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„PHD THESIS”
EXAMINING GENETIC VARIABILITY IN ANCIENT HUNGARIAN GOOSE POPULATION WITH MICROSATELLITES

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I. BACKGROUND OF THE RESEARCH

Changes in the past three century as a result of industrial evolution, which left a permanent mark in the world, didn't avoid agriculture. The production of agricultural products at commercial scales led to bigger production requirements. Selection only took high performance breeds into consideration. The appearance of the specialised breeds began to endanger old, traditional breeds. This phenomena can be detected especially in chicken husbandry, where due to large scale specialisation, the genetical substance is more homogeneous and narrower today (SECRETARIAT OF THE CONVENTION ON BIOLOGICAL DIVERSITY, 2000).

Hungary has always been a leader in sustaining native and traditional livestockbreeds. Efforts in this field were launched in 1960. At the beginning the official, Hungarian genetic reserve programs, efforts only concentrated on sustaining the number of the breeds and they only recently began propagating special and expensive genotypes, as well as evaluating the frequency of genetic variations and the distance between genotypes.

A Research consortium was set up and coordinated by the **University of Debrecen, Center of Agricultural Sciences, Department of Animal Husbandry** within the framework of a Széchenyi-plan (MIHÓK, 2006). The winning proposal entitled "Scientfic evaluation of the genetic and economic value of traditional livestock breeds" was led by Mr. Imre Bodó who is also involved in measuring the genetic variance in old, domestic animal breeds using modern, molecular and genetic methods. One aim of the program was to define the genetic variability in the existing gene reserve through **molecular genetic markers**.

In Hungary, the production of goose products and goose husbandry, have century-long traditions. This experience places Hungary among the world leaders in goose husbandry and goose product production (BOGENFÜRST, 2000). Sygnificant plume and live animal exports were made to neighbouring countries in the 19th century. Hungarian goose products gained a reputation primarily through white feathered field goose breeds. Two versions, the **plain** and **curled feather Hungarian goose** appeared at the beginning of 1800's, in the wetlands of the Great Plain (MIHÓK, 2000). The plain and curled feather Hungarian goose breeds were declared national treasures by the parliamentary decree of 32/2004 (IV.19.).

Though opinions are still split about its origin, most say that this breed is “unique of our country”.

This essay – as the part of the Széchenyi-plan entitled “Scientfic evaluation of the genetic and economic value of traditional livestock breeds” is aimed at evaluating the plain and curled feathered livestocks, and estimating the genetic distance between the populations as well as defining genetic variability within the populations through molecular genetic markers in-, and around Hungary.

II. OBJECTIVES OF THE RESEARCH

I. The goose sector is experiencing a worldwide decline, which is primarily due to economic causes were, did not only affect goose husbandry. Unfortunately goose-related research has also been overshadowed lately. Though most domestic animals (horse, pig, cow, sheep, chicken) have numerous, characterized microsatellites – moreover, they have developed microsatellite sets, which could be used for population-genetic examination – we didn't find any microsatellites in Domestic goose (*Anser anser domesticus*). Thus, our main objectives were as follows:

- **to adopt** microsatellites into domestic goose
- **to optimalize** the microsatellite primers for our examinations
- and, **characterizing** the microsatellites found in domestic goose from different species (Common Eider (*Somateria mollissima*) Mallard duck (*Anas platyrhynchos*), Canada goose (*Branta canadensis*)).

II. Our other objectives were

- to define the **genetic variability** of livestocks and
- to estimate the **genetic distance** with the adaptable microsatellites between the groups, which are claimed to be the curly and plain feathered Hungarian goose, but have no documentation of origin.

We used two species for control. One of them was the Greylag goose (*Anser anser*), the native domestic goose. The other one was the Emden goose, wich was brought to Hungary in the early 1900's. We examined the **genetic relation between the Emden goose and the Hungarian goose** as well, because there are more records from the past century regarding the crossing of the emden breed with the Hungarian goose (e.g.:HANKÓ, 1940).

III. METHODS OF THE RESEARCH

For the examination we took blood samples from 329 geese, from 14 different places which are not in genetic relation with each other. The **blood samples were taken** with the supervision of the University of Debrecen, Center for Agricultural Sciences, Faculty of Agriculture, Department of Animal Husbandry. The livestocks were from the area of Hungary and Transylvania (Romania). We used a Greylag goose population of 21 birds, and an Emden goose population for control. The DNA samples of the latter were given by the Veterinary University of Vienna. *Figure 1.* shows a map of the population's place of origin.

Figure.1.

