Apidologie 29 (1998) 481–490

Original article

A morphological and mitochondrial assessment of *Apis mellifera* from Palermo, Italy

Angela Sinacori[a], Thomas E. Rinderer[b]*, Vicki Lancaster[c], Walter S. Sheppard[d]

[a] Istituto di Entomologia Agraria, Università di Palermo, Palermo, Italy
[b] USDA-ARS, Honey-Bee Breeding, Genetics and Physiology Laboratory, 1157 Ben Hur Road, Baton Rouge, LA 70820-5502, USA
[c] Department of Statistics, Kansas State University, 101 Dickens Hall, Manhattan, KS 66502, USA
[d] Department of Entomology, Washington State University, 166 FSHN Bldg, Pullman, WA 99164-6382, USA

(Received 10 November 1997; accepted 7 October 1998)

Abstract – A characterization of the honey bees from western Sicily (Palermo, Italy) is presented. Morphological comparisons to *A. m. ligustica* were made using data taken from honey bee populations from southeastern (Bari) and central (Emilia Romagna) Italy. The honey bees of the Palermo area have distinct morphological differences compared to the mainland honey bees. The mtDNA haplotype common in subspecies within the African lineage of *A. mellifera* predominated in the Sicilian honey bee samples (13 out of 16). These results suggest both the potential and the desirability to expend efforts to conserve *A. m. sicula.* © Inra/DIB/AGIB/Elsevier, Paris

***Apis mellifera sicula* / *Apis mellifera ligustica* / morphology / mitochondrial DNA / Sicily / Italy / germplasm conservation**

* Correspondence and reprints
E-mail: trindere@asrr.arsusda.gov
With the technical collaboration of Rita Riggio (Department of Entomology, Louisiana State University) and J. Anthony Stelzer (USDA-ARS, Honey-Bee Breeding)

1. INTRODUCTION

The honey bees of Italy are well known. *Apis mellifera ligustica* Spinola has been imported to much of the apicultural world because of its handling and honey production characteristics. The ecotype 'standard' for *A. m. ligustica* is from northern Italy in the 'Liguria' area near Genoa [1]. However, *A. m. ligustica* may range in various ecotypes throughout the Italian peninsula [14]. The characterization of the ecotype found in the province of Bari (southern Italy) is particularly important since this population may have developed resistance to *Varroa jacobsoni* in suburban and urban regions isolated from organized beekeeping [10].

The honey bees of Sicily are equally interesting for different reasons. Although the island of Sicily is close to the mainland, the local honey bee has been recognized since 1911 as a distinct subspecies, *A. m. sicula* Montagano [11]. Aside from morphological distinctiveness, *A. m. sicula* is notable for its behavioral characteristics [14]. Swarm cell production is very high, colonies do not swarm until after virgins have hatched, and colonies do not fly during the hot part of the day when the predator *Vespa orientalis* is most active [14]. The status of *A. m. sicula* has been threatened by importations of *A. m. ligustica* from mainland Italy that began in the last century and have expanded within the past 20 years, especially in eastern Sicily [3–5]. Ruttner [14] reported the morphology of *A. m. sicula* collected from Sicily prior to the modern commercial trend to import *A. m. ligustica.* Hence, baseline data exist to compare the effects of importations and to guide conservation efforts.

This report presents a characterization of the honey bees from western Sicily (Palermo, Italy). Mitochondrial DNA restriction fragment length polymorphism characteristics and a standard set of morphometric measurements are used for these characterizations.

2. MATERIALS AND METHODS

Sixteen colony samples from the apiary of the University of Palermo were collected and stored in ethanol or liquid nitrogen pending analysis. These colonies originated from swarms collected from various Sicilian locations believed to be relatively free of introduced *A. m. ligustica.*

