



Regulatory Mechanisms in Biosystems

ISSN 2519-8521 (Print)
ISSN 2520-2588 (Online)
Regul. Mech. Biosyst.,
2024, 15(1), 92–96
doi: 10.15421/022413

Obtaining morphometric standards of drone wings of separate populations of honey bees (*Apis mellifera*) in Ukraine

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Article info

Received 04.01.2024

Received in revised form

05.02.2024

Accepted 23.02.2024

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Galatiuk, O. Y., Zastulka, M. V., Cherevatov, V. F., Yarovets, V. I., & Egoshin, L. R. (2024). Obtaining morphometric standards of drone wings of separate populations of honey bees (*Apis mellifera*) in Ukraine. *Regulatory Mechanisms in Biosystems*, 15(1), 92–96. doi:10.15421/022413

Today, there are no systematic studies on the wing phenotypes of drone populations of the honeybee widespread in Ukraine. Considering that drone genomes are haploid, this allows one to establish the correspondence between the phenotype and the drone genome, thereby roughly determining the queen's genome in the part responsible for the wing phenotype. This partially compensates for the lack of resources among domestic scientists to conduct genetic research on bees. The aim of the study was to examine the wings of drones from several apiaries in the Kharkiv, Sumy, Poltava, and Zhytomyr regions, identify typical phenotypes, and attempt their taxonomic identification. Using discriminant analysis, 4640 drone wings were classified into three clusters. A two-step scheme for forming significantly different phenotype clusters of wings was proposed. Initially, based on the similarity of Euclidean distances and Mahalanobis distances (<2.6) between clusters, three groups were obtained, which, for refinement, underwent a second classification. As a result, average values and confidence intervals of eight morphometric traits were established: Ci, Dbi, Disc.sh, Pci, Ri, Ci.3, Ci.2.1, Ci.2.2 for the three wing groups. It is suggested to accept the trait values of these groups as reference data: one as a local population of the *A. m. carnica* subspecies, and the other two as regional standards for Ukrainian bees. Based on the obtained standards, a significant presence of *A. m. carnica* subspecies bees was established in all studied apiaries, except for the apiary with the status of a breeding ground for Ukrainian steppe bees (Kuzemin village, Sumy region), where such presence is minimal. This fact indicates the need for special measures to reproduce and expand the ranges of existence of local populations of Ukrainian steppe bees. The example of creating local and regional morphometric standards provided in this work is specifically designed to address this issue.

Keywords: classical morphometry; bee wings; drones; discriminant analysis.

Introduction

One of the ways to determine the affiliation of the honeybee (*Apis mellifera* L.) population in Ukraine to specific subspecies is through wing morphometry of worker bees and drones. For this purpose, the cubital index Ci is most commonly used, occasionally along with the humeral index Dbi and the discoidal shift Disc.sh. The variation limits of these traits for populations of Ukrainian steppe bees, as reported by prominent Ukrainian scientists such as Polishchuk (2001, 2006a, 2007), Polishchuk et al. (2006b), Hryhorkiv (2018), and Brovarskyi et al. (2017), allow, with a certain level of confidence, the attribution of the wing phenotype to the *A. m. macedonica* subspecies. Research on the morphometry of Carpathian bees, initiated by Ukrainian researcher A.Haidar, is continued in the breeding and selection laboratory for Carpathian bees at the "P. I. Prokopovych Institute of Beekeeping", Mukachevo, Zakarpattia region. Through selective breeding based on exterior traits, phenotypic characteristics of four Carpathian bee types – "Vuchkivsky", "Rakhivsky", "Ho-verla", and "Synevyr" – have been sufficiently stabilized, as reflected in the works of Kerek et al. (2017, 2018, 2020), Pappa et al. (2017a), and Mertsina (2006). According to these publications, bees from this region are likely to belong to the *A. m. carnica* subspecies. The study of morphometric wing indicators of worker bees from selective crosses of Carpathian bees provides grounds to assume significant differences between the phenotypes of local populations and Western selection lines (Petko & Fedorovich, 2022).

