DOI 10.32900/2312-8402-2024-132-111-123
UDC 595.638.1.575.577

BIOLOGICAL NOMENCLATURE (TAXONOMY) AND CLASSIFICATION OF HONEY BEE. CURRENT STATE AND PROBLEMS

Iryna MASLII, CandVetSc., senior research assistant,
https://orcid.org/0000-0002-8671-3356
Yurij LIASHENKO, CandAgSc., senior research assistant,
https://orcid.org/0000-0003-2747-476X
Livestock farming Institute of NAAS of Ukraine, Kharkiv Ukraine

The chronology of scientific research achievements in the process of determining the biological nomenclature and classification of honey bees and the implementation of the results obtained for use in the practice of beekeeping in the selection and preservation of aboriginal breeds (races) of bees in modern environmental conditions is highlighted. An attempt is made to focus this study in the field of analysis of the chronology of methods used in the historical aspect of determining the taxonomy of insects, in particular bees. At the same time, the problems and prospects of scientific research in modern economic and natural and climatic conditions of the development of the industry are reflected. It is shown that initially only morphometry was used worldwide to identify bee breeds. However, morphometric features are not always informative in identifying subspecies, since they are subject to variability under the influence of environmental conditions. Later, biochemical methods for identifying bee subspecies based on polymorphism of allozyme loci were developed. It is shown that at the same time, methods for identifying bee subspecies based on polymorphism of mitochondrial DNA (mtDNA) loci were developed. This polymorphism was successfully used in phylogenetic and phylogeographic studies of honey bees. The disadvantage of mtDNA markers is the exclusively maternal type of inheritance. At the same time, methods for identifying bee subspecies were developed taking into account polymorphism of nuclear DNA (nDNA) loci. Recently, methods for identifying bee subspecies based on SNP analysis have been developed. These markers have become widely used in population, evolutionary and phylogenetic studies of bees due to the development of next-generation sequencing methods NGS (Next Generation Sequencing) Illumina. SNP markers are characterized by high resolution due to their number and stable inheritance over several generations, which can be successfully used in genetic mapping, population and evolutionary studies, selection of lines for economically useful traits and disease resistance, identification of taxonomic affiliation of bee families.

Keywords: *honey bee, taxonomy, morphometric, molecular genetic research methods.*

БІОЛОГІЧНА НОМЕНКЛАТУРА (ТАКСОНОМІЯ) ТА КЛАСИФІКАЦІЯ МЕДОНОСНИХ БДЖІЛ. СУЧАСНИЙ СТАН ТА ПРОБЛЕМАТИКА

Ірина МАСЛІЙ, к. вет. н., с. н. с., https://orcid.org/0000-0002-8671-3356
Юрій ЛЯШЕНКО, к. с-г. н., с. н. с., https://orcid.org/0000-0003-2747-476X
Інститут тваринництва НААН, Харків, Україна

Висвітлено хронологію здобутків наукових досліджень в процесі визначення біологічної номенклатури і класифікації медоносних бджіл та впровадження отриманих результатів для використання у практиці ведення галузі бджільництва щодо селекції та збереження аборигенних порід (рас) бджіл у сучасних умовах довкілля. Зроблено спробу зосередити дане дослідження в полі аналізу хронології методів, що застосовувались в історичному аспекті визначення таксономії комах, зокрема бджіл. Разом з цим відображено проблеми і перспективи наукових досліджень в сучасних економічних та природно-кліматичних умовах розвитку галузі. Показано, що для ідентифікації порід бджіл спочатку у всьому світі використовували лише морфометрію. Однак морфометричні ознаки не завжди інформативні при ідентифікації підвидів, оскільки під впливом умов довкілля схильні до мінливості. Надалі набули розвитку біохімічні методи ідентифікації підвидів бджіл на основі поліморфізму алозимних локусів. Відображено, що одночасно розроблялися методи ідентифікації підвидів бджіл на основі поліморфізму локусів мітохондріальної ДНК (мтДНК). Цей поліморфізм успішно застосовувався у філогенетичних та філогеографічних дослідженнях медоносної бджоли. Недоліком маркерів мтДНК є виключно материнський тип успадкування. У той самий час розвивалися методи ідентифікації підвидів бджіл з урахуванням поліморфізму локусів ядерної ДНК (яДНК). Останнім часом набули розвитку методи ідентифікації підвидів бджіл на основі аналізу SNP. Дані маркери набули широкого поширення у популяційних, еволюційних та філогенетичних дослідженнях бджіл завдяки розвитку методів секвенування наступного покоління NGS (Next Generation Sequencing) Illumina. SNP-маркери характеризуються високою роздільною здатністю в силу їхньої кількості та стабільної успадкованості у ряді поколінь, які можуть бути успішно використані в генетичному картуванні, популяційних та еволюційних дослідженнях, селекції ліній за господарсько–корисними ознаками та стійкістю до захворювань, ідентифікації таксономічної приналежності сімей бджіл.

Ключові слова*: медоносна бджола, таксономія, морфо метричні, молекулярно-генетичні методи дослідження.*

Beekeeping has existed for millennia. Pollination of crops by honey bees is even more important than its products from both a commercial and ecological point of view. Knowledge about the main pollinators of agricultural plants, in particular, bee breeds, is one of the modern sections that expand the understanding of the most valuable species of insects and encourage a deeper understanding of their role in the direct and indirect impact of both pollination activity on the reproduction of entomophilous plants and the production of food products for humans. Apis melliffera (honey bee) is one of the economically valuable species represented in Ukraine. It is characteristic that bees show the greatest adaptive efficiency precisely to those climatic conditions, species composition of honey plants, parasites and bee diseases, where their breed (race) was historically formed. (Metlytska O. I., 2016).

