

The wing coupling apparatus and the morphometric analysis of honeybee populations

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Significant differences between countries were found in the distribution of the number of hamuli within *Apis andreniformis*, *A. florea*, *A. cerana* and *A. koschevnikovi*. The mean hamuli numbers for *Apis mellifera intermissa* differed significantly among localities in Algeria. Significant differences in intercolonial variability between countries were found within *A. cerana*. There was no significant intraspecific variability within *A. andreniformis*, *A. florea*, *A. koschevnikovi* and *A. m. intermissa*. Significant differences in the mean number of hamuli occur between *A. m. intermissa* and *A. andreniformis*, *A. florea* and *A. cerana*; also between *A. cerana/A. koschevnikovi* and *A. andreniformis* and *A. florea*. Significant differences were found in the distribution and variability of the number of hamuli between species (populations). The mean numbers of hamuli for *A. andreniformis* differed from those of *A. florea*. Both these population means differed from those of *A. cerana*, *A. koschevnikovi* and *A. m. intermissa*. No significant differences were found between *A. cerana* and *A. koschevnikovi*. When the analysis included data for *A. dorsata*, *A. nigrocincta*, *A. m. carnica*, *A. m. caucasica* and *A. m. ligustica*, the results showed significant differences in hamuli numbers between *A. andreniformis/A. florea* and *A. cerana/A. koschevnikovi/A. nigrocincta* and *A. m. intermissa/A. m. carnica/A. m. caucasica/A. m. ligustica*. Hamuli numbers in *A. dorsata* significantly differed from those of other populations except *A. m. intermissa*. These results show that hamuli numbers are useful in the classification of honeybee populations. Whether hamuli would be useful in multivariate analysis depends on the correlation between the number of hamuli and the other characters used.

Introduction

The history of the classification of honeybees reflects several important changes in the definitions of categories, forms of measurement, and methods of analysis. A major advance was the formulation of a metrical set of morphological characters and the application of univariate statistical methods of analysis that emerged from the Russian school early in the last century.¹⁻³ Subsequently, some 60-odd morphological characters were gradually introduced into the literature on honeybee morphometrics, but the relative value or weight of characters had necessarily remained blurred until the polyandrous mating of honeybee queens was demonstrated,⁴ the genetic theory of natural selection developed,⁵ and the general application of multivariate methods of analysis⁶ had become commonplace.^{7,8}

One particular character, the hamuli, or wing-hooks, has become something of an enigma in honeybee taxonomy.⁹ These structures are located near the proximal end of the anterior margin of each hindwing and which couple it to a fold in the forewing to form a single, functional aerofoil during flight¹⁰⁻¹³ (Fig. 1). Long used in classification studies of honeybees, they

