm)

Time era	n	Hight at withers Mean ±SD P< 0.001		Chest depth Mean ±SD P< 0.001		Coxal distance Mean ±SD P< 0.001		Heart girth Mean ±SD P< 0.001	
Grey Alpine cattle 1940-1950	46	113.8^{a}	5.12	60.6^{a}	3.11	41.6^{a}	3.92	165.7^{a}	10.11
Grey Alpine cattle 2014	59	125.9^{b}	4.87	72.9^{b}	3.14	48.3^{b}	3.04	187.9^{b}	8.82
Total average	105	120.7	7.80	67.6	6.84	45.4	4.77	178.3	14.49

a, b – different letters mean significant differences (Tukey's post-hoc test)

Results on body indices investigated show us that almost all of them went through a change statistically significantly (Table 7). The mean values for index of compactness (p= 0.015) and index of strength (p< 0.001) decreased in good concordance with the target breeding programme for more milk production. So, the cows became less compact (slimmer) and less strong in front (thinner). At the same time, they became of longer legged (shallower body depth) as it is revealed in the significant lower figure of today index of leg length (p= 0.021). Tendencies in body indices are in causal connection with changes in body measurements.

Table 7. Results on body indices adjusted for 3 years of age according to the time era

Time era	n	Index of compactness Mean ±SD P= 0.015	Index of narrowness Mean ±SD P= 0.299	Index of leg length Mean ±SD P= 0.021	Index of strength Mean ±SD P< 0.001
Grey Alpine cattle 1940-1950	46	152.3^{b} 25.85	261.1 52.65	65.6^{a} 12.30	280.6^{b} 30.65
Grey Alpine cattle 2014	59	143.6^{a} 6.58	252.7 28.77	69.5^{b} 2.92	241.6^{a} 19.00
Total average	105	147.4 18.22	256.3 40.97	67.8 8.60	258.7 31.42

a, b – different letters mean significant differences (Tukey's post-hoc test)

Table 8 shows the age at first calving in the Tyrolean Grey Cattle. The cows born between 1946 and 1957 calved at about 42 month of age firstly, while the today representants of the breed do this much earlier, at about 34 months of age.

Table 8. Age at first calving in the investigated Tyrolean Grey Cattle populations (in months)

Time era	n	Mean	Median	Standard deviation	Lower quartile 25%	Upper quartile 75%
Grey Alpine cattle past (1946-1957)	48	42.2	38.8	14.8	32.2	47.8
Grey Alpine cattle present (2001-2012)	60	33.6	33.3	3.9	31.2	35.8
Overall mean	108	37.4	34.1	11.1	31.4	38.3

The Figure 1 is representing the cumulative proportion of cows calved firstly by age. The two most frequently used test in survival analysis are the generalized Wilcoxon test (Gehan test) and the log-rank test. The former test is more sensitive to discover the difference at the beginning, while the latter one is to reveal the differences at the end of functions (MCGRADY, 2005).

In our investigation the Gehan's Wilcoxon Test values were as follows WW = 1031.0, Sum = 4198E2, Var = 1046E2, Test statistic = 3.184264 and P< 0.002. This means that there is a strong, significant age difference between the past and present Tyrolean Grey Cattle populations in the beginning of first calving. In the Log-Rank Test we got the next values: WW = -21.17, Sum = 102.19, Var = 25.469, Test statistic = -4.19500 and P< 0.001. These values inform us a further strengthening of the difference between the cows being in age at first calving by ageing.

From the age at first calving we can state that the beginning of calving was/is still at later age on average; close to 3 years of age. However, a statistically proven decrease in the age at first calving was also detected.

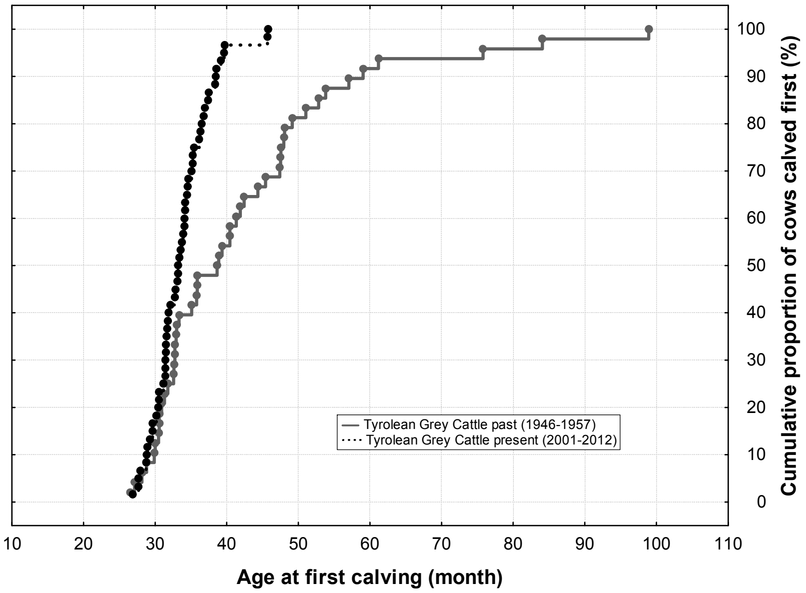

Figure 1. The cumulative proportion of cows calved first according to time era

Conclusion and recommendation

The conclusion of the investigation is that the Tyrolean Grey Cattle cannot be considered as an inbred breed. It is a satisfactory result. The inbreeding coefficient of 1.13%, shows that the assortative mating is under constant control and supervision of the Grey Alpine Cattle Association.

The inbreeding coefficient is in a continuous increase in the modern cattle breeds. Its actual value is the highest for the US- and Canadian Holstein-Friesians (5 and 4%, respectively). It is a little bit lower in Europe (UK: 3%, NL: 3%, I: 3%, and F: 2%). It elevates year by year by approximately 0.2 on average. Among the breeding bulls one can regularly see larger inbreeding coefficient than among cows.

The breed is still nowadays a robust cattle and related to the aboriginal form despite of some discernible modification proven. The physical aspects are described by the measurement of different body parts of a cattle. The body parts are the withers, the chest depth, the coxal distance and the chest circumference. As it was expected and looked for, in all comparisons (with the exception of index of narrowness) significant differences were determined between cattle of the 40´s-50´s and cattle of today.

Deviations in the height at withers and the leg length are consequences of target breeding to improve the milk performance. The enlargement of coxal distance can support a greater space for udder and calving ease.

Also the mean values of body indices altered with the target breeding programme, but the maintenance of the rustic fundament and the capability of locomotion on mountain terrain of that breed should also be treated as an aim. This later is related to protection of natural habitat of domestic and wild animals too, and draws attention to exploiting the benefits of heritage resources in rural tourism.

It was quite remarkable to find out during the research that the cattle from the past gave birth to their calves first at or over approximately 4 years of age only.

However, the results of the research show a steady decrease in the age of the first calving compare to the results of the present day. Nevertheless, this decrease is rather management-dependant due to the fact this was a result of a delayed start of utilization of the cattle as breeding animals.

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Ergebnisse der Sequenzanalyse des mitochondrialen Gens Cyt-b von Cikta Schafen

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Zusammenfassung

Das Ziel dieses Beitrages ist die mitochondriale Untersuchung von Cikta Schafen. Die Untersuchung gefährdeter Rassen ist eine der wichtigsten Aufgaben des Konservierungsprozesses auf der ganzen Welt.

In Bezug auf die Nukleotid- und Haplotyp-Diversität zeigt die Rasse einen gewissen Grad an genetischer Verengung, was eine Folge des Flaschenhalseffekt‘s sein kann. Die durchschnittliche Anzahl paarweiser Nukleotiddifferenzen ist jedoch relativ hoch, was auf unterschiedliche genetische Eigenschaften der in den Betrieben vorkommenden Familien hinweist.

Weder der TAJIMA D-Test noch die Fs-Statistiken von FU für die Cikta Schaf Herden wurden statistisch bewiesen, das heißt die einmal stark reduzierte Bestandgröße der Rasse, die aus der Rassengeschichte bekannt ist, verursachte keinen genetischen Drift, die Rasse befindet sich in einem genetischen Gleichgewicht.

Während unserer Arbeit konzentrierten wir uns auf die DNA-Analyse von Cikta Schafen und die Statistiken hinter den mathematischen Werten, die Prognose der Rasse anzeigen könnten. Das Auffinden gemeinsamer Gene bei Zaupel-Nachfolgern wird für Züchter auch in Zukunft von großer Bedeutung sein, kann jedoch mehr Zeit in Anspruch nehmen.

