

DOMESTIC CATTLE BREED DIVERSITY IN LITHUANIA

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Summary. Economical liberalisation, which started in 1989, led to a dramatic decrease of cattle numbers in Lithuania. From 1989 to 1995 the number of cattle decreased by about 50 % and the local native cattle breeds became a status of endangered breeds. International breeding programmes have intensified the economic competition among breeds. The promotion and facilitation of using a few universal breeds for dairy and beef production has led to the replacement of less productive breeds with more productive ones and increased the number of endangered breeds globally. However, traditional native cattle breeds are often well adapted to local environment, animal husbandry practices and feeding; the breeds can have resistance to local diseases and are important from historical point of view.

To change this situation, more attention is currently focused on the maintenance of animal genetic diversity than in the past, and activities have been initiated on scientific, political and administrative levels.

The N-EURO-CAD project, funded by Nordic Genebank for Farm Animals (NGH), was designed to analyse genetic diversity within North European, Baltic and Polish cattle breeds, to estimate relationships and genetic distances between them by using genetic markers. The results of studies will give better picture on the origin and relationships between North European, Baltic and Polish cattle breeds and their history, will promote preservation of endangered cattle breeds and conservation of cattle genetic resources. The studies on the origin of cattle breeds also can give more information on history and migration of human populations.

Keywords: cattle, conservation, diversity, livestock.

LIETUVOS GALVIJŲ VEISLIŲ GENETINĖS ĮVAIROVĖS TYRIMAS

Santrauka. Dėl intensyvios ekonominės plėtros žemės ūkyje, 1989-1995 metais Lenkijoje auginamų galvijų skaičius sumažėjo 30%, Lietuvoje, Latvijoje bei Estijoje - apie 50%, o šiose šalyse laikomų vietinių galvijų veislės atsidūrė ties išnykimo riba.

Ilgą laiką, tarptautinės veisimo programos buvo orientuotos į intensyvių galvijų produktyvumo didinimą, o šis procesas, savo ruožtu, lėmė ekonominę konkurenciją tarp komercinių ir vietinių galvijų veislių. Kelių, aukšto produktyvumo, universalių veislių naudojimas galvijų pieno, mėsos bei kitų produktyvumo savybių gerinimui, tiek Europoje, tiek ir visame pasaulyje lėmė ties išnykimo riba esančių veislių skaičiaus padidėjimą. Yra žinoma, kad vietinės, tipiškos tam tikram geografiniam regionui arba šaliai galvijų veislės, yra geriau prisitaikę prie esamų gamtinių bei aplinkos sąlygų, veisimo būdų bei auginimo tipo, šėrimo sąlygų bei paties pašaro, pasižymi aukštu atsparumu tai vietovei būdingų ligų atžvilgiu. Vietinės galvijų veislės yra svarbios ne tik ekonominiu, bet ir istoriniu požiūriu, kadangi kiekviena veislė turi savo unikalų kelią evoliucijos eigoje.

Pastaraisiais metais daug dėmesio yra skiriama gyvūnijos genetinės įvairovės išsaugojimui. N-EURO-CAD projekto tikslas yra ištirti šiaurės Europos šalių galvijų genetinę įvairovę ir nustatyti genetinius atstumus bei ryšius tarp atskirų veislių genetinių žymeklių pagalba. 1999 metais šis projektas buvo išplėstas, įterpiančias į jį Baltijos šalių – Lietuvos, Latvijos ir Estijos bei Lenkijos galvijų veisles. Iš viso į projektą yra įtrauktos 35 galvijų vietinės bei komercinės (pagerintos) veislės iš Suomijos, Norvegijos, Švedijos, Danijos, Islandijos, Lenkijos, Latvijos, Estijos ir Lietuvos. Pagal galvijų duomenų bazės (CadBase) rekomendacijas (<http://www.ri.bbcrs.ac.uk/cdiv/www/inform.htm>), genetinės įvairovės tyrimui buvo pasirinkta 20 skirtingų genetinių žymeklių-mikrosatelitų. Dalis tiriamų gyvulių jau yra ištirta kraujo grupių, kraujo plazmos baltymų bei pieno baltymų polimorfizmo atžvilgiu. Fenotipiniai požymiai, tokie kaip spalva, raguotumas bei atskiri, specifiniai kiekvienai iš tiriamų veislių, požymiai yra sukaupti duomenų bazėje (<http://www.neurocad.lva.lt>). Tyrimų tikslas yra ištirti keturių Lietuvoje veisiamų galvijų veislių: Lietuvos juodmargių, Lietuvos žaliųjų, Lietuvos šėmųjų bei Lietuvos baltnugarių genetinę įvairovę 20 genetinių žymeklių pagalba. Remiantis daugelyje šalių atliktais tokio pobūdžio tyrimų rezultatais, galima teigti, kad, tyrimų rezultatai suteiks daugiau informacijos apie veislių kilmę, kitimą evoliucijos eigoje, tarpusavio ryšius bei giminingumą, genetinę įvairovę bei atstumus tarp šiaurės Europos, Pabaltijo šalių bei Lenkijos galvijų veislių.