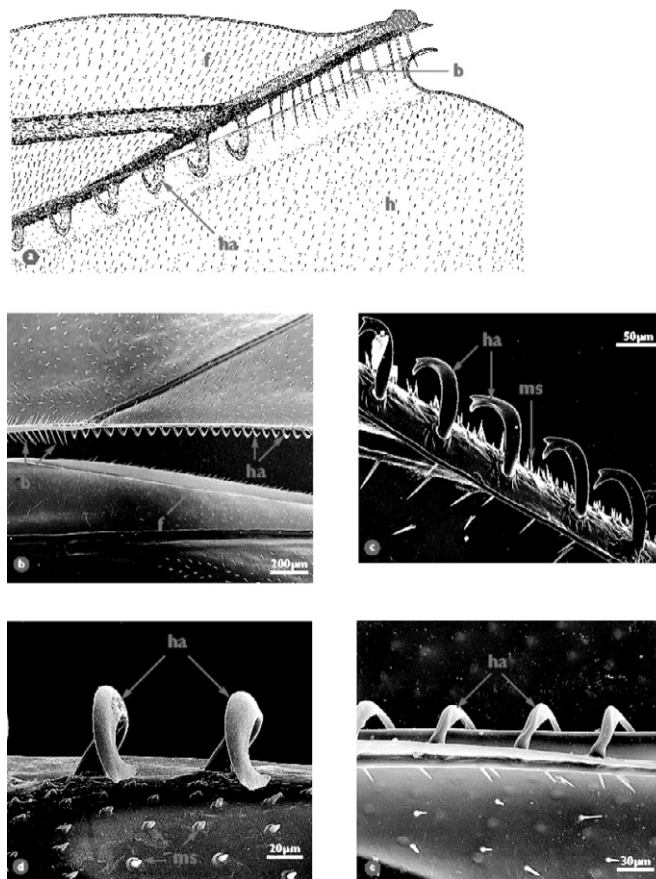


Fig. 1. Honeybee wing coupling mechanism: a, diagrammatic view from below forewing, hindwing, hamulus, and wing bristles; b, SEM micrographs of wings separated, hindwing at top, hamuli and bristles on leading edge of hindwing with fold in trailing edge of forewing; c, hamuli and small mechanoreceptor setae; d, hamuli and mechanoreceptor setae viewed from above; e) hamuli coupled with fold in forewing (symbols: f = forewing, h = hindwing, ha = hamulus, ms = mechanoreceptor setae). From Goodman¹³ with permission.

were judged to be of no use for taxonomic discrimination because within-bee variation was significantly greater than between-bees variation,⁹ despite having a high genetic heritability.^{14,15} Here we reassess and re-evaluate all of the relevant data (some previously published, other new) on the hamuli of the honeybee wing in terms of their suitability as probes in honeybee population structure as well as classification. The cardinal points of interest in these structures include developmental homeostasis, environmental effects, genetics, sexual and caste dimorphism, classification and population biology.

Materials and methods

Honeybees

The numbers of hamuli of worker honeybees used for the analyses in this study derive from: (1) raw data from the Institut für Bienenkunde at Oberursel; (2) new material collected for *A. andreniformis*, *A. florea*, *A. cerana* and *A. koschevnikovi* from

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Table 1. Mean number of hamuli and standard deviations (s.d.), coefficients of variation (CV), ranges and extent of hamuli from previously published papers.

