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Original article

The matter of sampling distance and confidence levels in the subspecific classification of honeybees, *Apis mellifera* L.

Sarah E. Radloff[a]*, Howard Randall Hepburn[b]

[a] Department of Statistics, Rhodes University, Grahamstown, South Africa
[b] Department of Zoology and Entomology, Rhodes University, Grahamstown, South Africa

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Abstract – The effects of variations in sampling distance and confidence levels on the subspecific classification of honeybees were analysed by subjecting colony means of morphometric characters to factor analysis and stepwise discriminant analysis procedures. Analyses of honeybees from a transect from Morocco through Spain and another from Tanzania through Sudan show that the greater the distance between samples, the more distinct the morphoclusters. The length of the transect may obscure small biometric groups if the between-group variation is considerably larger than the within-group variation. Varying the levels of confidence applied to the ellipses and the discriminant a posteriori probabilities from low to high decreased the number of colonies correctly assignable to morphoclusters. Thus, sampling distance, transect length, confidence levels and their a posteriori probabilities are all just as crucial to the structure and resolution of honeybees morphoclusters as are sample size and character suites. © Inra/DIB/AGIB/Elsevier, Paris

honeybee classification / sampling / confidence levels

1. INTRODUCTION

Contemporary classification of honeybees stems from multivariate methods of analysis as originally advanced by DuPraw [8, 9] and substantially developed by Ruttner [18]. This approach requires the control of several variables of which sample size and character suites have been well documented [7, 19]. However, there remains a degree of arbitrariness in the setting of confidence limits to define morphoclusters [6, 12, 13, 18]. That differing morphoclusters may be obtained by varying confidence limits is evi-

* Correspondence and reprints
E-mail: stsr@giraffe.ru.ac.za

dent in two groups of recent regional studies: the Iberian Peninsula [2, 11, 16, 18] and northwest Africa [4, 11, 15, 18]. It can also be inferred from these studies that morphocluster formation may also be sensitive to sampling distance. However, the effects of sampling distance and the confidence levels given to morphocluster ellipses and their discriminant a posteriori probabilities, on morphocluster formation of honeybees have not previously been assessed and this is the purpose of this report.

2. MATERIALS AND METHODS

Two transects, which had been previously studied, were chosen because they cut across areas in Africa where there are particular and biologically interesting uncertainties about population distribution and demarcation and/or hybridisation zones between adjacent populations. First, a transect from the western Sahara to the eastern Pyrenees, resulting in distinct morphoclusters, was selected. Worker honeybees were sampled from colonies of small fixed-site beekeepers at 13 different localities with an average distance between localities (mean sampling distance resolution) of approximately 155 km [11]. Ten morphometric characters used in the previous study [11] were measured. Their Ruttner [18] numbers are given in brackets as follows: length of cover hair on tergite 5 (1), length of proboscis (4), width and length of wax plate on sternite 3 (11) and (13), pigmentation of abdominal tergite 2 (32), scutellum (35) and scutellar plate (36), wing angles B4 (22), N23 (30), O26 and (31) (*table I*). Second, a transect from northern Tanzania in East Africa to northern Sudan in northeastern Africa, resulting in overlapping morphoclusters, was selected. The mean sampling distance resolution was approximately 164 km. Morphometric data from a previous study [17] and from the Institut für Bienenkunde (Ruttner collection, Oberursel, Germany) were combined. Measurements of six morphometric characters that were common to both databases were used in the analysis (*table I*).

The colony means of the morphometric characters were analysed using factor analysis and stepwise discriminant analysis procedures at different mean sampling distance resolutions (*table II*). Morphocluster ellipses were constructed at different levels of confidence, namely at the 90 and 95 % levels [1]. The number of correctly classified colonies in each morphocluster was investigated at different a posteriori probability levels.

3. RESULTS

3.1. Northwestern Africa to northeastern Spain transect (1 860 km)

The factor analysis using morphometric measurements from 73 colonies sampled at a mean distance resolution of approximately 155 km delineated three distinct clusters, the colonies from Tan Tan and S. Rabat forming one cluster (*Apis mellifera sahariensis*), those from Marrakech, Ez Zhiliga, Ksar-el-Kebir and Tetouan a second cluster (*A. m. intermissa*) and all the colonies of Spain forming the third cluster (*A. m. iberica*). A discriminant analysis using the means of the most discriminatory characters revealed 100 % correct classification of the colonies into the three established clusters. Confidence ellipses drawn at both the 90 and 95 % levels showed no overlap indicating that the clusters are distinct at both levels (*figure 1*). The a posteriori probabilities allocating each colony to a cluster were all equal to 1.0 except for one colony in cluster 1 with $P = 0.934$, one colony in cluster 2 with $P = 0.997$ and one colony in cluster 3 with $P = 0.980$. Hence if a 95 % level of confidence was used for the a posteriori probabilities, one colony from cluster 1 would have been unclassified.

