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## COMPARATIVE SEQUENCING ANALYSIS INTRON OF ELONGATION FACTOR EF1-ALPHA OF HONEYBEES FROM RUSSIAN URAL

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Comparative sequencing analysis of variability (>40 per cent) intron of elongation factor gene EF1-alpha of nuclear DNA can be used in phylogenetic reconstruction genus *Apis*. In this work we have for the first time shown possibility using this marker in phylogenetic reconstruction in *Apis mellifera* species, in spite of its low intraspecific variability (<2 per cent).

We were made sequencing analysis fragment intron of elongation factor gene EF1-alpha of honey bees from 3 colonies of a northern area of Bashkir population *Apis mellifera mellifera* (Russia, Birsky region of Bashkortostan republic). Comparative analysis was made with published in genebank sequences: *Apis andreniformis* (Ay721702, Ay721703, Ay721704), *Apis dorsata* (Ay721705, Ay721706, Ay721707), *Apis florea* (Ay721708, Ay721709), *Apis mellifera ligustica* (Ay721710), *Apis koschevnikovi* (Ay721711, Ay721712, Ay721713, Ay721714, Ay721715); *Apis mellifera lamarckii* (Ay721716); *Apis nuluensis* (Ay721717) (Arias, Sheppard, 2005).

Using cluster analysis we constructed dendrogram by neighbor-joining method. On the dendrogram bee samples differentiated into four branches. Samples of different bee species clustered in separate branches. The first branch included samples of western honeybee *Apis mellifera*. *Apis mellifera mellifera* from Ural located separately from other subspecies. Samples of gigantic Asian bees of genus *Apis* have differentiated into a second branch of *Apis dorsata*. Asian bees of species *Apis koschevnikovi* and *Apis nuluensis* were included into a third branch. These two bee species had low level of genetic variation among themselves. The fourth branch included bee species of Asian dwarf bees of species *Apis andreniformis* and *Apis florea*. Bee samples of each of them separated in different subgroups.