

Instytut Sadownictwa i Kwiaciarstwa  
Oddział Pszczelnictwa  
*Pszczelnicze Towarzystwo Naukowe*

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Avtor e-mail: [apismell@hotmail.com](mailto:apismell@hotmail.com)

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Classification of a honey bees (*Apis mellifera* L.) has been based on morphometrical methods before beginning of use of molecular methods in bees studying. Modern systematics and phylogenetics often use molecular methods. In particular, the methods based on polymorphism of DNA are applied to a honey bee. Initial researches based on a restriction analysis (RFLP) of mitochondrial DNA (mtDNA) (Smith 1991), sequencing analysis of mtDNA (Cornuet et al. 1991, Garnery et al. 1992), analysis of polymorphism of microsatellite loci (Estoup et al. 1995, Viard et al. 1998) have shown existence only three evolutionary branches – A, M and C. Following researches based on sequencing analysis of 2 subunit of gene NADH - dehydrogenase (ND2) mtDNA (Arias and Sheppard 1996), based on RFLP analysis intergenic site between 1 and 2 subunit of genes cytochrome-c-oxidase (COI-COII) of mtDNA by endonuclease DraI (Franck et al. 2000, Palmer et al. 2000), based on analysis of microsatellite loci polymorphisms (Franck et al., 2000) have shown existence fourth evolutionary branch O. Further, P. Franck et al. (2001) by DraI endonuclease perform RFLP analysis of the intergenic locus COI-COII mtDNA, has shown existence of five evolutionary branches A, M, C, O, Y.

In recent time all subspecies and population of *A. m. mellifera* of an evolutionary branch M are subject to intensive hybridization. Analysis of frequencies of combination PQQ of intergenic locus COI-COII mtDNA in populations of bees in Urals (Middle and Southern Urals) has been shown existence of four reserves of subspecies *A. m. mellifera* (Ilyasov et al. 2005).

Analysis of nucleotide sequences of a fragment of gene ND2 with average size 688 b.p. in 12 samples of four populations has shown transitions in positions 536, 621, 861, 1015, 1047 between sequences of gene ND2 of the analysed samples. Transition T>C in position 536 in samples DQ181614 and DQ181618 lead to replacement aminoacid isoleucine Ile by threonine Thr. Transversion was not revealed. Numbering of sequences is concerning sequence full mtDNA of *A. m. ligustica* from GenBank NCBI (NC 001566).

Analysed sequences of gene ND2 of bees from Ural population were deposited to GenBank (<http://www.ncbi.nlm.nih.gov>) at numbers DQ181611-DQ181622. Sequence comparison of gene ND2 of the Urals bee samples with bees from European populations *A. m. mellifera* (AY114495, U35758, U35759, U35760) has shown their big similarity that shows their unity of an origin and genetic relationship.

Thus, part of unique European population *A. m. mellifera* which is subdivided into four subpopulations described by significant similarity with European populations of *A. m. mellifera* was still kept in Urals. For successful preservation gene pool of *A. m. mellifera* and restoration of its initial area in Urals is necessary more detailed research of bees of this region.