Ten workers from each colony were dissected and 36 morphological measurements were made. These measurements and their alphabetical designations given in *table I* follow the methods and designations of Rinderer et al. [13]. Figures 1 and 2 of Rinderer et al. [13] illustrate the wing venation angles and the locations of various structures for which pigmentation was evaluated. The methods follow those of Rinderer et al. [13] and are a modified combination of those of Ruttner et al. [15], Ruttner [14] and Daly and Balling [6]. Numerical designations for wing angles in *table I* follow the synthesis of Rinderer et al. [13]. For the most part, numbers represent lengths or widths of various structures and are reported in millimeters. Interior angles of vein intersections in wing venation patterns are reported in degrees. Pigmentation characteristics of the second, third and fourth tergites are scored according to the procedures of Ruttner et al. [13] and Ruttner [14]. Scores represent the proportion of comparatively light areas to the total area of the tergite. Scores for the color intensity of the scutellum (Sc) range from 0 to 9, with 0 being completely black. A scale ranging from 0 to 5 was employed for the metatergum (B) and mesotergum (K); completely black being equal to 0, and completely yellow being equal to 5.

Forty-seven morphological comparisons to *A. m. ligustica* were made using data taken from honey bee populations from southeastern (Bari) Italy (*table I*). Forty-one measurements provided interval data, and six provided ordinal data. The mean of ten bees was calculated for each colony and these means were used to calculate descriptive and inferential statistics. Student's *t*-tests were used to test the null hypothesis that the means from the two sources were equal. Since that by chance alone one would expect at least two significant test results ($P \leq 0.05$), to maintain an overall experiment-wise significance level of 0.05, a Bonferroni-type adjustment was made whereby individual tests must have a significance level of ≤ 0.001.

In addition, 11 statistical comparisons (*table IV*) of morphological data were made

Table I. Descriptive and inferential statistics for the mean of ten bees per colony from ten colonies of *Apis mellifera ligustica* from Bari, Italy and 16 colonies of *Apis mellifera sicula* from Palermo, Italy.

Character	*A. m. ligustica*			*A. m. sicula*			Comparative statistics	
	Mean	S.D.	Min./ Max.	Mean	S.D.	Min./ Max.	*t*-value	*P*
Forewing length (F_L)	9.193	0.07	9.093 / 9.300	9.005	0.12	8.799 / 9.204	4.458	0.00
Forewing width (F_B)	3.222	0.02	3.207 / 3.254	3.124	0.08	2.998 / 3.263	3.952	0.001
Hindwing length (HW_L)	4.323	0.05	4.213 / 4.394	4.238	0.06	4.113 / 4.331	3.793	0.001
Hindwing width (HW_W)	1.89	0.02	1.864 / 1.927	1.812	0.06	1.697 / 1.931	3.696	0.001
Hamuli Number	21.59	0.84	20.1 / 22.6	22.71	1.08	20.9 / 24.4	2.797	0.010
Angle 20	13.3	0.76	12.4 / 14.6	14.1	0.53	12.9 / 14.9	–3.028	0.006
Angle 29	30.5	0.82	29.27 / 31.71	29.5	0.76	28.5 / 30.95	–3.175	0.004
Angle 30	109	2.97	102.4 / 113	109.5	3.55	102.9 / 116.3	–0.365	0.718
Angle 31	97.57	1.38	95.3 / 100.6	99.31	2.01	96.3 / 103.4	–2.401	0.024
Angle 32	23.97	1.19	21.94 / 25.46	22.00	1.12	20.61 / 23.96	4.266	0.00
Angle 33	91.65	1.29	89.99 / 93.84	92.83	2.14	88.82 / 96.85	–1.568	0.130
Angle 34	052.91	1.63	50.40 / 56.82	50.61	2.10	46.15 / 53.82	2.939	0.007
Angle 35	24.51	0.88	23.23 / 25.99	22.96	0.83	21.32 / 24.16	4.529	0.00
Angle 36	63.85	1.33	61.55 / 65.27	63.03	1.85	59.11 / 66.16	1.218	0.235
Angle 38	93.05	1.95	89.23 / 95.41	94.44	1.67	91.72 / 97.89	–1.948	0.063
Angle 39	43.37	1.12	41.48 / 44.49	42.26	1.85	39.45 / 44.84	1.701	0.102
Angle 40	34.00	1.19	31.86 / 35.87	35.59	2.34	31.91 / 39.09	–1.977	0.059
Angle 42	110.8	0.90	108.8 / 112.1	112.0	1.47	109.7 /114.6	–2.374	0.026
Angle 43	77.74	1.93	74.6 / 81.28	78.26	1.58	75.34 / 81.17	–0.236	0.462
Cubital vein A length (a)	0.581	0.03	0.544 / 0.634	0.551	0.03	0.508 / 0.603	2.837	0.009
Cubital vein B length (b)	0.23	0.01	0.213 / 0.254	0.225	0.01	0.205 / 0.249	0.281	0.380
Length of tibia (T_i)	3.157	0.04	3.113 / 3.215	3.199	0.04	3.13 / 3.266	–2.759	0.011
Length of femur (F_e)	2.633	0.02	2.599 / 2.662	2.647	0.03	2.588 / 2.706	–1.302	0.205

