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International Association for the Conservation of Animal Breeds in the Danubian Region

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LECTURES

1.
MOLECULAR APPROACH TO PRESERVATION OF ANIMAL GENETIC RESOURCES

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Traditional approach to estimate genetic diversity within animal populations and between them relies on phenotypic diversity. The main disadvantage of this approach represents the fact that phenotypic diversity only partially reflects real genetic diversity, due to dominance effects, lack of detectable phenotypes and environmental effects. Even prominent phenotypic differences are able to give only vague impression about the real genetic distance. A good example are apparently clear phenotypic differences among human races, which represent less than 15% of the global genetic variation, whereas more than 85 % of genetic variation remains phenotypically hidden within races. Similar situation is in different animal breeds, where only very small number of genes frequently causes prominent phenotypic differences, leading to overestimation of genetic distances. These facts emphasize the necessity of application of genetic markers into analysis of animal genetic resources.. In our laboratory we develop and apply different types of genetic markers for analysis of farm- and free living populations of different animal species for more than a decade. Selection of markers includes mitochondrial DNA sequence polymorphisms, microsatellites, RFLP, SSCP, RAPD and SCAR markers. The use of these markers enabled us in the past to resolve some phylogenetic problems related to salmonid species, pedigree ambiguities in the Lipizzan horse population and characterization of red deer, goat and sheep populations in Slovenia. Especially in the case of salmonid populations, where phenotypical plasticity is a serious obstacle for phenotypic characterization, we were able to shed new light on the phylogenetic classification of several extremely small populations inhabiting the river Neretva basin. The final goal of this research is to identify evolutionary significant populations which deserve special protection and to propose measures for sustainable management with animal genetic resources.

2.

MILK PROTEIN POLYMORPHISM AND GENETIC CHARACTERIZATION OF CATTLE POPULATION IN SLOVAKIA

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The study of genetic polymorphisms contributes to the genetic characterization of animals. The maintaining of genetic diversity become lately to a serious problem. Genetic variants of 4 polymorphous systems of milk proteins (alpha s_1 – casein, beta – lactoglobulin, beta – casein and kappa – casein) there were observed. The frequencies of milk protein alleles of the following cattle breeds from nucleus herds were determined. Slovak Pied, Slovak Pinzgauer, Holstein Friesian or German Black and White. We noticed differences between the breeds in kappa – casein system, namely in representation of hetero – and homozygous form. The frequencies of B allele were 21 % in the Holstein – Friesian cattle, 22 % German Black and White, 56 % in the Slovak Pied and 24 % Slovak Pinzgauer. The values of E allele frequency of kappa – casein were 0.0169 in nucleus of Holstein, 0.0164 Slovak Pinzgauer and 0.0077 in Slovak Pied breed.

Nei´s standard distance is considered as the suitablest method to evaluate the genetic distances among populations. The lowest values were calculated between Holstein: Black and White and highest among Pinzgauer and others breeds.

3.

GENOME TYPING OF AUTOCHTHONOUS BREEDS OF DOMESTIC ANIMALS IN CROATIA

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ABSTRACT

The national program protection the endangered breed of domestic animals requests reliable evidence of originality of breeds. Beside good knowings of the phenotypic features, necessarily is knowings of genetic structure of breeds, their variability, similarity and distance in relation to cognate populations. The genetic characterization in Croatia include autochthonous breeds bovines, horses, donkeys, pigs, sheep, as well as turkeys, fish and bees. Genetic polymorphisms at the protein- (blood groups, blood and milk proteins) and DNA-level (microsatellites, mitochondrial DNA) can be successfully used for population analysis and for establishing relationships within and among species. On the basis of the research blood protein polymorphism and microsatellite markers have been estimated the genetic distances among three cattle breeds (Istrian cattle, Slavonian-syrmian podolian cattle and Busha), three horse breeds (Posavina horse, Croatian Coldblood and Murinsulaner horse) and two donkey populations. On the basis of sequences mitochondrial DNA, we determined the genetic relationships of subpopulations of Lippizaner horse (Ergela and Field breeding), cold-blooded autochthonous breed of horses, type of donkeys and a few breeds of bovines. Rare breeds of sheep (Ruda sheep, Pag island sheep and Krk island sheep) has been typed using several methodological approaches: blood protein polymorphisms, microsatellite markers and mitochondrial DNA.

For Black Slavonian and Turopolje pig have been investigated blood protein polymorphisms and eight microsatellite locis. Endangered poultry populations (Zagorje turkey, Hen Hrvatica and Dravska goose) is for till the object of research of phenotypic characteristics. The international project with neighbouring countries try establish resistance to varoosis for Mediterranean ecotype of Grey bee. Using RAPD method will try to determine genetic diversity in four lines of carp. The molecular research does on endemic soft-muzzled trout using microsatellite markers and mitochondrial DNA. On the basis of the research microsatellite markers and mitochondrial DNA have been typed endemic soft-muzzled trout.

Introduction

Autochthonous breeds of domestic animals make the component of total national and global animal genetic resources. The genetic richness can be seen in the existence of a greater number of breeds and populations formed and adapted during past centuries in certain areas. Genetic and paragenetic influences (climate, soil, food, illnesses, management) profiled hundreds of breeds, types and subtypes adapted by specific ecological niches, with their own phenotype and genetic identity. The fact is that animal genetic resources have been decreasing around the world, which was in cattle-breeding, due to the expressed trend of “monoculture” (small number of economically active breeds). Local breeds without genetic and economic value were frequently pushed out. This is one of the main reasons of the sudden disappearance of many local breeds, population and subpopulations genetically adapted to local conditions. Together with the disappearance of breeds, the biological variety within species also disappears, which does an irreparable damage, since the variability is a precondition of survival and selection progress.

During the last decade in Croatia, there was a great progress in developing the awareness of professional and general public on the need of protecting autochthonous breeds of domestic animals as a unique cultural heritage. During the eighties, the professional audience concentrated on the autochthonous cattle breeds, Slavonian Syrmian Podolian and Istrian cattle, which has given certain results. During the mid-nineties, these breeds already experienced certain revitalisation. Though they are still endangered, they have a solid base for survival. At the beginning of the nineties of the last century, the programmes were concentrated on the autochthonous breeds of horses, sheep, pigs, donkeys, turkeys, fish and bees. The activities that were taken resulted in including genetically interesting breeds and populations in the system of state support for breeders (annual bonuses) and for some breeds adequate programmes of preserving their uniqueness were envisaged. Previous information on autochthonous breeds were mostly based on historical records, previous research of exterior and production features. Aware of the deficiencies in these information, the attitude of the public audience was to establish (confirm) the originality of autochthonous breeds, following the latest scientific achievements. Established information should, in a competent way, help in establishing justified and viable protection programmes, indicating the best way of preserving the genetic variability.

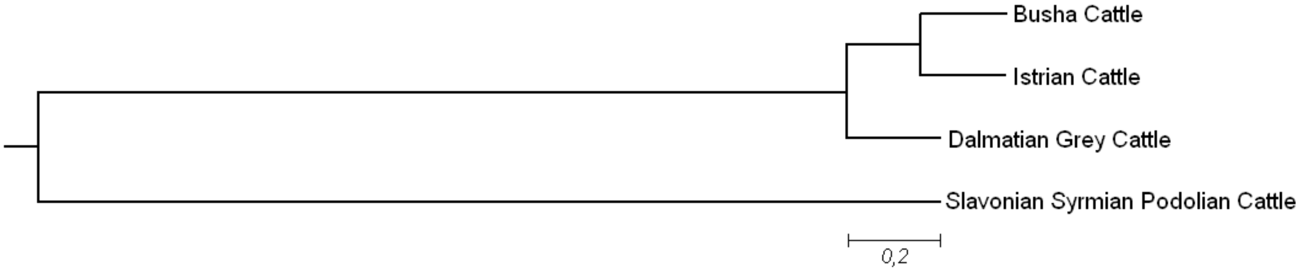
Fifteen years ago first studies on the polymorphisms of blood proteins of autochthonous cattle breeds. New development of molecular genetics methods imposed the need for the DNA structure research, as the most reliable method for confirming originality, i.e. phylogenetic relationship. During several past years, there were numerous phylogenetic studies on several domestic animal species. The collaboration project of determining genetic structure of horses, cattle, sheep and pigs has been in progress. Some of recent information have been included in the breeding programmes by which the autochthonous breeds are tried to be protected from extinction.

The latest molecularly genetic methods, out of which a microsatellite typing and mtDNA typing are an obligatory phylogenetic tool, have been used to complete our information on autochthonous breeds of domestic animals. But, previously researched frequencies of polymorphism proteins, which are used for completing previously established information have not been left out from the phylogenetic studies. The following survey will deal with some of the information on the phylogenetic originality of the Croatian autochthonous breeds, based on various phylogenetic markers.

Autochthonous cattle breeds

The programme of preserving autochthonous breeds in Croatia has been initiated on the Slavonian-syrmian podolian and Istrian cattle. At the same time, the idea of protecting Busha in Croatia by establishing a herd nucleus was initiated, but the then environment was not interested enough in such a kind of protection. The interest of the professional and general audience was concentrated on the Istrian cattle and Slavonian-syrmian podolian cattle, while Busha was “forgotten”. Today, when the protection of Busha has been initiated, it was realised that only a few dozens of Busha remained in the whole area, by which an effort will be made to revitalise the whole population.

The polymorphism research of blood and milk proteins has been carried out for decades, and it also started to be used in the genetic determination of the autochthonous cattle breeds. At the beginning of nineties, blood protein polymorphisms of the Slavonian-syrmian podolian cattle have been researched (Gašpert et al., 1990), the Istrian cattle (Caput et al., 1992), the Grey dalmatian cattle (Ivanković et al., 1997) and Busha (Ivanković et al., 2004). The research results were used for the construction of the dendrogram showing phylogenetic relations.



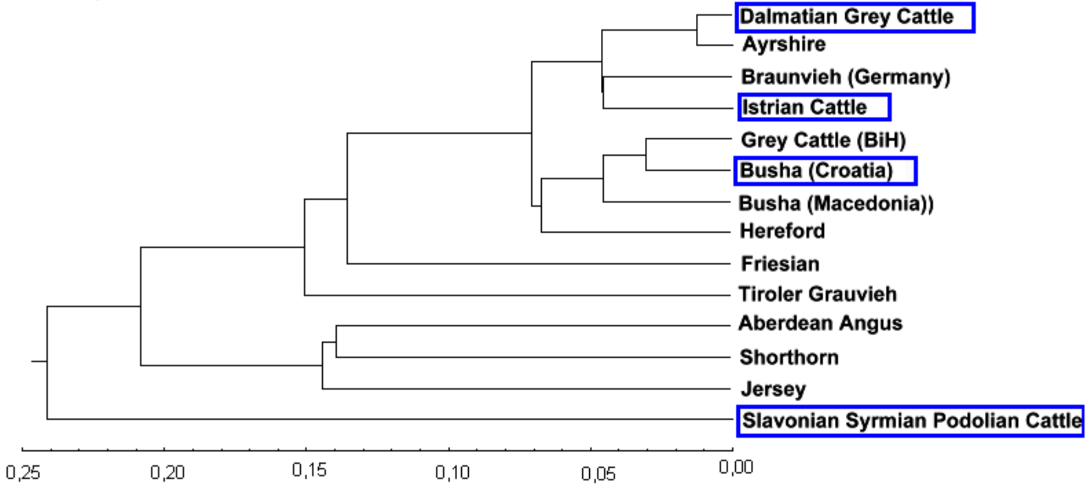
Graph 1. UPGMA tree of cattle breeds in Croatia, based on blood protein polymorphism (Ivanković *et al.*, in press; Gašpert *et al.*, 1990; Caput *et al.*, 1992, Ivanković & Caput, 1997).

It can be noticed that Slavonian-syrmian podolian cattle is significantly philogenetically distanced in comparison to other breeds, which, regarding the assumption of its genesis, is expected. The Grey dalmatian cattle is philogenetically related to Busha, since it emerged from merging Busha by the Austrian Tiroler Grauvieh.

