

**STELLATE STURGEON (*Acipenser stellatus*, Pallas)  
MICROSATELLITE DNA MARKERS POLYMORPHISM**

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Stellate sturgeon (*Acipenser stellatus*, Pallas) plays a key role in biodiversity Black Sea basin and recently was an important representative of fishing. Despite the commercial and environmental importance, information about the genetic status of the stellate sturgeon population and its biodiversity in the Azov-Black Sea basin is not enough.

We analyzed 32 individuals from breeding herds of stellate sturgeon populations from Azov-Black Sea basin, introduced into aquaculture in 2013. We analyzed the stellate sturgeon by four microsatellite DNA markers: LS-19, LS-39, LS-54 and Aox-27 and have identified total 21 alleles.

In analyzed locus LS-19 were found 5 allelic variants, with range from C (0.031) to E (0.437). Locus LS-39 was monomorphic, and has only one allelic variant J, which is typical for this species. For locus Aox-27 were found 6 allelic variants, with range from H (0.016) to M (0.250). For locus LS-54 there were detected 9 allelic variants, with range from variants H and N (0.031) to G and K (0.188).

Observed heterozygosity ( $H_o$ ) ranged from 0.875 for locus LS-19 and 1.000 for locus LS-54. Expected heterozygosity ( $H_e$ ) ranged from 0.704 from locus LS-19 to 0.872 for locus LS-54. The mean observed heterozygosity was 0.938, while the mean value of the expected heterozygosity was 0.790. The excess of heterozygous genotypes are due to result of reproduction of wild spawners of stellate sturgeon population of the Black Sea basin.

Polymorphic information content (PIC) for stellate sturgeon ranged from 0.642 to locus LS-19 and 0.842 for LS-54. The mean polymorphic information content was

0.743, confirming an adequate level of polymorphic markers selected for this type of species ( $PIC > 0,500$ ). The mean probability exclusion (PE) was 0.872, that confirming highly informative for these microsatellite DNA markers ( $PE > 0.600$ ).

Our result demonstrate, that in the stellate sturgeon population traced conservation heterozygous genotypes. This is proof that of these fish are enough diversity.