As in other branches of animal husbandry, in beekeeping, significant attention is paid to the breed resources of bees, the rational use of which in appropriate natural and climatic conditions ensures an increase in the received products and balances the multifaceted connections in wildlife. (Metlytska O.I, 2010).

The achievements of any science are the result of historical development, which is manifested in the concepts of leading representatives, through whose efforts it moves forward.

The goal was to generalize the issue of taxonomy and classification of honey bees, distributed throughout the territory of Ukraine through the analysis of population and molecular genetics methods.

Research methods. The methodological tools included both general scientific methods - logical analysis and synthesis, classification and systematization, generalization, and special ones - problem-chronological and source and terminological analyses, as well as analysis of literary sources.

Research results. According to the main taxonomic categories (ranks), bees – Apis – belong (Zlotin O. Z., 1988., Cherkasova A. I., 1991, Kotthoff U.et al., 2013) to:

- Phylum: Arthropoda / *Arthropoda*
- Class: Insecta / *Insecta*
- Order: Hymenoptera / *Hymenoptera*
- Family: Apidae / *Apidae*
- Genus: Bee / *Apis*

Hymenoptera is a large order of insects, consisting of bees, sawflies, ants and wasps. Currently, about 150,000 living and about 2,000 extinct species of hymenoptera have been described.

The only genus *Apis* of honey bees is included in the family *Apidae.* All species of honey bees of the genus *Apis* are very similar in behavior, social biology, morphology, nest architecture and nutrition. However, despite the great similarity between species of honey bees, differences in behavior and ecology are observed.

According to some authors, species of honey bees of the genus Apis are grouped into three lineages:

- dwarf - *Apis andreniformis* and *Apis florea*;
- giant - *Apis dorsata*;
- with closed nests - *Apis koschevnikovi, Apis cerana* and *A. Mellifera*.

Some scientists divide bees into four species:

- *A. mellifera* – western cryptic bee;
- *A. cerana* – eastern cryptic bee;
- *A. dorsata* – giant bee;
- *A. florea* – dwarf bee.

Each of these species occurs in a wide range of climatic conditions and habitats. Each lineage includes many ecologically and morphologically differentiated allopatric subspecies and related species that live in the same territory but occupy different ecological niche (Meixner et al., 2013). In particular, *A. mellifera* L. bees were distributed throughout Europe, Africa, and were divided into many subspecies, and are currently distributed on all continents except Antarctica.

Apis mellifera (honey bee) is one of the most well-studied species of honey bees, although many questions about its biology, taxonomy and evolution remain unanswered.

At the initial stage of the classification of honey bee subspecies, there were several identification methods, in particular, morphometric: morphometry of body parts; classical morphometry of the wing. It was used to establish the breed composition of bee colonies, starting from the first half of the 20th century. (Ruttner, 1973).

Some of the most important exterior indicators are listed below (Yarovets, 2022):

1. Length of the proboscis. This indicator is taken into account when determining the breed of bees. It also has independent breeding, biological and economic significance - bees with a long proboscis are able to extract nectar from deeply located nectaries.
2. Length and width of the right front wing. Some researchers associate wing size with the potential foraging capabilities of bees.
3. Number of hooks on the hind wing. This indicator is rarely used, but it is of interest because it is not associated with seasonal variability.
4. Cubital index. This indicator does not change during the season, weakly correlates with other exterior indicators.
5. Length and width of the third tergite. The dimensions of the tergite correlate well with the overall dimensions and body weight of the bee and can be a reliable criterion for determining the breed of bees.
6. Length and width of the third sternite.
7. Length and width of the wax mirror.
8. Tarsal index. The indicator is practically independent of seasonal influence, and it can be successfully used to determine the breed of bees.
9. Discoidal displacement.

Classical wing morphometry is an important and inexpensive method for determining the breed composition of bee colonies by phenotypic characteristics. The latter include the so-called indices - the values of the ratios of the lengths of certain segments on the wings. Over time, classical morphometry has developed, and the DAWINO discriminant analysis (Fig. 1) has appeared; geometric analysis of the wing shape.