In 2006, the complete genome sequence for the honeybee *Apis mellifera* was published with 328 co-authors (Weinstock et al., 2006). This event served as a starting point for the accumulation of whole-genome data for various bee populations. One of the directions in such research is the search for genetic markers that allow the identification of subspecies of the honeybee (Henriques et al., 2018). In Ukraine, as well as in Europe, amidst the backdrop of globalization, there is a threat of hybridization and loss of indigenous populations, which form the basis of the selection process in their respective locations (Cherevatov et al., 2014). This has led to the development of molecular genetic research, conducted under the guidance of Metlytska et al. (2010, 2011), Papp et al. (2017b) and Cherevatov et al. (2019). Recent studies confirmed that the Carpathian bee belongs to the evolutionary lineage C (Fan Han et al., 2012), derived from and representing an ecotype formed as a result of the eastward expansion of this subspecies into the Carpathian Mountains. Simultaneously, determining the subspecies of different populations of Ukrainian steppe bees requires additional research. Due to a series of unfavorable circumstances, Ukrainian scientists face limitations in conducting genetic research. An alternative to genetic research could be the study of drone wing phenotypes using the morphometric method, allowing for preliminary assumptions about the composition of chromosomal sets in the genomes of drones, queens, and worker bees. However, there are difficulties that prevent the extensive study of drone wings, as is done for worker bees. Primarily, this is due to the seasonality of their presence in apiaries and significant fluctuations in wing phenotypes compared to worker bee

wings, owing to the peculiarities of genetic deviations and their impact on drone wing phenotypes.

Today, there is a limited number of literary sources, complicating the procedure of establishing an exact correspondence between the wing phenotype of drone bees and the corresponding spectrum of taxonomic gradation for the honeybee. In the classical work of Ruttner (1988), it is stated that the values of the cubital index for drone bees of the honeybee range from 1.38 to 1.93, and for the subspecies *A. m. carnica*, it is 1.8 to 2.3. In the study by Groeneveld et al. (2020), experimental values of the cubital index for drone subspecies are provided: *A. m. mellifera* – Ci = 1.48, *A. m. ligustica* – Ci = 1.77, *A. m. carnica* – Ci = 1.95. Referring to the absence of reliable scientific research, these values are suggested as baseline data. Additionally, the absence of any reference data for important wing phenotype traits, such as the discoidal index (Dbi) and discoidal shift (Disc.sh.), is noted. It is also highlighted that due to significant anomalies in wing venation, drones are less suitable for establishing taxonomic affiliation compared to worker bee wings. Unfortunately, morphometric studies of drone wings by domestic scientists are not known to us.

The aim of our work was to conduct morphometric studies of drone wings in apiaries of Kharkiv, Sumy, Poltava, and Zhytomyr regions with the aim of obtaining primary data for creating phenotypic standards of drone wings for local bee populations. We also aimed to perform their breed interpretation and establish the effectiveness of the method.

Materials and methods

2585 wings were used (from 24 bee colonies, from O. Galatiuk apiaries: Chudniv village, Veresi village, and Zhytomyr city, Zhytomyr region), 797 wings (from 6 bee colonies, O. Kalashnikov apiary, Kharkiv city), 679 wings (from 7 bee colonies, L. Yehoshyna apiary, Sumy region, Okhlyrka district, Kuzemin village), 579 wings (from 9 bee colonies, L. Hryhorkiv apiary, Poltava region, Hadiach city). All bee families from O. Kalashnikov, L. Yehoshyna, L. Hryhorkiv apiaries, and part of the bee colonies from O. Galatiuk apiaries, which had local origin, were positioned as local populations of Ukrainian steppe bees. L. Yehoshyna apiary has the status of a breeding apiary. In addition, part of the studied bee colonies from O. Galatiuk apiaries, whose queens were acquired in Zakarpattia and Khmelnytsky regions for scientific purposes, were previously classified as subspecies *A. m. carnica* and *A. m. macedonica*, respectively.

Photos of the wings were processed using the TpsDig2 program. The preliminary preparation of the array of experimental data was carried out using the previously developed methodology (Yarovets et al., 2023a). The classification of drone wings was performed based on eight characteristics: Ci, Dbi, Disc.sh, Pci, Ri, Ci.3, Ci.2.1, Ci.2.2, as proposed in the work by Yarovets et al. (2022). This was done independently for each of the three apiaries, using discriminant analysis of data and the Statistica software suite (Yerina & Yerina, 2014). Initially, a general classification of drone wings into three or four clusters was performed separately for each of the four apiaries. As a result, the majority of drone wings for each bee colony were concentrated in two clusters, while a small portion was assigned to other clusters and excluded from further consideration. In the second stage, the remaining drone wings underwent classification into two clusters. Based on the obtained average values of cluster characteristics, using Euclidean distances between them and Mahalanobis distances (MD) between the centroids of individual clusters, three groups of clusters were formed, showing sufficient similarity within each group. The group formation procedure involved 1666 drone wings from 44 clusters belonging to 32 bee colonies. In the third stage, a reclassification of the 1666 drone wings into three clusters was carried out, improving the accuracy of classification by redistributing wings slightly between groups.