Tabele 1. Nei's original measures of genetic identity (*above diagonal*) and genetic distance (*below diagonal*).

	Busha	Dalmatian gray cattle	Istrian cattle	Slavonian syrm. pod. cattle
Busha Cattle	-	0.9956	0.9962	0.9687
Dalmatian Gray Cattle	0.0044	-	0.9962	0.9592
Istrian cattle	0.0038	0.0038	-	0.9575
Slavonian Syrm. Pod. Cattle	0.0318	0.0417	0.0434	-

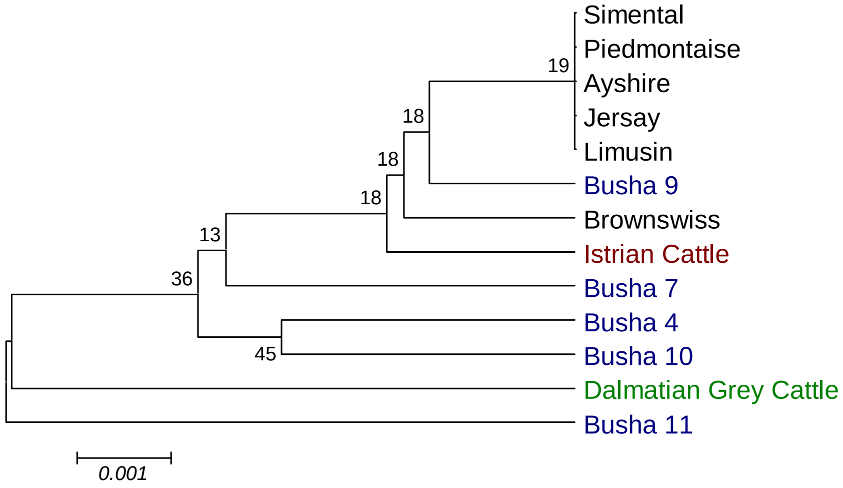
Frequencies of other breed polymorphs were given to established values of frequencies of poylmorph blood proteins of autochthonous Croatian cattle breeds in constructing dendrograms (Graph 1). The grouping of autochthonous Croatian cattle breeds with related and geographically closer breeds has been noticed. Thus, Busha shows the smallest genetic distance in comparison to the grey cattle from Bosnia and Herzegovina and a bit bigger in comparison to the Macedonian busha (Graph 2). The genetic distance of the Slavonian-syrmian podolian cattle regarding the polymorphism blood protein frequencies has a significant deviation from other cattle breeds.



Graph 2. UPGMA tree (*Euclidean linkage distance*) constructed on the basis of frequencies of polymorphism blood proteins of various cattle breeds

Due to comparatively simple isolation and organisation, maternal heritage, lack of recombinations and comparability of homologous nucleotide regions, mtDNA, the marker system in population and evolution biology has been suitable. That's why we have included it in the genetic studies of autochthonous breeds of domestic animals. Due to all the mentioned, D-loop mtDNA region has been sequenced of Busha, Istrian cattle and Grey dalmatian cattle. Sequences indicated the modest level of variability within the researched populations.

The variability of mtDNA sequencies can be noticed on constructed dendrograms in which, for comparison, we included sequences of some other cattle breeds, available in the NCBI database (AccNo. AF034442; AccNo. AF034439; AccNo. AF034446; AccNo. AF034443; AccNo. AF034440; AccNo. AF034438). The variability of Busha population is expected assuming its genesis based on available literature data. Significant spatial dispersion of collected samples contributed to this (Graph 3).



Graph 3. UPGMA Neighbor-joining tree constructed on the basis of D-loop mtDNA region sequences of various cattle breeds

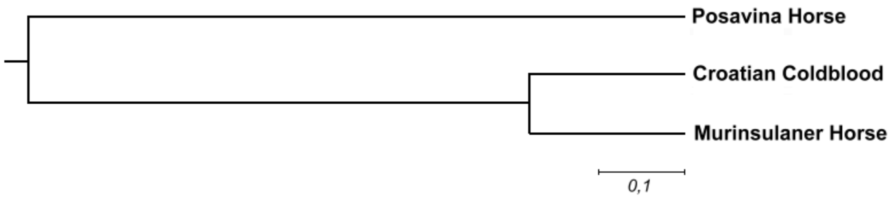
Previous information will be completed by the use of other marker systems, primarily microsatellites and established information will be included in the revision of the existing system of protection and designing a programme for protection of these breeds. Information will be the basis for establishing the adequate cooperation with institutions and services of neighbouring countries in order to avoid the inbreeding or other unwanted events which can be met in the revitalisation of critically endangered domestic animal populations.

Autochthonous horse breeds

Autochthonous cold-blooded Croatian horse breeds have been dominantly represented, by their share, in the total horse population in Croatia. Their systematic breeding started in the 19th century in Međimurje and then it spread to Podravina, Posavina and parts of Slavonia. They were bred on the then horse population “Bushak” which, depending on the climate, was differently conformationally and genetically profiled. The breeding trends imposed the need for improving working and production features of these horses, during the 20th century, quality stallions of heavy European horse breeds were imported, primarily of the Noric (the Noriker) , the Percheron and Belgian coldblood, which were used for “improving” the existing population. The differentiability of the base population and oriented selection approach conditioned the profiling of the then population into breeds which still exist in these areas. The Posavina horse and the Croatian Coldblood remained in the marginal pasture areas in a small number which demands a constant monitoring. Murinsulaner horse population is reduced to forty heads which are carefully monitored, while its revitalisation is questionable. It requires the international cooperation of countries in the area of the river Mura.

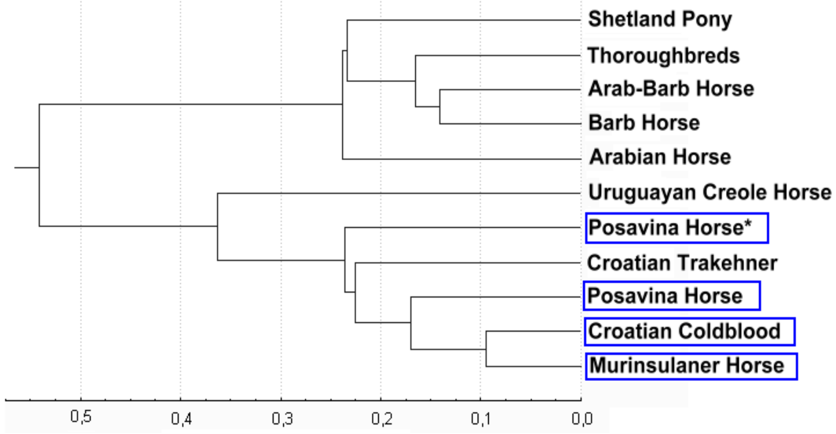
The state stimulates the preservation of autochthonous horse breeds by significant financial support. Its exterior features have been investigated several times, but there is the need for its typing on the genetic level. The information on the genetic originality helps in giving the concrete answer on the need and way of preserving these breeds. Some research of the genetic structures of autochthonous horse breeds on the level of polymorphism proteins have already been carried out, while the research of the chosen genetic markers (microsatellites and mtDNA) are in progress.

The research of polymorphism blood proteins showed the expectedly higher genetic closeness of the Croatian Coldblood and Murinsulaner horse (Graph 4), while the genetic distance to the Posavina horse is significantly bigger.



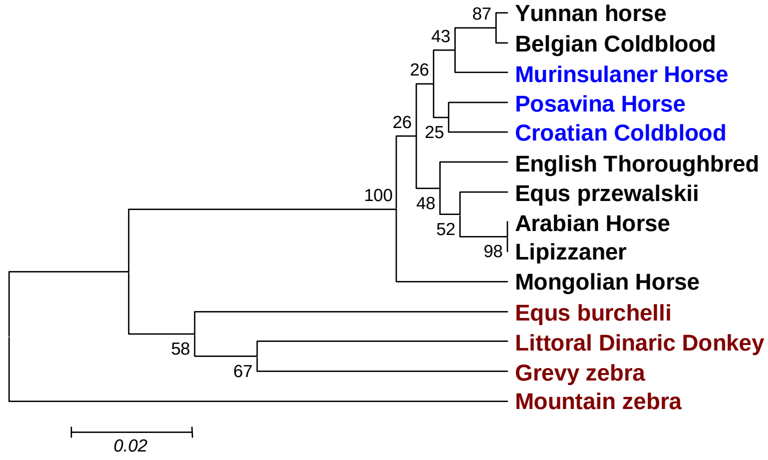
Graph 4. UPGMA Neighbor-joining dendrogram constructed on the basis of frequencies of polymorphism blood proteins of the autochthonous Croatian horse breeds

By including the phylogenetic relations of blood polymorph frequencies of some other breeds in the calculation, the grouping of autochthonous Croatian horse breeds can be noticed, in comparison to other breeds (Graph 5). These observations have to be taken with some restrictions, since the number of researched protein markers has been relatively small. The completion of existing information by including a higher number of microsatellite loci in studies will give more reliable picture of the phylogenetic relations of observed populations.



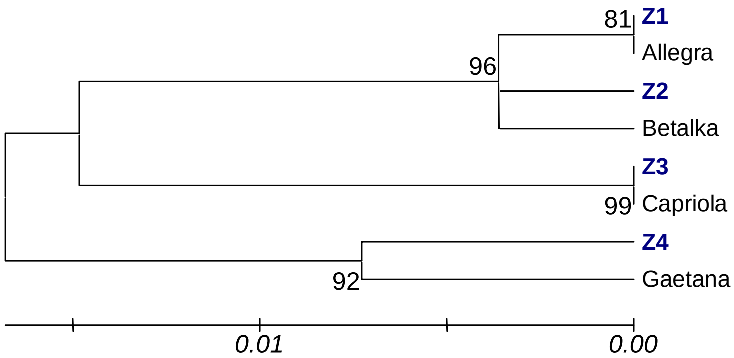
Graph 5. UPGMA tree (*Euclidean linkage distance*) has been constructed on the basis of frequencies of polymorphism blood proteins

The research of mtDNA sequences indicated a significant phylogenetic closeness of the Croatian autochthonous horse breeds, particularly the Croatian Coldblood and Posavina horse (Graph 6). The Murinsulaner horse shows greater closeness with the Belgian coldblood horse, which is expected due to its significant introduction to Croatian horse breeds and particularly Murinsulaner horse.



Graph 6. UPGMA Neighbor-joining tree constructed on the basis of D-loop region sequences of various *Equidae* mtDNA (Przewalskii horse - AccNo. AF014409; Thoroughbred horse - AccNo. AF072990; Arabian horse - AccNo. AF132591; Belgian horse - AccNo. AF064632; Lipizzan horse - AccNo. AF168690; Cheju horse - AccNo. AF014412; Mongolian horse - AccNo. AF014414; Yunnan horse - AccNo. AF014417; *Equus burchelli* - AccNo. AF220923; Grevy zebra - AccNo. AF220930; Mountain zebra - AccNo. AF220925; Litoral Dinaric Donkey – Croatia, Haplotype W).

In Croatia, the Lippizaner population consists of, apart from a stud, also of the country part of breeding. The genetic studies of the Lippizaner population in Croatia mostly included the stud part of breeding (COPERNICUS project), while the country part of population remained unresearched. Wanting to research the country part of the population and to clarify some doubts about the reliability of keeping the pedigree in country breeding, the research of D-loop sequences of mtDNA regions of several mare genders has been carried out. The mtDNA sequencing of unrecognised genders of Lippizaner mares showed mistakes in keeping stud-books. For some mares it has been established that they do not belong to genders that they belong according to their pedigree. For the gender *Liza-Cica-Pliva* (haplotype Z1) it has been established that it is identical to the gender Allegra, and the gender *Cura-Lela* (haplotype Z3) to the gender Capriola (Graph 7).



Graph 7. UPGMA Neighbor-joining tree constructed on the basis of D-loop sequences of mtDNA regions of the part of Lippizaner gender (Čačić, 2003; Kavar et al., 1999)

Since the gender *Pliva* (Bosnia and Herzegovina), recognised in LIF, recognising the gender *Liza-Cica-Pliva* by LIF, would complete already recognised gender of Lippizaner.