Table I. Continued.

Character	*A. m. ligustica*			*A. m. sicula*			Comparative statistics	
	Mean	S.D.	Min./ Max.	Mean	S.D.	Min./ Max.	*t*-value	*P*
Length of metatarsus (M_L)	2.039	0.03	2.002 / 2.105	2.045	0.02	2.011 /2.095	–0.550	0.588
Width of metatarsus (M_W)	1.119	0.01	1.105 / 1.142	1.126	0.02	1.095 / 1.179	0.72	0.405
Longitudinal distance of sternite 3 (S_3)	2.787	0.04	2.745 / 2.840	2.751	0.05	2.660/ 2.838	1.961	0.062
Longitudinal distance of wax mirror (W_L)	1.332	0.04	1.293 / 1.428	1.335	0.04	1.247 / 1.413	–0.141	0.889
Transversal distance of wax mirror (W_T)	2.397	0.05	2.320 / 2.482	2.344	0.06	2.260 / 2.449	2.473	0.021
Distance between wax mirrors (W_D)	0.263	0.02	0.226 / 0.309	0.271	0.03	0.204 / 0.309	–0.669	0.516
Length of the postmentum of the proboscis (P_M)	0.528	0.01	0.511 / 0.545	0.501	0.02	0.475 / 0.524	4.380	0.00
Length of the glossa of the proboscis (G_l)	5.769	0.06	5.650 / 5.869	5.748	0.10	5.554 / 5.863	0.606	0.550
Length of the left proximal segment of the proboscis	1.539	0.03	1.483 / 1.584	1.521	0.04	1.465 / 1.598	1.307	0.203
Length of the left distal segment of the proboscis	0.584	0.01	0.568 / 0.604	0.589	0.02	0.557 / 0.617	–0.771	0.448
Length of the right proximal segment of the proboscis	1.544	0.03	1.496 / 1.596	1.523	0.03	1.472 / 1.575	1.635	0.115
Length of the right distal segment of the proboscis	0.580	0.01	0.560 / 0.603	0.585	0.02	0.554 / 0.635	–0.571	0.573
Longitudinal diameter of tergite 3	2.212	0.03	2.189 / 2.278	2.207	0.04	2.127 / 2.256	0.396	0.695
longitudinal diameter of tergite 4	2.187	0.03	2.155 / 2.249	2.161	0.04	2.072 / 2.218	1.831	0.079
Width of tomentum A on tergite 4	0.272	0.03	0.231 / 0.309	0.297	0.05	0.158 / 0.390	–1.446	0.161
Width of tomentum B on tergite 4	1.571	0.05	1.483 / 1.661	1.526	0.09	1.407 / 1.787	1.384	0.179
Longitudinal distance of sternite 6	2.570	0.03	2.519 / 2.620	2.537	0.04	2.461 / 2.598	2.183	0.039
Transverse distance of sternite 6	3.04	0.05	2.981 / 3.112	3.027	0.07	2.920 / 3.152	0.587	0.563
Pigmentation of tergite 2	8.86	0.15	8.6 / 9.0	7.225	1.41	3.7 / 8.8	3.626	0.001
Pigmentation of tergite 3	8.32	0.66	6.8 / 8.9	6.88	1.19	4.1 / 8.4	3.493	0.002
Pigmentation of tergite 4	5.27	0.54	4.6 / 6.0	4.88	0.76	3.3 / 5.8	1.406	0.172
Pigmentation of the cupola of the scutellum (S)	4.72	1.50	3.0 / 8.0	4.28	2.48	0.8 / 8.5	0.502	0.619
Pigmentation of the metanotum of the scutellum (K)	0.05	0.13	0 / 0.4	0.025	0.08	0.006 0/0.3	0.627	0.537
Pigmentation of the mesonotum of the scutellum (B)	0.02	0.06	0 / 0.2	0.913	0.50	0.25 0/1.7	–5.540	0.00

Table II. Classification results of a linear discriminant analysis. Two hundred and sixty individual honey bees each were classified according to discriminant functions derived from an analysis of the other honey bees in the analysis.