The mean sampling distance resolution along this transect was then increased to approximately 310 km between localities. The factor analysis using 42 colonies again delineated three distinct clusters, the colonies from Tan Tan forming one cluster (*A. m. sahariensis*), those from Marrakech and Ksar-el-Kebir a second cluster (*A. m. intermissa*) and colonies from Alhaurin el Grande, Totana, Puerto de Sagunto and Montblanc forming the third cluster (*A. m. iberica*). The a posteriori probabilites were

Table I. Means and standard deviations of discriminant morphometric characters (measurements in mm, angles in degrees).

Transects and Countries	Locality	Morphometric characters (1)	(11)	(31)	(32)	(35)	(36)	(4)	(13)	(22)	(30)
1) Morocco	Tan Tan	0.19(0.01)	2.69(0.04)	34.2(1.1)	7.43(0.89)	3.17(0.77)	0.20(0.49)	6.06(0.08)	2.22(0.06)	103.9(3.4)	79.5(2.4)
	S. Rabat	0.19(0.02)	2.72(0.04)	34.3(1.2)	7.28(1.34)	2.37(1.17)	0.57(0.91)	6.08(0.06)	2.25(0.03)	108.4(2.6)	79.0(1.9)
	Marrakech	0.19(0.02)	2.68(0.04)	38.4(2.0)	2.50(1.11)	0.37(0.37)	0.22(0.29)	6.03(0.12)	2.21(0.05)	102.7(3.2)	75.9(2.1)
	Ez Zhiliga	0.25(0.02)	2.68(0.03)	33.8(2.6)	1.92(0.82)	0.14(0.21)	0.14(0.17)	6.27(0.10)	2.26(0.04)	110.8(3.6)	78.5(2.2)
	Ksar-el-Kebir	0.22(0.01)	2.78(0.02)	34.2(1.0)	1.37(0.38)	0.03(0.05)	0.18(0.26)	6.32(0.14)	2.34(0.03)	107.6(3.6)	74.6(2.2)
	Tetouan	0.26(0.01)	2.79(0.03)	33.4(1.7)	1.77(0.15)	0.03(0.06)	0.17(0.11)	6.53(0.02)	2.41(0.02)	104.9(2.2)	73.5(3.3)
Spain	Alhaurin el Grande	0.23(0.02)	2.94(0.04)	37.9(1.2)	1.18(0.19)	0.15(0.22)	0.28(0.23)	6.81(0.11)	2.50(0.02)	107.3(2.8)	82.1(4.5)
	Berja	0.27(0.03)	2.97(0.02)	37.3(1.4)	1.23(0.20)	0.55(0.24)	0.68(0.35)	6.63(0.09)	2.47(0.03)	108.7(2.9)	82.4(1.9)
	Totana	0.26(0.02)	2.94(0.02)	38.7(0.9)	1.20(0.09)	0.27(0.29)	0.33(0.25)	6.50(0.12)	2.47(0.04)	108.9(2.0)	80.8(2.4)
	Callosa d'Ensania	0.29(0.03)	2.96(0.04)	38.8(2.5)	1.32(0.43)	0.72(0.19)	1.17(0.34)	6.59(0.04)	2.50(0.02)	107.9(2.8)	80.9(2.3)
	Puerto de Sagunto	0.27(0.01)	2.97(0.04)	37.3(1.4)	1.32(0.17)	0.78(0.12)	1.25(0.21)	6.50(0.07)	2.51(0.01)	106.6(2.7)	81.7(1.7)
	Benicarlo	0.34(0.01)	2.92(0.01)	37.1(1.5)	1.26(0.31)	0.10(0.17)	0.06(0.09)	6.47(0.08)	2.50(0.03)	105.7(2.3)	82.6(2.1)
	Montblanc	0.38(0.03)	2.90(0.03)	38.0(1.6)	1.10(0.15)	0.12(0.12)	0.13(0.23)	6.44(0.05)	2.47(0.03)	108.4(2.1)	80.4(2.6)
2) Tanzania	Njiro-Arusha	0.23(0.02)	2.56(0.07)	37.7(1.7)	6.30(2.31)	4.92(1.95)	1.94(1.46)				
Kenya	Ngong and Nairobi	0.23(0.02)	2.52(0.05)	37.8(2.6)	6.31(1.56)	4.23(1.38)	1.65(1.07)				
	Lake Baringo	0.19	2.39	40.3	6.67	4.25	2.41				
	Kerio Valley	0.21	2.46	38.9	2.30	2.80	2.00				
Ethiopia	Mega	0.21(0.01)	2.54(0.07)	34.5(1.5)	6.21(2.05)	1.06(0.54)	1.42(0.64)				
	Agere Maryam	0.23(0.01)	2.54(0.01)	35.4(0.8)	1.36(2.35)	0.09(0.10)	0.39(0.68)				
	Shashemene	0.22(0.01)	2.62(0.02)	35.5(2.9)	2.15(1.40)	0.32(0.34)	0.18(0.31)				
	Addis Ababa	0.23(0.02)	2.62(0.05)	36.8(3.1)	0.99(0.56)	0.13(0.27)	0.16(0.31)				
	Debre Markos	0.22(0.01)	2.66(0.02)	34.9(1.1)	0.32(0.44)	0.10(0.14)	0.02(0.04)				
	Bahir Dar	0.19(0.01)	2.51(0.04)	35.0(1.8)	3.10(1.83)	1.13(0.86)	0.00(0.00)				
	Gonder	0.20(0.01)	2.67(0.05)	33.2(1.5)	3.67(2.74)	1.87(1.86)	0.02(0.04)				
	Adi Arkay	0.18(0.01)	2.55(0.06)	32.7(2.0)	6.90(0.71)	3.02(0.88)	0.03(0.04)				
Sudan	Wad Medani	0.18(0.03)	2.35(0.04)	35.7(3.7)	8.67(0.28)	6.98(1.03)	2.48(2.06)				
	Khartoum	0.18	2.45	36.2	8.55	6.65	0.50				
	Shendi	0.19	2.34	38.7	9.00	8.13	4.73				