Results

In order to illustrate the quality of the conducted classification, let's provide an example of the classification of drone wings from three points of O. Galatiuk apiary into four clusters (Table 1, 2). According to the values of the "Partial Lambda" column, the contribution weight of each feature to the classification increases in the following sequence: Ri, Disc.sh., Ci.2.1, Pci, Ci.2.2, Dbi, Ci, Ci.3. In other words, the least signifi-

cant feature is Ri, and the most significant one is Ci.3. Pairwise correlations between the values of all features range from 0 to 0.3 ($P < 0.05$). Thus, the correlation relationships between them are insignificant, indicating the importance of all the features used for data classification.

Table 1

Summary results of discriminant analysis of wings (n = 2585) of drone bees from bee colony (n = 31)

Indexes	Wilks' Lambda	Partial Lambda	F F _{0.05} = 3.26	P	Toler.	1-Toler. (R-Sqr)
Ci	0.115	0.839	164.34	<0.001	0.858	0.142
Dbi	0.112	0.862	137.48	<0.001	0.690	0.310
Pci	0.108	0.893	103.23	<0.001	0.774	0.226
Disc.sh.	0.104	0.928	66.95	<0.001	0.659	0.341
Ri	0.103	0.939	55.34	<0.001	0.521	0.479
Ci.3	0.139	0.696	374.40	<0.001	0.948	0.052
Ci.2.1	0.105	0.921	73.14	<0.001	0.680	0.320
Ci.2.2	0.111	0.871	127.16	<0.001	0.739	0.261

Table 2

Accuracy matrix classification of drone wings (n = 2585) in bee colony (n = 31)

Clusters	Percent correct	G_1:1 P = 0.304	G_2:2 P = 0.253	G_3:3 P = 0.185	G_4:4 P = 0.257
G_1:1	98.1	771	9	6	0
G_2:2	94.0	22	616	6	11
G_3:3	91.9	14	3	440	22
G_4:4	96.2	5	14	6	640
Together	95.4	812	642	458	673

The accuracy of the classification is 95.4% and is quite acceptable (Table 2). 797 wings (O. Kalashnikov, Kharkiv) from 6 bee colonies are distributed into three clusters with an accuracy of 95.8%, 679 wings (L. Yehoshyna, Sumy region, village Kuzemin) from 7 bee colonies are divided into four clusters with an accuracy of 95.4%. 579 wings (L. Hryhorkiv, Poltava region, city Hadiach) from 9 bee colonies are classified into three clusters with an accuracy of 95.8%.

Discussion

Formation of groups of similar clusters of drone wings. Based on the results of the initial classification, three groups of clusters of drone wing indices were formed using Euclidean distances of mean values. They are denoted as No. 1, 2, and 3. The final composition of data arrays was obtained based on Mahalanobis distances between cluster centroids in each group separately. Only those clusters with MD between centroids not exceeding 2.6 were included in the data groups. Group No 1 includes 11 clusters of drone wings from O. Galatiuk apiary, 2 from L. Egoshina apiary, and 6 from O. Kalashnikov apiary. Group No. 2 includes 7 (O. Galatiuk), 5 (L. Egoshina), and 1 (L. Hryhoruk). Group No. 3 includes 8 (O. Galatiuk), 4 (L. Egoshina), and 1 (L. Hryhoruk), totaling 1666 drone wings. For the purpose of refinement and verification of the correctness of the result of forming three arrays of morphometric data, their reclassification was carried out (Table 3, 4).

The classification accuracy was 96.9%. Coefficients of variation (C_V) for all features are <17.5%, except for the Disc.sh. feature, where C_V = 70–116%, which might initially raise doubts about the usefulness of this feature. However, its importance in overall classification is supported by the data in Table 1 and the analysis of confidence interval values for the three clusters of wings (Table 3). The confidence interval boundaries for the Disc.sh. feature, firstly, do not overlap, and secondly, are at significant distances from each other. The datasets obtained from the research corresponding to clusters 1, 2, and 3 are labeled as: No. 1.2, 2.2, and 3.2.

The confidence interval values can be used by beekeepers as reference ranges for the typical values of drone wing features, aiming for a rough assessment of the affiliation of investigated bee colonies to the formed drone wing groups. The next step involved checking the interrelationships between the finally formed groups No. 1.2, 2.2, 3.2 using Mahalanobis distances (Table 5, 6).