Schlüsselwörter: Zaupel, Cikta, Nukleotid- und Haplotyp-Diversität

Einleitung

Zaupel Schaf ist eine ausgestorbene Schafrasse mit überlebenden deutschen und österreichischen Nachfolgervarianten: das Waldschaf (Sumavska), das Steinschaf (Bovska) und das Bergschaf. Der vierte Nachkomme des Zaupelschafes ist das Cikta Schaf, welches mit schwäbischen Einwanderern aus dem 18. Jahrhundert nach Ungarn kam (KOPPÁNY, 2000). Sie sind genetisch am nächsten beieinander veranlagt. Jede dieser Rassen zeichnet sich durch starke Robustheit, gute Fruchtbarkeit und natürliche Resistenz gegen einige Krankheiten aus. Die Qualität der Wolle ist nicht so fein wie die von Merino Schafen, aber aufgrund der anderen Eigenschaften lohnte es sich sehr, sie in der Zucht zu behalten. In Bezug auf die Anzahl der Herden sind diese Rassen immer noch extrem gefährdet, aber die Anzahl der Individuen und Züchter nimmt zu.

Mitochondriale DNA (mtDNA) ist DNA in den Mitochondrien. Mitochondrien kommen in großer Zahl in allen Zellen vor und liefern Energie in Form von ATP (Adenosintriphosphat). Bei Säugetieren besteht die mitochondriale DNA aus einer relativ kleinen kreisförmigen Doppelhelix. Schafe haben, wie Menschen ungefähr 16.500 Basenpaare ihres eigenen Genoms für Mitochondrien, welches in der Evolutionsforschung verwendet wird, da mtDNA bei Säugetieren streng mütterlich veranlagt ist. Die väterliche Linie trägt nicht zur mtDNA bei den Nachkommen bei, da die väterliche mtDNA während der Penetration oder der ersten embryonalen Zellteilung verloren geht und eine Rekombination zwischen mütterlichen und väterlichen Varianten bisher unbekannt ist (SCARPULLA, 2005).

Schaf-mtDNA wird ebenfalls verwendet, um die Geschichte der Domestizierung und in diesem Falle die Entwicklung verschiedener Rassen zu untersuchen. Es gibt mehr verschiedene mitochondriale mütterliche Abstammungslinien (z.B. Haplotypgruppen A, B, C und D), davon kommt B hauptsächlich in Mufflons und in europäischen Rassen vor (TAPIO et al., 2016).

Cytochrom-b ist ein Protein, das vom Cyt-b-Gen der mitochondrialen DNA kodiert wird, die zu einer Gruppe gehört, die als Komplex III von elf Proteinen bezeichnet werden. Es fungiert als Teil einer Elektronentransportkette, welche Redoxenergie in eine Kraft umwandelt, die Protonen bewegen kann. Das mitochondriale Cyt-b-Gen wird in systematischen Studien verwendet, um die Unterschiede auf vielen taxonomischen Ebenen zu verifizieren. Bei Säugetieren ist dies eines der besten Gene für die Analyse, da die meisten Sequenzinformationen bereits bekannt sind. Aufgrund der hohen Sequenzänderung ist das Cyt-b-Gen ein vernünftiges Instrument zum Vergleich von Tieren derselben Art (CASTRESANA, 2001).

Bei dieser Verarbeitung ist es unser Ziel, die genetische Vielfalt der Rasse Cikta, basierend auf der Cytochrom-b-Region, zu bewerten.

Material und Methode

Die für die Blutentnahme ausgewählten Individuen wurden im Zuchtbuch der nationalen Cikta Herde aufgeführt und waren aus Sicht, der mtDNA-Analyse die Vertreter der ältesten 36 Familien mit 4-5-6 Ahnenreihen, entsprechend ihrer mütterlichen Abstammung. Um die biologische Probe zu sammeln, haben wir insgesamt drei Herden ausgewählt, in denen alle lebenden Vertreter der alten Familien zu finden waren: Nagydorog (mit 20 Familien und 40 Proben), Pénzesgyőr (11 Familien und 22 Proben) und in Szécsénke (mit 5 Familien und 10 Proben).

Im Herbst 2015 wurden Blutproben aus der Halsvene in Blutröhrchen entnommen, die EDTA-Antikoagulans enthielten. Sie wurden bis zur Verarbeitung bei -20°C gelagert.

Die mtDNA wurde unter Verwendung des SIGMA GenElute Blood Genomic DNA Kits gemäß den Anweisungen des Herstellers isoliert. Der Cytochrom-b-kodierenden Region (1140 bp) wurde eins von MEADOWS et al. (2005) entworfener Primerpaar zugewiesen. Ein programmierbares Thermal Cycler 2720 PCR-Instrument (Applied Biosystem) wurde verwendet, um das DNA-Segment zu amplifizieren.

Die Sanger-Sequenzierung des Cyt-b-Genes wurde in beide Richtungen durchgeführt, was zur Bewertung einer 990-bp-Region (14130-15119) aus 67 Probe führte.

Mit der Software DnaSP v6.0 haben wir die Anzahl der polymorphen Stellen in der gesamten Probe bestimmt und den mittleren Nukleotiddifferenz innerhalb und zwischen den Herden berechnet (ROZAS et al., 2017). Zur weiteren statistischen Verarbeitung verwendeten wir den von FU und LI vorgeschlagenen Test (1993), das JUKES und CANTOR-Methode (JUKES und CANTOR, 1969; JUKES, 1990) sowie TAJIMA-Test (1989).

Ergebnisse und Auswertung

Tabelle 1 zeigt die Anzahl der pro Herde bewerteten Individuen und Mutationen.

Tabelle 1. Individuen und Mutationen pro Herde

Parameter	Szécsénke	Pénzesgyőr	Nagydorog
Anzahl der Familien	5	11	20
Anzahl der Individuen	10	16	41
Anzahl der ausgewerteten Sequenzen	10	16	41
Anzahl der polymorphen Stellen	12	12	15
Anzahl der Mutationen	12	12	15

In der gesamten Population betrug die Anzahl der monomorphen Basen im Cyt-b-Mitochondriengenom 920, während die Anzahl der polymorphen (mutierten) Basen 16 betrug. Für letztere wurden eine einzelne (singleton) und 15 multiple (parsimony) informative Mutationen an den folgenden Basisstellen gefunden: 687 und 135, 237, 249, 339, 423, 426, 456, 506, 525, 613, 705, 726 743, 765, 843.

Der Bestand in Szécsénke teilt elf polymorphen Positionen mit dem Bestand in Pénzesgyőr und zwölf Positionen in Nagydorog; somit kann die genetische Identität zwischen den Cikta Herden als signifikant angesehen werden.

Die Gesamtzahl der Haplotypen betrug 10, während die durchschnittliche Nukleotiddiversität (π) war $2{,}96*10^{-3}$.

In einer anderen ungarischen einheimischen Schafrasse, Zigaya fand PÁSZTOR (2016) 22 variable Basenstellen in der Cytochrom-b-Region, von denen sich 11 einzelne und 11 multiple Mutationen aufwiesen. Daraus lässt sich schließen, dass Zigaya Schafe eine vielfältigere genetische Zusammensetzung zu haben scheinen als die Cikta Schafe.

Der Nachweis der durchschnittlichen Anzahl von Nukleotiddifferenz (k) und der Nukleotiddiversität (π) ist besonders nützlich bei der Bewertung verschiedener Bestände. Die Nukleotiddiversität (π) ist die Anzahl verschiedener Nukleotide an einer bestimmten Basenstelle auf zwei zufällig ausgewählten Chromosomen in einer Population. Dies bestimmt auch die genomische Vielfalt der Individuen in der Herde.

Tabelle 2. Werte von k und π pro Herde

Parameter	Szécsénke	Pénzesgyőr	Nagydorog
Durchschnittliche Anzahl von Nukleotiddifferenz,	4,067	2,258	2,961
Nukleotiddiversität, π	$4{,}34*10^{-3}$	$2{,}41*10^{-3}$	$2{,}99*10^{-3}$

Beide Anzeichen geben Auskunft über den Grad der Diversität innerhalb des Bestandes (Tabelle 2).