Autochthonous donkey breeds

In Croatia, especially in its coastal part, donkeys have been living for centuries, helping a man to survive in savage environmental conditions. During several centuries of adaptation and natural selection in certain regions, donkey populations of special phenotype features have been profiled. The intensification of agrarian production and economic-social movements in rural areas have caused a significant decrease in the number of donkeys. The present information shows that in Croatia there have been several thousands of donkeys, but some types are on the verge of extinction. In the nineties of the last century, the inevitable need for protection and preserving of donkeys in Croatia was realised.

In the first stage of the preparation of the donkey protection programme, several types within the total donkey population were noticed and defined exteriorly. In the later studies, these data were completed by research at the molecularly genetic level. The research of the genetic structure of the total donkey population that were carried out on the level of polymorphism proteins, microsatellites and mtDNA confirm the genetic differentiation of the total donkey population in three types. The research results of the polymorphism blood protein frequencies are shown in a diagram 2.

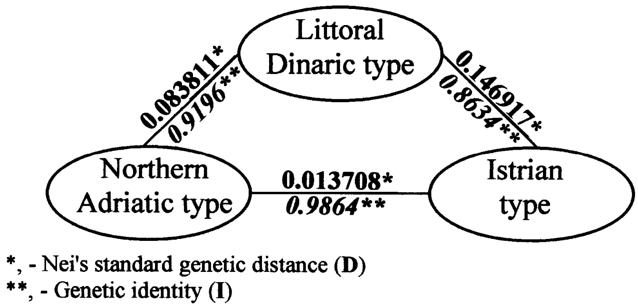


Diagram 2. Genetic distances and the genetic identity of donkey types in Croatia (Ivanković & Caput, 1997)

The DNA structure was completed by the analysis of microsatellite loci, chosen from the set recommended by ISAG for *Equida* typing. The research results confirmed observations noted on the basis of blood polymorphisms analyses.

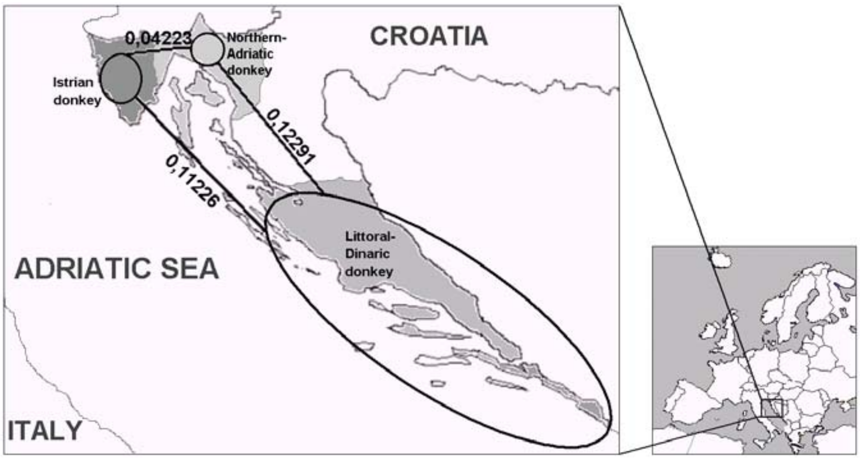
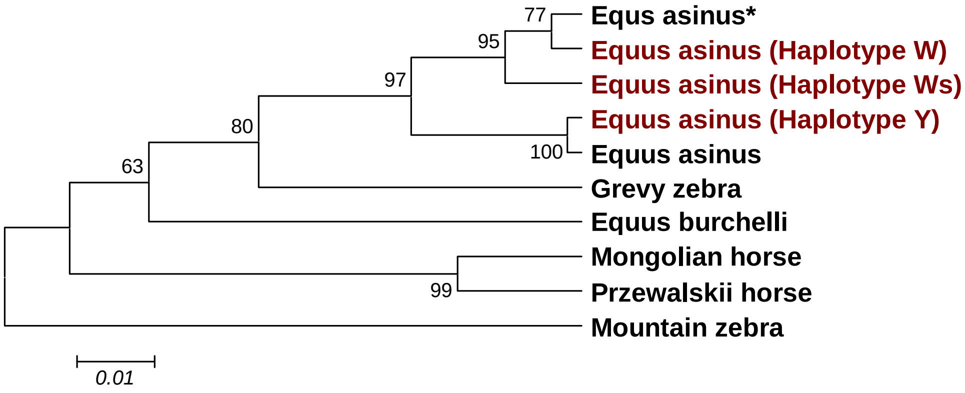


Diagram 3. Genetic distances of donkey types in Croatia established on the basis of microsatellite loci (Ivanković et al., 2003)

MtDNA sequencing confirmed the existence of several haplotypes (Y, W, Ws) within the total donkey population. The regional distribution of certain haplotypes has been noticed. The haplotype Y was represented in the Istrian donkey population, while W and Ws haplotypes were represented in the population of Littoral-Dinaric and Northern-Adriatic donkey (Graph 8).



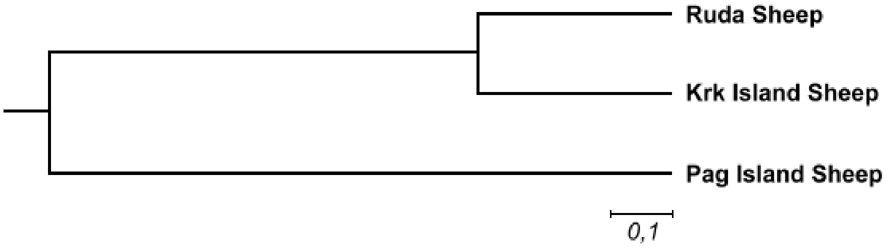
Graph 8. UPGMA Neighbor-joining tree constructed on the basis of D-loop sequences of mtDNA regions of donkeys in Croatia (Przewalskii horse - AccNo. AF014409; Mongolian horse - AccNo. AF014414; *Equus burchelli* - AccNo. AF220923; Grevy zebra - AccNo. AF220930; Mountain zebra - AccNo. AF220925, *Equus asinus* - AccNo. X97337; *Equus asinus** - Ishida et al., 1995; Donkey in Croatia - Haplotype W, Ws and Y).

Due to the applicability of established information in the breeding programme, the influence of certain restrictive endonucleases, it is possible in a relatively simple and fast way to determine the affiliation of individuals to a haplotype group. But, due to lack of adequate breeding programme for donkey population, the information about the molecularly genetic features have had no practical influence on profiling of breeding. The highest problem of revitalisation of donkey population in Croatia is a low level of animal fertility and insufficient motivation of relatively old breeders.

Autochthonous sheep breeds

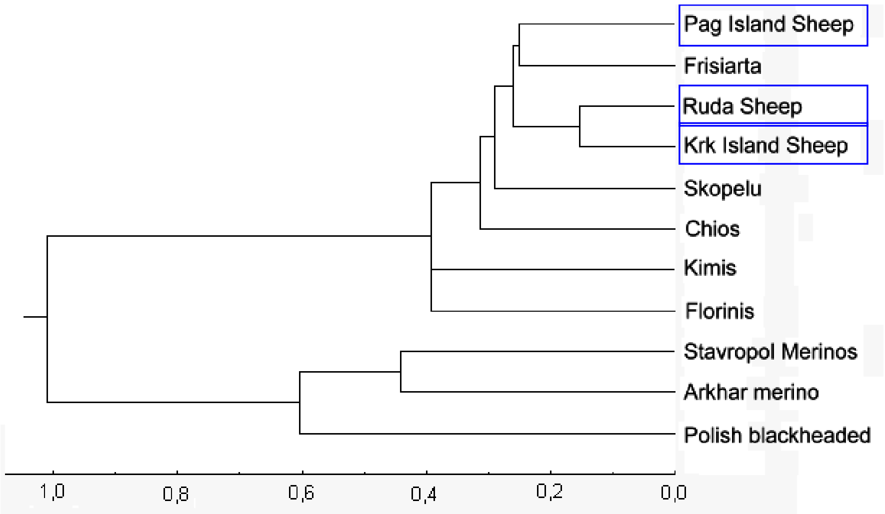
The sheep raising in Croatia has been based on traditional sheep breeds which are formed on Pramenka, merinized to a smaller or bigger extent, during last centuries. Regarding the phenotype, breeds have certain special features, but the real originality tries to be established by studies on the DNA level. The research included determining frequencies of polymorphism blood proteins, microsatellites and mtDNA sequences.

The research of polymorphism blood proteins indicates the special features of the Pag island sheep, while Ruda and Krk island sheep are genetically closer (Graph 9).



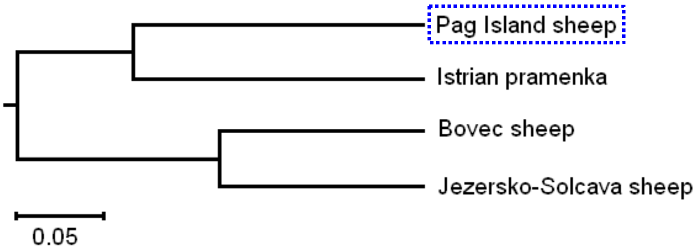
Graph 9. UPGMA Neighbor-Joining tree constructed on the basis of blood protein polymorphism of some autochthonous sheep breeds in Croatia

If frequencies of polymorphism blood proteins of other sheep breeds are taken into account in calculating genetic distances, the closeness, i.e. the specificity of autochthonous Croatian sheep breeds in comparison to other breeds can be noticed (Graph 10).



Graph 10. UPGMA tree (*Euclidean linkage distance*) constructed on the basis of frequencies of polymorphism blood proteins of sheep breeds.

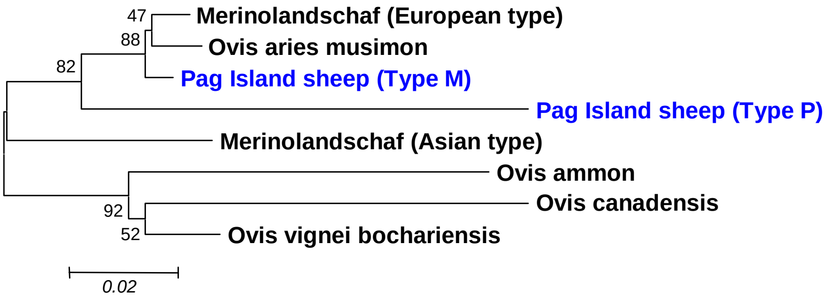
The analysis of microsatellite locus set of the Pag sheep is the first step in typing autochthonous sheep breeds on the DNA level. The research results were compared with the Slovenian autochthonous breeds (Graph 11). Nei's genetic distance (*D*) reveals a close relationship between two local Slovene breeds, Jezersko-Solcava sheep and Bovec sheep (0.2443), while the distance between Istrian pramenka and Pag island sheep was a bit greater (0.3606) (Ivanković *et al.*, 2004). Such a result is expected, since phylogenetically, the Pag island sheep represents a merinized pramenka of the island of Pag.



Graph 11. UPGMA Neighbor-Joining tree of the genetic relationships among three Slovenian sheep breeds and Pag island sheep (measured with seven microsatellite loci).

The study of the Pag sheep genetic structure included the sequencing of the proximal part (nt 15816-16153) of the D-loop region at mtDNA. After clustering D-loop mtDNA sequences of the Pag island sheep, their grouping into two main haplotypes was proposed (type M and P). The difference of the haplotype M in comparison to haplotype P (6.78 to 9.44 %) is higher than within haplotyes which suggests their previous separation, i.e. larger genetic distance. The difference within P haplotypes shows longer independent existence and stratification of the original Pag island sheep haplotype diversified by mutations (Ivanković *et al.*, 2004).