Analysis of the data in Table 5 is performed based on a slightly refined empirical similarity scale, as proposed in a previous study (Galatiuk

et al., 2022): if MD values are within 0–2, the similarity between the data is high; 2.0–2.6 indicates moderate similarity; 2.6–3.5 suggests low similarity, and >3.5 indicates no similarity. The MD values between the centroids of the data arrays for the three wing groups are >2.6, indicating significant differences between them (Table 3). This is confirmed by the distribution of individual wings from groups No. 1.2 and 2.2 among all three groups, except for group No. 3.2, where 27.8% of wings are assigned to group No. 2.2 (Table 6). This fact can be interpreted as the influence of the "breed" characteristic of the wing phenotype of group No. 2.2 on the primary phenotype typical of group No. 3.2.

Table 3

The summary values of indices and coefficients of variation for clusters (n = 3) of drone wings (n = 1666)

Clusters	Meaning	Indexes		Pci	Disc.sh.	N wings
		Ci	Dbi			
1	Means	1.918	1.031	2.841	2.899	602
	C _v (%)	16.1	7.2	5.9	69.4	
2	Means	1.634	0.81	2.945	-2.883	609
	C _v (%)	16.4	8.6	7.4	70.9	
3	Means	1.675	0.862	2.892	1.553	455
	C _v (%)	17.5	9	7	116	
Together						1666
Clusters	Meaning	Indexes				wings
		Ri	Ci.3	Ci.2.1	C.2.2	
1	Means	1.551	1.687	1.777	3.779	602
	C _v (%)	6	10.1	7.2	11.9	
2	Means	1.316	1.688	1.553	3.949	609
	C _v (%)	6.9	10.2	7.9	12.1	
3	Means	1.524	1.653	1.657	4.826	455
	C _v (%)	5.2	10.3	8.4	13.3	
Together						1666

Table 4

Confidence intervals for the mean values of features (n = 8) of clusters (n = 3) in the final classification of drone wings (n = 1666)

Clusters	Ci		Dbi		Pci		Disc.sh.	
	-95.0%	+95.0%	-95.0%	+95.0%	-95.0%	+95.0%	-95.0%	+95.0%
1	1.894	1.943	1.025	1.037	2.827	2.854	2.738	3.060
2	1.613	1.656	0.805	0.816	2.928	2.963	-3.046	-2.720
3	1.648	1.702	0.855	0.869	2.873	2.91	1.387	1.719
Clusters	Ri		Ci.3		Ci.2.1		Ci.2.2	
	-95.0%	+95.0%	-95.0%	+95.0%	-95.0%	+95.0%	-95.0%	+95.0%
1	1.544	1.558	1.674	1.701	1.767	1.787	3.743	3.815
2	1.309	1.324	1.675	1.702	1.543	1.563	3.911	3.987
3	1.517	1.531	1.638	1.669	1.644	1.67	4.767	4.885

Table 5

Mahalanobis distances between centroids of wing groups (n = 3)

Wing groups	No. 1.2	No. 2.2	No. 3.2
No. 1.2	–	4.1	3.0
No. 2.2	4.1	–	2.9
No. 3.2	3.0	2.9	–

Table 6

Distribution of individual wings between centroids of wing groups (n = 3)

Researchable benchmark	N		Standards comparison
	wings	%	
No 1.2	599	99.5	No. 1.2
	1	0.2	No. 2.2
Together	2	0.3	No. 3.2
	602	100	–
No 2.2	1	0.2	No. 1.2
	603	99	No. 2.2
Together	5	0.8	No. 3.2
	609	100	–
No 3.2	25	4.1	No. 1.2
	169	27.8	No. 2.2
Together	414	68.1	No. 3.2
	608	100	–

In order to reconcile the results of the wing study of bees from the Kharkiv, Sumy, Poltava, and Zhytomyr regions of Ukraine, a comparison was made between groups No. 1.2, 2.2, 3.2, and the reference data from previous research (Yarovets et al., 2023b) for a small region in the Carpathians, namely, the "CarnicaSk" population of the *A. m. carnica* subspecies and the "LocalCarpathic" micropopulation of Carpathian bees, the subspecies of which is currently not established (Table 5).