Es ist ersichtlich, dass die Herde in Szécsénke durch die größte Diversität mit der höchsten Anzahl an durchschnittlichen Nukleotiddifferenz (4,067) und Nukleotiddiversität ($4{,}34*10^{-3}$) gekennzeichnet ist. Diesem Bestand folgt der in Nagydorog, gefolgt von dem in Pénzesgyőr mit der geringsten Vielfalt.

Diese Nukleotid-Diversitätswerte sind jedoch ungefähr dieselben wie die beim Menschen ($3–11*10^{-3}$) und machen etwa ein Zehntel der Diversität der Essigfliege (*Drosophila melanogaster*) Populationen aus (LI und SADLER, 1991).

Tabelle 3 zeigt die Werte der durchschnittlichen Anzahl von Nukleotiddifferenzen (k) und der Nukleotiddiversität (π) im Vergleich nach Herde.

Tabelle 3: Werte von k und π in paarweisen Vergleichen von Herden

Parameter	Zwischen Szécsénke und Pénzesgyőr	Zwischen Szécsénke und Nagydorog	Zwischen Pénzesgyőr und Nagydorog
Durchschnittliche Anzahl von Nukleotiddifferenz, k	2,898	3,148	2,754
Nukleotiddiversität, π	$3{,}10*10^{-3}$	$3{,}18*10^{-3}$	$2{,}94*10^{-3}$

Im Vergleich von Szécsénke und Pénzesgyőr betrug die durchschnittliche Anzahl der Nukleotiddifferenz 2,898. Hier betrug die nach JUKES und CANTOR (Dxy (JC)) berechnete korrigierte Anzahl von Basensubstitutionen $3{,}27*10^{-3}$ mit einer Standardabweichung von $1{,}36*10^{-3}$.

Die durchschnittliche Anzahl der Nukleotiddifferenz zwischen Szécsénke und Nagydorog betrug 3,148, während die nach JUKES und CANTOR berechnete korrigierte Anzahl der Basensubstitutionen (Dxy (JC)) $3{,}47*10^{-3}$ mit einer Standardabweichung von $1{,}12*10^{-3}$ betrug.

Im dritten Vergleich (Pénzesgyőr und Nagydorog) betrug die durchschnittliche Anzahl der Nukleotiddifferenz 2,754, der Wert von JUKES und CANTOR (Dxy (JC)) $2{,}77*10^{-3}$ mit einer Standardabweichung von $0{,}68*10^{-3}$.

Gemäß dem in der gesamten Population durchgeführten TAJIMA-Test betrug die durchschnittliche Anzahl paarweiser Nukleotiddifferenzen (k) 2,926 und die Nukleotiddiversität (π) $3{,}13*10^{-3}$. Der Wert des TAJIMA D-Tests betrug -0,3751, statistisch nicht signifikant ($P> 0{,}10$). Ein signifikanter negativer Wert wäre ein Indikator für ein Übermaß an seltenen Variationen, oder eine demografische Expansion, während ein signifikanter positiver Wert ein Indikator für eine genetische Verengung (Flaschenhalseffekt) oder eine Fragmentierung in Subpopulationen wäre.

Der D*-Test von FU und LI ergab einen Wert von 1,1378 ($P> 0{,}10$), und der F*-Test von FU und LI ergab einen Wert von 0,7179 ($P> 0{,}10$) in der gesamten Population; keine waren signifikant.

Die FU- und LI-Testwerte für die Haplotyp-Diversität (Hd) betrugen 0,853 mit einer Standardabweichung von $0{,}61*10^{-3}$. Die FUs Fs-Statistik betrug 0,123.

In der Rasse Zigaya stellte PÁSZTOR (2016) fest, dass die Haplotyp-Diversität (Hd) 0,911 mit einer Standardabweichung von 0,077 beträgt; $\pi = 2{,}26*10^{-3}$. Auch aufgrund dieser Anzeichen weist das Cikta Schaf eine geringere genetische Vielfalt auf als Zigaya Schafe.

In der Variante der ungarischen Racka in Rumänien haben DUDU et al. (2016) höhere Werte festgelegt: Hd = 0,958 (Standardabweichung 0,009), $\pi = 7{,}00*10^{-3}$, wobei Cytochrom-b und Kontrollregion zusammen berücksichtigt werden. Die Kontrollregion, welche die Fähigkeit besitzt zu mutieren und nicht nur die vielfältigere Cytochrom-b-Sequenz der rumänischen Racka, können ebenfalls zum höheren Wert beitragen.

Weder der TAJIMA D-Testwert (-0,3751), noch der Wert der FU‘s Fs-Statistik (0,123) der Cikta Schaf Population wurden statistisch bestätigt. Dies weist darauf hin, dass sich die Rasse in einem genetischen Gleichgewicht befindet. Eine Abweichung davon gefährdet die Rasse jedoch nicht.

Schlussfolgerung und Empfehlung

Bei dieser Verarbeitung wurde die Cytochrom-b-Region der mitochondrialen DNA in Cikta Schafen anhand von 67 Individuen bewertet.
In Bezug auf die Nukleotid- und Haplotyp-Diversität zeigt die Rasse einen gewissen Grad an genetischer Verengung, was eine Folge des Flaschenhalseffekts sein kann. Die durchschnittliche Anzahl paarweiser Nukleotiddifferenzen ist jedoch relativ hoch, was auf unterschiedliche genetische Eigenschaften der in den Betrieben vorkommenden Familien hinweist.
Weder der TAJIMA D-Test, noch die Fs-Statistiken von FU für die Cikta Schaf Herden waren statistisch bewiesen, das heißt die einmal stark reduzierte Bestandgröße der Rasse, die aus der Rassengeschichte bekannt ist, verursachte keine genetische Drift, die Rasse befindet sich in einem genetischen Gleichgewicht. Die genetische Trennung der Familien in den Betrieben und der Zustand des genetischen Gleichgewichts bilden eine Grundlage für die Aufrechterhaltung der gegenwärtigen Vielfalt der Rasse.
Das Wissen und die konsequente Pflege alter Familien sind dafür unerlässlich.
Wir hoffen, dass die Berücksichtigung der mtDNA-Variabilität eine wichtige Rolle bei der Erhaltung der genetischen Vielfalt seltener einheimischer Rasse spielt.
Die verstärkte Betonung der mütterlichen Seite wird auch durch die Tatsache gerechtfertigt, dass Mutterschafe in einem höheren Anteil als Widder vorhanden sind und über einen längeren Zeitraum in der Zucht bleiben, so dass sie in größerem Umfang für die Umsetzung und Erhaltung der genetischen Vielfalt verantwortlich sein können.
Durch die Untersuchung der Vielfalt von mtDNA möchten wir auch eine Grundlage für eine effizientere Erhaltungszucht mit einer Auswahl innerhalb der Familie schaffen.
Das Auffinden gemeinsamer Gene bei Zaupel-Nachfolgern wird für Züchter auch in Zukunft von großer Bedeutung sein, kann jedoch mehr Zeit in Anspruch nehmen.

Danksagung

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Results of the sequence analysis of the mitochondrial gene Cyt-b from Cikta sheep

Abstract

The aim of this study is the mitochondrial examination of Cikta sheep. The investigation of endangered breeds is one of the most important tasks in the conservation process around the world.

In terms of nucleotide and haplotype diversity, the Cikta breed shows some degree of genetic narrowing, which can be a result of the bottleneck effect. However, the average number of pairwise nucleotide differences is relatively high, which indicates different genetic characteristics of the families occurring in the farms.

Neither the TAJIMA D test nor the Fs statistics from FU for the Cikta herds were statistically proven to be significant, i.e. the once greatly reduced population size of the breed, which is known from breed history, did not cause any genetic drift, the breed is in a genetic equilibrium.

During our work, we focused on DNA analysis of Cikta sheep and the statistics behind the mathematical values that could indicate breed prognosis. Finding common genes among Zaupel successors will continue to be of great importance for breeders in the future, but can take more time.

Key words: Zaupel, Cikta, nucleotide and haplotype diversity

Descriptive information of Transylvanian Naked Neck hen's egg production

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Abstract

Transylvanian Naked Neck chicken was a good farm animal having good egg production under suitable conditions. The egg production of the Transylvanian Naked Neck White, Black and Speckled population of the University of Debrecen Farm and Regional Research Institute of Debrecen was evaluated. Morphological traits (height, width and weight) and some composition parameters (weight of yolk/albumin and eggshell thickness) were measured during the experimental period. Transylvanian Naked Neck chickens have smaller and more peaked eggs compared to some (semi)-intensive genotypes, thought eggshell thickness is similar to those of, what can be important during transportation.