Since the Pag island sheep emerged by crossing the original island "Pramenka" and Merino, we assume that the determined P haplotype belongs to the original Pag sheep genotype, i.e. "the original island Pramenka". Similar or identical sequences were not found in available databases (NBCI, GenBank-Database, http://www.ncbi.nlm.nih.gov) and scientific papers. The low degree of sequence divergence of haplotype M from Merinolandschaf European type (2.58%) and *O. musimon* (3.16%)

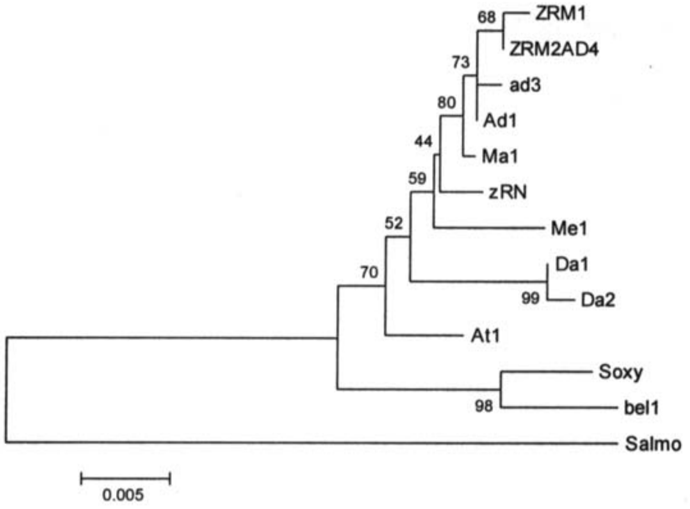


indicates that haplotype M entered the Pag sheep population by its merinisation (Ivanković *et al.*, 2004).

Graph 12. Neighbor-Joining tree of mtDNA D-loop sequence (nt 15816-16136) showing relations among the members of the subgenus *Ovinae*: Merinolandschaf European type (AccNo. AF039577); *O. aries musimon* (AccNo. AF039579); Pag island sheep (Haplotypes M and P; sequence i and j); Merinolandschaf Asian type (AccNo. AF039578); *O. canadensis* (AccNo. AF076917); *O. vignei bochariensis* (AccNo. AF039580) and *Ovis ammon* (AccNo. AJ251327).

Fish genotyping in Croatia

Croatia has been known in the ichthyological circles by the existence of endemic species and fish subgenders. There is a special scientific interest in the endemic fish species, particularly endangered ones. A molecularly genetic typing of the endemic soft-muzzled trout solinka (*Salmothymus obtusirostris salonitana*) and a stream trout from the rivers Jadro, Žrnovnica, Zrmanja and Krka have been carried out. It has been established that a stream trout from the Zrmanja belongs to the Adriatic trout lineage. The soft-muzzled solinka is significantly phylogenetically closer to the stream trout, than to the soft-muzzled trout from the Neretva (Bosnia and Herzegovina). The soft-muzzled trout solinka *(Salmothymus obtusirostris salonitana*) has a special branch within the phylogenetic lineages of the stream trout (Odak, 2004).



Graph 13. Neighbor-Joining tree of relationships among fish haplotypes included in the research (on the basis of cytochrome b gene and D-loop region) (Odak, 2004).

It is interesting that mtDNA and nucleus DNA sequencing results have been partly contradictory. The complete identity between the soft-muzzled solinka and the Neretva soft-muzzled trout has been established by the analysis of the nucleus DNA (the lactate dehydrogenase gene). Contrary to these observations, mtDNA sequences indicate a significantly higher closeness of Solin soft-muzzled trout with the Adriatic lineage of trouts than with a soft-muzzled trout from the Neretva.

Such contradictory sequencing results indicate the need of knowing advantages and lacks of certain gene-marking systems, which, depending on predispositions of the researched population have to be used adequately to get reliable data.

Together with sequencing of interesting regions of nucleus regions and mtDNA, a microsatellite typing of researched trouts has been carried out. It has been established that the soft-muzzled and a stream trout have a certain part of common alleles, which indicates that they might by hybrids (Odak, 2004).

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4.

MICROSATELLITE MARKER DIFFERENTIATION BETWEEN AUSTRIAN ENDANGERED SHEEP BREEDS

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Introduction

A great variety of different, more or less related, autochthonous sheep breeds exists in the eastern Austrian part of the Alps. A lot of them are endangered. A differentiation as clear as possible between breeds is necessary to decide if a population should be conserved as an independent breed within a separate conservation breeding programme or together with other subpopulations belonging to one larger breed. Genetic distances can help to distinguish between different populations more objectively and molecular genetic information might also be used to assign individuals correctly to their breed, especially when the phenotypical differentiation between breeds is difficult and the animals pedigree is obscure.

Material and Methods

Tissue samples taken from the ear of individuals belonging to the following 11 breeds were collected using the so called Typi Fix ® system

♦	Alpines Steinschaf	AST
♦	Montafoner Steinschaf	MST
♦	Tiroler Steinschaf	TST
♦	Krainer Steinschaf	KST
♦	Waldschaf	WAL
♦	Kärntner Brillenschaf	KBR
♦	Zackelschaf	ZAC
♦	Braunes Bergschaf	BRB
	Tiroler Bergschaf	TB (not endangered)
	Texel	TEX (Outgroup)
	Juraschaf	JUR (special interest of Juraschaf breeders)

♦ In Austria endangered sheep breeds

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* funded by ÖNGENE

With exception of the three latter breeds all breeds investigated are considered as endangered in Austria. Texel was used as „outgroup“. Because of a high breeder’s interest the Juraschaf was included. 25 microsatellite loci were genotyped. The selection of the investigated loci is based on ISAG/FAO (1998) recommendation. With the aid of special programmes (Raymond and Rousset 1995) a test for Hardy-Weinberg-Equillibrium was carried out. For estimation of the genetic distances between the sheep populations special distance matrices were used (Nei 1987, Reynolds 1983).

Based on the distance matrices, distance trees were constructed applying the Neighbour-Joining method. Further for the test of the possibility of a correct assignment of individuals to their breed the software package „GeneClass“ (Cornuet et al, 1999) was used.

Results and discussion

FAO (1998) recommends as a compatibility rule to use only loci with a minimum number of four alleles for genetic distance studies. This was fulfilled for all 25 loci chosen. On average the number of observed alleles per locus was 15 ranging from 7 at locus D5S2 up to 30 alleles at locus CSRD247. The observed heterozygosity was, higher than 0.50 in all except one of the 25 gene loci.

On four gene loci there was a significant dislocation from Hardy-Weinberg- equilibrium. They are not enlisted for calculation of genetic distances. Therefore the following results are just based on the remaining 21 gene loci .

Based on the genetic distance matrices shown in Table 1 an “average distance matrix” for the 11 investigated populations was calculated and breed distance trees constructed (Figure 1).

The relatively small distance especially between Waldschaf and Alpines Steinschaf might be partly explained through their common ancestor the Zaupelschaf (Sambraus, 1994), but also by more recent (known) incrossing from Waldschaf into the Alpines Steinschaf population. Other breeds belonging to the Steinschaf-group like Krainer Steinschaf originate from the Zaupelschaf as well, but have been more isolated geographically. This might be a reason for the larger distance between this breed and other Steinschaf-breeds.

For the Montafoner Steinschaf quite a large distance relative to all other breeds was found. The breed history of this breed is not well known; almost all living animals belong to just one flock. The Montafoner Steinschaf was not officially acknowledged as a separate breed in Austria before this study was carried out. Until now it used to be counted as Alpines Steinschaf. In future it will be a separate endangered breed.

As expected the distance between the outgroup Texel and all other breeds was quite large. This was also the case for Zackelschaf, which is no breed from the eastern part of the Alps, but from the Pannonic area. Nowadays this breed is mainly found in Hungary. In contrast to these two breeds the Juraschaf is a typical breed of the Alps. It is one of the main sheep breeds in Switzerland and stems geographically far away from the other breeds.

Results for the correct assignment of separate individuals to their real breed of origin are shown in Table 2. With the exception of Alpines Steinschaf quite high percentages of correct assignments (most probable and significant) were found for all breeds. For the large part of those animals without correct assignment we have found mistakes by the collection of Tissue samples or by breeding organisation.

Comparable good results for breed assignment also were found for Austrian sheep breeds by Schwend (2001) based on the information of just 11 microsatellite loci and by Simianer (2002) for closely related cattle breed in Germany.

At the moment we are working on a similar scientific investigation for genetic differentiation between Austrian endangered goat breeds.

Conclusions

The results show clearly that closely related breeds can be distinguished based on microsatellite loci information. Results of genetic distance studies provide arguments for an official acknowledgement of breeds and might have a direct impact or influence on conservation breeding programmes.

In conservation breeding the question whether an animal belongs to a certain breed or not is of a certain importance to decide whether it should contribute to the gene pool of a highly endangered breed or not. For such decision the significant assignment should be considered, because an animal with unknown origin will always be assigned most probably to one of the reference populations, even if its real population of origin is not included. In case an animal is assigned significantly to more than one population this might be a hint for being a crossbred animal. The results allow to trace back crossbred animals and might also be helpful to detect errors in a database.

Summary

Eleven in some cases closely related sheep breeds being native in Austria could be clearly distinguished through genetic distances based on the information of 21 polymorph microsatellite loci. The shortest genetic distance was found between Alpines Steinschaf and Waldschaf. Within the so called “Steinschaf”-group (Alpines Steinschaf, Montafoner Steinschaf, Krainer Steinschaf and Tiroler Steinschaf) the Montafoner Steinschaf has got a special status with regard to the large distance to the other breeds in the group. This is of high relevance, because this population was not acknowledged as an independent breed before the study was carried out. A correct breed assignment using a Bayesian approach was possible for only 66 % of all individuals belonging to Alpines Steinschaf, but for at least 90 up to 100 % of individuals for all other breeds investigated.

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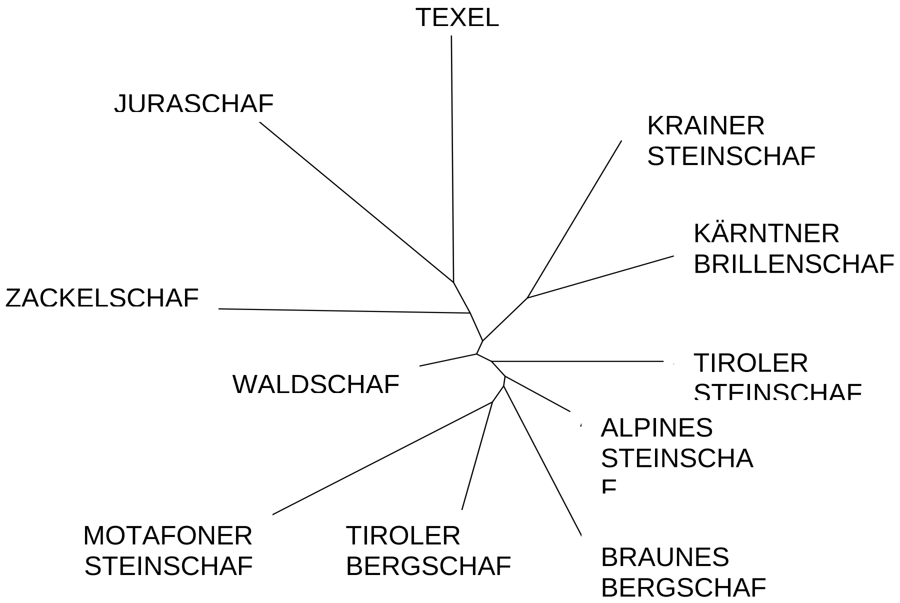
Table 1: Distanc matrix for 11 investigated populations based on Nei’s minimum distance (lower triangle) and Reynolds’ distance (upper triangle)

	AST	**TB**	**BRB**	**JUR**	**KST**	**KBR**	**MST**	**TEX**	**TST**	**WAL**	**ZAC**
AST		,028	,039	,071	,072	,061	,063	,083	,031	,020	,068
TB	,030		,049	,115	,081	,074	,072	,107	,066	,043	,101
BRB	,038	,044		,114	,081	,075	,091	,128	,065	,050	,107
JUR	,062	,095	,091		,126	,111	,133	,098	,094	,080	,098
KST	,065	,071	,071	,103		,057	,109	,110	,082	,054	,097
KBR	,055	,066	,065	,094	,050		,103	,110	,083	,052	,086
MST	,055	,061	,077	,109	,089	,085		,130	,102	,070	,130
TEX	,073	,090	,106	,081	,092	,094	,105		,103	,070	,109
TST	,034	,059	,057	,079	,070	,070	,086	,087		,034	,089
WAL	,020	,040	,045	,069	,048	,045	,060	,061	,036		,068
ZAC	,063	,089	,090	,086	,083	,075	,108	,094	,078	,062	

Table 2: Relative and absolute number of correctly assigned animals based on 21 microsatellite loci

breed	N	Relative (absolute) number correkter...	
		most probable	significant
		assignments	
Alpines Steinschaf	41	65,8% (24)	80,5% (33)
Texel	58	91,4% (53)	86,2% (50)
Montafoner Steinschaf	66	93,9% (62)	84,8% (56)
Krainer Steinschaf	62	98,4% (61)	91,9% (57)
Kärntner Brillenschaf	109	94,5% (103)	89,0% (97)
Waldschaf	91	90,1% (82)	87,9% (80)
Zackelschaf	49	95,9% (47)	79,6% (39)
Tiroler Steinschaf	53	92,4% (49)	84,9% (45)
Braunes Bergschaf	58	89,7% (52)	84,5% (49)
Tiroler Bergschaf	53	92,4% (49)	83,0% (44)
Juraschaf	77	100,0% (77)	94,8% (73)

Fig. 1: Reconstructed phylogenetic distance tree for the 11 breeds based on averaged distance matrix (Reynold's distance) from 100 Bootstrap-samples with 50 individuals within each breed.