Collected as	Classified as	
	A. m. sicula	*A. m. ligustica* from Bari
A. m. sicula	154	6
A. m. ligustica from Bari	1	99

Table III. Mitochondrial haplotypes of ten colonies of *Apis mellifera ligustica* from Bari, Italy and 16 colonies of *Apis mellifera sicula* from Palermo, Italy. Mitochondrial haplotype classifications are based on *Eco*R 1 RFLP patterns [9, 19].

Subspecies	Mitochondrial haplotype		
	African	mellifera	carnica/ligustica
A. m. sicula	13	3	0
A. m. ligustica	0	10	0

between our collection of honey bees from Sicily and the collection of *A. m. sicula* reported by Ruttner [14]. These comparisons (*table V*) were also made between our collection of honey bees from Bari and the collection of *A. m. ligustica* reported by Ruttner [14]. An F-test for variance equality was performed prior to making between group comparisons for the equality of means. When the variance test gave a significant result ($P \leq 0.05$), an adjusted *t*-test was performed based on an adjustment made to the number of degrees of freedom associated with the *t* statistic [12].

A linear discriminant analysis was carried out using the individual bees and the 41 interval scale measurements. Although individual bees are more likely to be misclassified than the mean of ten bees from a colony, individual bees were used to increase the number of observations. The six ordinal scale measurements were not used since they did not meet the assumption of normality.

Total nucleic acids were extracted from one individual worker from each colony following the method of Sheppard and McPheron [17]. Extracted DNA was digested with the restriction enzyme *Eco*R I according to the manufacturer's instructions. Digestion products were processed by electrophoresis on 1 % agarose gels and the mtDNA fragments were visualized using ethidium bromide following the procedures of Sheppard et al. [18] and Shiff and Sheppard [16]. Gels were photographed for documentation. Classification of mitochondrial DNA haplotypes was either 'African' 'mellifera' or 'carnica/ligustica' according to the procedures of several authors [9, 16, 18, 19].

3. RESULTS

3.1. Morphology

The honey bees of the Palermo area have distinct morphological differences compared to honey bees of mainland Italy (*table I*). Linear wing measurements are all significantly smaller for the honey bees of Sicily. Some wing venation angles are strongly different, and the cubital vein A length is somewhat larger ($P = 0.009$) in the Sicilian honey bees. In contrast, the linear measurements of leg parts are not significantly different between the groups. Indeed, each of the four leg part measurements are slightly larger

for the Sicilian honey bees. The length of the postmentum of the proboscis is distinctly shorter in the Sicilian honey bees. However, the other five mouth part measurements are quite similar between the two honey bee stocks. The six tergite and sternite measurements indicate that the general body size of the two groups of bees is quite similar. The areas of pigmentation on tergites are generally greater or much greater for the Sicilian honey bees, corresponding to the general impression that they are darker bees. However, scutellum colorations are similar. Overall, the two groups of bees are clearly distinct. The linear discriminant analysis correctly classified 253 of the 260 individual bees, thus providing a probability of correctly being classified of 0.97 (*table II*).

Morphologically, the honey bees of Bari are similar to Ruttner's [14] descriptions of *A. m. ligustica* (*table V*) and the honey bees of Palermo are similar to Ruttner's [14] description of *A. m. sicula* (*table IV*). However, statistical comparisons within the two groups provide a few significant differences. Angle G18 is smaller and the color of tergite three is lighter for our collections in comparison to Ruttner's measurements. Also, the hind leg length is shorter for the honey bees of Bari in comparison to Ruttner's *A. m. ligustica.*

3.2. Mitochondria

The mtDNA haplotype common in subspecies within the African lineage of *A. mellifera* [7] predominated in the Sicilian honey bee samples (13 out of 16). Three of the 16 had an *Eco*R I pattern generally associated with *A. m. mellifera* [14], but also known from *A. m. ligustica* from the Bari region of southeastern Italy [2; Arias et al. unpublished data].