Keywords: Transylvanian Naked Neck, egg production

Introduction

Up to the beginning of th 20th century, the Transylvanian Naked Neck chicken was supposed to be a good farm animal as they were extraordinarily hard, firm and resistant. Previously, they were respected as good winter layers, having good egg production under suitable conditions.

Relationship between egg quality and genotype was identified by several researchers so it can be concluded that all characteristics have a genetic basis. PARMAR et al. (2006) found differences among various populations of Kadaknath breed. BÓDI et al. (2015) found that the unselected indigenous Yellow Hungarian chicken was similar or maybe better performance in physical traits (e.g.: egg yolk ratio, eggshell strength) compared to those of selected or layer hybrids.

The aim of this research study was to collect descriptive information from the egg production of the Transylvanian Naked Neck White, Black and Speckled breeds.

Material and methods

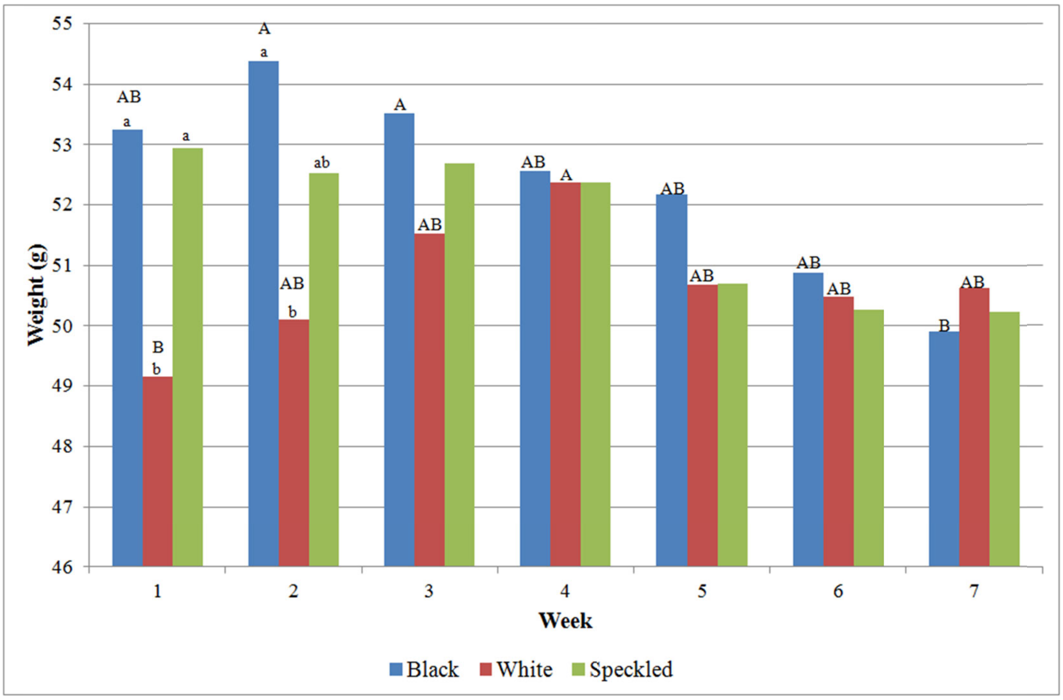
The egg production of the Transylvanian Naked Neck White, Black and Speckled population of the University of Debrecen Farm and Regional Research Institute of Debrecen was evaluated. The experimental data was collected in 2018. Within all weeks, 30 eggs were randomly chosen from the weekly laid eggs and morphological parameters (height, width and weight) were measured. In the next step, five eggs were again randomly chosen among the 30 to measure weight of yolk/albumin and eggshell thickness.

The differences among breeds and weeks of performance were evaluated with analysis of variance. The homogeneity of group variances was checked with Bartlett test, and because of homogenous variances, Tukey-test was used to discover the significance differences ($P<0.05$) among experimental groups. Statistical analysis was carried out using R software (R Core Team, 2014).

Results and discussion

There were significant difference among breeds only in the beginning of the data collection (Figure 1). Black Transylvanian Naked Neck hens had heavier eggs compared to whites in the first two weeks. During the evaluation of within breed performance, significant differences were found for the Black and White varieties whereas egg weight was similar for Speckled hens.

Egg weights of Transylvanian Naked Neck breeds were lower compared to Yellow Hungarian and (semi-)intensive genotypes (BÓDI et al., 2015) and reported by SZALAY-LENCSÉS (2004). Transylvanian Naked Neck breeds had heavier eggs than Kadaknath breed (PARMAR et al., 2006).



^{a,b}: Significant difference ($P<0.05$) among breeds within weeks,
^{A,B}: Significant difference ($P<0.05$) among weeks within breeds

Figure 1. Changing of egg weight during the data collection period

There were no significant differences found for the height of the eggs neither among breeds nor among weeks during the data collection period (Figure 2). The average egg height changed within a small interval and was smaller than reported by BÓDI et al. (2015) for Yellow Hungarian chicken and (semi-)intensive genotypes.

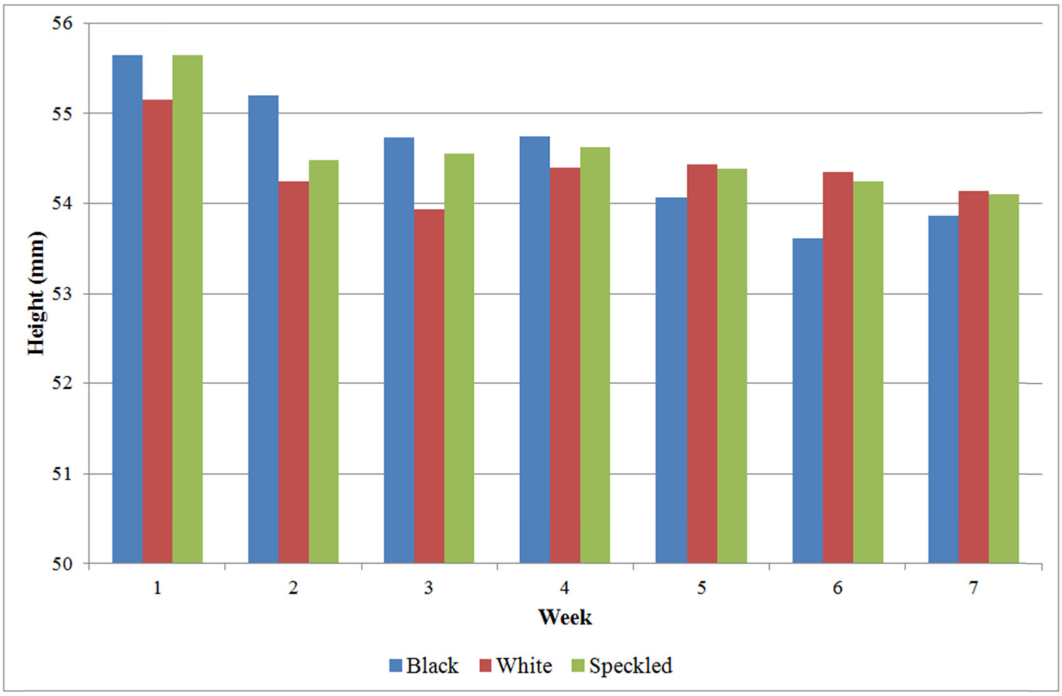
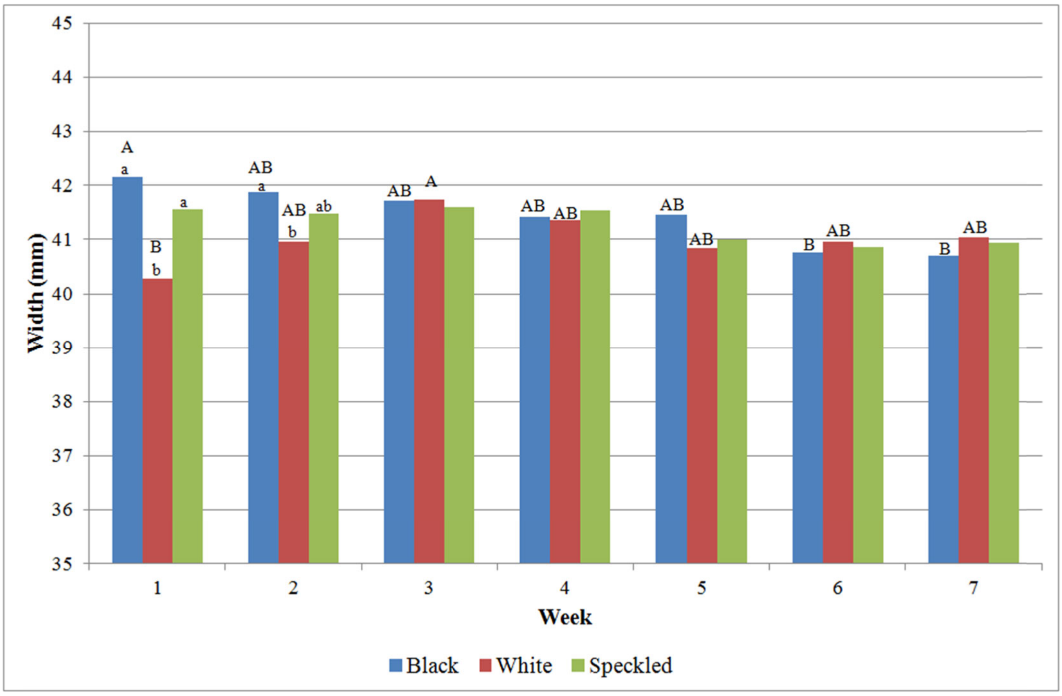