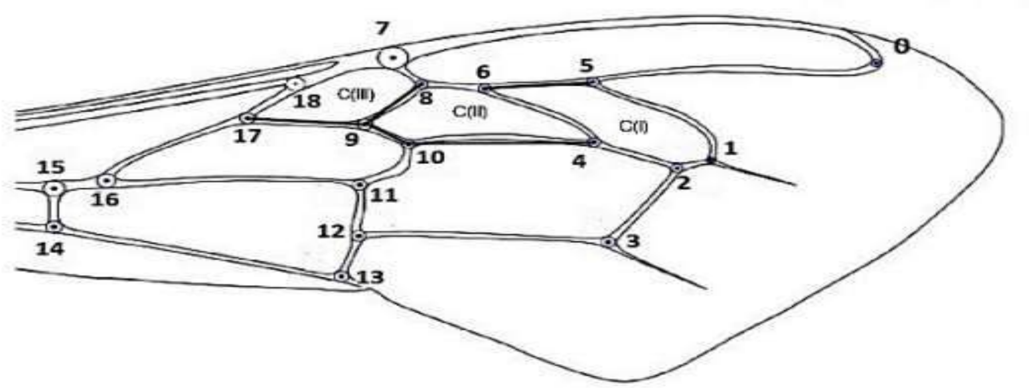


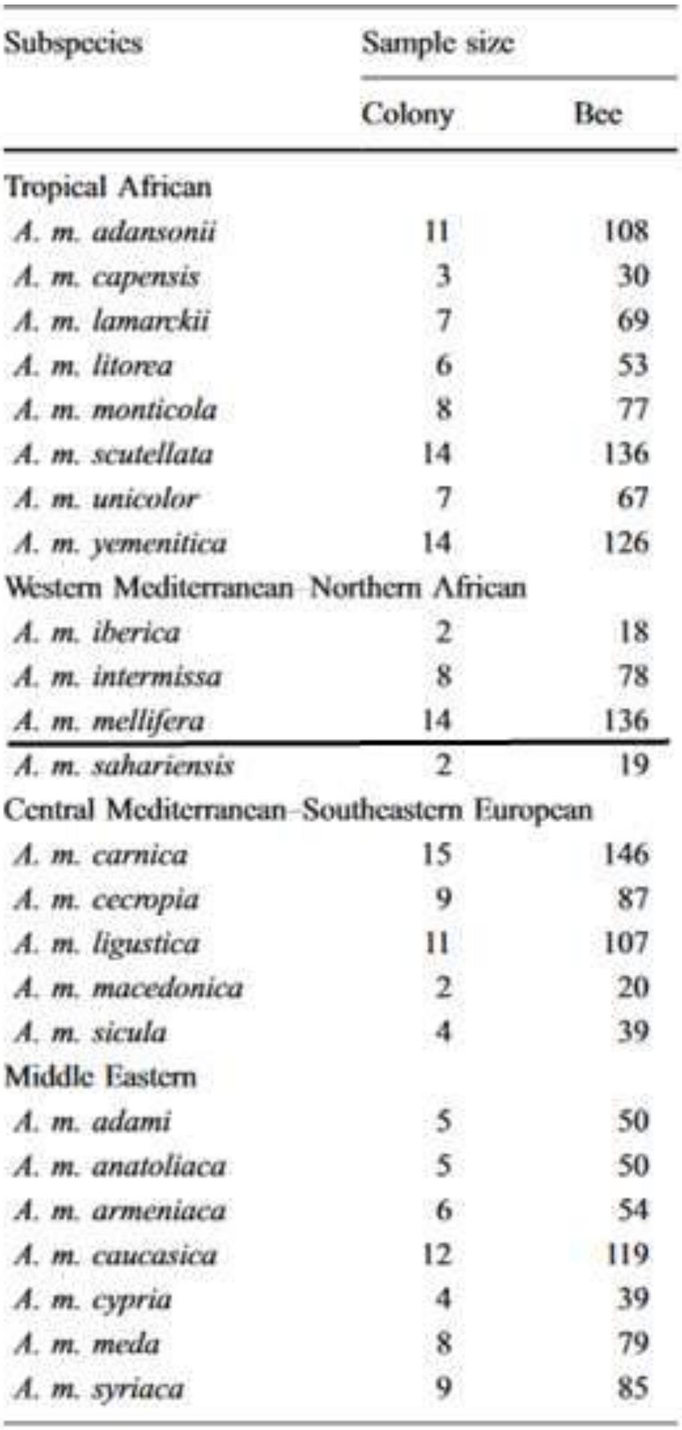
Fig. 1. **Scheme of drawing and numbering points on the wing according to the DAWINO method**

Morphometric methods are based on numerous measurements of many individuals. From a large number of characters for the analysis of honey bees from a wide range of geographical locations, researchers selected 42. This set of characters was called the “standard morphometric” indicators. They have stood the test of time and continue to remain relevant and used in a wide range of studies of geographical variations (Diniz-Filho et al, 2000, Bouga M., 2011, Vinutha R Bhatta et al, 2022,).

The biodiversity of the honey bee *Apis mellifera* L was first assessed using morphometry. After the development of multivariate statistical methods, they were used by Ruttner (1988) to systematize the taxonomy of honey bees of the genus *Apis.*

Initially, the biodiversity of honey bees was determined using the morphometric method, which was entirely based on a large collection of samples with subsequent multivariate analysis of morphometric characters. This identification method was long considered definitive among honey bees.

The systematics and nomenclature of honey bees of the genus *Apis* are quite complex (Sheppard, Meixner, 2003; Chen., 2016,). Maa T.C., (1953) distinguished 24 species of honey bees and three genera. Kanderir, Fuchs et al., 2011, provide tabular data obtained from the Oberurse Database and used in their works for 24 names of subspecies of honey bees (Fig. 2).



Subspecies	Sample size	
	Colony	Bee
Tropical African		
A. m. adansonii	11	108
A. m. capensis	3	30
A. m. lamarckii	7	69
A. m. litorea	6	53
A. m. monticola	8	77
A. m. scutellata	14	136
A. m. unicolor	7	67
A. m. yemenitica	14	126
Western Mediterranean–Northern African		
A. m. iberica	2	18
A. m. intermissa	8	78
A. m. mellifera	14	136
A. m. sahariensis	2	19
Central Mediterranean–Southeastern European		
A. m. carnica	15	146
A. m. cecropia	9	87
A. m. ligustica	11	107
A. m. macedonica	2	20
A. m. sicula	4	39
Middle Eastern		
A. m. adami	5	50
A. m. anatoliaca	5	50
A. m. armeniaca	6	54
A. m. caucasica	12	119
A. m. cypria	4	39
A. m. meda	8	79
A. m. syriaca	9	85

Fig. 2. **List of honey bee subspecies**

Based on a large volume of samples and multivariate analysis, a classification was proposed, the basis of which is the division of bee subspecies into branches. Initially, three branches were distinguished - A (from South and Central Africa), M (North Africa and Northern Europe), C (Eastern Europe and the Mediterranean). The classification was further refined by adding a fourth evolutionary branch - O (Near and Middle East).