| Species | Form [#] | No. of bees | Mean \pm s.d. | CV (%) | Range | Extent (mm) | Extent CV (%) | Region | References |
|--------------------------|-------------------|-------------|------------------|--------|-------|-----------------|---------------|------------------------------|------------|
| <i>A. cerana</i> | W | 40 | 18.50 \pm 1.38 | 7.45 | 15–21 | | | Japan | 18 |
| | W | 1075 | 18.23 \pm 1.87 | 10.27 | 13–24 | | | E. China | 18 |
| | W | >25 | 18.09 \pm 0.90 | 4.97 | | | | India | 39 |
| | W | ? | 18.04 \pm 0.65 | 3.60 | | | | India | 40 |
| | W | 420 | 18.05 \pm 1.55 | 8.59 | | 1.15 \pm 0.05 | 4.28 | Nagaland, NE India | 61 |
| | W | 420 | 18.52 \pm 2.13 | 11.50 | | 1.14 | 5.36 | Brahmaputra Valley, NE India | 61 |
| | W | 300 | 18.29 \pm 1.48 | 8.09 | | 1.16 | 4.20 | Himalayas, NE India | 61 |
| | W | 40 | 17.20 \pm 1.04 | 6.05 | 16–19 | | | N. Borneo | 19 |
| | W | ? | 19.35 \pm 0.83 | 4.27 | | 1.25 \pm 0.02 | 1.63 | N. India | 59 |
| | W | 3 | 18.16 \pm 0.39 | 2.15 | | | | Sulawesi, Indonesia | 21 |
| | W | 200 | 17.90 \pm 1.47 | 8.24 | 14–21 | | | N. India | 10 |
| <i>A. dorsata</i> * | W | 410 | 25.31 \pm 0.58 | 2.30 | 20–30 | 1.65 \pm 0.03 | 1.82 | India | 58 |
| | W | ? | 24.43 | | 18–29 | | | Central Myanmar | 64 |
| | W | 200 | 24.62 \pm 1.73 | 7.00 | 21–29 | | | N. India | 10 |
| <i>A. andreniformis</i> | W | 180 | 10.38 \pm 0.92 | 8.86 | | | | Thailand | 20 |
| | W | 40 | 10.88 \pm 1.07 | 8.38 | | | | Philippines | 20 |
| <i>A. florea</i> | W | 200 | 11.81 \pm 1.14 | 9.63 | 9–15 | | | N. India | 10 |
| <i>A. koschevnikovi</i> | W | 90 | 17.70 \pm 0.60 | 3.39 | | | | N. Borneo | 19 |
| <i>A. nigrocincta</i> * | W | 10 | 17.86 \pm 0.68 | 3.80 | | | | Sulawesi, Indonesia | 21 |
| <i>A. m. carnica</i> * | W | 148 | 19.53 \pm 1.62 | 8.29 | 16–24 | | | E. USA | 31 |
| | W | 154 | 19.60 \pm 1.60 | 8.15 | 16–24 | | | Europe | 18 |
| <i>A. m. caucasica</i> * | W | 106 | 20.69 \pm 0.42 | 2.01 | 16–29 | | | Central Russia | 31 |
| | W | 474 | 21.08 \pm 0.31 | 1.46 | 17–26 | | | S. Russia | 31 |
| | W | 201 | 20.38 \pm 1.84 | 9.02 | 16–26 | | | Russia | 36 |
| | W | 256 | 20.61 \pm 1.49 | 7.24 | 16–25 | | | N. Caucasus, Russia | 31 |
| | W | 142 | 21.37 \pm 1.61 | 7.54 | 18–26 | | | Caucasus Mtns, Russia | 31 |
| | W | 212 | 20.91 \pm 1.68 | 8.05 | 14–25 | | | Abchasia, Russia | 31 |
| | W | 69 | 21.71 \pm 1.56 | 7.19 | 18–27 | | | Transcaucasia, Russia | 31 |
| | W | 506 | 21.49 \pm 0.36 | 1.65 | | | | Bulgaria | 31 |
| | W | 150 | 21.51 \pm 1.54 | 7.18 | 17–25 | | | China ex Italy | 18 |
| | W | 402 | 21.01 \pm 1.64 | 7.83 | 17–25 | | | E. USA ex Italy | 31 |
| <i>A. m. ligustica</i> * | W | ? | 22.64 \pm 1.74 | 7.69 | | 1.42 \pm 0.07 | 4.72 | India | 59 |
| | W | 699 | 20.56 | 8.10 | 16–26 | | | Australia ex Italy | 36 |
| | W | 374 | 21.45 \pm 1.60 | 7.47 | 17–26 | | | Manchuria ex Italy | 18 |
| | W | 200 | 20.09 \pm 1.72 | 8.56 | 15–25 | | | India ex Italy | 10 |
| | W | 200 | 20.09 \pm 1.72 | 8.56 | 15–25 | | | India | 39 |
| <i>A. cerana</i> | Q | 100 | 16.10 | | 15–17 | | | India | 39 |
| <i>A. dorsata</i> | Q | 3 | 23.00 | | 22–27 | | | India | 38 |
| <i>A.m.caucasica</i> ? | Q | 139 | 18.46 \pm 1.89 | 10.25 | | | | Bulgaria | 31 |
| | Q | 27 | 18.67 | | | | | Russia | 31 |
| <i>A. m. carnica</i> | Q | 8 | 16.25 | | | | | Germany | 31 |
| <i>A. m. ligustica</i> | Q | 10 | 18.00 | | | | | Canada | 31 |
| <i>A.m.caucasica</i> | D | 118 | 20.57 \pm 0.28 | 1.37 | | | | Russia | 31 |
| | D | 997 | 21.39 \pm 1.20 | 1.65 | | | | Bulgaria | 31 |
| | D | 200 | 20.91 \pm 2.13 | 10.17 | | | | Australia ex Russia | 36 |

*Data used in the analysis. #W, workers; Q, queens; D, drones.

Borneo, Cambodia, Malaysia, Myanmar, Nepal, the Philippines, Thailand and Vietnam – referred to as the Grahamstown database; (3) raw data from a previous study of *Apis mellifera intermissa* from Algeria were obtained from Barour *et al.* (unpubl.); (4) data from previously published papers (Table 1). Morphometric analyses were performed on 11 065 individual worker bees from 639 colonies across the distributional areas of *A. andreniformis*, *A. florea*, *A. cerana*, *A. koschevnikovi* and *A. m. intermissa*.