Figure 2. Changing of egg height during the data collection period

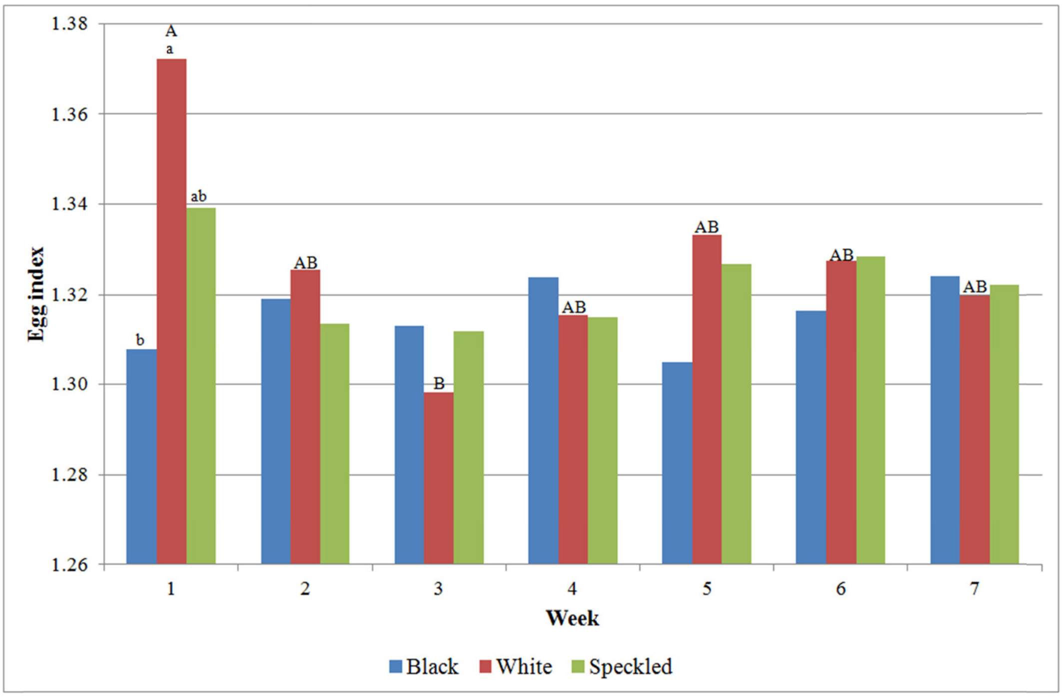
The tendency of egg width was quite similar to the weight of the eggs (Figure 3). White Transylvanian Naked Necks laid narrower eggs than Blacks in the first two data collection week. There were no significant differences among breeds within weeks in the remaining time period. The within breed comparison was not significant for Speckled hens and the significant differences for Black and White chickens were within a small interval. Transylvanian Naked Neck hens had narrower eggs than Yellow Hungarian chicken and (semi-)intensive genotypes (BÓDI et al., 2015).



^{a,b}: Significant difference (P<0.05) among breeds within weeks,
^{A,B}: Significant difference (P<0.05) among weeks within breeds

Figure 3. Changing of egg width during the data collection period

There was statistically significant difference between White and Black Transylvanian Naked Neck chickens in the first week of data collection as eggs of White hens were more peaked compared to those of Blacks (Figure 4). Speckled and Transylvanian Naked Neck hens had quite similar shaped eggs like Yellow Hungarian chickens and slightly peaked compared to (semi-) intensive genotypes (BÓDI et al., 2015) and more rounded than the Indian indigenous Kadaknath breed (PARMAR et al., 2006).



^{a,b}: Significant difference (P<0.05) among breeds within weeks,
^{A,B}: Significant difference (P<0.05) among weeks within breeds

Figure 4. Changing of egg index during the data collection period

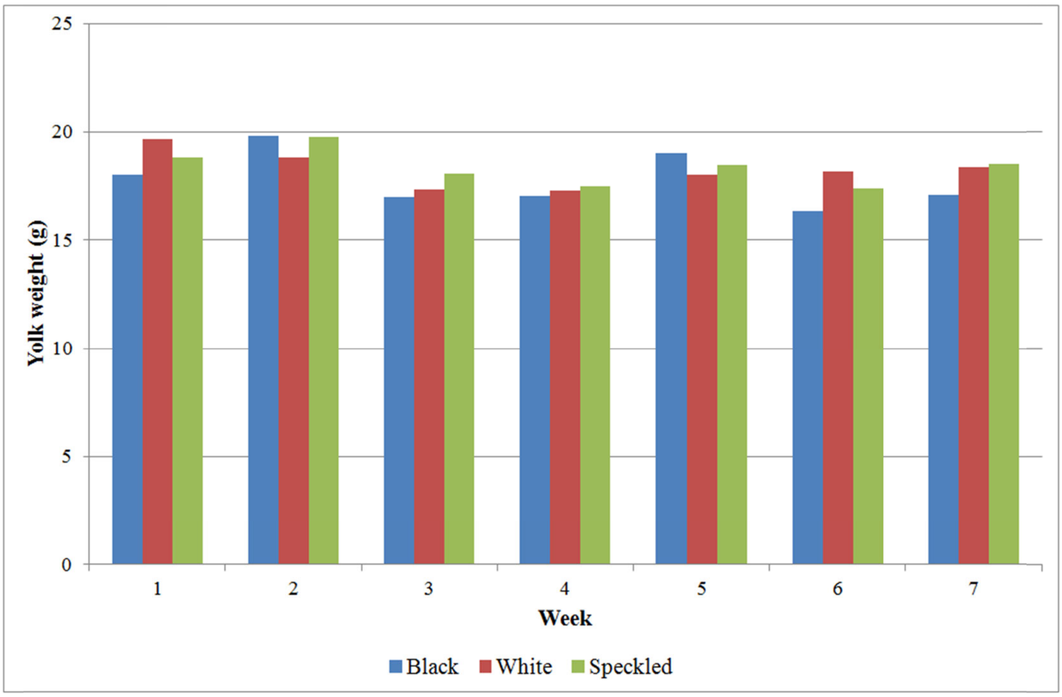
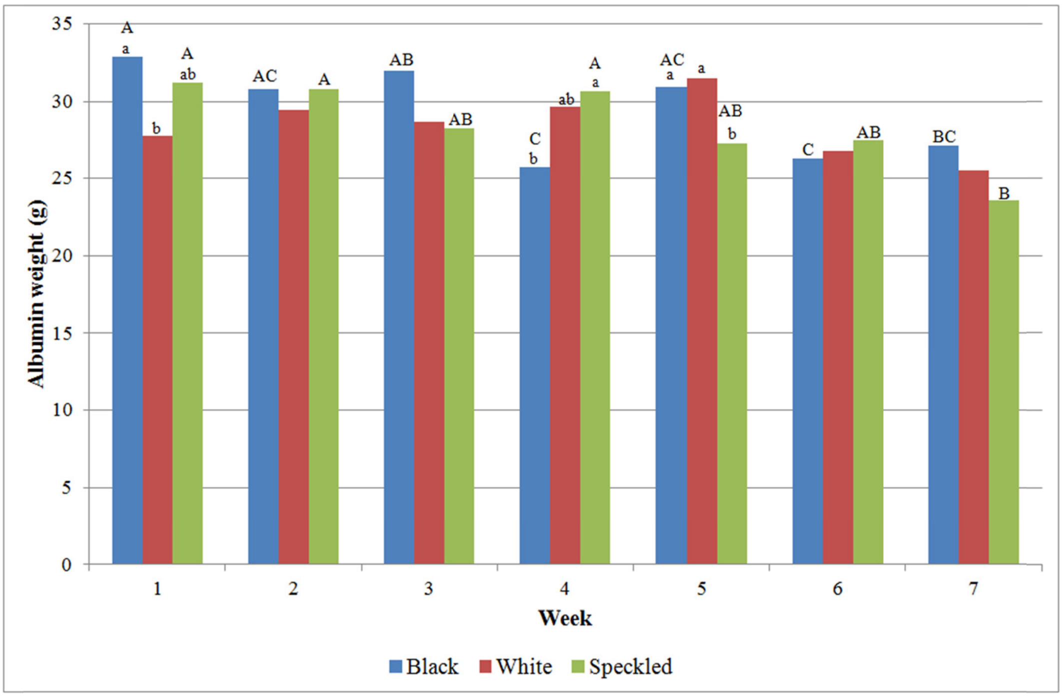