The provenance of the population

*Curledplume:*1.=Curly1(n=64); 2.=Curly2 (n=24); 3.=Curly (n=7); 4.=Curly4 (n=10); 5.=Curly5 (n=12); 6.=Curly6 (n=11); 7.=Curly7 (n=6); 8.=Curly8 (n=7);

Lank plume: 9.=Oroshaza (n=8); 10.=Oroshaza x Curly (n=21); 11.=Parlag (n=9); 12.=Babat1 (n=64); 13.=Babat2 (n=23); 14.=Emden goose (n=63); 15.=Greylag goose (n=21)

The most important thing was to prevent blood clot when collecting blood samples because the method we used for **cleaning the DNA** is not suitable for gore blood. Preparation

of DNA samples were done based on the NAGY (2002) method. The efficiency of the DNA isolation and the semiquantitative estimation of DNA quantity was carried out by using agarose gel electrophoresis.

Microsatellites are those genetic markers, which are effective tools for genetic mapping, examining the place of origin, genetic examining the population, showing the polimorphisms or to comparing breeds, populations, species. Although finding microsatellites in the case of numerous domestic and wild animals is advanced, only a few microsatellite markers are provided in the case of different waterfowl species (SLATE et al., 1998, MAAK et al., 2000). Our greatest concern during the selection of microsatellites was the low number of the microsatellites in the case of waterfowl. In Domestic goose we didn't find previously isolated or characterized microsatellites. The genetic analysis had been carried out with microsatellites from some other waterfowl species. That method was used for examining the possibility of the adapting different waterfowl microsatelites into geese. In the examination, we tried to identify 23 different microsatellites *(table 1.)* in Domestic goose breeds.

The method which is regularly used to demonstrate microsatellite markers, is called **polymerase chain reaction**. The polymer-chain reaction, or PCR allows fast, in vitro propagation to create thousands of the originally existing quantity, from any kind of DNA's optional section. A pre-condition of the application is that, the succession of the 10-20 nucleotids at the two ends of the section in question must be known (MULLIS et al., 1986). Because we adopted the used primers from other animal species we had to make sure of their functioning in the examined animals, prior to application. Therefore we had to optimise PCR conditions. During the optimization of the reaction we determined the sticking temperature of primers in the examined breeds and determined the numbers of PCR cycles. To do so, we carried out a test PCR in the case of every microsatellite. *Table 1.* indicates the names, origin, and sticking temperature along with the number of PCR- cycles before and after optimisation. The working primers were highlighted in the table.

Table 1.

Used microsatellite

No.	Microsatellite	Provenance	Annealing temperature	PCR-Cycles	Referent
1.	**Smo1**	Somateria mollissima	**54 °C**	**38**	*1.*
2.	Smo4	Somateria mollissima	55 °C	38	*1.*
3.	Smo6	Somateria mollissima	65 °C	38	*1.*
4.	**Smo7**	Somateria mollissima	**60 °C**	38 →**29**	*1.*
5.	Smo8	Somateria mollissima	54 °C	38	*1.*
6.	Smo9	Somateria mollissima	61 °C	38	*1.*
7.	Smo10	Somateria mollissima	50 °C	38	*1.*
8.	**Smo11**	Somateria mollissima	**61 °C**	**38**	*1.*
9.	**Smo12**	Somateria mollissima	**49 °C**	38 →**29**	*1.*
10.	**Smo13**	Somateria mollissima	**65 °C**	**38**	*1.*
11.	APH02	Anas platyrhynchos	62 °C	29	*2.*
12.	APH08	Anas platyrhynchos	58 °C	29	*2.*
13.	**APH12**	Anas platyrhynchos	**52 °C**	**30**	*2.*
14.	**APH13**	Anas platyrhynchos	**52 °C**	**30**	*2.*
15.	**APH16**	Anas platyrhynchos	**52 °C**	**29**	*2.*
16.	**TTUG-1**	Branta canadensis	**55 °C**	35 →**30**	*3.*
17.	**TTUG-2**	Branta canadensis	**55 °C**	35 →**30**	*3.*
18.	TTUG-3	Branta canadensis	53 °C	35	*3.*
19.	TTUG-4	Branta canadensis	55 °C	35	*3.*
20.	**TTUG-5**	Branta canadensis	**59 °C**	35 →**27**	*3.*
21.	**Bcaμ1**	Branta canadensis	56 °C → **57 °C**	**27**	*4.*
22.	**Bcaμ3**	Branta canadensis	56 °C → **57 °C**	**27**	*4.*
23.	**Bcaμ9**	Branta canadensis	**56 °C**	**26**	*4.*

1.= PAULUS et al.(2003), 2.= MAAK et al.2003) , 3= CATHEY et al (1998), 4.=BUCHHOLZ et al.(1998)

The fragment-length has been determined with laser **capillar electrophoresis.** The machine, used for the analysis is an *ABI PrismTM 3100* genetic analyzing device (Applied Biosystems, Vienna). The ABI PrismTM 3100 genetic analyzer is an automatic fragmentation

device with capillar electrophoresis, which enables one to determine the length-, and the base succession of a DNA section.