Recently, two more branches have been described as lineage Y from Ethiopia and lineage Z from Syria (table 1) (Franck et al., 2001; Ruttner, 1988 .; Alburaki et al., 2013, Whitfield, 2006, Wallberg, 2014, Chen C. et al.,2016).

According to other literature data, currently about 30 subspecies of the species *A. Mellifera* are recognized by most scientists. In particular: Species: *Apis mellifera. Subspecies: A. m. adami; A. m. adansonii; A. m. anatoliaca; A. m. artemisia; A. m. capensis; A. m. carnica; A. m. caucasia; A. m. cecropia; A. m. cypria; A. m. iberica; A. m. intermissa; A. m. jemenitica; A. m. lamarckii; A. m. ligustica; A. m. litorea; A. m. macedonica; A. m. meda; A. m. mellifera; A. m. monticola; A. m. remipes; A. m. ruttneri*; *A. m. sahariensis; A. m. scutellata; A. m. siciliana; A.m. sicula A. m. simensis; A. m. sinisxinyuan; A. m. sossimai; A. m. syriaca; A. m. taurica; A. m. unicolor* (Linnaeus, C. 1758, Engel, M.S. 1999,).

Table 1

Classification of *Apis* subspecies by morphological characteristics and distribution area

№	**Name**	
	Branch, distribution area	**Subspecies**
1	**A,** Africa	*A. м. adansonii*
2		*A. м. capensis*
3		*A. м. lamarckii*
4		*A. м. litorea*
5		*A. m. monticola*
6		*A. м. scutellata*
7		*A. m. unicolor*
7		*A. м. yemenitica*
9	**M,** Western and Northern Europe	*A. м. ibericensis*
10		*A. м. intermissa*
11		***A. м. mellifera***
12		*A. м. sahariensis*
13	**C,** Mediterranean. Eastern Europe	*A. м. carnica*
14		*A. m. cecropia*
15		*A. м. ligustica*
16		*A. m. macedonica*
17		*A. m. caucasia*
18		*A.m. sicula*
19	**O,** Near and Middle East	*А. м. адамі*
20		*A. м. anatoliaca*
21		*A. м. armeniaca*
22		*A. m. cypria*
23		*A. m. meda*
24		*A. м. syriaca*
25	**Z,** Syria	*A. m. syriaca*
26	**Y,** Yemen	*A. m. jemenitica*

Ilyasov R. et al. (2017) provide a list of subspecies of honey bees, the names of which differ somewhat from the data of previous authors (Table 2).

Table 2

Division of *A. Mellifera* subspecies into branches

№	Branch	Subspecies	№	Branch	Subspecies
1	**A**	*A. m. sahariensis*	*16*	**C**	*A. m. ligustica*
2		*A. m. intermissa*	*17*		*A. m. carnica*
3		*A. m. lamarckii*	*18*		*A.m. carpathica*
4		*A. m. litorea*	*19*		*A. m. macedonica*
5		*A. m. scutellata*	*20*		*A. m. cecropia*
6		*A. m. monticola*	*21*		*A.m.sicula*
7		*A. m. adansonii*	*22*		*A.m. pomonella*
8		*A. m. unicolor*	*23*		*A. m. ruttneri*
9		*A. m. capensis*	*24*		*A. m. caucasia*
10		*A. m. simensis*	*25*	**O**	*A. m. remipes*
11		*A.m. nubica*	*26*		*A.m.armeniaca*
12	**M**	***A. m. mellifera***	*27*		*A. m. adami*
13		*A. m. iberiensis*	*28*		*A. m. meda*
14	**Z**	*A. m. syriaca*	*29*		*A. m. cypria*
15	**Y**	*A. m. jemenitica*	*30*		*A. m. anatoliaca*

They differ in many features, both behavioral and morphological. Initially, the recognition of subspecies was based on a descriptive basis, but they turned out to be insufficient.

Important remarks regarding the use of classical, standard wing morphometry were expressed by A. Tofilski (2008), emphasizing the possibility of using different options in terms of the number of wing features, which, as a rule, lead to classification results that differ little from each other.

In addition, the use of stepwise discriminant analytics allows you to reduce the number of features and leave only those that make a significant contribution to the discrimination of wing phenotypes.

However, there are several circumstances that prevent the effective use of this method to its full extent. The use of segment lengths and segment areas requires studying only bees of the same age, which is extremely problematic, especially if a significant number of colonies from different regions and apiaries are being studied, and the use of segment areas requires the presence of specific technological and software, to which most Ukrainian beekeepers do not have access (Cherevatov V.F. et al., 2023).

The difficulty also lies in the further use of the obtained classification data for the purpose of correct comparison of wing phenotypes from different apiaries or regions. From this point of view, the use of a set of 8 indices has the advantage that it allows creating sufficiently compact banks of reference index data. According to the authors, such banks must meet certain requirements - contain the minimum number of signs that would be sufficient for reliable classification of bee wings; signs must be unified; signs must be established without technological difficulties. The use of such reference data banks is the key to reliable identification of the breed composition of bees by wing phenotype. Thus, morphometric research methods, despite their low accuracy, allow for a quick and inexpensive preliminary assessment of the taxonomic affiliation of bee colonies. Additional assessments of biological and ethological signs of bee colonies allow for increasing the accuracy of identification of their taxonomic affiliation. These facts make morphometric methods of studying bees widespread in the practical activities of beekeepers today.