Figure 5. Changing of yolk weight during the data collection period

There were no significant differences found for the yolk weight of eggs neither among breeds nor among weeks during the data collection period (Figure 5). The average yolk weight changed within a small interval and was higher than reported by PARMAR et al. (2006) in their study.

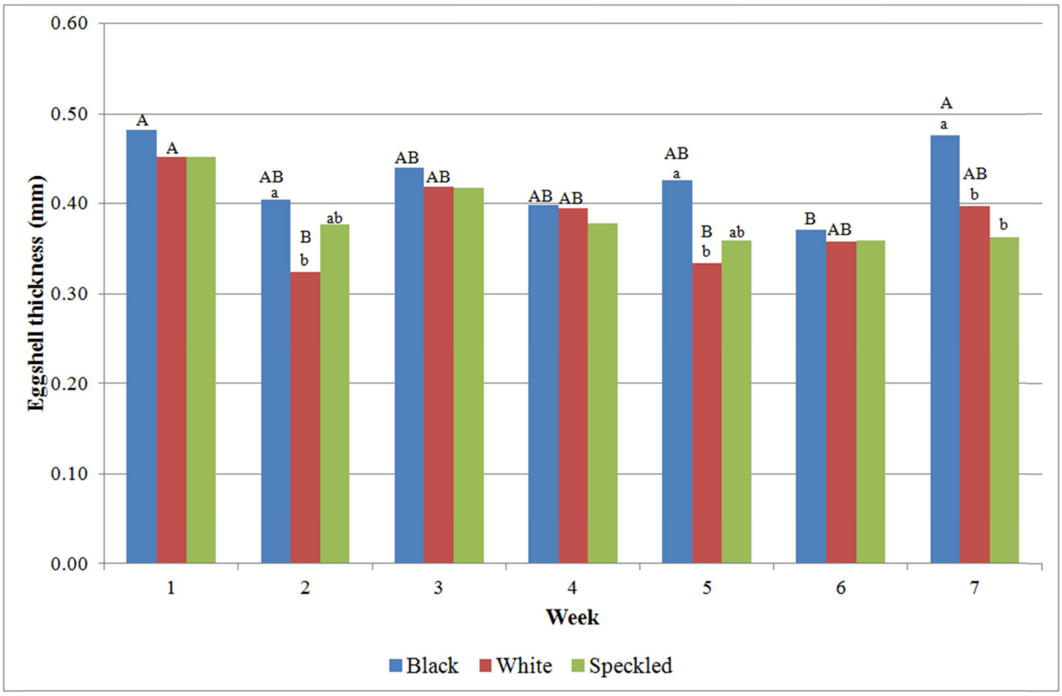
Significant differences were found among breed in the first, fourth and fifth week of data collection (Figure 6). Speckled hens produced more albumin in the fourth week than Blacks, whereas Blacks exceeds performance of Whites in the first and Speckled had lower albumin weight in the fifth week than the other breeds. Albumin weight of White hens was not significantly different during the examined time period whereas some differences were found for Black and Speckled chickens. The albumin weight of Transylvanian Naked Neck chicken breeds were higher compared to PARMAR et al. (2006) results of an Indian indigenous breed.



^{a,b}: Significant difference ($P<0.05$) among breeds within weeks,
^{A,B}: Significant difference ($P<0.05$) among weeks within breeds

Figure 6. Changing of albumin weight during the data collection period

There were significant differences among breeds in the second, fifth and seventh weeks as Black Transylvanian Naked Neck chickens had thicker eggshell compared to the Whites (Figure 7). The eggshell thickness of the Speckled hens was not changed significantly during the examined time period. Significant difference was found between first and sixth week for the Black hens, whereas eggshell thickness of White hens in the first week was differed from those of in the second and fifth weeks. Transylvanian Naked Neck chickens eggshell thickness is in agreement with SZALAY-LENCSÉS (2004) results reported for Hungarian indigenous chickens and BÓDI et al. (2015) found for Yellow Hungarian chicken and (semi-)intensive genotypes. Eggshell thickness was continuously higher for all breeds during the examined time period than it was presented in PARMAR et al. (2006) study for Kadaknath chicken breed.



^{a,b}: Significant difference (P<0.05) among breeds within weeks,
^{A,B}: Significant difference (P<0.05) among weeks within breeds

Figure 7. Changing of eggshell thickness during the data collection period

Conclusion and recommendation

It can be concluded that Transylvanian Naked Neck chickens have smaller and more peaked eggs than some (semi)-intensive genotypes, thought eggshell thickness is similar to those of, what can be important during transportation.

Acknowledgement

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Slovak national rabbit breeds − A review

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Abstract

A rabbit breed is a distinct variety created through natural selection or selective breeding for specific characteristics, including size, fur, feed conversion ratio, climate adaptability or temperament. Due to the varied genotype, a large number of varieties became breeds in a relatively short period of time. In Slovakia, the coordinator of rabbit breeding is the Slovak Union of Small Animal Breeders. There are two main types of rabbit breeding - for production purposes and purebred rearing. The national rabbit breeds arose out of the fixation of specific genetic traits in fur colour, type and body shape in consequence of mutation and combination. Some of breeds are present as very small populations consisting of approximately 20 breeding females and of 10 to 15 males. The aim of our work was to describe the characteristic features of the Slovak national rabbit breeds generated by Slovakian breeders.

Keywords: Slovak, rabbit, national breed

Introduction

Rabbit husbandry is well-known and widespread throughout the world. A rabbit breed is a distinct variety created through natural selection or, more often, through selective breeding for specific characteristics, including size, fur (length, quality, or colour), feed conversion ratio, climate adaptability or temperament. Due to the varied genotype, a large number of varieties with a varied gene pool became breeds in a relatively short period of time.

There is a long year's tradition of rabbit husbandry in Slovakia established already in the mid-19th century. At the turn of the 19th century, numerous breeder societies were founded, which brought significant social and economic contributions to the husbandry of the existing breeds and creation of new ones. First breeding organization was found in the 1923 in Holíč.

There are two main types of rabbit breeding - for production purposes (meat, skin, fur) and purebred rearing (exhibition). Nowadays, rabbit population in Slovakia consists of about 70 purebred breeds, including many colour varieties. The national rabbit breeds arose out of the fixation of specific genetic traits in fur colour, type and body shape in consequence of mutation and combination. The coordinator of rabbit breeding is the Slovak Union of Small Animal Breeders. Some of breeds are present as very small populations consisting of approximately 20 breeding females and of 10 to 15 males. Rabbit is, after poultry, the most

efficient converter of proteins in cellulose rich plants into food with high-value animal protein. With the current societal focus on sustainability and avoidance of competition between food and feed, rabbit meat production is thus especially interesting.
The aim of our work was to describe the characteristic features of the Slovak national rabbit breeds generated by Slovakian rabbit breeders.