We used *GeneScan® 2.1.* and *Genotyper® 2.1.* (Applied Biosystems, Vienna) softwares for **evaluating the standardization**. The *GeneScan® 2.1.* software is used to define the length of the detected DNA fragments from crude data according to the standard of length. We collected the defined allels into a Microsoft Excel table, for each animal. The received genotype-matrixes of every animal and DNA microsatellitemarkers provided the base of further evaluation.

We estimated the genetic diversity of the population through the numbers-, and distribution of the alleles. The more allels were found in the population the more varied was the distribution. We used the *MSA 4.00* (DIERINGER and SCHLÖTTERER., 2003) software to determine the occurance and the numbers of the allels per locuse (EWENS 1972; KIMURA et al., 1975).

The **expected** (He=expected heterozygosity) and **observed** (Ho=observed heterozygosity) **heterozygosity -** which means the partial number of the heterozygosity within the population indicates genetic variability. We calculated the expected heterozigosity from the occurance of the allel. The actual heterozigosity was determined based on the numbers of the observed animals inside the population. We also used *MSA4.00* software (DIERINGER and SCHLÖTTERER., 2003) to receive the values.

The **PIC-value** (Polymorphic information content = PIC) is suitable for determining the information content and the degree of polymorphism of the marker. It is based on the number and the frequency of the alleles (BOTSTEIN et al., 1980). So the information content and the quality of a marker depend on the number of allels and its frequency within the population. We defined the PIC-values with *MSA 4.00* software (DIERINGER and SCHLÖTTERER., 2003).

In view of a given locus' number of allels we examined how the **Hardy-Weinberg balance (HWE)** works. In case of significant deviation from the Hardy-Weinberg balance, we can assume that the population is not ideal, in point of the examined locuses so e.g. mating is not random (assortative mating), the number of the birds are very low (genetic drifting), or

the chances for zygots to staying alive depends on which allel of the locus they are carrying (selection) (BLOCK, 2004). We defined if the Hardy-Weinberg balance prevails in the given population for each and every locus as well as for the entire population. We used the *Genepop v.3.4d*. software for this examination (RAYMOND et al., 1995).

We examined the occurrence and the frequency of the **private allels** in each population**.** Those allels are called private allels, which could be identified only within one specific population. We determined the private allels with the *MSA 4.00* software (DIERINGER and SCHLÖTTERER., 2003).

The rates of the **F- statistic** consist of the *F*is, *F*it, *F*st fixation indexes. With these rates we can evaluate the genetic difference among the populations. The three rates can be used to define the heterozygote loss as well (HARTL et al., 1997). The rates of the F-statistic are calculated with the *MSA 4.00* software (DIERINGER and SCHLÖTTERER., 2003). We counted the *F*st averaging in point of each locus and population, and we compared the populations in pairs. Therefore, we also defined the genetic distance between the examined populations with the *F*st rate.

We calculated the **genetic analogy/difference** among the examined populations with the Nei-standard genetic distance (NEI, 1978) and based on the shared allels („proportion of shared alleles „= POSA) (BOWCOCK et al., 1994). The **philogenetic tree** is able to demonstrate the genetic distance. We designed the populations' philogenetic tree, or dendrogram, according to the genetic distances based on shared alleles (POSA) (BOWCOCK et al., 1994). The philogenetic tree is based on the analogy with the Neighbor-Joining procedure (SAITU et al., 1987). We used the *Phylip* software (FELSENSTEIN, 1993) to design the dendrogram and for displaying we used the *TreeViewPPC' v.1.6.5.* software (PAGE, 1996).