Determining the breed of bees by studying exterior features using the classical method is complicated by the fact that the indicators of some measurements of body parts in breeds are within the same or close limits. In addition, some authors indicate that the results of morphometric measurements carried out using the standard method are influenced by subjective factors.

However, phylogeographic studies have shown that variations in the morphological features of these subspecies as a result of adaptation to local conditions often complicate their correct identification. Therefore, molecular methods based on DNA markers, such as mitochondrial DNA (mtDNA), microsatellites and single nucleotide polymorphisms (SNP, Single Nucleotide Polymorphism), have been developed. Molecular genetic studies have generally confirmed the previously obtained morphometric data for branches A, M, C; O. More recently, the Y branches, which include the subspecies *A. m. yemenítica* from Ethiopia (Franck et al.,2000, 2001) and the Z branches, which include the subspecies *A. m. syriaca* from Syria (Alburaki et al., 2013, Meixner et al., 2013, Babu K. N. et al., 2020), have been isolated.

Among molecular markers, non-recombinant and maternally inherited mtDNA is one of the most widely used objects of study. PCR-based assays for bee typing were first used in connection with the Africanization of honey bees in the Americas. The introduction of the African subspecies *A.m.scutellata* in Brazil, and its subsequent hybridization with previously imported European subspecies (Michener, 2000), led to the rapid spread of wild populations of the new hybrid strain (Africanized honey bee) over a large area covering most of South America, Central America, Mexico, and the southwestern United States (Texas, New Mexico, Arizona, Nevada, and California) (Pinto et al., 2012).

A feature of mtDNA as a molecular marker is that it is inherited from only one parent: it is transmitted through the maternal line (from mother to offspring) during fertilization. Due to maternal inheritance, there are no genetic recombinations in the mitochondrial genome, thus a single haplotype is inherited - a set of closely linked loci. The mutational process acts as the only factor in the formation of mtDNA polymorphism, and mutations that are stored and accumulate in the mitochondrial genome can be a trace of the evolutionary history of a species or an individual (Metlitskaya et al. 2012).

One of the first molecular genetic studies to identify Africanized bees in California was based on polymorphisms of three mtDNA loci and required the use of three restriction enzymes (Hall Smith, 1991. Smith, 1995). Later, the analysis methodology was improved, and today the most informative for typing is the intergenic locus located between the genes of cytochrome oxidase subunits I and II (COI-COII) of the mitochondrial genome of *Apis mellifera*.

Proposed by Garnery et al. (1993) PCR protocol involves the use of one pair of primers and restriction endonuclease Dra I. Classification of mitotypes of the COI-COII locus is carried out on the basis of a complex analysis, which includes the length of the amplification fragment and polymorphism of the Dra I restriction endonuclease sites. Based on the Dra I restriction of the COI-COII locus of bee mtDNA, 91 mitotypes of the evolutionary branch M, 30 of the branch A, 5 of the branch C and 7 of the branch O mitotypes have been identified to date (Ilyasov et al., 2016). As an alternative approach to determining the mitochondrial genome of African bees, an analysis method based on the polymorphism of the cytochrome b gene of mtDNA can be considered. Crozier et al.

(1992) developed primers within cytochrome b and proposed to diagnose Africanized bees by the presence/absence of the Bgl II restriction site. The advantage of this method is its simplicity and ease of interpretation of the results (convenient for analysis of amplification 485 nucleotide pairs (bp) and restriction 291/194 bp fragments, use of agarose gel). However, this method does not allow to distinguish the mitotypes of bees from the southern part of Africa *A. m. scutellata* from *A. m. intermissa* (Northeast Africa) and the genetically related *A. m. iberica* (Southern Spain).

In addition, the intergenic region of cytochrome oxidase subunits I and II (COI-COII) of the *Apis mellifera* mitochondrial genome is also widely used as a simpler, but less informative method for classifying mitotypes of bee subspecies, which is based on the analysis of inertias/deletions in this region. At least 7 variants of the lengths of the amplified fragments PoQ, PoQQ, PoQQQ, PQ, PQQ, PQQQ and Q are known, which can be explained by a combination of 3 sequences: Po (67 bp), P (54 bp) and Q (192-196 bp). For their analysis, primers 5’ CAKATTTAГAAATCCATAT 3’ and 5’ ATAAATATAAATCATGTGGA 3’ are used, which flank the 3’- and 5’-terminal sequences of the COI and COII genes, respectively. The size of the amplified fragment using the specified pair of primers is 350 bp for the case of the simplest combination Q (*A. m. sausasica* and other southern subspecies of *A. mellifera*) and 600 bp for the case of a more complex combination PQQ in *A.m.mellifera*. Mitotype classification is carried out using agarose gel electrophoresis.

In addition to the mitochondrial genome, to confirm breed affiliation, analysis of allelic polymorphism of microsatellite loci is used according to the recommendations of the Food and Agriculture Organization of the United Nations (FAO) and the International Foundation for Animal Genetics (ISAG). The use of a set of microsatellites allows you to successfully determine the main genetic and population parameters of the study groups and carry out breed differentiation, assess the level of inbreeding/outbreeding, the level of population cross-breeding, etc. (Grygorchuk D.I. et al., 2020).