Table II. Number of colonies sampled at each locality at different mean sampling distance resolutions.

Transects and Countries	Locality	Distance km[1]					
			155 km	310 km	465 km	620 km	775 km
1) Morocco	Tan Tan	273	6	6	6	6	6
	S. Rabat	176	6	–	–	–	–
	Marrakech	245	6	6	–	–	–
	Ez Zhiliga	190	5	–	5	–	–
	Ksar-el-Kebir	102	6	6	–	6	–
	Tetouan	143	3	–	–	–	3
Spain	Alhaurin el Grande	106	6	6	6	–	–
	Berja	153	6	–	–	–	–
	Totana	102	6	6	–	6	–
	Callosa d'Ensania	120	6	–	6	–	–
	Puerto de Sagunto	102	6	6	–	–	6
	Benicarlo	148	5	–	–	–	–
	Montblanc		6	6	6	6	–
	Total	1860	73	42	29	24	15
			164 km	328 km	492 km	656 km	820 km
2) Tanzania	Njiro-Arusha	222	21	21	21	21	21
Kenya	Ngong and Nairobi	222	16	–	–	–	–
	Lake Baringo	226	1	1	–	–	–
	Kerio Valley	169	1	–	1	–	–
Ethiopia	Mega	179	4	4	–	4	–
	Agere Maryam	173	5	–	–	–	5
	Shashemene	214	6	6	6	–	–
	Addis Ababa	141	8	–	–	–	–
	Debre Markos	141	5	5	–	5	–
	Bahir Dar	121	5	–	5	–	–
	Gonder	117	6	6	–	–	6
	Adi Arkay	101	5	–	–	–	–
Sudan	Wad Medani	141	3	3	3	3	–
	Khartoum	125	1	–	–	–	–
	Shendi		1	1	–	–	–
	Total	2292	88	47	36	33	32

[1] The value next to a locality is the distance to the locality immediately below it.