5.

POPULATION GENETIC STUDIES IN THE HUNGARIAN MANGALICA BREEDS USING MICROSATELITE MARKERS

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The genetic structure and relationships among Mangalica breeds and farms at different geographical locations have been studied by microsatellite markers, in order to characterise the populations and to give sound scientific basement for managment practices.

The estimated distances were the smallest between *swallow bellied* and *blonde*, while *red* showed the largest genetic distance from the previous two breed. This approach is capable of distinguish subpopulations within breeds as well.

The present work can be extended to handle mating, to control conservation and to maintain genetic variability and viability of the breeds.

6.

ESTIMATION OF GENETIC DISTANCE BETTWEEN TRADITIONAL HORSE BREEDS IN HUNGARY

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Molecular genetic investigations are important for both to study the differences between horse breeds and to clarify the relations within breeds (lines, familes).
In this repect in Danubian region the Hucul, the Bosnian pony, the Noriker (Murinsulaner, Posavina) cold blooded horses are interessant as old native breeds of the region. The old native Hungarian horse is extinct as an important component of modern warm blooded horses of the country.

The other here improved breeds are also important for registration and preservation. The oldest one is the Lipizzan horse breed established at Lipica in 1580. The Mezőhegyes breeds Nonius, Gidran, Furioso should be considered basic horse breeds as well as the Kisbér Half bred and the Shagya Arabian. The moders Sport horse breeds and new cold blooded breeds (e.g. Hungarian Cold Blooded horse, or the Semigreu Romanesca). are improved by West European breeds, first of all by English Thoroughbreds or Belgian Draught Horse.

Because the original stud book of these breeds in Danubian countries can be found, and the cradle of them is here, these populations should be considered independent breeds which can be distinguished from the other breeds by their pedigrees, conformation, measurement and hopefully by molecular genetic investigation also in the future.

INCO-COPERNICUS project in Lipizzan breed gives a good example for the investigation within the breed in order to clarify relationship among studs, lines and families by microsatellite and mitochondrial methods.

7.

PHYSICAL AND MICROSATELLITE BASED CHARECTERIZATION OF ANATOLIAN WATER BUFFAO RAISED IN TURKIYE

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SUMARY

One indigenous water buffalo population to Anatolia were characterised with 11 cattle autosomal microsatellite loci. A set of 4 cattle microsatellite loci was found to be polymorphic in the Anatolian buffalo genome. Genotyping of these polymorphic microsatellite loci revealed alleles ranging from 3 to 9. The observed heterozygosity ranged from 0.550 to 0.775 and the expected heterozygosity ranged from 0.494 to 0.815. The F_{IS} value changed from –0.101 to 0.205. This result shown that, Anatolian water buffalo population samples seemed to be in Hardy- Weinberg expectation.

INTRODUCTION

The number of water buffaloes in the world has decreased rapidly over the past three decades *(Georgoudis et al., 1998).* Most of world buffaloes live in Asia, Egypt, Southern and south-eastern Europe. Also buffaloes have played an important role in the rural economy of developing Asian country from ancient times.

According to FAO (2000) data, there are about 166 million domesticated buffaloes raised in the five world continents. However, there are about 158 million buffaloes left in the world *(FAO statistics, 2003).* Roughly 97 percent of them or 153 million heads are water buffaloes essentially found in the Asian region.

Also, in Turkey the buffaloes population have declined dramatically over the last decades. The total population according to FAO statistics is 164.000 heads (2003). Their breeding areas are especially middle of Black sea region in Turkey. These animal are mainly used for milk and meat production in this areas. The creamy part of milk fat of water buffaloes milk is populer accompanies to famous Turkish desert. Water buffaloe milk is preferably take place at least in some persantage in Turkish sausage making ındustry.

It is estimated that, 4-5 % of total milk and meat production comes from buffaloes sources. 3.65 % percent of red meat production sources from buffaloes genotypes. Total 40-60 % of buffaloes population are raised in Middle of Black Sea region. The largest number of buffalo population existed in Black sea region. Eastern Anatolian buffalo population has second biggest number of population. Third biggest number of population in the Marmara region existed in Istanbul and surroundings this city. Feeding is based on grazing, straw and concentrates. Their purpose of raising is firstly milk and secondly meat production.

Table 1 shown that several characteristics about Anatolian water buffalo raised in Turkey. This study was estimated to examine the within population genetic diversity using microsatellite markers.

MATERIALS AND METHODS

The numbers of animals sampled from the Anatolian water buffalo were 40 individuals. Blood samples of unrelated animals were collected in slaugterhouse in Silivri of Marmara region. Bloods were collected in 10 ml tubes containing K_2EDTA and stored at –20 ^{0}C until the DNA was extracted by the standart Phenol – Chloroform technique *(Sambrook, J. et all, 1989).* The microsatellite loci used in the study and their characteristics are given in Table 2.

The PCR analyses were carried out using an Applied Biosystems GeneAmp® PCR System 2700 thermal cycler. The reaction mixture was composed of genomic DNA (100 ng), 200µm dNTPs, 2.0 mM $MgCl_2$, 1X PCR buffer, 5 pmol forward and reversed primers and Taq DNA polymerase (0.5 u/sample) in a total volume of 20 µl. All samples were amplified in a reaction volume of 20 µl containing 11.7 µl of (dH_2O) distilled water.

The PCR reactions were carried out in 0.2 ml PCR plates with the following PCR conditions: 1 cycle of initial denaturation for 5 minutes at 94 ^{0}C, 30 cycle of 45 seconds at 94 ^{0}C, 45 seconds at annealing temperature, 1 minute at 72 ^{0}C and 1 cycle of final extension for 10 minutes at 72^{0}C. In order to minimize the artifacts caused during the amplification leading to false size estimations, one or more positive controls were used in each PCR reaction together with a negative control. The PCR product were checked on a 2% Agarose gel together with DNA size markers standards. For all microsatellites allele size was determined on all samples with a Perkin Elmer ABI Prism 310 Genetic Analyzer using the GeneScan Software (Perkin Elmer).

DATA ANALYSIS

For the population and for each locus number of alleles (n_A), observed heterozygosity (H_0) and unbiased expected heterozygosity (H_e) were calculated using Genetix 4.0 Programs.

Also the averages of n_A, H_0, H_e based on four loci were also computed. The population F_{IS} value of Wright’s F statistics based on four loci were estimated and used to test the deviation from the Hardy Weinberg equilibrium. All of the above computations were performed by using Genetix 4.0 statistical programs.

RESULTS AND DISCUSSION

Heterologous cattle microsatellite markers have been tested on Anatolian buffalo genome. A set of 11 (TGLA227, ILSTS005, CSSM66, BM1818, ETH10, ETH225, ETH3, HAUT24, HEL5, TGLA122, TGLA126) cattle microsatellite loci was analysed in Anatolian buffalo samples. Four cattle microsatellite loci was found to be polymorphic in the anatolian buffalo genome. Allele frequencies for each of four microsatellite loci in each of the individuals are reported. The number of alleles Per locus varied from 3 (ILSTS005) to 9 (BM1818). The mean number of alleles Per locus is about 6.75. Allele numbers distribution at the four analysed loci is given in Table 3. The observed heterozygosity ranged from 0.550 to 0.775, and the expected heterozygosity ranged from 0.494 to 0.815.

Arora et al (2003), was studied physical and microsatellite characterization of Tarai Buffalo of India. The Tarai buffalo is riverine with 50 chromosomes, which is similar to Anatolian water buffalo population which is called as subgroup of Mediterrenean water buffaloes. Arora et al (2003), had studyed on heterologous cattle microsatellite loci and were used them for molecular genetic characterization of Tarai genome. A set of 22 cattle microsatellite loci was found to be polymorphic

in the Tarai genome. Genotyping of these polymorphic microsatellite loci revealed alleles ranging from two to seven. Observed heterozygosity of changed from 0.1316 to 0.9231. Mean observed heterozygosity of 0.60 in the Tarai buffalo population. Expected heterozygosity of changed from 0.1246 to 0.8149. BM1818, CSSM66 and ILSTS005 microsatellite loci was found polymorphic in the Tarai buffalo population and also Anatolian water buffalo population. Anatolian water buffalo population heretozygosity was found to similar in Tarai buffalo population.

Moioli et al (2001) was studied genetic diversity between Greek, Italian and Egyptian buffalo populations with using 13 polymorphic microsatellite loci. The number of alleles Per locus varied from two (ILSTS005) to 19 (ETH03). Only for two loci (CSSM33 and ILSTS005), all detected alleles were found in all three country populations (Italian, Greek and Egyptian). ILSTS005 loci was shown 3 alleles in Anatolian water buffalo population. Observed average heterozygosity was 0.135, 0.151 and 0.158 in the Italian Greek and Egyptian populations, respectively. It was lower, although not significantly different from the expected heterozygosity (0.173, 0.176 and 0.190 respectively for the Italian, Greek and Egyptian). But Anatolian water buffalo population observed and expected heterozygosity was found very high.

The Anatolian water buffalo population F_{IS} value changed from –0.101 to 0.205. This result shown that, Anatolian water buffalo population samples seemed to be in Hardy Weinberg expectation. As a conclusion, it can be said that the present study revealed the presence of high degree of genetic diversity within the water buffalo populations of Turkey.