Raktažodžiai: vietiniai galvijai, genetinė įvairovė, išsaugojimas.

Introduction. The changes in agricultural system, which started in Lithuanian after 1989, led to a decrease in a cattle number. Two Lithuanian native cattle breeds, which were less competitive under current market conditions, were interbred with more productive Black and White and Red cattle or replaced by improved cattle breeds and became a risk to be extinct. Awareness of

loosing of these breeds and their value of genetic resources initiated the conservation of Lithuanian indigenous cattle, which started with native cattle recording and foundation of special preservation herds. Studies of evaluation of the genetic diversity of local cattle breeds were also started. Knowledge about the genetic diversity and variability of small breeds is needed

for the management of small populations (Baumung et al., 2000). The studies of genetic variation provide an understanding of the current and historical evolutionary processes that have generated biodiversity patterns, the preservation of which should be an important component of conservation plans (Smith et al., 1993). By using microsatellite markers, it is possible to verify the genetic diversity of cattle breeds and through that evaluate the level at which genetic variation is being lost or restructured in these populations.

In this paper, we describe current stage of domestic cattle breed diversity globally and in Lithuania, and usefulness of molecular genetic characterization of cattle genetic resources in decision making in conservation.

Worldwide situation in cattle genetic diversity

Worldwide there are more than 790 breeds of cattle; about 270 of which exist in Europe (EAAP 1993; FAO 1995). For more than 100-200 years, many European breeds have been genetically isolated and this geographic separation promoted the divergence of populations. There are tools to practice more intensive selection in commercial cattle breeds. However, the genetic diversity of cattle is decreasing. Local cattle breeds have become almost totally displaced by commercially high productive cattle breeds, mostly as a result of the needs of high-input farming system. Wars and other forms of socio-political instability led made the owners move their livestock out of their original area, which increased the possibility of mixing animals with other breeds, thereby potentially losing a local specific breed.

The change in agricultural technology and in economic ability of traditional livestock production system is leading to the changes of farming system. The predominance of sires from a few selected high productive breeds in breeding programmes has a negative effect on the level of genetic diversity. As an example, Holstein cattle have become the pre-dominant dairy breed worldwide, which is used for milk production improvement, but only at the cost of declining genetic diversity within the improved breed.

Extensive use of artificial insemination has reduced the number of breeding sires and also may result the high level of inbreeding or restriction in excess of effective population size. In many European countries, the leading sire may account for up to 25% of pedigree inseminations in some breeds (FAO, 2000).

FAO estimates that at least one breed of traditional livestock becomes extinct every week and more than 30% of European livestock are currently estimated to be endangered (FAO 1995).

Many traditional breeds have disappeared because of farmers focus on the new cattle breeds. Around 16% of them have become extinct and 15 % - are rare (FAO, 2000). Many breeds become rare either because their characteristics do not meet contemporary demand or because their qualities have been not recognized. However, the multipurpose local and traditional breeds are often well adapted to local conditions, climate, diseases, and nutritional environment throughout many years. Such breeds may also be better adapted to locally

produced forage, or be more resistant to geographically localized pathogens and pests. The native breeds have been also selected for different objectives, depending on the traits that were important to the local human communities. We can assume that livestock breeds represent the outcome of socioeconomic development and are unlikely to survive outside the social and agricultural systems having formed them.