One of the promising areas of work using molecular genetic markers is the possibility of a comprehensive assessment of the level of hybridization of bees (using the types of molecular genetic markers listed above) to address the issue of their adaptive abilities. As a result of all this, continuous hybridization leads to greater mortality and corresponding economic costs.

Timely assessment of bee colonies using different types of molecular genetic markers (primarily using microsatellites and analysis of mitochondrial genome variability) allows you to determine with a high level of probability the level of genetic variability and, accordingly, the degree of hybridization. All this allows you to effectively control the selection process (Shaibi, 2008).

Regarding the study of the genetic foundations of the adaptive qualities of bees at this stage of the development of molecular genetics, researchers' attention is focused on finding a set of allelic variants of genes, the functioning of which is directly related to the regulation of the adaptive properties of the organism. The ability to identify a molecular genetic marker associated with an economically useful trait, in particular, hygienic behavior, etc., provides the broadest prospects for the application of marker-associated selection (MAS) methods in beekeeping. However, at this stage of genetics development, there are no effective DNA tests for assessing the polymorphism of quantitative trait loci (QTL), which significantly complicates the possibility of using MAS. In this direction (search for potential QTL for the needs of MAS), a lot of work is being done to study the expression features of various candidate genes (associated with any economically useful trait); a search for single-nucleotide polymorphisms in the nuclear and mitochondrial genomes is being conducted; DNA markers are being searched / developed that could be used in breeding programs (primarily in the areas of bee resistance), etc.

Today, uncontrolled hybridization of bees belonging to different races (breeds) of *Apis mellifera mellifera* has reached an alarming pace in Ukraine. Preservation of the gene pool of local (aboriginal) bees well adapted to local natural conditions is an urgent area of scientific research, which cannot be solved without the use of molecular genetic methods for monitoring local populations (Van der Zee, R. et al, 2009, Brodschneider, 2016, Cherevatov et al., 2019).

Correct identification of these subspecies is important for sustainable beekeeping and the preservation of honey bee biodiversity, since the artificial movement of subspecies/breeds between different regions leads to the loss of purity of the aboriginal gene pool as a result of hybridization. Until recently, beekeeping used mainly morpho-physiological criteria to assess the degree of genetic characteristics of subspecies (purebredness): body color, length of the proboscis, features of wing venation, cubital index, egg production of queens, etc. However, they vary greatly in hybridized colonies, which significantly reduces the reliability and even makes it impossible to determine breed affiliation using traditional morphometric analysis. Phylogeographic studies have shown that variations in morphological features as a result of adaptation to local conditions often complicate their correct identification.

In solving important issues of establishing the breed affiliation of bees, preserving its unique gene pool within natural ranges, there is an urgent need to apply molecular genetic methods (Magnus, 2014).

Preservation of the gene pool of local forms of *Apis melliffera* seems to be particularly relevant for Ukraine due to the significant diversity of natural conditions and the prevalence of several races (breeds) of the honey bee. During the last years of the late 20th and early 11th centuries, queens of different breeds were massively imported to Ukraine from abroad, then a hybrid of several breeds began to be imported, in particular *Backfast.* Uncontrolled crossing of different species led to the loss of useful traits by bees and a decrease in their adaptability to the environmental conditions of the territory in which this species is widespread. It also creates obstacles to the selection of bees and the preservation of their purebredness. To prevent this, it is necessary to establish and monitor the genetic structure of bee populations kept in Ukraine today.

Conclusions. The material presented above argues that each individual indicator does not allow for a full assessment of the state of the population. Only by taking into account the results of applying a set of indicators can one draw the right conclusions. The prospects of using different types of molecular genetic markers for solving a number of practical problems in selection and breeding work in Ukrainian beekeeping are undeniable. Summarizing all of the above, we can conclude that the prospects of using different types of molecular genetic markers for solving a number of practical problems in selection and breeding work in Ukrainian beekeeping are undeniable.

Referenses

Alburaki, M., Bertrand, B., Legout, H., Moulin, S., Alburaki, A., Sheppard, W. S. and Garnery, L. (2013). A fifth major genetic group among honeybees revealed in Syria‘, *BMC Genetics,* 14. doi: 10.1186/1471-2156-14-117.

Babu K. N., Sheeja Th. E., Minoo D., Rajesh M. K., Samsudeen K, Suraby E.J., Payatatti I., Kumar V. (2020). Random Amplified Polymorphic DNA (RAPD) and Derived Techniques Molecular Plant Taxonomy. *Methods and Protocols* DOI: 10.1007/978-1-0716-0997-2_13

Bouga M, Alaux C, Bienkowska M, Bü chler R, Carreck NL, Cauia E, Chlebo R, Dahle B, Dall'Olio R, De la Rú a P, Gregorc A, Ivanova E, Kence A, Kence M, Kezic N, Kiprijanovska H, Kozmus P, Kryger P, Le Conte Y, Lodesani M, Murilhas AM, Siceanu A, Soland G, Uzunov G& Wilde J. (2011). A review of methods for discrimination of honey bee populations as applied to European beekeeping. *J. Apicult. Res.* 50(1): 51–84. https://doi.org/10.3896/IBRA.1.50.1.06).