4. DISCUSSION

The population of honey bees we studied in Sicily retains a majority of the characteristics of *A. m. sicula.* However, the presence of a mitochondrial haplotype common in mainland Europe may reflect genetic pressure from introduced *A. m. ligustica.* If so, the introduced bees may have been similar to those of Bari or other regions having the 'mellifera' haplotype. Alternatively, the persistence of this particular mitochondrial pattern in southeastern Italy (Arias et al. unpublished data) and its presence in *A. m. sicula* raises the possibility that it was established in one or both of the subspecies before human-mediated honey bee movements. Assessment of the phylogeographic distribution of this particular mitochondrial haplotype in Italy may resolve this question.

The color shift to lighter bees in the Sicilian collection may be an artifact of differences in methodology between our study and Ruttner's [14] study since a similar shift was seen in the comparison of our Bari collection of *A. m. ligustica* and Ruttner's collection of *A. m. ligustica.* However, the difference for the Sicilian honey bees is 2.3 fold, much more than the 1.2 fold difference seen in the comparison of *A. m. ligustica* ecotypes. This stronger difference seen between the two collections of honey bees from Sicily might in part arise from the intrusion of genes from importations of non-*A. m. sicula* stock.

These results suggest both the potential and the desirability to expend efforts to conserve *A. m. sicula.* This subspecies has unique adaptations to the Sicilian environment, and may be critical as a pollinator of some of the region's flora. In addition, the unique evolutionary history of *A. m. sicula* is cause to consider the subspecies as a valuable genetic resource that could be utilized in future honey bee breeding efforts.

Previous research based on mtDNA restriction fragments [8] and mtDNA ND2 gene sequences [2] has suggested a phylogenetic association between *A. m. sicula* and honey bees of Africa and southern Spain. The predominance of the 'African' mtDNA RFLP pattern in our samples of *A. m. sic-*

Table IV. A comparison of morphometric characteristics of honey bees from Sicily representing *Apis mellifera sicula* provided by Ruttner [14] and our 1996 collection of honey bees from Palermo.

Morphometric characteristic	Ruttner [14] (n = 10)		This collection (n = 16)		Statistical comparison		
	Mean	Variance	Mean	Variance	t-test	df	P
Proboscis length	6.234	0.066	6.249	0.010	0.059	11*	0.477
Hind leg length	7.951	0.051	7.892	0.006	0.799	10*	0.222
T3 + 4	4.376	0.019	4.368	0.005	0.172	12*	0.433
Forewing length	8.976	0.158	9.005	0.015	–0.525	24	0.302
Cubital index	2.467	0.176	2.456	0.038	0.078	11*	0.470
Sternite 6 index	82.80	12.320	83.830	1.824	–0.888	11*	0.197
Angle E9	21.29	14.440	22.000	1.261	–0.575	10*	0.289
Angle G18	97.34	14.440	92.830	4.601	3.427	13*	0.002
Angle I10	50.54	16.16	50.610	4.410	0.051	12*	0.480
Angle L13	14.54	1.638	14.08	0.572	1.030	13*	0.161
Color of tergite 3	2.94	1.464	6.881	1.408	–8.178	24	0

* Indicates a test for equal variances at a P value of ≤ 0.05 was rejected. For these cases, a t-test for equality of means performed done using a Satherthwait approximation [12] which adjusts the degrees of freedom.

Table V. A comparison of morphometric characteristics of honey bees from Italy representing *Apis mellifera ligustica* provided by Ruttner [14] and our 1996 collection of honey bees from Bari.

