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GENETIC IMPROVEMENT OF HONEY BEES FOR KEEPING IN EXTREMAL CLIMATIC CONDITIONS

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Abstract. Genetic improvement of honey bee populations based on molecular genetics features is faster and precision in comparison with morphometry and behavior-based methods. We developed the method based on nine nuclear microsatellite loci that allow a selection of most adaptive honey bee colonies by genetically defined features. Our study the heterozygosity of the dark European bee *A. m. mellifera* inhabiting the extremely cold region of the Ural Mountains to provide a marker-assisted selection for revealing the high adapted to extremely cold climate honey bee population can be applied for marker-assisted selection of honey bees adapted to beekeeping in extremal climatic conditions.

Keywords: Honey bee, molecular genetic method, adaptation, breeding.

ГЕНЕТИЧЕСКОЕ УЛУЧШЕНИЕ МЕДОНОСНОЙ ПЧЕЛЫ ДЛЯ РАЗВЕДЕНИЯ В ЭКСТРЕМАЛЬНЫХ КЛИМАТИЧЕСКИХ УСЛОВИЯХ

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Аннотация. Генетическое улучшение популяций медоносных пчел с использованием молекулярно-генетических методов происходит быстрее и

точнее по сравнению с морфометрическими и этологическими методами. Мы разработали метод, основанный на девяти ядерных микросателлитных локусах, который позволяет отбирать наиболее адаптивные колонии медоносных пчел по генетически определенным признакам. Наше исследование гетерозиготности темной европейской пчелы *A. m. mellifera*, обитающей в холодном климате Урала, позволяет проводить селекцию семей, хорошо адаптированных к экстремальным климатическим условиям.

Ключевые слова: Медоносная пчела, молекулярно-генетический метод, адаптация, разведение.

The honey bee, *Apis mellifera*, is an essential pollinator that plays a positive role in both agriculture and ecology. About 30 allopatric subspecies have been identified throughout Africa and Europe, 24 of which live in Europe [1]. Climatic condition is the first factor of the natural selection of honey bees. Harsh climates as over cold or over hot make honey bee survival impossible without human assistance [2].

Heterozygosity is of major interest to scientists of genetic variation in natural populations. It is often one of the first parameters that one presents in a data set. It can tell us a great deal about the structure and even the history of a population. A very low level of heterozygosity indicates severe effects of small population sizes like bottlenecks, genetic drift, and little genetic variability. A very high level of heterozygosity indicates isolate-breaking effects like migration and lots of genetic variabilities. Often, the observed level of heterozygosity compared with expected under Hardy-Weinberg equilibrium. If the observed heterozygosity is lower than expected it means the inbreeding, and vice versa - an outbreeding.

Based on the polymorphism of the nine microsatellites loci (ap243, 4a110, A24, A8, A43, A113, A88, Ap049, and A28) in 192 worker bees from 12 colonies (Bort 01 – 16 bees; Bort 02 – 16 bees; Bort 03 – 16 bees; Kush-Elga-Bash (hive 07) – 16 bees; Kush-Elga-Bash (hive 25) – 16 bees; Kush-Elga-Bash (hive 29) – 16 bees; Kapova Peshera (hive 15) – 16 bees; Kapova Peshera (hive 24) – 16 bees; Kapova Peshera (hive 31) – 16 bees; Baisalyan (hive 01) – 16 bees; Baisalyan (hive 13) – 16 bees; Baisalyan (hive 14) – 16 bees) the heterozygosity have been analyzed.

It is known, that 15–20 unrelated drones fertilize the queens increasing the genetic diversity of their colonies [3, 4]. Therefore, the offspring from different drones may be present in each colony simultaneously. This phenomenon should be manifested in the form of substantial genetic diversity among individuals working for the honey bee colony. It can lead to significant genetic diversity in the population of worker bees in one colony. Therefore, we calculated the average heterozygosity of the honey bee colony based on polymorphism of nine microsatellite loci.

The populations are characterized by an optimal level of genetic diversity. The deficit of genetic diversity can lead to the loss of ecological plasticity and adaptability to the environment. The excess of genetic diversity can lead to a loss of balance of the genome. In the literature, the average heterozygosity of six microsatellite loci varied from 0.43 to 0.47 in the population of *A. m. iberiensis* in Spain (De la Rúa et al., 2004); heterozygosity of six microsatellite loci varied from 0.22 to 0.29 in the population of *A. m. ligustica* in Portugal [5]; heterozygosity of nine microsatellite loci varied from 0.32 to 0.41 in the population of *A. m. mellifera* in the Republic of Bashkortostan [1]. The level of average heterozygosity among colonies of *A. m. mellifera* in the current study was varied from 0.12 to 0.40, which matched the results from the literature.