Data analysis

Colony sample means and inter- and intracolony coefficients of variation were computed for hamuli numbers from 15–20 bees

per colony. Univariate statistical analysis of the data included ANOVA and Tukey multiple comparison procedures for means and Levene's test procedure for variances.¹⁶

Results and discussion

Classification

The number of hamuli, their frequency distribution and linear extent on the edge of honeybee wings have generally been an adjunct to classification, since the work of Koschevnikov.¹ Hamuli numbers were also shown to be species-specific and the frequency distributions bimodal in *A. cerana* and *A. mellifera* workers.^{17,18} This point was also established for *A. florea* and

Table 2. Mean and range of hamuli numbers, inter- and intra-colony variations by species.

| Species | Mean* | n | Intercolony CV (%) | No. of bees | Intracolony CV (%) | Range |
|--------------------------------|--------------------------------------|-----|-----------------------------------|-------------|-----------------------------------|-------|
| <i>A. andreniformis</i> | 10.29 ^a | 16 | 4.19 ^a | 310 | 9.04 ^a | 7–14 |
| <i>A. florea</i> | 11.18 ^b | 104 | 5.51 ^b | 1 872 | 8.87 ^{ab} | 8–16 |
| <i>A. cerana</i> | 17.56 ^c | 475 | 4.96 | 8 027 | 7.85 ^{ac} | 10–24 |
| <i>A. koschevnikovi</i> | 18.40 ^c | 5 | 5.40 | 100 | 8.36 ^a | 14–22 |
| <i>A. mellifera intermissa</i> | 22.56 ^d | 39 | 5.11 | 756 | 7.84 ^a | 16–29 |
| | $F_{4,634} = 1910.6$ $P < 0.0001$ | 639 | $F_{4,634} = 9.8$ $P < 0.0001$ | 11 065 | $F_{4,634} = 7.3$ $P < 0.0001$ | |

*Means with the same superscript letter do not differ significantly ($P > 0.05$).

A. dorsata.¹⁰ Similarly, Rinderer *et al.* showed that the hamuli means and coefficients of variation differ significantly between *A. florea* and *A. andreniformis*, but did not differ significantly between *A. koschevnikovi* and *A. cerana* (Table 1).^{19,20} The lack of significant differences in hamuli numbers between *A. cerana* and *A. nigrocincta* has also been reported (Table 1).²¹ Somewhat surprisingly, Gromisz²² and Ruttner⁹ excluded hamuli from their morphometric character suites because they did not obtain clear-cut geographical variation in very large samples of *A. mellifera* and *A. cerana* and concluded that they have little value in subspecific classification ('subspecies' in honeybees is a highly suspect concept anyway).^{23,24} Perhaps so, but in studies of honeybee population structure they are a rich source of information, particularly if one considers their genetic properties (see below).

Between-species analysis

In this study, we confirm these results for the mean number of hamuli (Table 2). Significant differences between the mean number of hamuli were also found between *A. m. intermissa* and *A. andreniformis*, *A. florea* and *A. cerana*; also between *A. cerana/A. koschevnikovi* and *A. andreniformis* and *A. florea* (Table 2). Significant differences were found in the distributions in the number of hamuli and variability between species (populations) (ANOVA: means: $F = 1910.6$, (4, 634) d.f., $P < 0.0001$; Levene: variability: $F = 9.9$, (4, 634) d.f., $P < 0.0001$). The mean number of hamuli of *A. andreniformis* hamuli mean numbers differed from those of *A. florea*. Both these population means differed from those of *A. cerana*, *A. koschevnikovi* and *A. m. intermissa* (Table 2). No significant differences were found between *A. cerana* and *A. koschevnikovi*.

When the analysis included data for *A. dorsata*, *A. nigrocincta*, *A. m. carnica*, *A. m. caucasica* and *A. m. ligustica* (Table 1), the results showed significant differences in hamuli numbers between *A. andreniformis/A. florea* and *A. cerana/A. koschevnikovi/A. nigrocincta* and *A. m. intermissa/A. m. carnica/A. m. caucasica/A. m. ligustica* (ANOVA: $F = 150.3$, (9, 56) d.f., $P < 0.0001$). Hamuli numbers of *A. dorsata* significantly differed from those of other populations except *A. m. intermissa*.