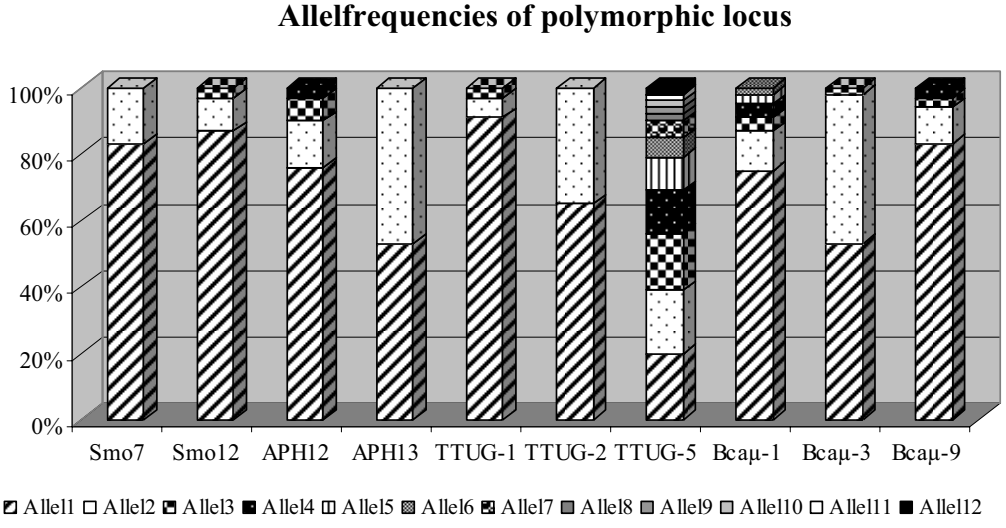
IV. MAIN FINDINGS OF THE THESIS

Results of Microsatellite-adoption

The rate of adapting microsatellites into duck-, and Canada goose- to the Domestic and Greylag goose species, was an important aspect for further population genetic examinations.

From the examined 23 microsatellites we adapted fourteen (61%) to the examined Hungarian-, and Emden goose breeds. Five from the examined ten microsatellites (50%) of the teal, three from the five duck microsatellites (60%) and six from the eight Canada goose microsatellites (75%) were adapted into the Greylag goose and other Domestic goose species. Ten out of the fourteen microsatellites were polimorph (71%), and four were monomorph (29%). In the case of the ten locus the number of alleles were between 2–12 in the examined fourteen Domestic goose population. We detected an allele number between 2-9 (average 3.7) in case of the ten polimorph microsatellites, what we used for the observation of the thirteen Hungarian goose population of 277 birds. We found 2-8 alleles on the examined ten locuses in 63 birds from the Emden goose population with an average of 3.2 alleles. Two microsatellites in 21 birds proved to be monomorph from the observed Greylag goose population, the allele number was between 1-10. We defined the allele frequency from the number of alleles on each locuses, shown on *figure 2*.

Figure.2.



We have calculated the observed and the expected heterozygote rate of the polimorph microsatellites in the average of a population of 15. The expected heterozygote rate was 3 %-78 %, the observed heterozygote rate was 1 %-72%. The microsatellite locuses haven't been used in population genetic examinations before in the currently examined goose-breeds, so we had to determine the PIC rate (Polimorphism Information Content) of each locus. The rates were between 0.42 and 0.83. *Table 2.* indicates the allele number of polimorph microsatellites, heterozygosis, and PIC-rates according to locuses.

Table 2.

Characteristic of microsatellites

Microsatellite	Allele number	Heterozygosity	PIC
Smo7	2	29%	0.25
Smo12	2	9%	0.17
APH12	4	31%	0.35
APH13	2	38%	0.37
TTUG-1	3	1%	0.12
TTUG-2	2	39%	0.34
TTUG-5	12	72%	0.83
Bcaμ1	6	40%	0.40
Bcaμ3	3	47%	0.39
Bcaμ9	4	30%	0.28

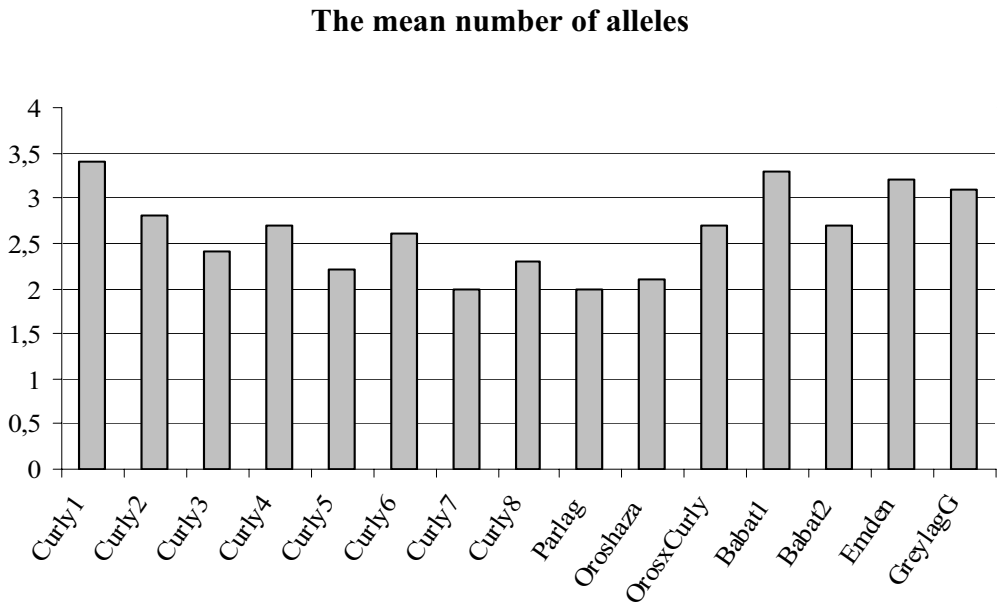
Higher heterozygosis is often in relation with the high allele numbers of the microsatellites (BOWCOCK et al., 1994, YANG et al., 1999), WIMMERS et al., (2000) reject the idea of only using high-variability markers in the population-genetic research. The heterozygosis of the population could be easily overestimated, the reason for that being that high-polimorphism microsatellites could alter results (WIMMERS et al, 2000).