The highest level of heterozygosity comes out in the following apiaries: Kush-Elga-Bash 07, Kapova Peshera 31, Baisalyan 14, Bort 02, Kush-Elga-Bash 25, and Kapova Peshera 15. The lowest level of heterozygosity comes out in the following apiaries: Bort 01, Bort 03, Kush-Elga-Bash 29, Kapova Peshera 24, Baisalyan 01, and Baisalyan 13. The differences between observed and expected heterozygosities in all colonies are not significant which means that no deviation from the Hardy Weinberg equilibrium.

Harpur et al. (2013) showed that the genetic diversity of honey bees in wild populations higher than in commercial populations, which helps them to adapt to the harsh environment and survive without human assistance [4]. Thus, we assumed that honey bee colonies with a higher level of heterozygosity possessed the greatest ability to the adaptation to harsh environmental conditions. This can be explained by the fact that heterozygous organism contains a bigger number of gene alleles, than homozygous. Each allele has owned specific advantage and a combination of many alleles allow honey bees to precisely tune their adaptability to a different environment. The ability to the adaptation to various environments is adaptive plasticity. Adaptive plasticity allows organisms to cope with environmental change, thereby increasing the population's long-term fitness. According to this definition, we can state that heterozygosity is a basic indicator of adaptive plasticity - heterozygosity less than average allows less adaptability, but heterozygosity more than average allows more adaptability of honey bee colonies. Based on the strategy of marker-assisted selection we selected honey bee colonies with a higher than average level of heterozygosity.

References

1. Ilyasov R.A., Poskryakov A.V., Petukhov A.V., Nikolenko A.G. Genetic differentiation of local populations of the dark European bee *Apis mellifera mellifera* L. in the Urals // Russian Journal of Genetics. 2015. 51 (7). P. 677–682. DOI: 10.1134/S1022795415070042.

2. Ilyasov R.A., Poskryakov A.V., Petukhov A.V., Nikolenko A.G. Molecular genetic analysis of five extant reserves of black honeybee *Apis mellifera mellifera* in the Urals and the Volga region // Russian Journal of Genetics. 2016. 52 (8). P. 828–839. DOI: 10.1134/S1022795416060053.
3. Oxley P.R., Hinshumpatch P., Gloag R., Oldroyd B.P. Genetic evaluation of a novel system for controlled mating of the honeybee, *Apis mellifera* // Journal of Heredity. 2010. 101 (3). P. 334–338. DOI: 10.1093/jhered/esp112.
4. Harpur B.A., Minaei S., Kent C.F., Zayed A. Admixture increases diversity in managed honey bees: Reply to de la Rúa et al // Molecular Ecology. 2013. 22 (12). P. 3211–3215. DOI: 10.1111/mec.12332.
5. De la Rúa P., Galián J., Pedersen B.V. and Serrano, J. Molecular characterization and population structure of *Apis mellifera* from Madeira and the Azores // Apidologie. 2006. 37. P. 699–708. DOI: 10.1051/apido:2006044.

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ТЕМНАЯ ЛЕСНАЯ ПЧЕЛА *APIS MELLIFERA MELLIFERA* L. В СИБИРИ: СОВРЕМЕННОЕ СОСТОЯНИЕ И ПУТИ СОХРАНЕНИЯ ПОПУЛЯЦИЙ

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Аннотация. Скрининговые исследования медоносной пчелы, проведенные на территории Сибири, позволили выявить популяции темной лесной пчелы *Apis mellifera mellifera* в Томской области, Красноярском и Алтайском краях, Республике Алтай. Сравнительный анализ генетического разнообразия темной лесной пчелы популяций Сибири, Урала и Европы, выполненный по данным молекулярно-генетического исследования митохондриального и ядерного геномов, позволяет предположить существование сибирского экотипа среднерусской породы. Изученные пчелиные семьи характеризуются высоким адаптационным потенциалом (высокая степень «акклиматизации») и хорошими хозяйственными значимыми показателями. С целью сохранения генофонда среднерусской породы сибирских популяций проводятся как мониторинговые исследования и эколого-генетический анализ пчелиных семей, так и селекционно-племенная работа в пчелорепродукторе Томской области.

Ключевые слова. *Apis mellifera mellifera*, темная лесная пчела, генетическое разнообразие, адаптация, Сибирь.