Within-species analysis

Significant differences were found in the distribution in the number of hamuli between countries within *A. andreniformis*, *A. florea*, *A. cerana* and *A. koschevnikovi* (ANOVA: *andreniformis*: $F = 3.7$, (4, 11) d.f., $P < 0.0373$; *florea*: $F = 14.9$, (11, 92) d.f., $P < 0.0001$; *cerana*: $F = 11.0$, (23, 451) d.f., $P < 0.001$; *koschevnikovi*: $F = 124.4$, (1, 3) d.f., $P = 0.0015$; Table 3(a)–(d)). The mean numbers of hamuli for *A. m. intermissa* differed significantly among locali-

Table 3. Mean numbers of hamuli, inter- and intra-colonial variations for within-species analysis.

| (a) <i>A. andreniformis</i> | | | | | |
|------------------------------------|----------------------|-------------|---------------------|----------|--------------------|
| Country | Mean* | No. of bees | Intracolony CV (%) | <i>n</i> | Intercolony CV (%) |
| Malaysia | 9.83 ^a | 60 | 9.58 | 3 | 1.78 |
| Myanmar | 10.03 ^a | 60 | 9.17 | 3 | 2.92 |
| Borneo | 10.23 ^{a,b} | 60 | 9.06 | 3 | 1.57 |
| Vietnam | 10.62 ^b | 110 | 9.46 | 6 | 4.01 |
| Philippines | 10.85 ^b | 20 | 8.60 | 1 | – |
| | $F_{4,305} = 9.5$ | 310 | $F_{4,305} = 1.3$ | 16 | $F_{3,11} = 1.76$ |
| | $P < 0.0001$ | | | | $P = 0.2569$ |
| | $P = 0.2129$ | | | | |
| (b) <i>A. florea</i> | | | | | |
| Saudi Arabia | 12.93 | 15 | 6.18 | 1 | – |
| Oman | 13.15 | 60 | 8.26 | 3 | 3.63 |
| Iran | 12.20 | 49 | 11.59 | 3 | 7.46 |
| Pakistan | 11.67 | 6 | 7.00 | 1 | – |
| Nepal | 11.40 | 20 | 6.61 | 1 | – |
| India | 10.50 | 18 | 7.48 | 1 | – |
| Sri Lanka | 11.43 | 40 | 8.38 | 2 | 2.17 |
| Myanmar | 10.62 | 220 | 10.86 | 11 | 4.50 |
| Thailand | 11.19 | 895 | 9.13 | 52 | 2.94 |
| Cambodia | 11.38 | 120 | 8.69 | 6 | 2.66 |
| Vietnam | 10.98 | 409 | 9.46 | 22 | 3.77 |
| Malaysia | 10.10 | 20 | 9.58 | 1 | – |
| | $F_{11,1860} = 38.0$ | 1872 | $F_{11,1860} = 2.1$ | 104 | $F_{8,92} = 1.5$ |
| | $P < 0.0001$ | | $P = 0.0166$ | | $P = 0.1937$ |
| (c) <i>A. cerana</i> | | | | | |
| Afghanistan | 18.20 | 137 | 8.08 | 8 | 3.82 |
| Japan | 18.50 | 160 | 8.42 | 8 | 3.92 |