In this dissertation, the different variability, adapted microsatellites were perfectly suitable for defining the variability of goose-livestocks diversity and to difference the populations.

Genetic diversity of the observed populations

We have found 40 different alleles on ten locuses in the 15 population all together. The average of the alleles in the population of 15 was 2.6. The average allele number is shown on *figure 3.*

Figure.3.

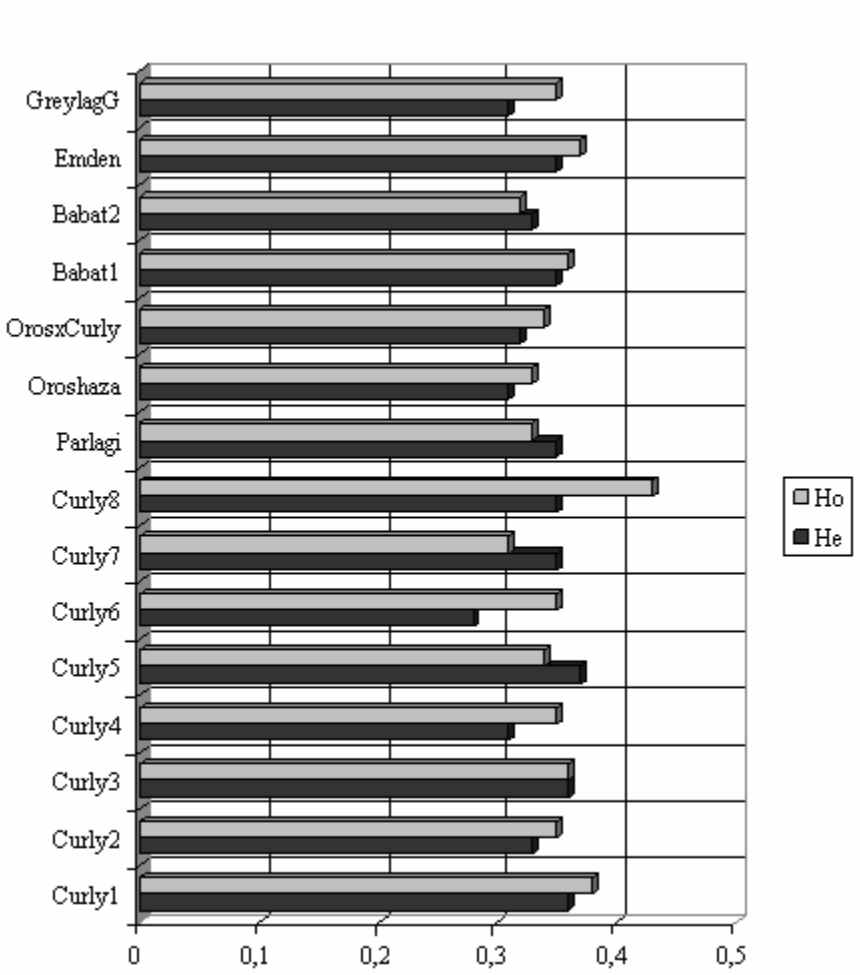


Most of the alleles (3.4) occured in the *Curly1* population, the least alleles (2) were in *Parlag* and *Curly7* population. We detected that the average number of alleles was below three in the *Curly2* (2.8), *Curly3* (2.4), *Curly4* (2.7), *Curly5* (2.2), *Curly6* (2.6), *Curly8* (2.3), *Oroshaza* (2.1), *Oroshaza x curly* (2.7) and *Babat2* (2.7) populations. In the *Babat1* population the average allele number was 3.3 and in the *Emden* population it was 3.2. In the *Wild goose* population we found 3.1 alleles in the average of ten microsatellites.