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***Table 1.** Several Characteristics About Anatolian Water Buffalo Raised in Turkey*

	Maximum	**Minimum**	**Sources**
Lactation Yield (kg)	1070.5±279.9	709.6±23.0	Şekerden et al (2000b) Uslu, N.T. (1970b)
Lactation Length (day)	269.2±70.0	222.0±44.2	Şekerden et al (2000a) Şekerden et al (2000b)
Fat (%)	8.1±0.205	6.6±0.68	Kök, S., (1996) Şekerden et al (2000a)
Adulty Body Weight	518.6±17.2	411.0±9.07	İlarslan et al (1983) Uslu N.T, (1970a)
Calving Interval	434.3±57.1	365.2±17.5	Şekerden et al (2000a) İlarslan et al (1983)
Ageat first Insemination(day)	679.7±210.9		Şekerden et al (2000a)
Age at first calving (day)	1313.2±234.8	964.1±3.94	Şekerden et al (2000b) İlarslan et al (1983)
Birth Weight (Male)	34.3±1.20	26.7±0.52	Alaçam et al. (1992) Uslu N.T; (1970b)
Birth Weight (Female)	31.6±0.90	22.1±0.48	Alaçam et al. (1992) Uslu N.T., (1970b)
Servis Periyodu	112.45	70.8	İlarslan et al (1983) Şekerden et al (2000b)
Gestation Lenght (day)	326.5±5.8 (artificial ınsemination)	317.0±51.5 (natural insemination)	İzgi and Asker, (1989) İzgi and Asker, (1989)
Daily Live Weight Gaining (gr) (0-3 Month)	(Male)	(Female)	Şekerden et al. (2000c)
Male	0.483		
Female		0.456	
Daily Live Weight Gaining (gr) (3-6 Month)	(Male)	(Female)	Şekerden et al. (2000c)
Male	0.305		
Female		0.294	
Daily Live Weight Gaining (gr) (6-9 Month)	(Female)	(Male)	Şekerden et al. (2000c)
Male		0.314	
Female	0.357		
Daily Live Weight Gaining (gr) (9-12 Month)	(Male)	(Female)	Şekerden et al. (2000c)
Male	0.504		
Female		0.360	
Fat Content of Milk	8.1	6.1	Kök, S. (1996) (Soysal and Kök, 1997)
Total Solid Matter of Milk	17.7 (3. Lactation)	15.3 (1. Lactation)	Şekerden et al.(2000b)
Ash % of Milk	0.830	0.743	Şekerden et al.(2000a) Şekerden et al.(2000b)

Water of Milk	82.3		Kök, S.; (1996)
Protein % of Milk	4.6	4.2	Şekerden et al. (2000a) (Soysal and Kök, 1997)(Kök, S., 1996)
Caseine % of Milk	3.4 (3. Lactation)	3.0 (1. Lactation)	Şekerden et al.(2000b)

Table 2. *The table shows the name of the microsatellite loci used in the study, their primer sequences, Polymorphism information contents (PIC), annealing temperature, the chromosome number the belong to, and the references articles.*

Locus Name	**Primer Sequence**	**PIC**	**Annealing Temp. (^{0}C)**	**Chromosome Number**	**Reference**
TGLA227	CGAATTCCAAATCTGTTAATTTGCT ACAGACAGAAACTCAATGAAAGCA		55	18	Steigleder et al, (2004)
ILSTS005	GGAAGCAATGAAATCTATAGCC TGTTCTGTGAGTTTGTAAGC	0.42	55	10	Arora et al, (2003)
CSSM66	ACACAAATCCTTTCTGCCAGCTGA AATTTAATGCACTGAGGAGCTTGG	0.49	58	14	Arora et al, (2003)
BM1818	AGCTGGGAATATAACCAAAGG AGTGCTTTCAAGGTCCATGC	0.40	58	23	Arora et al, (2003)

Table 3. *Characteristics of Bovine Microsatellite Markers Tested on Anatolian Water Buffalo Population.*

LOCUS	**Number of alleles (n_A)**	**Observed Heterozygosity (H_O)**	**Expected Heterozygosity (He)**	**$H_{n.b.}$**	**F_{IS}**
TGLA227	7	0.600	0.743	0.753	0.205
ILSTS005	3	0.550	0.494	0.500	-0.101
CSSM66	8	0.775	0.707	0.716	-0.084
BM1818	9	0.750	0.815	0.825	0.092
Mean	6.75	0.668	0.689	0.698	0.043

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8.

NATIVE GENETIC ANIMAL SOURCES IN TURKIYE

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The total area used in agricultural production in Turkey is about 27 million hectares. Economically irrigable agricultural land in the country is about 8.5 million hectares. Cultivated land is dominated by cereal production, which accounts for nearly 50 % of cultivated area. Farmland is privately owned. Average farm size is 6.5 ha; however 62% of farms are under 5 ha.

STRUCTURE OF ANIMAL PRODUCTION SYSTEM

Historically, livestock and livestock products have played important roles in the Turkish agricultural economy and rural society.

Turkish livestock products such as leather products, wool carpets, mohair, soft cheese, yogurt, buttermilk and honey are worldwide known. However, contribution of livestock industry to Gross National Product (GNP) has been drastically declined in last two decades. The share of agriculture in GNP was 26 % in 1980, but it decreased to 13.6 % in 2002. The same trend can be observed for agricultural export.

Livestock industry accounts about 25 percent of the agricultural GNP in the country.

Recently, Turkey has become a net importer of livestock products and is increasingly dependent on the world market. While productivity has risen over the last decade, the Government's protective measures have not resulted significant production gains.

Cattle and Water Buffalo Husbandry

With respect to the figures of 2000, 89% of total milk and 30.7% of meat production is provided by cattle in Turkey. A significant proportion like 84% of the dairy enterprises in livestock sector has 1-4 heads of dairy cattle. Likewise, 87 % of cattle fattening enterprises have less than 10 animals.

The geography, socio-economic and cultural structure, presence of livestock improvement projects has had a significant impact on the distribution of cattle breeds and their population throughout Turkey.

Anatolian Black (Yerli Kara), which is one of the local breeds of Turkey, had a high population and was very common in Central Anatolia, due to intensive crossbreeding in recent decades, its population dramatically declined and become a threatened breed in the region.

Eastern Anatolian Red (Doğu Anadolu Kırmızısı) is a breed of Eastern and North Eastern Anatolia and it has the second largest distribution area after Anatolian Black.

Anatolian Gray (Boz Irk) is widespread in Aegean and Marmara regions. South Anatolian Red (Güney Anadolu Kırmızısı) is extended in EastMediterranean region and Southeast Anatolia.

All these local breeds used to have rather large populations and extension areas, but the number of purebreds has declined and even their populations have come to the threshold level of extinction due to crossbreeding in recent decades.

Holstein Friesian, Brown Swiss and Turkish Brown Swiss are wide-spread from west to east. Jersey is especially common in Black Sea region and Simmental can be seen throughout the country.

The Swiss Brown was first crossed with Anatolian Gray and new crossbred was called as Karacabey Brown (Karacabey Esmeri). Later on, a definition was made for the Anatolian Black and Eastern Anatolian Scarlet or Brown, including the crossbreds of them called as Turkish Brown Swiss.

Sheep and Goat Husbandry

According to data belonging to the year 2000, 11.48 percent of meat and 10.15 percent of milk production of Turkey provided by sheep and goat species.

Sheep breeding in Turkey is generally carried out by small structured native sheep breeds having low fertility and milk yield and rough fleece production. Native breeds constitute 97.3% of the total sheep population in the country.

Akkaraman (White Karaman) mainly located in Central Anatolia is ranking in the first order as its population among the native sheep breeds.

Morkaraman, which is widespread in Eastern Anatolia and Dağlıç in Western Anatolia are the 2nd and the 3rd. Kıvırcık exists in Aegean and Marmara regions, Karayaka breed in Black Sea region, Gökçeada in Gökçeada-Çanakkale region, Sakız (Chios) in coastal parts of Aegean-Marmara, Turkish Merino in South Marmara-Central Anatolia regions, Ivesi (Awassi) in South East Anatolia and Tuj (Tushin) breed in Kars province and premises.

As native hair goat constitutes 94.8% of the goat population of Turkey while Angora goat comprises 5.2 % of it.

Poultry Husbandry

According to the data belonging to the year 2001, there are total 10 555 poultry enterprises in Turkey. As distribution of total numbers of enterprises; there are 57 layer and 198 broiler breeding, 1 439 layer production and 8 861 broiler enterprises in the country.

Poultry farming is intensively practiced especially in Marmara, Aegean, Central Anatolia, Black Sea and Mediterranean regions. Poultry production is an integrated sector.

Turkey husbandry, which showed a rapid development in a short time, is densely practiced in Marmara, Central Anatolia and Southeast Anatolia regions.

Türkiye has a great potential for animal production and the topographic and climatic conditions are favorable for animal husbandry in general . Even though Türkiye is among the leading countries in the nımbers of some of the livestock , the animal productivity sometimes can be quite low due to the high numbers of low producing , umimproved native animals. Nevertheles , the adaption capacity of these indigenous animals , to the local conditions is higher than cultural breeds.

Native farm animal genetic resourches constıtute an important resource in total number of farm animal population .

Production systems in Türkiye vary from chances in international and national agricultural policies and in the milk and beef markets had greatest effect to the production systems and changing the content of population from native breeds to the exotic breeds.

9.

PIGEONS BREEDS

Wil J. van Eijsden

Pigeons get very little attention as a gene reserve. Their history with mankind goes back thousands of years. They were and are as much part of the Egyptian and Mesopotamian land fertility as the well known fertile river sludge because of their manure which is collected from pigeon towers. Today large pigeon farms for meat production exist in Italy and the USA. Pigeons are highly esteemed by fanciers globally for their different types of flying abilities and their beauty. They are a cheap and important additional food in subsistence farming situations.

In a private investigation I found that in the Hungarian language area about 75 breeds were once present. Of these around 30 are still reasonably common and not endangered. Another 25 were found to be still present but in low numbers and are probably endangered. No evidence was found of around 20 breeds. These might be extinct already.

The collected data are not complete and the result is also complicated by the use of synonym names.

It would be important to do a proper scientific study about the real situation. This study could then be used to develop a necessary gene conservation programme and to get support for the implementation of such programme before another 20 or 25 breeds disappear.

10.

AN-GR CONSERVATION STRATEGIES TO DEVELOP LOW INPUT MIXED FARMING IN SOUTH-EAST ASIA

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Abstract

The low agricultural production level in South-East Asia forces rural people for all day survival type work and does not allow focusing and exploring the natural values. Conservation of domestic AnGR is sustained spontaneously through the daily life of traditional, mixed type family farming system, without any direct conscience.

Vietnam – as a tropical and sub-tropical country – is a typical South-East Asian country with an elongated „S" form of length, borders China to the North, Laos and Cambodia to the West, and the Pacific Ocean to the East and the South. The traditional farming base of South East Asia – as well of Vietnam – is an integrated system of rice, root crops, fruit, vegetables, livestock and poultry. Majority of rural population are farmers, 75% of them practice animal husbandry. Animal production in Vietnam takes 20–25% of total agricultural production. Only 1% of meat is exported. Livestock enterprises are very small and comprise pigs, cattle, buffalo, chickens and ducks. The main agricultural areas of the country are the Red River Delta (North) and the Mekong Delta (South). A considerable part of Vietnam, however, is characterized by much poorer conditions for agricultural activities, where contribution to the development of low input mixed farming should be of major importance.

Being the home of valuable domestic animal genetic resources (AnGR) such as:"I" pig, "Bau Quy" duck, "U Riu" cattle and others species, Central Vietnam – endowed with poor soil and some of the worst weather in the country – is the most destitute, food deficit region in Vietnam. Development of animal breeding adapted to specific local conditions in Central Vietnam can highly contribute to improve the quality of life of rural people. It is obvious that local breeds have to be conserved and used for traditional farming. However, because of the great differences of breeds in different areas of the country, introduction of animal breeds may threaten local breeds, and varieties in the case of crossings. Their breeding would need a very strict control to avoid loss of local breeds and varieties, just if foreign breeds were imported *("physical isolation").*

Certain animal breeds however, would not endanger local breeds directly, if imported breeds have no relatives there, and therefore, no crossings with local breeds can happen *("biological isolation").* To enlarge choice of animal breeds in Central Vietnam, introduction of landrace varieties of Guinea-fowl, or goose and turkey to some extent, suitable for extensive type of farming, can be considered. Species mentioned, have no local varieties in Vietnam and therefore can be introduced, if gene conservation aspects of local breeds are concerned.

The local types of Guinea-fowl were exported from KATKI, Godollo, Hungary, to the National Institute of Animal Husbandry, Hanoi, Vietnam for testing its acclimatization to the Vietnamese conditions. The following potential risks should be evaluated, tested and proper solution developed by the adaptation process of Guinea-fowl: (1) response of Guinea-fowl to climatic conditions (seasonality, productivity, growth, veterinary issues), (2) use of natural resources (fodder) by Guinea-fowl, its competition with "local users"; (3) impact of Guinea-fowl keeping on the environment, (4) impact of Guinea-fowl keeping on local "food chain", (5) conditions to develop organizations to control high quality production for the market (example: Label type production for export), (6) possibilities to extend breeding to other South-East Asian countries.