| Pakistan | 19.00 | 120 | 9.58 | 6 | 2.66 |
| Korea | 19.45 | 20 | 6.35 | 1 | – |
| Hong Kong | 18.59 | 240 | 8.59 | 12 | 3.80 |
| China | 18.06 | 471 | 8.86 | 31 | 4.21 |
| Nepal | 17.86 | 91 | 10.14 | 6 | 5.78 |
| N. India | 18.09 | 296 | 8.34 | 17 | 3.19 |
| Myanmar | 17.48 | 1201 | 10.95 | 63 | 5.25 |
| Vietnam | 17.64 | 1270 | 8.64 | 57 | 3.59 |
| Java | 18.21 | 365 | 7.69 | 9 | 2.97 |
| Bali | 18.37 | 97 | 6.95 | 5 | 2.04 |
| Cambodia | 17.46 | 325 | 8.88 | 17 | 4.34 |
| Papua New Guinea | 17.37 | 270 | 7.22 | 11 | 2.52 |
| Thailand | 17.96 | 97 | 7.71 | 6 | 2.59 |
| Sri Lanka | 17.87 | 159 | 7.94 | 19 | 2.92 |
| Sumatra | 17.83 | 120 | 6.93 | 6 | 1.53 |
| Sulawesi | 17.74 | 90 | 8.34 | 6 | 3.83 |
| Indonesia | 17.20 | 119 | 7.00 | 21 | 4.16 |
| Philippines | 17.03 | 1788 | 8.68 | 126 | 4.39 |
| Malaysia | 16.75 | 128 | 8.54 | 6 | 3.23 |
| Borneo | 16.70 | 463 | 8.02 | 34 | 3.29 |
| | $F_{21,8005} = 43.8$ | 8027 | $F_{21,8005} = 9.2$ | 475 | $F_{20,453} = 1.7$ |
| | $P < 0.0001$ | | | | $P = 0.2569$ |
| | $P = 0.0310$ | | | | |
| (d) <i>A. koschevnikovi</i> | | | | | |
| Malaysia | 19.48 ^a | 40 | 7.80 | 2 | 0.91 |
| Borneo | 17.68 ^b | 60 | 8.62 | 3 | 0.99 |
| | $F_{1,98} = 33.3$ | 100 | $F_{1,98} = 0.003$ | 5 | $F_{1,3} = 0.002$ |
| | $P < 0.0001$ | | $P = 0.9543$ | | $P = 0.9702$ |
| (e) <i>A. m. intermissa</i> | | | | | |
| Berrahel | 24.15 | 100 | 8.25 | 5 | 3.26 |
| Selawa | 22.72 | 36 | 7.77 | 3 | 5.41 |
| Ain Essel | 21.97 | 60 | 7.16 | 3 | 2.81 |
| Drean | 23.17 | 60 | 7.79 | 3 | 5.11 |
| Tawra | 23.00 | 60 | 10.00 | 3 | 1.88 |
| Souk Ahras | 22.52 | 60 | 8.40 | 3 | 3.34 |
| Mewna | 22.45 | 60 | 10.19 | 3 | 3.67 |
| Bri Metrane | 22.55 | 60 | 7.98 | 3 | 1.77 |
| Serraidi | 22.60 | 80 | 8.01 | 4 | 1.41 |
| El Hadeykes | 23.03 | 40 | 5.52 | 2 | 2.30 |
| Bni Isguen | 21.50 | 100 | 9.08 | 5 | 4.27 |
| Bni Isguen | 20.10 | 40 | 8.72 | 2 | 3.87 |
| | $F_{11,744} = 16.9$ | 756 | $F_{11,744} = 2.4$ | 39 | $F_{11,27} = 1.4$ |
| | $P < 0.0001$ | | | | $P = 0.0058$ |
| | $P = 0.2180$ | | | | |