Besides allele diversity, the heterozygosis inside the population also gives you information about the genetic variability of the population. This comes from the number of the heterozygote animals inside the population. The expected and the observed rates of the heterozygotes per populations are shown on *figure 4*.

Figusre.4.

Heterozygosity of the population



There were no significant differences among the heterozygosis of the populations. The highest heterozygosis rate was 0.37 (*Curly5*), the lowest was 0.26 (*Curly6*). There were three different populations from the Hardy-Weinberg balance (*Curly1, Curly6, Curly8*), which indicates overweight homozygote birds inside the population. In three curly feathered (*Curly3, Curly5, Curly7*), two plain feathered (*Oroshaza, Parlag*) and the crossed (*Curly x oroshaza*) populations we can assume that, they are at the early phase of the „bottle-neck" phenomena based on the low rates of the allele numbers and the relatively high rates of the heterozygosis. In two curly feathered (*Curly2, Curly4*) and two plain feathered Hungarian (*Babat1, Babat2*) populations the allele number and heterozygosis were above the average (2.6). There were no significant differences from the Hardy-Weinberg balance. In the *Greylag goose* and *Emden goose* populations, which are used for control we detected the allele number to be above the average compared to the high heterogeneity of other populations.

Genetic distance among populations

We counted the **allele frequency** from the number of alleles found in the population by locuses. The difference can not be declared as obvious, which is fixed in the allele frequency, because there were a lot of common alleles in the different populations. There were some alleles on each gene place which only occurs at very low frequencies in the observed stocks.

The **private alleles** in one breed or population can be defined as genetic distance as well. The more private alleles the specific population has and the less similar alleles they have in contrast with the other populations, the bigger the difference between them and other populations. We only found private alleles in the *Greylag goose* and *Curly1* population.

The **F-statistics** are suitable to studying the genetic variability structure, in which the whole variance ($\boldsymbol{F}_{\mathbf{IT}}$) of the populations are dividible into components such as within population ($\boldsymbol{F}_{\mathbf{IS}}$) and among population ($\boldsymbol{F}_{\mathbf{ST}}$). According to the results, the largest part of the whole genetic variance ($\boldsymbol{F}_{\mathbf{IT}}$ = 0,158126) was the component in between the populations ($\boldsymbol{F}_{\mathbf{ST}}$ = 0,114574; $\boldsymbol{F}_{\mathbf{IS}}$ = 0,049187) showing that some populations stand apart from each other. Observing each microsatellite, the $\boldsymbol{F}_{\mathbf{ST}}$- rates were higher in most of the locuses. The populations shown higher variance within the populations, than among one other in case of these locuses (Smo12, APH13, TTUG-1, TTUG-2, Bcaμ1, Bcaμ9).

The $\boldsymbol{F}_{\mathbf{ST}}$ rates calculated by populations are able to define the separation-rate of each population and counting the genetic difference between the populations. We defined them by populations and compared the rates in pairs. The significancy table as a result of the **homogenity test** is shown in *Table 3.*

Table 3.

Results of pairwise homogenity test

	C 1	C2	C 3	C4	C5	C6	C7	C8	Oros	OxC	Parl	B1	B2	Emd
C2	n.s.													
C3	n.s.	n.s.												
C4	n.s.	n.s.	n.s.											
C5	n.s.	n.s.	n.s.	n.s.										
C6	n.s.	n.s.	n.s.	n.s.	*									
C7	*	*	*	*	*	*								
C8	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	*							
Oros	n.s.	n.s.	*	n.s.	*	*	*	n.s.						
OxC	n.s.	n.s.	n.s.	n.s.	n.s.	*	*	n.s.	n.s.					
Parl	*	*	*	*	*	*	*	*	*	*				
B1	n.s.	n.s.	n.s.	n.s.	*	n.s.	*	n.s.	*	n.s.	*			
B2	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	*	n.s.	n.s.	*	*	n.s.		
Emd	n.s.	n.s.	n.s.	n.s.	*	*	*	n.s.	*	n.s.	*	n.s.	n.s.	
GG	*	*	*	*	*	*	*	*	*	*	*	*	*	*

C1 =Curly1; C2=Curly2; C3=Curly3; C4=Curly4; C5=Curly5; C6=Curly6 C7=Curly7; C8=Curly8; Oros=Oroshaza; OxC=Oros x Curly; Parl=Parlag; B1=Babat1; B2=Babat2; Emd=Emden; GG=Greylag goose; * = (p > 0,05). n.s. = not significant

The curly feathered populations were very homogeneous, only the *Curly7* stock was significantly different from the other curly feathered birds. Inside the plain-feathered populations the *Parlag* population was different from all others. We found differences between the *Babati1- Oroshaza* and *Babat 2- Oroshaza x Curly* populations as well.