Brodschneider, R., Gray, A., Van der Zee, R, Adjlane, N., Brusbardis, V., Charrière, J.D., Chlebo R.,Coffey, M.F., Crailsheim, K., Dahle, B., anihlík, J., Danneels, E., De Graaf, D.C., Draži M.M., Fedoriak, M., Forsythe, I., Golubovski, M., Gregorc, A., Grzda, U., Hubbuck, I., Tunca, R.., Kauko, L., Kilpinen, O., Kretavicius, J., Kristiansen, P., Martikkala, M., Martín-Hernández, R., Mutinelli, F., Peterson, M., Otten, C., Ozkirim, A., Raudmets, A., Simon-Delso, N., Soroker, V., Topolska, G., Vallon, J., Vejsnæs, F., and Woehl, S. (2016). Preliminary anlysis of loss rates of honey bee colonies during winter 2015/16 from the COLOSS survey, *J. Apicult. Res.* vol. 55, no. 5, pp. 375–8. doi: 10.1080/00218839.2016.1260240

Chen C., Liu Z., Pan Q., Chen X., Wang H., Guo H. (2016). Genomic analyses reveal demographic history and temperate adaptation of the newly discovered honey bee subspecies Apis mellifera sinisxinyuan n. ssp. // Molecular Biology and Evolution.. 33: 1337-1348. doi: 10.1093/molbev/msw017

Cherevatov O.V., Panchuk I.I., Kerek S.S., Volkov R.A. (2019). Molekulyarne rIznomanIttya speysernoYi dIlyanki SOI-COII mItohondrialnogo genomu ta pohodzhennya karpatskoYi bdzholi / O.V.Cherevatov, I.I.Panchuk, S.S.Kerek, R.A. Volkov // TsitologIya ta genetika., T. 53. № 4. – S.13–19

Cherevatov V.F., Babenko V.V., Galatyuk O.E., Yarovets V.I. (2023). Klasichna morfologIya kril bdzholi medonosnoYi (Apis mellifera L.) z vikoristannyam protokolu DAWINO / V.F.Cherevatov, V.V.Babenko, O.E.Galatyuk, V.I. Yarovets // BIologIchnI sistemi. T. 15. Vip. 2. 179–187

Cherkasova A. Y. Davidenko Y. K. Huba P. A. (1991). Slovar-spravochnyk po pchelovodstvu. K. 416 s.

Crozier RH, Crozier YC. (1992). The cytochrome b and ATPase genes of honeybee mitochondrial DNA. *Mol Biol Evol*. May; 9 (3):474-482. doi: 10.1093/oxfordjournals.molbev.a040729.

Diniz-Filho H.R, Radloff S, Fuchs S. (2000). Spatial analysis of morphometrical variation in African honeybees (Apis mellifera L.) on a continental scale. *Apidologie*. 31(2): 191–204.

Engel, M.S. (1999). The taxonomy of recent and fossil honeybees (Hymenoptera: Apidae; Apis). *Journal of Hymenoptera Research* 8(2): 165–196. BHL

Franck, P., Garnery, L., Solignac, M. and Cornuet, J. (2000). Molecular confirmation of a fourth lineage in honeybees from the Near East‘, *Apidologie*, 31,: 167–180. doi:10.1051/apido:2000114.

Franck P, Garnery L, Loiseau A, Oldroyd BP, Hepburn HR, Solignac M, Cornuet JM, (2001). Genetic diversity of the honeybee in Africa: microsatellite and mitochondrial data, *Heredity*, 86, 420-30.

Garnery L., Solignac M., Selebrano G., Cornuet J., (1993). A simple test using restricted PCR-amplified mitochondrial-DNA to study the genetic-structure of Apis mellifera L. Experientia 49(11): 1016–1021. doi.org/10.1007/BF02125651

Hall A., Slack T., Smith G., Whitson D. (1991). Sport in Canadian Society. Toronto: McClelland & Stewart,. Pp. 281.

Huzenko E. V., Tsar A. Y., Lemesh V. A. (2022). Metody identyfikatsii taksonomichnoi prynalezhnosti medonosnykh bdzhil Apis Mellifera. *Molekuliarna i prykladna henetyka.* Tom 32, doi.org/10.47612/1999-9127-2022-32-107-120

Ilyasov R.A., Poskryakov A.V., Nikolenko A.G. (2016). Organizatsiya genoma medonosnoy pchelyi. *Biomika,* Tom 8, 2, 97–99

Ilyasov R.A., Dar S.A., Dukku U.H.3, Kandemir I., Li M.L., Ozkan Kosa A., Nikolenko A.G., Kvon H.V. (2019). Obzor sovremennoy taksonomii evropeyskiy pchel roda Apis. *Biomika,* Tom 11 # 2, S. 212-241

Kandemir, Özkan A., Fuchs S. (2011). Reevaluation of honey bee (Apis mellifera) microtaxonomy: a geometric morphometric approach. *Apidologie.* 42: 618-627. doi: 10.1007/s13592-011-0063-3

Kotthoff U., Wappler T., Engel M.l S._(2013). Greater past disparity and diversity hints at ancient migrations of European honey bee lineages into Africa and Asia // *Journal of Biogeography.* V. 40 P. 1832–1838. doi: 10.1111/jbi.12151.

Linnaeus, C. 1758. Systema Naturae per regna tria naturae, secundum classes, ordines, genera, species, cum characteribus, differentiis, synonymis, locis. Editio Decima, Reformata. Tomus I. Holmiæ (Stockholm): impensis direct. Laurentii Salvii. 824 pp. DOI: 10.5962/bhl.title.542 BHL Reference page. [first availability, see p. 576]

Maa T.C. (1953). An enquiry into the systematics of the tribus Apidini or honey bees (Hymenoptera). *Treubia.* 21: 525-640.

Magnus R. M., Amber D. T., Szalansky A. L. (2014). Mitochondrial DNA diversity of Honey Bees (Apis mellifera) from unmanaged colonies and Swarms in the Unated States. R.M. Magnus,. *Biochem. Genetic* V. 52. 245 – 257.

