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Genetic characterization of the Czech Spotted cattle breed using panel of 10 microsatellite markers

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Introduction:

The Czech Spotted cattle, originated from spotted cattle growed in Switzerland, came to the Czech Republic in the second period of the 19th century. After its enlargement, there was applied a crossbreeding with Ayrshire, Red Holstein and Simmental cattle in sixties and eighties years of the 20th century. These crossbreedings increased both of milk and beef production efficiency.

The aim of our work was an evaluation of molecular-genetic diversity of the Czech Spotted cattle breed in present by using common methods, data space reduction and clusterig methods.

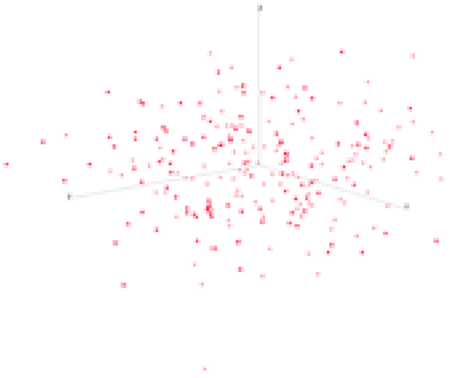
Material and methods:

- The analysed group consisted of 240 unrelated individuals of the Czech Spotted cattle breed.
- Genomic DNA was isolated using the JETQUICK Blood & Cell Culture DNA Spin Kit (Genomed GmbH, Germany) from individual blood samples.
- Amplification of the microsatelittes was performed using the StockMarks Cattle Bovine Genotyping kit (Applied Biosystems, UK). The genotyping of microsatelitte markers was performed by fluorescent fragment analysis on ABI PRISM 310 Genetic Analyzer (Applied Biosystems) and detected by software GeneScan 3.7 NT.
- The parameters of genetic diversity were evaluated by application of PowerMarker v3.28 analysis tools. After that, we used PCA and hierarchical clustering method to evaluate the genetic homogenity.

Table 1: Molecular-genetic characterization of the Czech Spotted cattle

Marker	MA freq.	GN	AN	Gene Diversity	Heterozygosity	PIC	f
BM1824	0.255	13	5	0.757	0.736	0.713	0.030
BM2113	0.352	25	8	0.771	0.803	0.739	0.000
ETH3	0.394	17	6	0.720	0.754	0.673	0.000
ETH10	0.422	16	6	0.718	0.717	0.676	0.003
ETH225	0.359	24	9	0.764	0.800	0.730	0.000
INRA023	0.333	30	10	0.771	0.776	0.737	0.000
SPS115	0.555	16	6	0.641	0.636	0.608	0.011
TGLA122	0.354	32	9	0.780	0.703	0.750	0.100
TGLA126	0.454	20	7	0.683	0.699	0.634	0.000
TGLA227	0.257	44	11	0.849	0.865	0.832	0.000
Mean	0.374	24	8	0.745	0.749	0.709	0.000

MA freq. - Major Allele frequency
GN - Genotype number
AN - Allele number
PIC - Polymorphism information content
f - inbreeding coeficient



Graph 1: Czech Spotted cattle - graphical illustration of reduced data space of 10 tested microsatellite loci (3 main PCA components of genotype data)

Results:

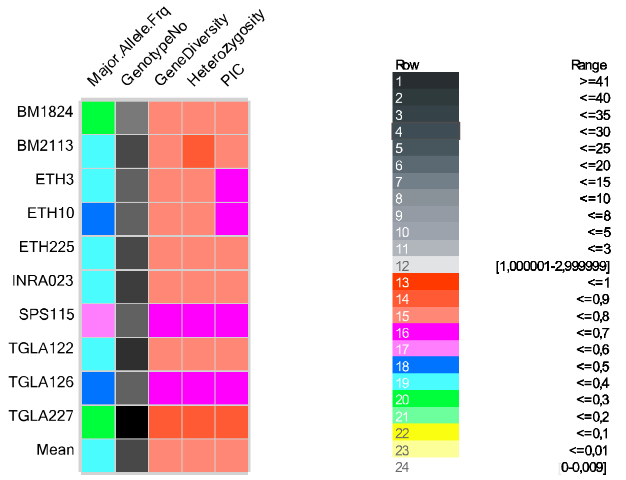


Figure 1: Czech Spotted cattle - graphical illustration of genetic variability

Summary:

We performed analysis of 10 microsatellite loci on the Czech Spotted cattle breed: BM1824, BM2113, ETH3, ETH10, ETH225, INRA023, SPS115, TGLA122, TGLA126, TGLA227. In group containing 240 unrelated individuals, the allele frequencies, observed and expected heterozygosity, test for deviations from Hardy-Weinberg equilibrium and Polymorphism information content (PIC) have been calculated. We found out gene diversity (H_E) = 0.745. The observed heterozygosity (H_O) across all loci was 0.749, the highest (was) 0.865 for the TGLA227 and the lowest 0.636 for the SPS115. The average PIC was 0.709. The joining distance of clustering of 3 PCA components, by which the cluster contained 95 % of all genotype combinations obtained by microsatellite loci analysis, was 0.319, opposite to even 0.788 by 100 % data combinations (minimal joining distance of clustering is 0, maximal is 1). These results refer to considerable genetic homogenity of the Czech Spotted cattle.

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