We found more differences upon comparing the curly-feathered with the plain-feathered populations. We detected differences between the *Oroshaza* and four other curly feathered (*Curly3, Curly5, Curly6, Curly7*) populations. It was a significant difference from the *Oroshaza x Curly* the *Curly6* and *Curly7*. The *Curly7* was significantly different from the *Babat1* the *Curly5*, and from *Babat2.*

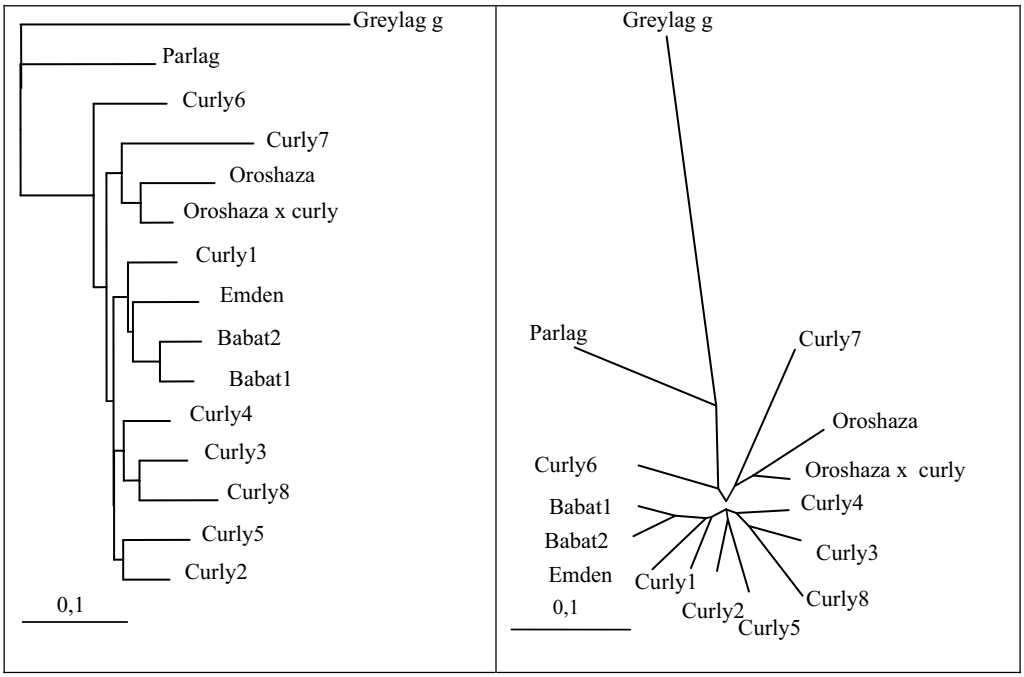
The effect of crossing with the emden breed in the 19001S (HREBLAY, 1909) is even traceable today in the Hungarian populations, because no significant differences were detected between most Hungarian and *Emden goose* populations. Five curly feathered (*Curly1, Curly2, Curly3, Curly4, Curly8*) and three plain feathered goose populations (*Oroshaza x Curly, Babat1, Babat2*) did not show significant difference from the *Emden goose*. From the *Greylag goose* population as we expected, every domestic stock showed significant difference.

We calculated the **genetic distance** between the populations from the allele frequency using the *MSA 4 00* software with the method of *POSA* and *Nei* (BOWCOCK et al., 1994; NEI, 1978). Although the Nei- distance rates were lower, than the ones we received by using the *POSA*, they led to the same result and they confirmed the genetic differential rates during the homogenity test.

The filogenetic tree, in other words **dendrogram,** is the graphical view of the genetic distances between populations. We chose the *POSA* genetic distancy rates, which represents the close relationships and also the genetic ties (BOWCOCK, 1994) between the subpopulations, like the ones we observed. The philogenetic tree indicating the rates is on *figure 5.* In the „A" dendrogram the *Greylag goose* population, which is used for control is considered as a separate group, so the software displayed the genetic distance between the populations compared to the external group. In the „B" dendrogram we did not choose any external groups, the software displayed the dendogram in relation to the populations based on the *POSA* rates.

Figure 5.

Dendrogram of the populations



V. NEW SCIENTIFIC RESULTS

1. We adapted succesfully 14 from 23 microsatellites to domestic and wild goose species, ten of which proved to be polymorph. The adaptation rate was 61 %. Based on the results we can state that the microsatellites we chose are suitable for analysing the genome of the geese. As we can see the result, the microsatellites are easy to adapt among the different waterfowl breeds and races, so this again underlines that it is worth trying to adapt microsatellites in the future.

2. We determined *the allele number*, the *expected and observed heterozygosis* and the *PIC rates* of the polymorph microsatellites.