The situation of cattle genetic resources in Lithuania

In Lithuania there are two main breeds - the Lithuanian Black and White and the Lithuanian Red, which form, respectively, some 62% and 32% of country's cattle population. The Lithuanian Black and White cattle breed is found in south-western parts of Lithuania and was developed from Lithuanian local black and white cattle by crossing them mostly with Dutch Black and White, Holstein-Friesian and German Black and White cattle. This breed is of dairy type and known for its adaptation to the locally prevailing climate and producing milk of good quality. The Lithuanian Red cattle breed is found in north-eastern parts of Lithuania and was formed early in this century from local red Lithuanian cattle by assortative mating, mass selection and crossing with the improved breeds: Ayrshire, Angeln, Dutch, Danish Red, Swiss Brown and Shorthorn. The hybrids were selected for milk production. Most animals are of clearly defined dairy type (FAO, 2000). In the south-western, south-eastern and, partly, in the central part of Lithuania most native cattle are either light grey or white-backed in coat colour. Over the period of last decades, Lithuanian native cattle, such as Lithuanian Light Grey and Lithuanian White-Backed, were almost replaced mainly by Black and White and Red high-productive cattle breeds. It is known that Lithuanian Light Grey and Lithuanian White-Backed cattle were bred in Lithuania from the ancient times and are specific to the country. Nowadays, the Lithuanian White-Backed, Lithuanian Grey and old type of Lithuanian Black and White cattle comprise very small populations and still have a status of an endangered breed. In the first half of the 20th century the number of animals was rather high. After the second World War and in the second half of the 20th century, as a result of industrialization and intensification of agriculture and partly, because of distribution of a few high productive and well selected breeds, the Lithuanian native cattle decreased in number very strongly and both these breeds were almost extinct. Although long time native cattle were kept only by private holders and bred without any breeding system, both breeds still have characteristics common to each native breed: typical coat color, body constitution, productivity qualities common to dairy or dairy-beef cattle, high resistance against some local diseases. It is known from the literature that for long time Lithuanian native cattle had a high importance in the agriculture and social life of Lithuanian rural population. It is also known that local breeds in the areas where they are farmed still are a reference point of ancient local traditions, linked to agricultural production and other sectors, such as food

and folklore (Villa et al., 2000).

The aim of the N-EURO-CAD project

The awareness of the importance of maintaining animal genetic resources has increased over the last years. Many European countries have or are developing national programmes for the preservation and conservation of farm animal biodiversity. The N-EURO-CAD project was founded by the Nordic Gene Bank for Farm Animals (NGH) in 1994 for the characterization of genetic diversity of cattle breeds in the North European countries and extended in 1998 with Baltic and Polish cattle breeds. Selected cattle breeds are genotyped and analysed for their genetic variation and compared with the already examined breeds of the Nordic countries using microsatellite markers.

The aim of the project is to provide information about the genetic diversity of Nordic, Baltic and Polish cattle breeds, to establish relationships among North European cattle breeds; and to provide information for decisions on management and conservation of cattle genetic resources.

Microsatellite markers in research on genetic diversity

Different cattle breeds may have similar phenotypic characters, but still can be different genetically; conversely, breeds may look very different but be genetically closely related. Breeds, which share the same alleles at similar frequencies, are genetically close related, whereas those having the same alleles at different frequencies or carrying many different alleles are genetically distant. It has been shown that European cattle breeds represent separate gene pools. Gene flow among breeds has not been sufficient to prevent the breeds becoming genetically differentiated (Blott et al. 1998).

A more reliable measure of differences among breeds is genetic distance, which can be estimated from the differences in the frequencies of different genetic variants (alleles) at a number of marker loci. From the patterns of within-population genetic variation at marker loci, it is possible to deduce demographic factors important to the conservation of domestic cattle diversity (Cornuet and Luikart 1996; Kantanen et al. 1999).