Table 7

Mahalanobis distances between the centroids of the obtained wing groups (n = 3) with local standards of local populations of the Carpathian region (n = 2)

Wing groups	No. 1.2	No. 2.2	No. 3.2	Carnica Sk	Local Carpathic
No. 1.2	–	4.1	3	0.8	3.7
No. 2.2	4.1	–	2.9	3.9	1.2
No. 3.2	3	2.9	–	2.7	3.2
Carnica Sk	0.8	3.9	2.7	–	3.5
Local Carpathic	3.7	1.2	3.2	3.5	–

The data presented in Table 7 indicate that group No. 1.2 is extremely similar to the "CarnicaSk" reference. Considering this fact, as well as the inclusion of clusters of drone wings from queens purchased in the Zakarpattia region and positioned as "Hoverla" and "Vuchkivsky," into group No. 1.2, it can be reasonably interpreted that the wing phenotypes of drone in this group belong, with sufficient probability, to the *A. m. carnica* subspecies. This assumption aligns well with Ruttner (1988) for the *A. m. carnica* subspecies, where the Ci values are indicated to be within the range of 1.8–2.3, and with our research data (Table 3, 4).

The similarity of group No. 2.2 to the "LocalCarpathic" reference indicates the prevalence of bees with the established phenotype over a significant part of Ukraine. Therefore, the authors suggest interpreting it in a territorially broader sense and transliterating it as "Ukrainian bees" ("Ukr-Bee"). Taking into account the data from previous studies on worker bees in Ukraine, where the simultaneous presence of bees from several evolutionary branches O and C was asserted (Meixner et al., 2007), a decision was made to verify the mentioned assumptions. For this purpose, the previously obtained local standard of drone from a bee colony originating from Georgia (Kutaisi), subspecies *A. m. caucasica*, labeled as "Cc307" (Galatiuk et al., 2023), was used. The result of the comparison between the arrays of feature values for the three groups and the local standard of the *A. m. caucasica* subspecies using Mahalanobis distances indicates a high similarity between group No. 2.2 and Cc307 (Table 8).

Table 8

Mahalanobis distances between the centroids of the obtained wing groups (n = 3) with the local standard of the subspecies *A. m. caucasica*

Wing groups	No. 1.2	No. 2.2	No. 3.2	Cc307
No. 1.2	–	4.1	3.0	5.2
No. 2.2	4.1	–	2.9	1.6
No. 3.2	3.0	2.9	–	3.1
Cc307	5.2	1.6	3.1	–

The obtained result forced an additional classification of the combined array of wings into four clusters (Table 9). The classification accuracy was 95.2%.

Table 9

Distribution of drone wings (n = 1739) in the classification model into four clusters

Wing groups	Cluster 1	Cluster 2	Cluster 3	Cluster 4	N wings
No. 1.2	4	586	0	12	602
D _s *	0.66%	97.34%	0.00%	1.99%	
No. 2.2	1	0	347	261	609
D _s *	0.16%	0.00%	56.98%	42.86%	
No. 3.2	368	7	7	73	455
D _s *	80.88%	1.54%	1.54%	16.04%	
Cc307	6	0	58	9	73
D _s *	8.22%	0.00%	79.45%	12.33%	
All groups	379	593	412	355	1739

Note: * – the degree of similarity of the part of the wings of the studied group to the corresponding cluster.

The degree of similarity (D_S) values may be considered as an evaluative characteristic of the similarity of the phenotype of certain wings to the phenotypes of wings in clusters obtained as a result of the final classification. As indicated by the analysis of Table 9 data, the majority of wings from groups No. 1.2, 3.2, and Cc307 are consistently assigned to one of the three clusters, with the exception of group No. 2.2, where 57% of wings are assigned to cluster 3. The latter characterizes the phenotype of the *A. m. caucasica* subspecies. Taking this into account, it can be asserted that the *A. m. caucasica* subspecies significantly influences the phenotype of the "UkrBee" population in Ukraine. The values of D_S can also characterize the degree of probable genome hybridization between the bee population "UkrBee" and the *A. m. caucasica* subspecies.

It is important to note that group No. 2.2 includes wing clusters from apiaries in the Zhytomyr region, as well as wings of drones from queens acquired from the Khmelnytsky and Sumy regions. The identification of the wing phenotype of group No. 3.2 remains the least defined. Commenting on the data in Table 6, the similarity of some wings of this group to the phenotype of group No. 2.2 was noted. It should be mentioned that group No. 3.2 includes wings of drones from apiaries in the Zhytomyr and Sumy regions. Perhaps, this is the phenotype that beekeepers attribute to the "Ukrainian steppe bees" population of the *A. m. macedonica* subspecies; however, its subspecies affiliation still needs to be confirmed through genetic studies.