3. Based our results we can state that some populations are at the beginning of the „bottleneck" phenomena. In these cases, we should increase the number of the stocks in order to avoid the losses of alleles and the decrease of heterozygosis.

4. By using the F-statistics we determined the genetic variance in the entire population (F_{IT}), within the population (F_{IS}) and between populations (F_{ST}) rates. These subpopulations showed very close relations with each other, because the genetic variance in most of the microsatellites (Smo12, APH13, TTUG-1, TTUG-2, Bcaμ1, Bcaμ9) was bigger within the population than between the subpopulations.

5. The fixation index rates are being confirmed by further (F_{ST}-values, POSA-, calculations Nei distance. Based on the results there were no significant differences between smaller groups of birds. This would be practical to add these homogeneous populations to avoid the Wahlund-effect (WAHLUND, 1928). Due to the random mating in the bigger population the heterozygosis would not decrease to such an extent as if they were kept in small subpopulations.

6. With our examination we found that the effect of the Emden crossing (HREBLAY, 1909 b.) in the early 1900's still exists in the Hungarian population, because from the thirteen Hungarian populations only five (*Curly5, Curly6, Curly7, Oroshaza, Parlag*) indicated significant differences from the German breed.

VI. FUNCTIONAL APPLICATIONS OF THE RESULTS

For developing the genereserve programmes the gene frequency of the gene reserved breeds and the scientic exploration of the distance among the different genotypes are needed. For the exact definition, we need the large concentration of information genetic markers, like the microsatellites. Although most of our domestic animals (cow, sheep, horse, chicken, pig) have numerous isolated and characterized microsatellites, the molecular genetic research in connection with goose were neglected. In this dissertation the adopted and characterised microsatellites could be the basis of an easily used marker-set in the future. Repeating the observations frequently with the microsatelites we applied, changes in genetic failure can be detected in ancient and traditional livestocks. Furthermore with the calculated markers there is an opportunity to characterise not only the ancient Hungarian goose, but also some other domestic goose breeds.

Genetic research of the curly-, and plain feathered versions of Hungarian goose, wich is declared to be our National treasure has never been carried out before. Although the birds decreased to an endangered number, (under 1000) so it is highly unlikely to sustain the livestocks without the much needed population genetic information background. There is an opportunity to work out a strategy for the long run by determining the homogeneity of a population without the documentation of origin.

VII. LIST OF PUBLICATIONS

Proofread publications

- **Aliczki,** K. (2005): Réghonosult magyar lúdpopulációk genetikai változatosságának a felmérése. (Examining the genetic variability of ancient, Hungarian goose populations.) XI. Ifjúsági Tudományos Fórum, Keszthely. Kiadta: Veszprémi Egyetem, Georgikon Mezőgazdaságtudományi Kar. Megjelent: CD formájában.

- **Aliczki,** K. (2005): Őshonos magyar lúdpopulációk genetikai változatosságának a felmérése mikroszatellitekkel. (Examining the genetic variability of ancient, Hungarian goose populations using microsatellites.) In.: Tavaszi Szél 2005. Konferencia kiadvány. Kiadta: Doktoranduszok Országos szövetsége. 8.-11. p.

- **Aliczki,** K. (2005): Réghonosult magyar lúdpopulációk vizsgálata molekuláris genetikai módszerekkel. (Examining ancient, Hungarian goose populations using molecular, genetic methods.) In.: Közép-Európa mezőgazdasága, lehetőségek és kockázatok. XLVII. Georgikon Napok és 15. ÖGA találkozó. (Szerk.: Palkovics M.-Weisz M.). 87. p.

- **Aliczki,** K., Dieringer, D. (2006): A genetikai variabilitás vizsgálata magyar lúd populációkban. (Examining genetic variability in Hungarian goose populations.) In.: Tavaszi Szél 2006. Doktoranduszok Országos szövetségének kiadványa. p. 4.-7.

- Mihók, S., **Aliczki,** K., Hidas, A. (2006): Molekuláris markerekkel történő fajtaazonosítás és fajtavédelem a réghonosult lúdfajtákban. (Type identification and preservation with molecular markers in ancient goose types.) In.: Génmegőrzés. Debreceni Egyetem, Agrártudományi Centrumának kiadványa. (Szerk.: Mihók S.) 86.-94. p.

- **Aliczki,** K., Dieringer, D. (2006): Réghonosult magyar lúdállományok populációgenetikai vizsgálata mikroszatellitek segítségével. (Population-genetic examination of ancient, Hungarian goose stocks with microsatellites.) Àllattenyésztés és Takarmányozás. (Szerk.: Gundel J.).