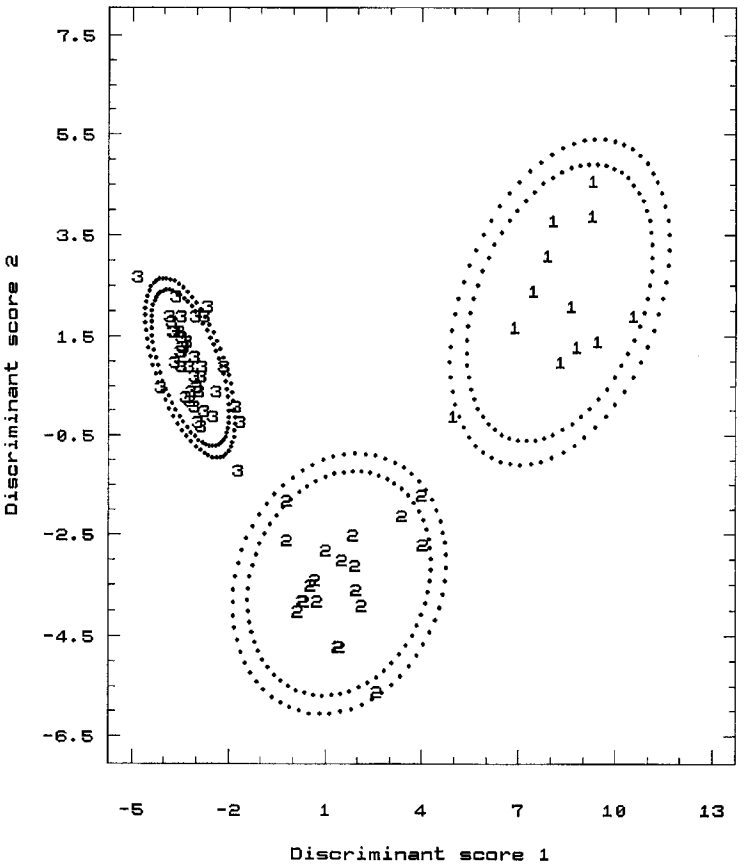

Figure 1. Discriminant analysis plot using a sampling distance resolution of 155 km along the transect from Morocco through Spain: cluster 1 comprises colonies from Tan Tan and S. Rabat, cluster 2 comprises colonies from Marrakech, Ez Zhiliga, Ksar-el-Kebir and Tetouan, cluster 3 comprises colonies from Alhaurin el Grande, Berja, Totana, Callosa d'Ensania, Puerto de Sagunto, Benicarlo and Montblanc. Confidence ellipses are at the 90 and 95 % levels.

in all cases equal to 1.0 except for two colonies from cluster 2, where $P = 0.999$.

When the mean sampling distance resolution between the localities was increased to approximately 465 km, the factor analysis using 29 colonies revealed the same three clusters except that the third cluster (*A. m. iberica*) was separated into two smaller groups. Colonies from Alhaurin el Grande formed one group and colonies from Callosa d'Ensania and Montblanc another. The a posteriori probabilities of assigning colonies to the three main clusters were, in all cases, equal to 1.0. Similar results were obtained when the mean sampling distance resolution between localities was increased to 620 km and then 775 km. A factor analysis showed three distinct morphoclusters in both cases. The a posteriori probabilities were all equal to 1.0.

A significant relationship was found between the eigenvalues obtained from the

first canonical variable and the mean sampling distance resolution ($r = 0.98$, $P = 0.0036$; *figure 2*). This result demonstrated that increasing the sampling distance increased the discimination among the morphoclusters.

A factor analysis carried out using the 41 colonies from Spain alone and a mean sampling distance resolution of approximately 155 km showed morphological differences amongst the localities. Three biometric groups were found, group 1 comprising colonies from Alhaurin el Grande, group 2 comprising colonies from Berja, Totana, Callosa d'Ensania and Puerto de Sagunto and group 3 comprising colonies from Benicarlo and Montblanc. A discriminant analysis confirmed these three biometric groups with 100 % correct classification results in each group except one group 2 colony being classified as group 3. Three a posteriori probabilities were between 0.90 and 0.95, two from group 2 and one from group 3. The percentages of classification would decrease to 88 % for group 2 and 91 % for group 3 if a 95 % level of confidence was used for the a posteriori probabilities. The separation of the three biometric groups from the *A. m.*