Slovak rabbit breeds

Slovak Gray Blue Rex − the first Slovak national breed of rabbits was bred by Mr. Imrich Vanek of Holič, the assessor and breeder. For the first time, the new breed was presented to the public at the 2nd district exhibition of rabbits in Holič in 1956. In 1959, the breeder submitted an application for recognition of the breed, but the recognition took place only in 1965 and it entered the European Standard of Breeds a year later under the name of Pearl Rex. In the European Standard of Breeds it was classified among small rexes. Mr. Miloš Supuka modified Slovak Grey-Blue Rex into an attractive type of medium-sized short-haired rabbits as we know him today. Nowadays, the Slovak Grey Blue Rex is successful at all breeding exhibitions at home and abroad (Brno, Prague, Bratislava, Nitra, Leipzig, Wales, Budapest, Belgrade), and its breeding extends beyond the borders of the Slovak Republic. In Slovakia 700-900 animals are reared.
Dwarf Slovak Gray Blue Rex has begun to appear in our exhibitions in 2000 and since then has been a very popular breed especially for beginning breeders.

Blue of Holic Rabbit – breeding of this second Slovak national rabbit is attributed to Mr. Imrich Vanek of Holič. It was recognized on 15 October 1975 at the National Exhibition of Rabbits and Fur animals in Nitra. Since then, it has spread throughout the country, but it is also reared in the Czech Republic, Germany, Hungary, Belgium, the UK and currently in the USA. Its quality improvement and present attractive appearance is a result of a long-year activity of several breeders (Mr. Stecz, Mr. Hrabovský, Mr. Šuster, Mrs. Miča and Žák from Záhorie and, currently, Mgr. Novák, the Supuka family and Mr. Pôsa). Breeders of Blue of Holic Rabbits are associated in the Club of breeders of national breeds and rexes. In Slovakia, there are 260 - 390 of these animals kept.

Nitra Rabbit − the third Slovak national breed of rabbits. A substantial contribution to its creation was make by the team of the Research Institute of Animal Production in Nitra under the leadership of Jaroslav Zelnik. For the breeding, Russian, French silver and Californian Rabbits were used. The Nitra Rabbit was recognized on November 16, 1975 at the Nitra´s National exhibition. At present, it is reared in a blue and a wild-blue colour, and it is a favourite breed of rabbits especially for its very good utility properties. Breeders of Nitra Rabbits are associated in the KANINO Club. Currently, 1,300-1,500 animals are reared in Slovakia.

Zobor Rabbit − one of the youngest national breeds of rabbits in Slovakia. Its breeding was carried out by the team of breeders led by Zelnik, Rafay and Malík. The first rabbits with this special appearance were obtained already in 1976. Although this group of rabbits was kept, the activities for the breed recognition continued only after 2000. Zobor Rabbit was recognized at the State exhibition in 2005 in black colour pattern. Nowadays, breeders have also been trying to reach blue colour pattern, and even rabbits with a rex-like coat. Its breeders are associated in an autonomous Club of rabbit’s breeders. At present, there are 100 - 120 rabbits reared in Slovakia.

Zemplin Rabbit – the creation of our fourth national breed of rabbits is attributed to Jozef Jonek from the municipality of Soľ, assisted by Miloš Supuka. The name of the breed is derived from the location of its origin, namely the Zemplín region.
Zemplin Rabbit was recognized at the State exhibition in Nitra on 22 November 1987. However, the first rise in its popularity among breeders occurred only in the 1990s. In 2006 Ze rabbit won the „Golden Kosák“ award at the Agrokomplex Exhibition in Nitra. The Zemplin Rabbit is included in the European Standard of Breeds and currently, in addition to Slovakia, it is also reared in the Czech Republic and Hungary. Breeders of Zemplin Rabbits are organized in the Club of breeders of Zemplin rabbits. At present, there are 800 -1,000 animals breeding in Slovakia.

Liptov Bold-Spotted Rabbit – one of the youngest Slovak national breeds of rabbits. The first colour pattern was wild, which was recognized at the Nitra National Exhibition in 2005 and later, in 2008 it was in a wild-blue colour. However, the recognition itself was preceded by the long-term work of the breeder, the most difficult part being fixing the head drawing. At its breeding the following combinations were proved successful: Vienna wild-coloured and Dutch wild-coloured, or Vienna Wild-Blue and Dutch Pearl. It is a smaller to medium breed with good productivity and fertility, which appears more and more on exhibitions of all kinds. There are several colour patterns in Liptov Bold-Spotted Rabbit: wild-coloured, grey-blue, black and blue.

Zemplin Rex – belongs among the most recent Slovak national breeds of rabbits. This breed was recognized at the State exhibition in Nitra in 2007, and its founder was the Supuka family from Vyšný Žipov. This is a short-haired form of the Zemplin Rabbit, in which the uniqueness of this colour was emphasized under influence of rex-like coat. The breeding basis is still relatively small, but new breeders are coming every year, and thus the incidence of these rabbits in different types of exhibitions is increasing.

Slovak Pastel Rex – bred by the Supuka family. The Slovak Pastel Rex was recognized on the State exhibition in Nitra in 2007, and since then it became more popular among the breeders both at home and abroad. The Slovak Pastel Rex attracts attention by its irredeemable pastel colour, resembling white coffee. The rearing of this rabbit breed is coordinated through the Club of Breeders of National Breeds and Rexes.

Dwarf Slovak Pastel Rex – the breeding of this Slovak national breed of rabbits is attributed to the Supuka family, who applied for its recognition on December 2, 2005 at the IX. National animal exhibition in Nitra. Since then, this breed has been regularly exhibited at all kinds of exhibitions and its breeding is organized via the Club of Breeders of National Breeds and Rexes.

Štrba Gepard Rabbit and Štrba Gepard Rex – the first one was recognized as a breed at the State exhibition of animals in Nitra on December 3, 2015. The breed ranks among medium-sized ones. The coat is relatively dense, elastic with a distinctive gloss and rich undercoat. The ideal coat length is 2.5-3.0 cm. The drawing consists of a combination of coat drawing and Japanese drawings, which are modified from stripes to individual spots.
Štrba Gepard Rex is a short-haired, rex-shaped form of the Štrba Gepard Rabbit recognized at the National exhibition of animals in Nitra on November 26, 2016.

Chrabrany Rabbit – the breeding of this unique rabbit breed is attributed to Peter Šípoš the farmer, assessor and breeder. It is essentially a Siamese Rabbit with red signs, brown eyes and the palest body of the meat type. The standard Chrabrany Rabbit has the length of the auricles between 11 and 12 cm. The drawing consists of a mask and coloured auricles. The mask covers the nose part; it has a regular oval shape, reaching the eye level. Drawing of auricles is sharply bordered at the root. The limbs are coloured up to the elbow joint. The tail is only coloured on the surface, the bottom of the tail is pale to white (GG allele); under intense colouration the bottom of the tail may be slightly fiery. The colour of the drawing is yellow-red. The coat colour of the white base is white or slightly yellowish-red. The eye colour is brown.

Slovak Pastel Rabbit – the creation of one of the newest breeds of rabbits is attributed to the farmer Ján Petrik from Dlhý Klčov, district Vranov nad Topľou. He began breeding on the basis of an approved research breeding. In 2013, at the occasion of a national exhibition, he applied for the breed recognition. The breed was recognized on November 22, 2013 at the State exhibition in Nitra. It is a medium-sized breed of rabbits with very good body musculature and interesting colouring.

Marten Blue Rabbit – the rabbit resembles the colour of pine marten, only in blue. It is a medium breed of a meat type with ideal weight of 4.00 to 5.00 kg, with good carcass maturity and yield. The basic colour is blue, with a backbone stretching from the root of the ear to the tail, with a dark blue stripe about 8 to 10 cm wide. The stripe is a part of the marten´s features, which include the dark colour of the auricle, nasal mask, eye rounds, tail and limbs.

Until 1993, this breed was recognized only in brown colour. For the creation of blue pattern, Big Marten Brown and Nitra Rabbit breeds (at that time with the genotype allele "gg") were used. In 1993, the breed was subjected to the recognition execution at the State animal exhibition, and the rabbit was classified in the European Standard of Breeds for rabbit assessment among the medium breeds in blue colour. In 2017, 120-140 rabbits of the "Marten" breed were registered.

Saris Giant Rabbit – the breeders from Prešov, under the direction of Ján Palisko, have been trying to create a large breed of rabbits weighing over 6 kg, with irregular Dutch drawing. As a result of the breeding process, black (Šoč), blue (Šom), wild (Šodiv) and yellow (Šož) rabbits were created. The breeding of this newly-bred rabbit is of relatively great interest for its very good slaughter yield and interesting colouring.