11.
STATE OF ANIMAL GENETIC RESOURCES IN THE CZECH REPUBLIC IN 2003

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Numbers of farmed and protected breeds, as well as trends in protected and supported breeds in 2003 are given in the Table 2 below.
Molecular genetic analyses were performed during 1997 – 2003 in following range:

Cattle

Reconstruction of Czech Red Cattle, by absorptive crossing of Czech Pied cows (originated from the Czech Red Cattle) with red bulls, derived in 1970-80 from the last original Czech Red cows through insemination with closely related Polish and German Red cattle. During 1997-2003 there were molecular genetic analyses performed to estimate genetic distance between these breeds.
Study has been carried using microsatellites and protein markers to estimate genetic distances among Czech Red cattle, Czech Spotted cattle, Black and White cattle, German Black and White cattle, and F1 crosses Czech Red x Czech Spotted cattle. Ten microsatellite loci were used plus the polymorphisms of kappa-casein, beta-lactoglobulin, prolactin and growth was involved into the computations. Minimal genetic distance as measured by the method of Nei`s standard was found between Black and White and German Black and White cattle (0.042). Also the distance between Czech Spotted and Black and White cattle was low, it reflects their mutually relationship, Black and White cattle has come into being by crossing of Czech Spotted cattle and Black and white bulls both European and American origin, the distance between Czech Red and Black and White cattle was low too. On the other hand, relatively low distance between Czech Spotted and German Black and White cattle was less expected. The distance between Czech Spotted and Czech Red cattle ranged rather in the middle like the distance between F1 crosses and Czech Spotted or Czech Red cattle. The phylogenetic non-relationship between Czech Red and German Black and White cattle found its reflection in the high genetic distance 0.138. The distances as measured by the method of Nei`s minimal and Manhattan matrix ranged similarly as the Nei`s standard. Further, the dendrograms were constructed using statistic package Phylip. Finally, the usefulness of polymorphous loci in quantification of distances among breeds was confirmed. Namely microsatellites offer great potential thanks to their extent polymorphism. Any singularity of the Czech Red breed was confirmed, and the necessity to save this endangered gene *reserve.*

Pigs

Genetic distance among five pig breeds currently farmed in the Czech Republic was estimated based on results of testing 11 polymorphic proteins, blood groups, alotypes and immunoglobulin markers. Distances between the Prestice Black Pied Pig and Landrace, White Improved, Czech Meaty, Duroc and Hampshire was 0,051 – 0,051 - 0,172 – 0, 231 and 0,247 respectively.

Sheep

Only differences among Shumavska, Valachian, Improved Valachian and Merinolandschaf breeds which are the most farmed dual-purpose breeds in the Czech Republic in the b-lactoglobulin locus (A, and B alleles) were tested so far, with the frequency 0,20-0,33-0,44 and 0,38 for the A-allele and 0,80-0,67-0,56 and 0,62 for the B allele in the above mentioned breeds.

Goats

Seven microsatellite markers (ILST011, MAF65*, OarFCB48, SR-CRSP-9, MHCIIDR, OarAE54, INRABERN172) were used for estimation of genetic variability of both national breeds. The numbers of detected alleles ranged from 4 to 13 and was lower in White Goat (4 to 8 only) and calculated genetic distance between the White and Brown Goat $D_N = 0,0517$.

Horses

13 microsatellite loci are continuously analyzed for of all breeds (AHT4*, AHT5*, ASB2*, HMS1, HMS2**, HMS3*, HMS6*, HMS7*, HTG4*, HTG6**, HTG7**, HTG10*, VHL20*). Results in 2003 for the two cold-blooded breeds (Silesian Noric, n=100 and Bohemio-Moravian Belgic, n=188) were calculated, $D_N = 0,0517$.

The genetic relationship between Moravian warm-blooded, Czech warm-blooded and Trakehner horse was investigated in a total of 17 gene-tic polymorphism markers (10 protein and enzyme loci, 7 blood groups) and in 62 alleles. The degree of heterozygosity was as follows: Czech warm-blooded horse 0.367, Trakehner horse 0.319, Moravian warm-blood horse 0.353. The closest genetic relationship was found between the Czech warm-blooded and the Trakehner horses *D* = 0.027; between the Czech warm-blooded and Moravian warm-blooded horse the genetic relationship was more distant *D* = 0.076 while the most distant genetic relationship was observed between the Trakehner and Moravian warm-blooded horses *D* = 0.102.

Estimation of distances among other farmed breeds (Silesian Noric SN, LanyNoric LN, English Fullblood A1/1, Czech warm-blooded CT, Latvian Zemaituka Z, Hutsul H, Old Kladruby White KB and Old Kladruby Black) based on 12 microsatellite loci analyse in 2002 showed following results:

Table 1 : genetic distances among different horse breeds farmed in the Czech Republic

Population	**A1/1**	**SN**	**LN**	**Z**	**CT**	**H**	**KB**	**KV**
A1/1	*****	0,020	0,003	0,026	0,017	0,017	0,021	0,033
SN	0,547	*****	0,014	0,014	0,012	0,019	0,033	0,030
LN	0,486	0,122	*****	0,021	0,006	0,016	0,032	0,024
Z	0,694	0,405	0,377	*****	0,021	0,016	0,038	0,030
CT	0,153	0,407	0,371	0,546	*****	0,014	0,018	0,035
H	0,447	0,352	0,293	0,479	0,414	*****	0,018	0,021
KB	0,568	0,409	0,484	0,488	0,411	0,564	*****	0,021
KV	0,672	0,371	0,512	0,434	0,621	0,594	0,273	*****

Table 2: Numbers of farmed and protected breeds, as well as trends in protected and supported breeds in the Czech Republic in 2003

Species	**Number of farmed breeds :**			**Names of protected breeds (names in bold critically endangered, < 100 breeding dams)**
	Indigenous and locally adapted	**Exotic and recently introduced**	**Protected genetic resources**	
dairy cattle	3	15	**2**	***Czech Red Cattle*** Czech Red Pied Cattle
sheep	8	18	**2**	Shumavska ***Valachian***
goats	2	4	**2**	White Shorthaired Brown Shorthaired
pig	4	5	**1**	Prestice Black Pied
horse	6	12	**4**	Old Kladruby Horse Hutsul ***Silesian Noric*** Czech-Moravian Belgic
poultry	27	23	**2**	Czech Gold Brindled Hen Czech Goose
rabbit	20	2	**7**	Moravian Blue, Bohemian Albinotic, ***Bohemi*** ***Lofer***, Bohemian Spotted, ***Moravian Brown-*** ***Bohemian Red***, ***Bohemian Black Kemped***
nutria	12		**3**	***Standard*** ***Silver*** ***Prestice Tricolor***
freshwater fish	32	23	**7**	local lines of: carp, tench, salmon trout, rainbow trout. catfish, whitefish, sturgeon
honey bee	1		**1**	Carniolan

++ increase > 10%
+ increase 1-10%
S = stable
- decrease up to 10%
-- decrease > 10%
n.a. not applicable

12.

APPLICATION OF DNA-MARKERS TO DISTINGUISH TSIGAI SHEEP VARIANTS

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Hungarian Tsigai (Berke) sheep breed formed geographically isolated populations on the course of its spread in Carpathian basin. These days, two different main variants of the Tsigai are distinguished. One of them is the original (native), being the gene reserve, while the other is selected for milking (dairy). In addition to the information of breed history, observable constitution and performance differences, blood and protein samples proved the distinction of these two variants.

A microsatellite (CSRD247, HSC, INRA063, MAF214, OarAE129, OarCP49, OarFCB11 and OarFCB30) comparison has been started to improve our knowledge in breed description by using ABI PRISM 310 Genetic Analyzer apparatus. Data evaluation was carried out by Genotyper and GENEPOP software programs.

Table 1.: **Nei's unbiased measures of genetic identity (above diagonal) and genetic distance (below diagonal)**

Population	Jákotpuszta	Kardoskút	Cegléd	Akasztó	Makó
Jákotpuszta	-	0.6570	0.6201	0.7009	0.7166
Kardoskút	0.4200	-	0.4485	0.7283	0.7801
Cegléd	0.4779	0.8019	-	0.4060	0.5640
Akasztó	0.3554	0.3170	0.9014	-	0.8276
Makó	0.3332	0.2483	0.5726	0.1892	-

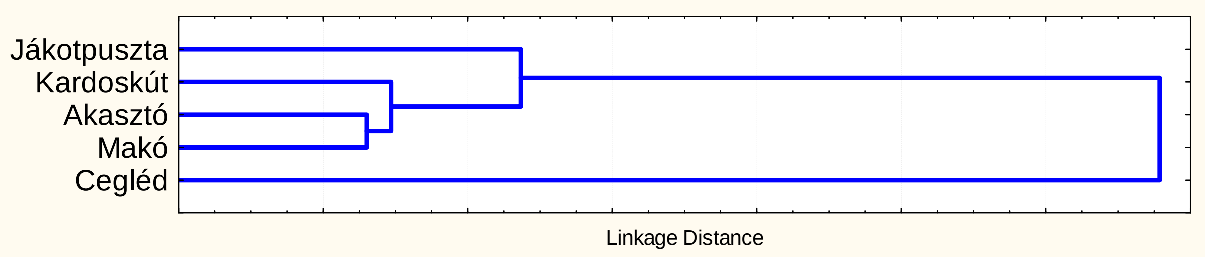

Figure 1.: **Tree diagram for Tsigai variants according to Nei’s genetic distances**

According to the results (Table 1., Figure 1.), it is obvious that the milking Tsigais (Cegléd) are seriously differing from the others. This variety came from the Southland, and has been mated continuously to rams from this region (Zombor and Plivniča) ever since. It is believed that the genetic difference is caused not only by selection, but by some blood from other breeds. At the same time, the native Tsigais could be further partible into a “mountain” (Jákotpuszta) and into a “lowland” (Kardoskút, Akasztó and Makó) eco-types. Jákotpuszta flock considered to be the ancient or Transylvanian type of Hungarian Tsigai. On the Hungarian Great Plain, the animals grew taller and differentiated from this in the last century.

13.
MUTTON PRODUCTION WITH HISTORICAL HUNGARIAN SHEEP BREEDS

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The Danubian region houses several ancient multipurpose sheep breeds like the Hungarian Racka (in Zackel-group) and Hungarian Berke (in Tsigai-group).

The aim of this study was to evaluate their utilisation in mutton production by using the conventional Hungarian Merino of wool-type as a control breed. Comparing the growth of young weaned lambs the daily gain was taken into consideration. The following parameters were collected: initial weight (20 Kg), final weights (30 and 40 Kg, in two slaughter weight categories, 10 males and 10 females in each), and length of intensive fattening.
To calculate the daily gain and the fattening days a multiple trait General Linear Model was applied, where fix effect was the sex and covariate was the age (StatSoft, Inc. (2003). STATISTICA (data analysis software system), version 6. www.statsoft.com.).

As it is presented in Table 1., the Racka had the weakest daily gain, however, the Berke and the Merino reached the same performances in both final weight categories. The results can be explained partly with the size of the breeds. The slower development of the Rackas caused their sole lighter slaughter weight category.

Table 1.: **Preliminary results in growth of lambs**

Initial weight, Kg		20			20	
Final weight, Kg		30			40	
Daily gain, g	n	LSM	Std.Err.	n	LSM	Std.Err.
Racka	40	227	11.2	-	-	-
Berke	10	310	5.6	10	350	11.1
Merino	10	293	11.3	10	362	11.1
Length of fattening						
Racka	40	63	1.5	-	-	-
Berke	10	38	2.9	10	54	1.8
Merino	10	36	2.9	10	54	1.8
p		<0.001			=0.812	

Within the frame of a larger project all the available parameters – beside the growth, the carcass traits as well as the meat and tallow properties - are recorded and evaluated. In this project, in year 2004, we can investigate three types of fattening: during the suckling period, and during intensive and extensive fattening. In the case of extensive one wethers are fattened on pasture only, and will be slaughtered in fall.