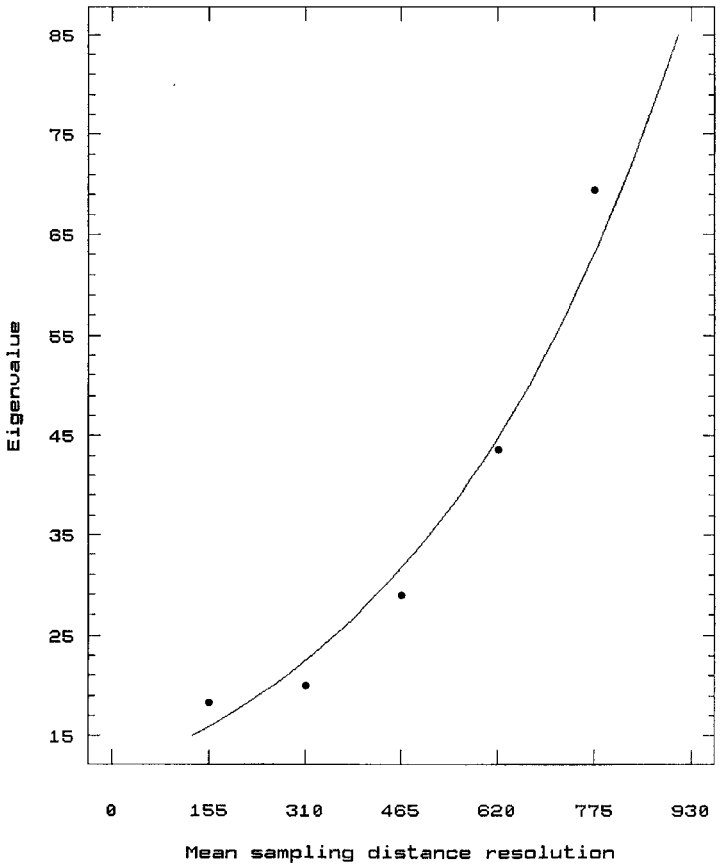

Figure 2. Relationship between the eigenvalues obtained from the first canonical variable and the mean sampling distance resolution for the northwestern Africa to northeastern Spain transect.

iberica cluster was not evident when all the colonies along the transect were analysed together. This is because the variation between the three distinct morphoclusters was larger than the within-cluster variations. Only when the colonies from Spain were analysed separately, were the three biometric groups detected.

When the 32 colonies from Morocco alone were analysed, the factor analysis revealed three clusters. Colonies from Tan Tan and S. Rabat formed cluster 1 (*A. m. sahariensis*), colonies from Marrakech and Ez Zhiliga the second cluster, and colonies from Ksar-el-Kebir and Tetouan the third cluster. One hundred per cent correct classification results were obtained for clusters 2 and 3, whilst one colony in cluster 1 was misclassified. A number of a posteriori probabilities of cluster 2 were not equal to 1.0, seven of the eleven colonies had probabilities equal to 1.0, two were between 0.75 and 0.90 and two between 0.65 and 0.70. This division of the *A. m. intermissa* cluster was not evident when the colonies from Spain were included in the analysis.

3.2. East Africa to northeastern Africa transect (2 292 km)

A factor analysis using 88 colonies delineated four morphoclusters, the colonies from Tanzania and Kenya forming one cluster (*A. m. scutellata*), those from southern (Mega, Agere Maryam) and central Ethiopia (Shashemene, Addis Ababa, Debre Markos) forming a second cluster, those from northern Ethiopia (Bahir Dar, Gonder, Adi Arkay) a third cluster and the colonies from Sudan a fourth cluster. Confidence ellipses drawn at both the 90 and 95 % levels showed overlapping of the clusters. A discriminant analysis resulted in 90 % (four misclassified), 93 % (two misclassified), 88 % (two misclassified) and 100 % correct classification for clusters 1, 2, 3 and 4, respectively. If the assigning of colonies to the various clusters was based on the a posteriori probabilities being greater than 0.90, then the percentages of classification would reduce to 46, 43 and 50 % for clusters 1, 2 and 3, respectively, and remain at 100 % for cluster 4.

The mean sampling distance resolution was increased to approximately 328 km between localities. The factor analysis using 47 colonies delineated only three clusters, the colonies from Njiro-Arusha and Lake Baringo forming one cluster, those from Mega, Shashemene, Debre Markos and Gonder a second cluster, and those from Wad Medani and Shendi a third cluster. The percentages of correct classification for the three clusters were 95.5 (one misclassified), 100 and 100 %, respectively. Using a 90 % level of confidence for the a posteriori probabilities would result in 77 (one misclassified, four unclassified), 100 and 100 % correct classification for the three clusters. Confidence ellipses drawn at the 95 % level showed overlapping of the morphoclusters whilst at the 75 % level the morphoclusters were distinct (*figure 3*).

Similar results were again obtained when the mean sampling distance resolution between localities was increased to approximately 492, 656 and then 820 km. Factor analyses showed three distinct clusters with 100 % correct classification in each cluster except that one colony from cluster 3 was misclassified into cluster 2. Again the level of confidence placed on the a posteriori probabilities of assigning colonies to the various clusters reduced the percentages of classification for clusters 1, 2 and 3. The relationship between the eigenvalues obtained from the first canonical variable and the mean sampling distance resolution was not significant ($r = 0.58$, $P = 0.3049$).

When the 39 colonies from Tanzania and Kenya alone were analysed, the factor analysis revealed no separation of the cluster into smaller biometric groups. Analysis of the colonies from Ethiopia only showed three biometric groups [17].