The presented results, along with the previously established similarity between individual wing groups of worker bees from different parts of Ukraine (Galatiuk et al., 2022), allow us to conclude that there are at least two populations of bees in the specified territory with clearly defined phenotypes of drone wings. These populations can be attributed to local populations of Ukrainian bees. This also provides grounds to assert that the haploid chromosomal sets of drones in both populations are similar in the part corresponding to the wing phenotype. The wing phenotype in this study is defined as the set of values for the eight external characteristics mentioned above.

Out of the 4640 wings obtained at the initial stage of the study, 1666 wings (36%) were involved in forming three wing groups. From the remaining 2980 wings, only 735 were sufficiently similar in phenotype to the formed groups but were intentionally not included in any group due to the small number of wings in clusters (<24). Among the other 2245 wings, approximately 50% had moderate similarity in phenotype to one of the three groups. However, individual characteristics showed significant differences from the mean group values, leading to a C_V imbalance (>20%). This was the reason for not using them to form groups. The clusters of the remaining 50% of wings were significantly different in phenotype from the three formed groups. Attempts to create additional groups based on them were unsuccessful due to a small representation (<=3 clusters per group) or insufficient similarity in the phenotypes of clusters within groups, controlled by C_V values <20% for seven characteristics. The presence of wings significantly different in phenotype from the three obtained standards may indicate considerable variability in the genomes of drones, and consequently, queens, or the presence of genomes of other subspecies, accounting for approximately 38% of the studied wings.

The representation of the *A. m. carnica* subspecies wing phenotypes was recorded on all studied apiaries. The highest number of wings classified as *A. m. carnica* subspecies was identified on O. Kalashnykov apiary in Kharkiv, as well as on O. Galatiuk apiary. It should be noted that a significant number of samples from O. Galatiuk apiary were intentionally taken from bee colonies with queens purchased in Zakarpattia for scientific purposes. A considerable number of drone wings classified as populations of Ukrainian bees were found in L. Egoshin and O. Galatiuk apiaries. However, we cannot currently assess the ratio between the phenotypes characteristic of the three obtained wing groups on individual apiaries. To do this, a detailed study of each apiary separately is necessary, with the examination of a much larger number of bee colonies. After obtaining reference data based on the results of this study, such a task is entirely realistic and does not require a significant number of drone wings, as in the case (approximately 100 each from each bee colony) when we were just starting our research.

As a result of our research, the fact of queens producing drones with significant anomalies in wing venation, which typically constitute about

5% of the total number, has been confirmed. This often led to the exclusion of such wings from consideration. For individual queens, the number of unsatisfactory wings reached 20%. Considering this, it can be anticipated that a significant number of wings contain deviations that experimenters may not notice but could affect the results of morphometric studies. This provided the basis for Groeneveld et al. (2020) to argue against the practicality of using drone wings for taxonomic analysis of bees. However, summarizing the discussion, we can assert that morphometry of drone wings can reliably and credibly form arrays of reference data and determine the taxonomic affiliation of bees, despite significant variability in wing venation. Therefore, the authors' use of 100 or more wings from each queen helps mitigate errors and inaccuracies that could arise due to poor wing venation in drones. Considering this, for the improvement of breeding work in beekeeping apiaries in Ukraine, it is advisable to conduct drone wing morphometry to control the purebredness of maternal and parental colonies.

Conclusions

The comparative analysis of drone wing phenotypes based on eight morphometric characteristics for four regions of Ukraine allowed the formation of three significantly different datasets that can be used as phenotypic wing reference standards: one for the local population of the subspecies *A. m. carnica* and the other two for regional standards of local populations of Ukrainian steppe bees.

The use of drone wing standards allows a quick and reliable identification of phenotypes in local bee populations and provides preliminary information about the approximate composition of drone and queen genomes. The high similarity in the phenotypes of drone wings between the Carpathian region and the Kharkiv, Sumy, Poltava, and Zhytomyr regions suggests their common origin and distribution. The significant influence of the subspecies *A. m. caucasica* on the phenotype of drone wings in one of the two populations of Ukrainian bees suggests a probable hybridization of genomes in the part responsible for the wing phenotype.

The authors express their gratitude to beekeepers O. Kalashnykov and L. Hryhorkiv for providing samples of drone wings, which contributed to the expansion of the study and the significance of the obtained results.

The authors declare no conflicts of interest.

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