Morphometric characteristic	Ruttner [14] (n = 35)		This collection (n = 10)		Statistical comparison		
	Mean	Variance	Mean	Variance	t-test	df	P
Proboscis length	6.359	0.016	6.297	0.005	2.004	27*	0.0276
Hind leg length	7.969	0.031	7.830	0.008	3.385	30*	0.001
T3 + 4	4.348	0.022	4.399	0.003	–1.674	40*	0.051
Forewing length	9.208	0.031	9.193	0.004	0.418	40*	0.339
Cubital index	2.551	0.168	2.540	0.037	0.119	33*	0.453
Sternite 6 index	83.480	10.956	84.482	1.189	–1.525	42*	0.067
Angle E9	23.49	3.684	23.970	1.410	–0.751	43	0.228
Angle G18	93.460	7.508	91.650	1.656	2.936	33*	0.003
Angle I10	52.130	9.302	52.91	1.627	–1.192	37*	0.120
Angle L13	13.570	2.220	13.310	0.572	0.749	30*	0.230
Color of tergite 3	7.140	1.562	8.55	0.437	–4.744	29*	0

* Indicates a test for equal variances at a P value of ≤ 0.05 was rejected. For these cases, a t-test for equality of means was performed using a Satherthwait approximation [12] which adjusts the degrees of freedom.

ula supports this hypothesis and also indicates that the honey bees of western Sicily remain relatively free from *A. m. ligustica* matrilines. Allozyme analysis of Sicilian honey bees also found that western populations were relatively free from genetic influence by *A. m. ligustica* [3].

There is continuing importation of honey bees from the mainland and we have detected some evidence that these importations have had a genetic effect. However, in addition to isolated locales in western Sicily, additional beekeepers on outlying islands are thought to have *A. m. sicula* not influenced by importation (Sinacori, unpublished data). The National List of Queen Bee Breeders includes a section for *A. m. sicula.* This program represents an effort to preserve this subspecies. Ongoing breeding could be enhanced with timely conservation efforts establishing refugia for *A. m. sicula* on one or more of these islands, even with selected colonies from the population we studied. Refugia populations would serve as source for genetic material for outcrossing to selected stock. The use of multiple refugia would help reduce inbreeding problems in the breeding programs.

ACKNOWLEDGMENTS

We thank Cristina Arias, Raphael Monaco and Antonio Nanetti for collections of honey bees. This study was in cooperation with the Louisiana Agricultural Experiment Station.

Résumé – Caractérisation morphologique et mitochondriale d'*Apis mellifera* de Palerme, Italie. Bien que la Sicile soit une île proche du continent, l'abeille locale a été reconnue dès 1911 comme une sous-espèce distincte, *Apis mellifera sicula* Montagano [11]. Outre ses caractères morphologiques distinctifs, *A. m. sicula* est remarquable par son comportement [14]. Ruttner [14] a décrit la morphologie d'abeilles *A. m. sicula* prélevées en Sicile avant la tendance commerciale moderne à importer *A. m. ligustica*. Les données de bases existent donc. En comparant avec la situation présente il est par conséquent possible de connaître l'influence des importations et d'orienter les efforts pour la conservation de cette race. Ce travail présente une caractérisation des abeilles de Sicile occidentale (Palerme). Pour cela on a utilisé les caractéristiques du polymorphisme de longueur de fragments de restriction de l'ADN mitochondrial (ADNmt), ainsi qu'un ensemble standard de mesures morphologiques.

Des échantillons ont été prélevés dans 16 colonies du rucher de l'Université de Palerme et conservés dans l'éthanol ou l'azote liquide en attente des analyses. Dix ouvrières de chaque colonie ont été disséquées et les mesures de 36 caractères morphologiques ont été prises. Les mesures et leur dénomination alphabétique données dans le *tableau I* suivent les méthodes et dénominations de Rinderer et al. [13]. Les mesures ont été comparées à celles de collections similaires à Bari et aux descriptions morphologiques publiées pour *A. m. sicula* et *A. m. ligustica* [14]. D'un point de vue morphologique, les abeilles de Bari et d'Italie centrale sont semblables aux descriptions d'*A. m. ligustica* faites par Ruttner [14] (*tableau III*) et les abeilles de Palerme à celles d'*A. m. sicula* faites par le même auteur [14] (*tableau IV*).

Dans chaque colonie on a prélevé une ouvrière dont on a extrait les acides nucléiques totaux selon la méthode de Sheppard et McPheron [17]. L'ADN extrait a été digéré avec l'enzyme de restriction *Eco*R I et classé selon les méthodes de Sheppard et al. [18] et de Shiff et Sheppard [16]. L'haplotype d'ADNmt commun dans les sous-espèces de la lignée africaine d'*A. mellifera* [8] prédomine dans les échantillons d'abeilles siciliennes (13 sur 16).