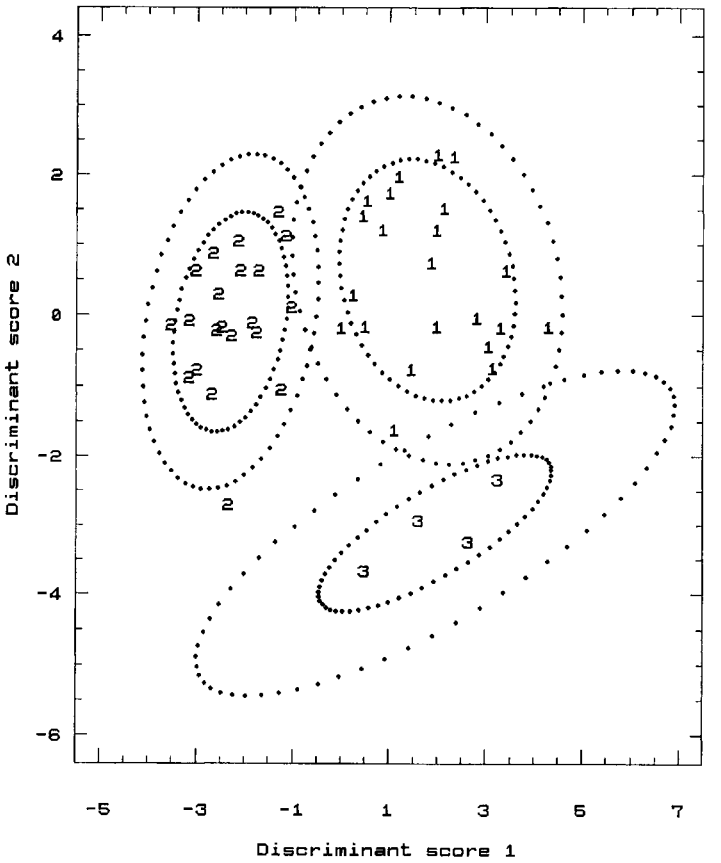

Figure 3. Discriminant analysis plot using a sampling distance resolution of 328 km along the transect from Tanzania through Sudan: cluster 1 comprises colonies from Njiro-Arusha and Lake Baringo, cluster 2 comprises colonies from Mega, Shashemene, Debre Markos and Gonder, cluster 3 comprises colonies from Wad Medani and Shendi. Confidence ellipses are at the 75 and 95 % levels.

4. DISCUSSION

Varying sampling distance along the transects examined had two pronounced effects on morphocluster formation. First, the greater the distance between samples, the more distinct the morphoclusters. Second, the length of the transect itself may obscure smaller biometric groups within a morphocluster when the between-group variation is considerably larger than the within-group variations. Varying the discriminant a posteriori probabilities from low (0.75) to high (0.90) decreased the number of colonies assignable to a specific morphocluster. Varying the level of confidence given to the confidence ellipses had the same effect as changing the discriminant a posteriori probabilities. The narrower the confidence ellipses (low confidence level) the less the overlapping of morphocluster ellipses.

These results demonstrate that sampling distance, transect length and operative confidence levels are crucial to the structure and resolution of honeybee morphoclusters. Sample size and character suites remain, of

course, of the utmost importance. The significance of the latter in morphocluster formation is especially well documented for the honeybees of northwest Africa [4, 11, 14, 18], the Iberian Peninsula [2, 10, 11, 16] and southern Africa [5, 18]. All of these variables individually contribute to the final statistical product that serves to morphometrically delineate subspecies of honeybees. While the multivariate analysis of morphometric characters is a robust and powerful adjunct to honeybee classification, it imposes important constraints that ultimately colour our perceptions as to the distinctiveness of natural honeybee populations.

The above analyses of the effects of distance and confidence levels on morphocluster formation readily explain the origins of the various discrepancies that emerge from a detailed comparison of the recent studies on the honeybees of northwestern Africa and the Iberian Peninsula cited in the Introduction. The situation for northeastern Africa is perhaps somewhat different. In this case, the decrease in the percentages of correct classification of colonies in a series of overlapping morphoclusters is greater than that seen in the Mediterranean region. This may result from the possibility that the African group of honeybee races are less distinct than those of Europe, an interpretation consistent with available data on allozymic and mitochondrial DNA differences among honeybee lineages [3, 20].

Whatever the sample size and character suite, sampling distance, confidence levels or transect length employed in population studies of honeybees, it remains inescapable that the classification of honeybee subspecies based on morphometric techniques alone will of necessity be arbitrary in nature until such time as the effective genetic populations and breeding systems of naturally occurring honeybee populations are more precisely defined. Whatever the methodological approach and statistical robustness, the results reported here are a common consequence of the spatial structure of natural populations. This being so, subspecific classification is of necessity an arbitrary set of operations because of the ways in which gene flow and microevolutionary processes lead to population differentiation.