14.

CO-EXISTENCE OF DOMESTIC ANIMAL GENETIC SOURCES AND RESSOUCES IN THE CARPATHIAN BASIN

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Abstract

Co-existence of animal genetic sources and resources is still the case in the Carpathian basin. It is due first of all to the comparatively high level of agro-biodiversity in that region, which can be explained by several factors, such as: (1) different environment, (2) different climate, (3) different nations, (4) different level of economical development, (5) different types and traditions of agriculture, (6) different conservation programmes (if any), (7) several local breeds and (8) several purposes of animal breeding and production.

In this context, the term "*animal genetic resources*" is used for domestic animal breeds which are well described and kept in large quantities or under strict conservation programmes. Nevertheless, the breeds are often chosen randomly, and conservation is based on the actually available breeding stock, or on a small region of collection. There are, however, a lot of local breeds or varieties, kept and maintained naturally by local people, according to their needs and traditions. For them we use the term "*animal genetic sources*" here. Characteristics and even existence of these breeds and varieties are usually unknown by conservationists and therefore the breeds may exist and disappear without any consciousness or conservation programme, depending on their use in sub-regional or local agriculture.

Poultry can be a good example for the co-existence of animal genetic sources and resources. Starting in the 1960-ies, decline of local breeds was very quick, parallel with the rise of poultry industry. The trends of decline, however, are different by species, regions and types of agriculture. Field studies were made by KATKI and MGE – the two main organizations of Hungarian gene conservation of indigenous and adapted poultry breeds – to localize both known and unknown varieties of poultry in different regions and conditions. First results of the study show that several breeds and varieties in different species exist in the Carpathian basin at least in poultry, kept by local people. Further studies are needed to reveal existence of animal genetic sources of other species, e.g. ruminants, as well as the special relations between breeds and breeders in local agriculture. To enhance the progress of gene conservation of both animal genetic sources and resources, the following conclusions and proposals should be considered:

(1) Several animal genetic sources (local breeds and varieties) still exist in the Carpathian basin. Main reasons for the co-existence of animal genetic sources and resources are the relatively high environmental, economical and traditional differences of regions and sub-regions.

(2) Gene conservation programmes of AnGR in certain species represent only the top of the iceberg, since animal genetic sources are usually excluded. This fact has to be taken into consideration to ensure equal importance of animal genetic sources and resources in conservation.

(3) Existence of several local breeds and varieties depend on the changes of local agricultural activities. Therefore, aspects of rural development and conservation of agricultural traditions are vital for conserving any local breed.

15.

ENSURING AND REVITALIZING THE LOCAL BAZNA BREED OF SWINE

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Abstract:

The study focuses on the Bazna swine breed, a race formed at the end of the 19th century in our country and, due to its qualities, still much appreciated. There are three main criteria that we have taken into consideration in order to appreciate it to its fullest. Thus, the general aspect refers to height, length and perimeter, characteristics that constitute important marks in the evaluation of any specimen. Secondly, we have analyzed the reproduction characteristics, which conclude that we are dealing with a good rate of productivity, and thirdly, the growth and fattening performances are also such as to ensure a good quantity of product (meat).

An important role in obtaining the best results in the case of this breed is held by the pure breed raised as a selection nucleus within the Station for Agricultural Reseach Turda, county of Cluj. This is made clear by the comparative analyses of the specimens' characteristics in small farmsteads and in the Station. Together with a few other improved swine breeds, the Bazna swine breed represents a very efficient solution for a modest environment and modest feeding conditions.

The Origin and Formation Mode of the Bazna breed

The Bazna breed is part of the native breeds group, which was formed in our country as a result of crossing performed between the Mangalita and Berk breeds.

In the year 1872, while building the railroads from Transylvania, for which purpose several English engineers were in the country (stationed in the locality of Bazna, county of Sibiu), a number of swine from the Berkshire (Berk) breed were brought from England, a breed that was considered at the time precocious and having tender meat.

A pair of such swine were ceded to Francois Ehrlich, former administrator of the Bazna resorts, in the vicinity of Medias. The boar was also used by him for mating with the sows of the Mangalita breed from the locality, thus resulting products that presented completely new qualities, convenient to the breeders, as compared to the known qualities for the Mangalita breed. These products stand at the basis of the present Bazna breed, whose name is due to the locality that it was formed in.

From the Medias center it was then spread into other areas around Sighisoara, Sibiu, and especially Fagaras, where it was kept as a predominant swine breed ever since the first decades of the twentieth century.

In general, the conditions under which the Bazna swine was formed and evolved were those ensured by the small breeder, namely very varied nourishment, largely based on grazing, kitchen leftovers, etc., and merely completed by concentrates, in particular corn. Thus, during its course of formation, it acquired the traits characteristic to a less particular animal, who consumes and assimilates well the most varied food types, nevertheless being quite precocious and having satisfactory prolification for the individual small farmstead, where, traditionally, it represents a preferred breed even to the present time.

At present, the Bazna breed is kept as a pure breed for the purpose of a selection nucleus within the Station for Agricultural Research from Turda, county of Cluj, in order to keep the existing gene pool and for the usage of small breeders with breeding stocks having a high degree of productivity, adapted to a breeding system specific to family farms in our country.

The General Aspect of the Bazna Breed of Swine

The Bazna swine is a mid-sized swine, with a harmonious conformation. The head is somewhat smaller as compared to other breeds, having large ears bent forward, thus partially covering the cheeks. The head profile is slightly concave. The neck is rather short and well connected to the nape and barrel.

The barrel is mid-sized, almost cylyndrical, with the spine line slightly convex and quite large. The abdominal line is also large enough and almost straight, having on the average 12 nipples symetrically arranged.

The croup is average as far as development is concerned, slightly flattened, with mid-sized hams. The members are average-sized, quite thin, but strong, ensuring good mobility of the animal.

The hair is straight, approximately 4 cms long.

The colour is made up of two nuances, forming a black-based characteristic drawing, with a white girdle, which envelops the barrel body at the level of the withers and is continued on the forelimbs. The width of the girdle varies between quite generous limits, however the robe typical to the breed is considered the one between 20-25 cms. The typical girdle specimens are more productive (significantly more as compared to the atypical ones), a reason that leads to the conclusion that for the purpose of reproduction typical girdle specimens should be selcted. Ever since the breed was initially formed, this morphological characteristic has been a selection criterion for breeders.

A smaller number of Bazna swine are either completely black, or speckled (from white, black and yellow or red), or the head and the neck are black and the rest is white. All these colous, as well as the completely white, are considered faulty and constitute reasons for the exclusion of reproduction specimens.

The typical robe specimens have a smoky colour at the edges of the girdle, which shifts the colour gradually from white to black. This area of transition is characteristic to the Bazna swine in pure breed. With cross-breds that sometimes have the girdle, this transition area is never noticeable, the limit between black and white being clear.

The dimensions of the most important body dimensions are rendered in Table 1.

Table 1

The main dimensions of the body and of the body mass for adult boars and sows belonging to the Bazna breed.

Specification		***Sex***	***Value***
Height (cm)	At withers level	boars	77.2
		sows	71.5
	At croup level	boars	85.2
		sows	78.6
Length (cm)	Of the barrel body	boars	130.2
		sows	117.4
	Of the body	boars	156.3
		sows	142.7
Perimeter (cm)	Of the thorax	boars	145.8
		sows	138.7
	Of the shin	boars	20.8
		sows	19.3
Bodily weight (kg)		boars	195.5

A farm's rentability relies greatly on the value of the existing biological material and on the efficiency of the use of reproduction animals.

Large productions, of superior quality, with low production expenses, is only possible if there is a continual improvement of certain physiological traits extremely useful from the economical point of view.

Characteristics of reproduction

The main characteristics of reproduction for the Bazna breed swine are rendered in Table 2.
The Bazna sows are generally good milk producers and good mothers, which explains the high number of weaned suckling pigs, in this respect outnumbering certain breeds with better prolification.

In the conditions provided by the farms in the private systems and within farmsteads, the suckling pig production rates are somewhat lower than the ones mentioned above, a fact due especially to the early introduction of sows and boars for reproduction (7-8 months or even earlier), when they haven't yet reached the necessary bodily development. However, as a consequence of common usage of improved reproductors purchased from the Station for Agricultural Research Turda, the respective rates can be sensibly improved (together with the breed in general) for the material in these farms as well. According to the poll data, the prolification of the Bazna swine, considered in general, is of approximately 9 suckling pigs at littering. At weaning, their number is extremely variable, depending not so much on the characteristics of the breed, but on the conditions existing in each farmstead (shelter, nourishment, care). We should emphasize that, under less appropriate conditions, the Bazna swine yields a greater number of suckling pigs per sow annualy than other prolific breeds (The Great White, Landrace or crossings between these breeds), a fact that constitutes one of the reasonswhy the Bazna breed is still preferred in certain areas.

Table 2

The reproduction performances of Bazna sows in different farms.

Reproduction performaces		***Small farms***	***Station for Agricultural Research Turda***
Prolification	Total (head)	9.5	10.6
	Of which live	8.7	9.2
Average weight of suckling pigs at birth		1.4	1.35
Number of suckling pigs at 21 days (head)		7.9	8.4
Suckling capacity (kg)		34.2	35.7
Average weight at 21 days (kg)		4.3	4.3
Number of weaned suckling pigs (head)		7.7	8.1
Average weight at weaning (kg)		8.1^{x}	9.1^{x}

X - weaning performed after 45 days

Growth and fattening performances

As far as the characteristics of fattening are concerned for the Bazna breed, it is noticed that these act diffferently depending on the farms.

These results are more influenced by the conditions for the keeping and nourishment of the breed, which differs from one breed to another. The Bazna young stock destined for reproduction, raised under normal conditions, has an average rhythm of development, depending on which the breed can be appreciated as semiprecocious.

The Bazna swine is suitable both for early fattening, starting with the age of approximately 3 months, until it reaches the weight of 100-110 kg, and for mixed fattening, starting at 5-6 months up to the weight of approximately 80 kg, after which the increase is significantly reduced. Thus, according to the control data, it results that the daily average increase up to 80 kg is of 630 g, and starting from this, up to 110 kg, the daily average increase only reaches 560 g. It is therefore recommendable from the economic point of view that the pigs from this breed, unlike the ones from the Great White and Landrace breeds should be fattened up to 80-90 kg, a weight they can reach at the age of approximately 7 months, after which it is recommendable that they be slaughtered.

Table 3

The evolution of growth and slaghtering performances achieved by the Bazna breed young stock during different periods

Growth performance	***Small farms***		***SAR Turda***	
	M	***F***	***M***	***F***
Daily average growth (g)	537	523	604	562
Thickness of lard (mm)	26.8	26.1	26.2	29.6
Average weight at 90 days (kg)	18.8	18.3	18.2	18.2
Average weight at 180 days (kg)	67.3	66.8	70.8	70.1
Specific consumption (kg forage/kg increase)	3.58	3.56	3.3	3.28

This suits also the point of view of the product resulted upon slaughtering (the meat), which, in the case of animals heavier than 80-90 kg has too much fat.

The thickness of the lard in the Bazna breed manifests the tendency for growth, but maintains itself below 30 mm on the average, many individuals thus falling within the limits characteristic to the white breed. The presented results might, over a very short period of time, place the Bazna breed among the maternal breeds in obtaining crossings, being known as a strong breed, given that sows are good mothers, and the reproduction quotas are constant all year long.

Production at slaughtering is generally mixed, irrespective of the type of fattening that the Bazna swine is subject to. Even after temporary fattening it produces a larger quantity of fat than the meat breeds (the Great White). This characteristic, parallel to its hardiness and perfect adaptability to modest living conditions , contributed to the large spread and the maintainance of the Bazna swine within family farms.

Through the value of the reproduction characteristics and mainly of the prolification and capacity for suckling, closely connected to the other characteristics observed over different periods, in the conditions of semi-intensive growth, specific to family farms, the breed reaches a level close to the improved swine populations raised in the country under the same conditions.

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