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The polymorphism of the population of the Ukrainian river buffalo at
microsatellite DNA loci

According to the zoological classification Asian water buffaloes (*Bubalus bubalis*) are divided into two subspecies i.e. river buffalo and swamp buffalo. The river buffalo is bred in Ukraine.

The water buffalo is a kind of farm animals, which has been used by the mankind as draft-cattle and for obtaining milk and meat for food since ancient times. Buffaloes have adapted to living in countries with hot humid climate, they are bred around the world, from tropical to temperate regions and even in highland areas. In many Asian countries they are used as financial guarantors for loans and as a financial asset that can be sold if necessary.

The breeding of water buffaloes of Asian origin in livestock production does not compete with mankind in the food chain, because these farm animals are undemanding to fodder; they efficiently convert poor quality fodder, such as reed, sedge, shrub vegetation, straw of rice, of rye, of triticale, and of flax etc., and waste products of food and sugar industries caused by processing in foods with high biological value and production of biofertilizers for improving soil fertility and structure.

Buffaloes are resistant to pyroplasmosis, anaplasmosis, tuberculosis, brucellosis, hoofed rot, diseases of the reproductive system and other diseases distributed within the species *Bos Taurus taurus*.

Nowadays there are more than 182 million head of the buffalo in the world. Most of their population is concentrated in Asia and is 96.99% (174 mil. head) of the world number; the number in Egypt is 2.24% (3.7 mil. head), in America – 0.64% (4.3 mil. head) and in Europe – 0.15% (459 tsd. head). In Australia, the swamp buffalo is mainly bred, its number is from 70 tsd. to 200 tsd. head.

Regardless of the geographical location of countries the buffalo population is intensively increasing in all the continents. During the period of 1961 – 2007 the number of buffalo increased by 54.05% or 85.84 mil. head in Asia, by 37.69% (2.48 mil. head) in Africa, by 6.14% (1.07 mil. head) in America. In Europe, the number of buffalo has declined from 0.73 to 0.25 mil. head or by 270.37%.

Unfortunately, the trend of growth of the species *Bubalus bubalis* in North America and Europe is not observed, the main reason for that is still excessive enthusiasm to the breeding of Holstein cattle. The number of buffaloes in these two continents is less than 1% of the global number of the buffaloes, but thanks to the Italian breeders the reduction of the buffalo population in Europe could be stopped.

Developed European countries, the USA, Canada, Israel etc. are gradually increasing buffalo herd and forming a new branch of cattle husbandry i.e. buffalo-breeding. In Ukraine, the number of buffaloes is not significant, but on the total amount of derived milk it is not inferior to the "supermilk" Holstein breed. Milk and

meat derived from buffalo may be the basic foundation of organic products for the Ukrainian population.

Therefore, the study of genetic diversity of buffaloes is particularly important. One way to study it is to use molecular genetic markers, including sequences of DNA polymorphism of which is caused by differences in the nucleotide sequences of different alleles at one locus. One of these types of genetic markers is microsatellite loci of the DNA. In recent years genetic characteristics of buffaloes with using microsatellites has acquired special distribution. This is confirmed by numerous studies of foreign authors.

Despite a number of existing microsatellite loci used for research, genetic analysis with using buffalo microsatellite loci for cattle is very efficient.

This paper presents the results of studies of genetic diversity of domestic buffalo population (*Bubalus bubalis*), the number of which decreased significantly in the recent decades in Ukraine. The material for these studies was 64 buffalo head, which are bred in «Goloseevo» farm, Kyiv region, and private households of residents of the Transcarpathian region. Genomic DNA was isolated from cartilage tissues from ears. Genetic analysis was performed using 11 microsatellite loci (BM1818, BM2113, BM1824, INRA023, ILST006, ETH10, ETH185, ETH225, SPS115, TGLA126, TGLA227), which are recommended by ISAG for genotyping of cattle.

The results of studies showed that the average number of alleles per locus was 6.55. The value of observed heterozygosity ranged from 0.260 to 0.980, expected one ranged from 0.291 (BM2113) to 0.753 (TGLA227). All microsatellite loci except BM1818, ETH185 and BM2113 showed high level of polymorphism. The most polymorphic locus was TGLA227. Despite the limited number of buffaloes, in the studied population an excess of heterozygous genotypes at the level of 5.5% was established. It indicates the existence of high genetic variability of population. For TGLA126 was determined the largest excess of heterozygous genotypes – 34.2%, while for BM1818 was fixed maximum deficit of heterozygotes – 27.3%.

Despite the use of microsatellite loci, which are recommended for cattle genotyping, the efficiency of their use for genetic analysis of buffaloes was very high (more than 99.99%). It indicates the ability and efficiency of use of selected microsatellite loci for allele pool evaluation and genetic diversity characterization of Ukrainian buffalo population.

Keywords: buffalo, genetic diversity, population, microsatellite loci, alleles