2Meixner M. D, Pinto M. A., Bouga M., Kryger P., Ivanova E., Fuchs S. (2013). Standard methods for characterising subspecies and ecotypes of Apis mellifera. *Journal of Apicultural Research* 52(4): DOI 10.3896/IBRA.1.52.4.05

Michener, C. D. (2000). The Bees of the World. 2715 North Charles Street Baltimore, Maryland 21218-4363: The John Hopkins University Press. Available at: www.press.jhu.edu.

Metlitska O.I. PolIschuk V.P., Taran S.I. (2010). Zastovuvannya metodIv morfometrIYi ta molekulyarno-genetichnoYi otsInki pri viznachennI chistoporodnostI ukraYinskih bdzhIl / BIlologIya tvarin (naukovo-teoretichniy zhurnal): zb. nauk. pr. LvIv: IBT NAAN UkraYini, 12, №1. P. 254-259.

Metlitska O. I., Kopilova K. V., (2012). PolImorfIzm mItohondrialnoYi DNK dlya otsInki genetichnoYi strukturi I pIdvidovoYi klasifIkatsIYi ukraYinskih bdzhIl Visnik PoltavskoYi derzhavnoYi agrarnoYi akademIYi. № 2 113-117

Metlytska, O. I., Kopylov K. V., Berezovskyi O. V. (2016). Suchasni molekuliarno-henetychni pidkhody dlia pidvyshchennia efektyvnosti selektsiinoho protsesu v tvarynnytstvi Ukrainy. *Rozvedennia i henetyka tvaryn*. Vyp. 51. S. 193-200. - Available at: http://nbuv.gov.ua/UJRN/rgt_2016_51_28

Pinto M A., Muñoz I., Chávez-Galarza J., Pinto M A. (2012). The Atlantic side of the Iberian peninsula: a hot-spot of novel African honey bee maternal diversity. *Apidologie* 43: 663-673. doi.org/10.1007/s13592-012-0141-1

Ruttner F. (1973). Zuchttechnik und Zuchtauslese bei der Biene: Anleitungen zur Aufzucht von Königinnen und zur Kör- und Belegstellenpraxis. Ehrenwirth Verlag; 138 p.

Ruttner F. (1988).Biogeography and taxonomy of honeybees. Springer: Berlin/Heidelberg, Germany; 284 p.

Shaibi T., Lattorff H., Moritz R. (2008). A microsatellite DNA toolkit for studying population structure in Apis mellifera. *Mol. Ecol. Resour.* V. 8, № 5. P. 1034 – 1036.

Sheppard W. S., Meixner M. D. Apis mellifera pomonella, a new honey bee subspecies from Central Asia Apidologie 34 (2003) 367-375 DOI: 10.1051/apido:2003037

Smith D.R, Glenn T.C. (1995) Allozyme polymorphisms in Spanish honeybees (Apis mellifera iberica). Journal of Heredity. 86(1):12-16

Tofilski A. (2008) Using geometric morphometrics and standard morphometry to discriminate three honeybee subspecies. Apidologie.; 39: 558–563. http://10.1051/apido:2008037).

Van der Zee, R., Pisa L., Andonov, S., Brodschneider, R., Charrière, J.D., Chlebo, R., Coffey, M.F., Crailsheim, K., Dahle, B., Gajda, A., Gray, A., Drazic, M.M., Higes, M., Kauko, L., Kence, A., Kence, M., Kezic, N., Kiprijanovska, H., Kralj, J., Kristiansen, P., Hernandez, R.M., Mutinelli, F., Nguyen, B.K., Otten, C., Özkrm, A., Perna, S.F., Peterson, M., Ramsay, G., Santrac, V., Soroker, V.,Topolska, G., Uzunov, A., Vejsnæs, F., Wei, S., Wilkins, S. (2009). Managed honey bee colony losses in Canada, China, Europe, Israel and Turkey, for the winters of 2008–9 and 2009–10, J. Apicult. Res., vol. 51, no. 1, pp. 100–14. doi:10.3896/IBRA.1.51.1.12.

Wallberg, A., Han, F., Wellhagen, G., Dahle, B.,(2014). A worldwide survey of genome sequence variation provides insight into the evolutionary history of the honeybee Apis mellifera, Nat. Genet., , vol. 46, pp. 1081–8. doi: 10.138/ng.3077.

Whitfield, C.W., Behura, S.K., Berlocher, S.H., Clark, A.G., Johnston, J.S., Sheppard, W.S., Smith, D.R., Suarez, A.V., Weaver, D., and Tsutsui, N.D., (2006). Thrice out of Africa: ancient and recent expansions of the honey bee, Apis mellifera, Science, , vol. 314, pp. 642–5. doi: 10.1126/science.1132772.

Yarovets V.I.,Babenko V.V., Galatyuk O.E. (2022). MorfometrIya kril bdzhIl za vIsmoma oznakami (Indeksami): CI, DBI, DISC.SH., PCI, RI, CI.2, CI.2.1, CI.3 doi.org/10.46913/beekeepingjournal..8.10 65-71.

Vinutha R Bhatta, Naresh Kumar A. (2022). Morphometric Characters of Apis cerana indica Worker Bees under Urban, Rural and Wild Habitats. Applied Ecology and Environmental Sciences. 2022; 10(10): 614-621. doi.org/10.12691/aees-10-10-3).

Zlotin O. Z. (1988). Sviiski komakhy [Relative insects]. K.: Radianska shkola (in Ukrainian)