Conclusion

The main producing countries (Spain, France and Italy) highlight the importance of rabbit farming in maintaining rural communities, supporting the local economy and providing jobs outside urban areas. However, after many years of downturn in the consumption of rabbit meat and the low prices of rabbit fur, the commercial rabbit sector is facing fundamental challenges which will shape its future and threaten its sustainability.

Slovak national breeds of rabbits belong to the cultural biological heritage, and our aim is to preserve and raise it for future generations of breeders. It is really necessary to conserve and maintain animal genetic resources as a safeguard with respect to climatic changes, occurrence of diseases, social changes, genetic problems, selection errors and unexpected catastrophic events that can markedly affect biodiversity.

At present in Slovakia the use of biotechnological and genomic techniques allowed the development of new methods, which expanded the existing knowledge on gene structure, function and expression. Nowadays this knowledge is extensively implemented in the development of rabbit husbandry.

Acknowledgement

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Use of genomics tools in the conservation programmes in Slovenia

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Extended summary

The conservation of Slovenian autochthonous breeds is regulated by the National agricultural law and was implemented by the Public Service for Animal Genetic Resource Conservation. The obligations of the Public service are defined within the long term and annual programmes. The programme includes various actions with the goal to protect autochthonous endangered breeds and different genomic tools are used for genetic characterisations and paternity tests. One of the main activities of the programme is collecting and storing the biological material, which is essential for genetic relationship and genetic diversity analyses. Such studies are extremely important for maintaining genetic variability and diversity within endangered populations and to analyse the population structure of each autochthonous breed. In the past five years, different biological material, such as blood and hair tissue was collected. Likewise, some endangered autochthonous breeds were genotyped with different genomic tools (SNP, microsatellites), like Krškopolje pig, Cika cattle, Jezersko-Solčava sheep, Bovec sheep, Istrian Pramenka, Bela Krajina Pramenka and Drežnica goat.

The Krskopolje pig is the only autochthonous pig breed in Slovenia and its population has increased from 320 animals in 2003 to 2500 animals in 2019 (Register, 2019). Despite the population increased the breed is still considered as endangered. The monitoring of the genetic diversity and genetic relationship within the population is therefore extremely important. For that reason, the genetic relationship and the population structure based on the 11 molecular markers from 30 animals of the Krškopolje pig were studied. The analysis showed inconsistencies between the pedigree data in the herd book and the genomic relationship among animals based on the microsatellite markers. Consequently, pedigree data were improved (Annual report, 2015).

The only Slovenian cattle breed, the Cika cattle, is endangered breed and its population increased from 680 in 2003 to 5.200 in the last year (Register, 2019). The public service together with insemination centre and breeding organization for Cika cattle is conserving the sire semen for genetic reserves and artificial insemination of breeding dams. Each year, the breed structure of the selected 8-10 potential sires and genetic relationship between them and the rest of the population is analysed, prior they are included in the insemination centre. For each potential sire the genetic relationship and inbreeding coefficient is calculated and the breed structure is determined, based on the BovineSNP50 BeadChip (Illumina). According to the results, the most appropriate sire candidates are selected for the artificial insemination in the population and for the long term conservation of genetic material (Annual report, 2019).

There are four autochthonous sheep breeds conserved in Slovenia. The Bovec sheep and Istrian Pramenka as well as the Bela Krajina Pramenka have critically endangered status while Jezersko-Solčava sheep has vulnerable status. The population of Istrian Pramenka is

remaining constant from 2003 till today, while the population of the Bela Krajina Pramenka increased from 600 in 2003 to 1.060 in 2019. The Bovec sheep population increased from 1.700 to 2.800 breed animals while Jezersko-Solčava sheep have stable population size, approx. 4.300 animals (Register, 2019). The genetic diversity parameters and the breed structure was studied on the 44 unrelated animals of Bovec sheep and 24 Istrian pramenka, while Bela Krajina Pramenka and Jezersko-Solčava sheep were represented with five animals each. All samples were genotyped with Illumina OvineSNP50 BeadChip. The results shown that Bovec sheep is closely related to the Jezersko-Solčava sheep, while the Istrian Pramenka is related to the Bela Krajina Pramenka, what was expected due to the common geographical area. Likewise, the phylogenetic and admixture analyses showed the unique genetic identity of the Bovec sheep and the Istrian Pramenka. (SIMCIC et al., 2017)

Drežnica goat is the only Slovenian critically endangered goat breed. Their population is slightly increasing from 550 in 2003 to 720 in 2019 (Register, 2019). The population structure and genetic identity of Drežnica goat was preliminary analysed and compared with other goat breeds. Samples of 135 animals were genotyped with Illumina GoatSNP50 BeadChip with 53.347 genetic markers. The genetic diversity parameters were calculated and the relationship with other Alpine goat breeds was studied. Preliminary results showed that Drežnica goat is an authentic breed with almost no introgression of other breeds (POGOREVC et al., 2019).

In the past, the genetic diversity parameters have been analysed using pedigree data. The introduction of modern methods and genomic tools allowed us more accurate calculations and more accurate results compared to pedigree data methods. Such genomic studies are important support for the breed conservation decisions and the population management, especially for critically endangered autochthonous breeds. Some studies also shown, that analysed Slovenian autochthonous breeds are authentic and have independent origin compared with other breeds. The results are important also to support the decision making within breeding programmes as well as to support the conservation program decisions.

Key words: breed conservation programmes

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In memoriam
Honor. Assoc. Prof. Dr. László Radnóczi (1949-2020)

László Radnóczi has been a committed supporter, helper, innovator and builder of Hungarian animal husbandry since the beginning of his career. He gained timeless merits in laying the foundations of modern animal production, and then in building them, such as the breeds, the pedigree system, the Pig Uniform Identification and Registration System (ENAR), the performance tests and the breeding value estimation (BLUP). He was the initiator of the introduction of computer technology in pig registration.

László was born in January 24th, 1949 in a small village in Western Hungary (Lövő). He graduated from the Széchenyi István Grammar School in Sopron in 1967.
He graduated from the Agricultural University Gödöllő (1973). In the years following his graduation, he began to engage in game management and game breeding. Between 1977 and 1979, he turned to pig farming, where he was involved in housing and breeding technology consulting.
From 1979 he was an employee of the National Animal Husbandry and Feed Inspectorate (then, through reorganizations to its later successors), and from 1990 until 2010 he was the head of the pig breeding department which was supplemented in later years by sheep and goats. Meanwhile, he received his doctorate (1988) for his work on breeding value estimation in pigs. He was the head of the breeding commission at the Hungarian Breeders' Association for Purebred Pigs (1990-2010). He was awarded an honorary associate professor at the University of Debrecen.
From 2010, he was the head of the Animal Husbandry Department, and later became the deputy head of the Agricultural General Department of the Ministry of Agriculture. He was awarded the title of administrative Chief Adviser in 2012, and retired in 2015.
In 2017, his four decades of work in pig breeding was recognized by the Association of Hungarian Livestock Breeders for the Hungarian Animal Husbandry Award. In 2019, dr. István Nagy, Minister of Agriculture, awarded him with the Bronze Degree of the Tree of Life Memorial Plaque. Once a year, the most prestigious award given to the best pig farmer, the award-winning Breeder of the Year award was won in 2019 by him with the unanimous consent of the membership, based on the recommendation and suggestion of his colleagues.

In addition to the intensive breeds and hybrids, his attention also turned to the old domestic animal breeds. Thus, he dealt with the establishment of the gene pool of protected Mangalica pig; the tasks of breed recognition for all animal species (breeding organizations included) and general conservation of the endangered breeds.
Following the official registration of our DAGENE Association, he served as its first secretary for several cycles (1998-2010).

Late evening on April 29, 2020, the livestock society suffered a great loss: in the 72nd year of his life, due to an incurable disease, the emblematic personality of the agricultural administration, our colleague, our friend, dr. László Radnóczi passed away. His loss is touched by the Ministry of Agriculture at a personal level.

On May 18, 2020, - in view of the emergency situation due to coronavirus epidemic, in a small family circle - he will be escorted to his last trip in the Farkasréti cemetery (Budapest), according to the ceremony of the Roman Catholic Church. Our Association poured out its grace with a wreath.