For the analysis of genetic diversity in Lithuanian cattle breeds we chose the analysis on microsatellite markers. The microsatellite marker is a sequence of varying numbers of short tandem repeated segments of 1-5 base pairs at a unique physical location in the genome, which varies among individuals sufficiently to have its pattern of inheritance tracked through families. A marker may or may not be part of a gene (Hartl and Clark, 1997). Microsatellite markers have also important qualities that make them very practical as molecular markers:

1. They are variable and exhibit a high level of allelic variation;
2. They are codominantly inherited;
3. All codominantly inherited alleles in an individual are visible, which is not the case for dominant markers, such as blood groups;
4. They are very versatile in their application; they may be used to detect genetic variability and population structure differentiation among populations, phylogeny;

they allow paternity testing and evaluate recent genetic and demographic history, such as population bottleneck;

5. They are easily analysed and occur regularly throughout the genome, making them especially suitable for genetic analysis.

For the N-EURO-CAD project 20 microsatellite markers were chosen from the CadBase recommendation list (http://www.ri.bbcrs.ac.uk/cdiv_www/inform.htm) (chromosomal location in parentheses): INRA063 (18), INRA005 (12), INRA035 (16), INRA023 (3), INRA032 (11), INRA037 (11), ETH225 (9), ETH152 (5), ETH10 (5), ETH3 (19), ILSTS005 (10), ILSTS006 (7), HEL5 (21), HEL1 (15), HEL9 (8), HEL13 (11), BM2113 (2), BM1824 (1), BM1818 (23), CSSM66 (14). As the same set of markers is used in the European cattle diversity project RESGEN

(<http://www.androclus.vet.uu.nl/resgen/>), it will be possible to allow the international comparison of the analysed breeds. The genotyping using microsatellite markers involves Polymerase chain reaction (PCR) amplification of the microsatellite region and measurement of the sizes of the amplified fragments. Microsatellite alleles are differentiated and visualised using A.L.F. DNA Sequencer and ABI PRISM® 3100 Genetic Analyser or similar molecular biology techniques. The exact alleles sizes are estimated according to agreed size standards of international reference animals.

The final statistical analysis will be performed by using computer programmes and the results will be published in international journals of genetics.

Discussion and conclusions N-EURO-CAD is the first study where microsatellite markers are used to estimate genetic diversity of Lithuanian cattle breeds. A loss of breeds or different strains may lead to a reduction in genetic diversity, which would restrict the ability of farmers to meet agricultural requirements in the future (Barker et al., 1993; FAO 1996) and has serious consequences for current livestock production and future capacity to manage the challenges and opportunities. The loss of indigenous breeds that, having high resistance against many diseases and tolerance to different environmental conditions, enable to exploit existence in more extreme environments also seriously affects the capacity of human society to live in large areas of the world in a sustainable manner. Without local breeds and the traditional farming methods, which were used for keeping them, many cultural aspects would disappear and the human population would lose a part of its own history and traditions.

It is not possible to conserve all genetic variations in all populations. The first step is the evaluation of genetic resources and the selection of appropriate populations for conservation. A strategy is then required that will maintain the widest possible level of genetic variation across the species (FAO 1996), nevertheless, more attention has to be paid to the need for genetic conservation and an evaluation of the breeding strategies accordingly. First, it is needed to understand the present position of the breed, which can be determined from an

analysis of historical records supplemented with data from genetic markers. The use of genetic markers provides the information on population genetic structures of the indigenous cattle breeds even if they lack detailed pedigree recording data. It is necessary to verify the biological value of Lithuanian cattle in contents of the whole Lithuanian cattle population. The comparison of genetic diversity among Nordic, Baltic and Polish cattle breeds would clarify the origin and relationships among these breeds. The studies on the genetic diversity can show the differentiation of breeds; and individual breeds may have unique combinations of genes as a result of the action of these different evolution ways. Breed preservation is important from a socio – economic point of view, as the farming of many local breeds supports local economies in marginal areas (Maijala et al., 1987). Local breeds help maintain the identity of local human populations in areas where they were or are still kept. Maintaining of genetic variation within a breed is important for historical and commercial future.

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