Résumé – Influence de la distance d'échantillonnage et des niveaux de confiance sur la classification des sous-espèces d'abeilles mellifères, *Apis mellifera* L. La taille de l'échantillon et l'assemblage des caractères mesurés sont des variables fondamentales dans la classification morphométrique multivariée des sous-espèces d'abeilles mellifères. Des publications récentes sur les abeilles mellifères du nord-ouest de l'Afrique et de la péninsule Ibérique suggèrent que des variations dans la distance d'échantillonnage et dans les niveaux de confiance affecteraient la formation des morphogroupes (= sous-espèces). Nous avons examiné ces facteurs en analysant des abeilles mellifères le long de deux transects, l'un à travers le Maroc et l'Espagne, l'autre à travers le Soudan à partir de la Tanzanie. Les moyennes par colonie des caractères morphométriques *(tableau I)* ont été analysées à l'aide des procédures de l'analyse factorielle et de l'analyse discriminante pas à pas, à différentes distances moyennes d'échantillonnage *(tableau II)*. On a construit autour des morphogroupes des ellipses à différents niveaux de confiance, à partir desquelles le nombre de colonies classées correctement dans chaque morphogroupe était estimé à différents niveaux de signification à posteriori (*figures 1* et *3*). Les résultats des analyses des deux transects montrent que, lorsque la distance d'échantillonnage entre localités augmente graduellement, les morphogroupes sont plus distincts (*figure 2*). La longueur du transect peut aussi cacher des groupes biométriques plus petits à l'intérieur d'un morphogroupe, lorsque la variation entre groupes est plus grande que la variation au sein du groupe. Faire varier le niveau des limites de

confiance utilisées pour définir les ellipses a eu le même effet que de changer les probabilités discriminantes a posteriori. Plus le niveau de confiance est bas, moins les ellipses des morphogroupes se chevauchent (*figure 3*). Les résultats montrent que la distance d'échantillonnage, la longueur du transect, les niveaux de confiance et les probabilités a posteriori sont aussi importantes pour la structure et la définition des morphogroupes que ne le sont la taille de l'échantillon et l'ensemble des caractères. Ceci explique facilement les désaccords entre les études récentes (cf. Introduction) portant sur les abeilles mellifères du nord-ouest de l'Afrique, et de la péninsule Ibérique. Les résultats suggèrent également que les sous-espèces d'abeilles mellifères d'Afrique définies morphométriquement ne sont peut-être pas aussi distinctes les unes des autres que ne le sont celles d'Europe.

***Apis mellifera* / classification / échantillonnage / niveau de confiance**

Zusammenfassung – Der Einfluβ von Entfernung zwischen den Probenorten und von Vertrauensgrenzen auf die Klassifizierung der Unterarten der Honigbienen, *Apis mellifera*. Die multivariate morphometrische Klassifizierung der Unterarten der Honigbienen wird grundlegend durch die Größe der Proben und die Zusammenstellung der vermessenen Merkmale beeinflußt. Neuere Untersuchungen der Honigbienen des nordöstlichen Afrika und der iberischen Halbinsel legen nahe, daβ auch Änderungen der Entfernung zwischen den Probenorten oder der Vertrauensgrenzen die Berechnung von Morphoklustern (= Unterarten) mitbestimmen. Der Einfluβ dieser beiden Faktoren wurden anhand einer Analyse von Honigbienen entlang einer Schnittlinie durch Marokko und Spanien, sowie einer weiteren von Tansania durch den Sudan untersucht. Hierzu wurden Volksmittelwerte der morphometrischen Merkmale (*Tabelle I*) unter Verwendung von Faktorenanalysen und schrittweiser Diskriminanzanalysen bei unterschiedlichen mittleren Entfernungen zwischen den Probenorten untersucht (*Tabelle II*). Daraufhin wurden um die Morphokluster Ellipsen mit unterschiedlichen Vertrauensniveau berechnet, aus diesen wurde die Anzahl korrekt klassifizierter Völker in jedem Morphokluster bei unteschiedlichem a posteriori Signifikanzniveau ermittelt (*Abb. 1* und *Abb. 3*). Das Ergebnis zeigt für beide Schnittlinien, daβ schrittweise Vergrößerung der mittleren Sammeldistanz die Morphokluster deutlicher werden läβt (*Abb. 2*). Zudem kann die Länge der Schnittlinie kleinere biometrische Gruppen innerhalb eines Morphoklusters verdecken, falls die Variation zwischen den Gruppen größer ist als die innerhalb der Gruppen. Die Änderung des Signifikanzniveaus der Konfidenzellipsen hatte den gleichen Effekt wie die Änderung der a posteriori Wahrscheinlichkeitsgrenzen in der Diskriminanzanalyse. Je niedriger der Vertrauenslevel war, um so weniger überlappten die Ellypsen um die Morphokluster (*Abb 3*). Diese Ergebnisse zeigen, daβ die Entfernung zwischen den Probenorten, die Länge der Schnittlinien, die Vertrauensgrenzen und die a posteriori Wahrscheinlichkeiten ebenso stark auf die Struktur und Auflösung der Morphokluster bei den Honigbienen Einfluβ nehmen wie Probengröβe und Zusammenstellung der vermessenen Merkmale. Diese Befunde könnten Unterschiede zwischen den neueren Untersuchungen der Honigbienen des nordwestlichen Afrika und der Iberischen Halbinsel erklären. Die Ergebnisse legen zudem nahe, daβ die morphometrisch definierten afrikanischen Unterarten der Honigbienen weniger deutlich voneinander abgesetzt sind als die europäischen Unterarten.