Les principales caractéristiques d'*A. m. sicula* sont encore conservées dans la population d'abeilles que nous avons étudiée. Ces résultats montrent qu'il est possible et

souhaitable de renforcer les efforts pour conserver cette race. Des mesures opportunes consisteraient à créer des zones refuges pour *A. m. sicula* sur une ou plusieurs îles proches, même à partir de colonies sélectionnées parmi la population étudiée.

***Apis mellifera sicula* / *Apis mellifera ligustica* / morphologie / ADNmt / maintien de la biodiversité**

Zusammenfassung – Eine morphologische und mitochondriale Einordnung von *Apis mellifera* von Palerma, Italien. Obwohl die Insel Sizilien nahe am italienischen Festland liegt, wurden die dort vorkommenden Honigbienen seit 1911 als deutlich unterschiedene eigene Unterart erkannt, *Apis mellifera sicula* Montagano [11]. Neben den morphologischen Unterschieden ist das Verhalten von *A. m. sicula* bemerkenswert [14]. Ruttner [14] beschrieb die Morphologie von *A. m. sicula,* die in Sizilien noch vor dem modernen kommerziellen Trend zur Einführung von *A. m. ligustica* gesammelt wurden. Daher gibt es Basisdaten für einen Vergleich des Einflusses der Importe und für eine Richtlinie bei der Bemühung des Erhalts dieser Rasse. In diesem Bericht werden Eigenschaften der Honigbienen vom westlichen Sizilien (Palermo, Italien) auf Grundlage typischer Polymorphismen in der Länge von Restriktionsfragmenten der mitochondrialen DNA und einer Standardgruppe von morphometrischen Messungen beschrieben. Von 16 Völkern des Bienenstandes der Universität Palerma wurden Proben genommen und in Ethanol oder flüssigem Stickstoff aufbewahrt, entsprechend der jeweiligen Analysemethode. Zehn Arbeiterinnen pro Volk wurden seziert und 36 morphologische Eigenschaften gemessen. Diese Messungen und ihre alphabetische Anordnung in *Tabelle I* erfolgt nach der Methode und Kennzeichnungen von Rinderer et al. [13]. Diese Messungen wurden mit ähnlichen Proben von Bari und den publizierten morphologischen Beschreibungen von *A. m. sicula* und *A. m. ligustica* verglichen [14]. Morphologisch ähneln die Honigbienen von Bari und Zentral -Italien den Beschreibungen von *A. m. ligustica* von Ruttner [15] (*Tabelle III*), die Honigbienen von Palermo ähneln Ruttners (*ibid*) Beschreibung von *A. m. sicula* (*Tabelle IV*). Die gesamten Nukleinsäuren wurden von einzelnen Arbeiterinnen aus jedem Volk nach der Methode von Sheppard und McPeron [17] extrahiert. Die extrahierte DNA wurde mit dem Restriktionsenzym *Eco*R I verdaut und nach der Methode von Sheppard et al. [18] und Shiff und Sheppard [16] klassifiziert. Der mtDNA Haplotyp, der allgemein in den Unterarten der afrikanischen Subspezies von *A. mellifera* vorkommt, dominierte in den sizilianischen Bienenproben. In der Population der Honigbienen, die wir in Sizilien untersuchten, waren noch die meisten Eigenschaften von *A. m. sicula* erhalten geblieben. Diese Ergebnisse zeigen, daβ es möglich und wünschenwert ist, die Anstrengungen zum Erhalt der *A. m. sicula* zu verstärken. Rechtzeitige Maβnahmen könnten in der Schaffung eines Rückzuggebietes für *A. m. sicula* auf einer oder mehreren nahegelegenen Inseln liegen, dies wäre sogar auf Grundlage ausgewählter Völkern der von uns untersuchten Population noch möglich.

***Apis mellifera sicula* / *Apis mellifera ligustica* / Morphologie / mitochondriale DNA / Sizilien / Italien / Erhalt genetischer Vielfalt**

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