Klassifikation von Honigbienen / Probenentfernung / Vertrauensgrenzen

REFERENCES

[1] Cornuet J.M., Représentation graphique de populations multinormales par des ellipses de confiance, Apidologie 13 (1982) 15–20.

[2] Cornuet J.M., Fresnaye J., Étude biométrique de colonies d'abeilles d'Espagne et du Portugal, Apidologie 20 (1989) 93–101.

[3] Cornuet J.M., Garnery L., Mitochondrial DNA variability in honeybees and its phylogeographic implications, Apidologie 22 (1991) 627–642.

[4] Cornuet J.M., Daoudi A., Mosshine E.H., Fresnaye J., Étude biométrique de populations d'abeilles Marocaine, Apidologie 19 (1988) 355–366.

[5] Crewe R.M., Hepburn H.R., Moritz R.F.A., Morphometric analysis of 2 southern African races of honeybee, Apidologie 25 (1994) 61–70.

[6] Daly H.V., A statistical and empirical evaluation of some morphometric variables of honey bee classification, in: Sorensen J.T., Footit R.J. (Eds.), Ordination in the Study of Morphology, Evolution and Systematics of Insects: Applications and Quantitative Genetic Rationals, Elsevier, Amsterdam, 1992, pp. 127–155.

[7] Daly H.V., Balling S.S., Identification of Africanized honeybees in the Western hemisphere by discriminant analysis, J. Kansas Entomol. Soc. 51 (1978) 857–869.

[8] DuPraw E.J., Non-Linnean taxonomy, Nature 202 (1964) 849–852.

[9] DuPraw E.J., Non-Linnean taxonomy and the systematics of honeybees, Syst. Zool. 14 (1965) 1–24.

[10] Goetze G.K.L., Die Honigbiene in natürlicher und künstlicher Zuchtauslese. Teil I, II, Parey, Hamburg, 1964.

[11] Hepburn H.R., Radloff S.E., Morphometric and pheromonal analyses of *Apis mellifera* L. along a transect from the Sahara to the Pyrenees, Apidologie 27 (1996) 35–45.

[12] Hepburn H.R., Radloff S.E., Honeybees of Africa, Springer-Verlag, Berlin, 1998.

[13] Kauhausen-Keller D., Ruttner F., Keller R., Morphometric studies on the microtaxonomy of the species *Apis mellifera* L., Apidologie 28 (1997) 295–307.

[14] Kerr W.E., Abejas Africanas su introduccion y expansion en el continente Americano. Subespecies y ecotipas Africanos, Indust. Apic. 13 (1992) 12–21.

[15] Lebdi-Grissa K., M'Sadda K., Cornuet J.M., Fresnaye J., Relations phylogénétiques de l'abeille tunisienne *A. m. intermissa* avec les races d'abeilles voisines africaines et ouest méditerranéennes, Rev. Agric. 44 (1991) 1231–1238.

[16] Orantes-Bermejo F.J., Garcia-Fernandez P., Morphological variability of *Apis mellifera iberica* in different apiaries of southern Spain, J. Apic. Res. 34 (1995) 23–30.

[17] Radloff S.E., Hepburn H.R., Multivariate analysis of honeybees, *Apis mellifera* Linnaeus (Hymenoptera: Apidae), of the Horn of Africa, Afr. Entomol. 5 (1997) 57–64.

[18] Ruttner F., Biogeography and Taxonomy of Honeybees, Springer-Verlag, Berlin, 1988.

[19] Ruttner F., Tassencourt L., Louveaux J., Biometrical-statistical analysis of the geographic variability of *Apis mellifera* L., Apidologie 9 (1978) 363–381.

[20] Smith D.R., Mitochondrial DNA and honeybee biogeography, in: Smith D.R. (Ed.), Diversity in the Genus *Apis*, Westview, Boulder, Colorado, 1991, pp. 131–176.