*Means with the same superscript letter do not differ significantly ($P > 0.05$).

Table 4. Correlation coefficients (r) between hamuli numbers and altitude and forewing length.

| Species | Altitude | | Forewing | |
|-------------------------|----------|-----------------|----------|-------------|
| | r | No. of colonies | r | No. of bees |
| <i>A. andreniformis</i> | -0.460 | 6 | 0.085 | 310 |
| <i>A. florea</i> | -0.135 | 95 | 0.149 | 1 863 |
| <i>A. cerana</i> | 0.045 | 414 | 0.250 | 8 027 |
| <i>A. koschevnikovi</i> | - | - | 0.168 | 100 |
| <i>A. m. intermissa</i> | -0.308 | 27 | 0.176 | 756 |
| All groups | 0.089 | 544 | 0.898** | 11 056 |

** $P < 0.01$.

ties within Algeria (ANOVA: $F = 4.9$, (11, 27) d.f., $P = 0.0004$; Table 3(e)). Significant differences in intercolonial variability between countries were found within *A. cerana* (Levene: $F = 1.6$, (23, 451) d.f., $P = 0.0337$), whereas no significant differences in variability were found within *A. andreniformis*, *A. florea*, *A. koschevnikovi* and *A. m. intermissa*.

Sexual and caste dimorphism

Casteel and Phillips reported that variability in the number of hamuli was greater in drones than in workers of *A. mellifera*, which they prematurely ascribed to environmental effects.²⁵ While others established the breadth of individual variation,^{18,26-30} substantial progress was made by Alpatov^{2,31} and Narayanan,³²⁻³⁴ who analysed large samples of *A. mellifera* and showed that the intercolonial means (all normally distributed) and coefficients of variation in hamuli number for drones, workers and queens were statistically significantly different and that greatest variability occurred in drones (Table 1). But, while queens had significantly fewer hamuli than drones or workers, their coefficients of variation were very similar to drones'. Despite their greater size, the numbers of hamuli in drones and workers are much the same.² Woyke³⁵ demonstrated that while most structures were larger in diploid drones than haploid ones, the number of hamuli in the former was significantly lower than the latter and workers' were significantly lower than queens'.³⁵

Experiments by Lee³⁶ confirmed that variation in the number of hamuli is greater in drones than in workers^{2,25} and also that drones raised in worker cells did not significantly differ from those of drone cells, a result pointing to a lack of environmental influence over the phenotype and a lack of dominance homeostasis in haploids. Contradictory results were reported for a correlation between hamuli and the cubital index,^{10,30} but it was established that hamuli number is proportional to hindwing size.³⁰ That queens and workers showed caste dimorphism for both means and variances of a quantitative character like hamuli suggests developmental differences (see below). The numbers, frequency distributions, linear extent of hamuli distribution along the edge of the hindwing and coefficients of variation for hamuli in *A. cerana* differ significantly for queens and workers. Likewise, queens of *A. dorsata*, *A. mellifera* and *A. cerana* differ significantly in these respects (cf. Table 1).^{31,37-41}

Environmental effects

Kellogg²⁶ reported that variation in several features of the wings of drones, reared in large drone or small worker cells, did not differ significantly; in more comprehensive experiments, however, Grout⁴² noted significant changes in the wing length and width in workers bees reared under similar conditions. But, there remained questions about wing symmetry and the possibility of environmental and/or developmental effects in the final expression of the phenotype. Petrov and Ankinovich calculated

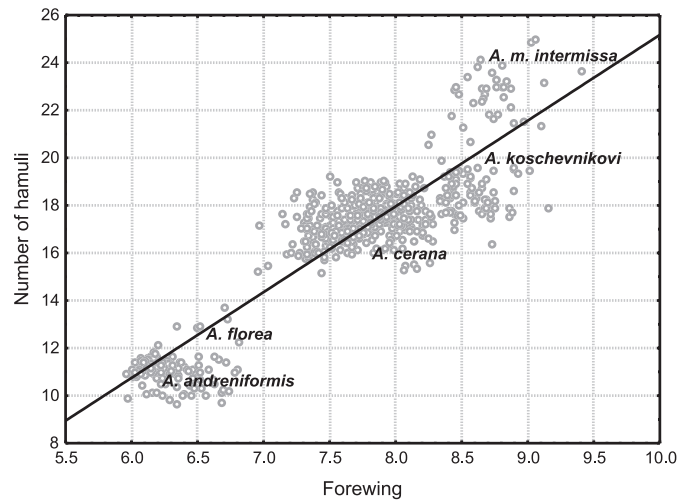


Fig. 2. Number of hamuli versus forewing length in five *Apis* species.

that the symmetry of the hamuli between left and right wings had a correlation close to unity (0.996).⁴³

Petrov subsequently reported that the numbers of hamuli in both drones and workers of *A. mellifera* were not affected by queen age, or the age of nurse bees⁴⁴ (but nutrition significantly affects hamuli number),³¹ nor did they vary seasonally as do other traits in honeybees such as pigmentation.⁴⁵

The susceptibility of wing size in *A. mellifera* to environmental effects was analysed by Alpatov for bees that were normally fed and under-fed; the coefficients of variation did not differ significantly but underfed bees had significantly fewer hamuli than the others.³¹ Further analyses of wing size and number of hamuli in different species of *Apis* have been developed. Saini *et al.* reported that the mean numbers of hamuli in workers of a given species are simply proportional to the size of the hindwing.¹⁰ Lee had earlier calculated the correlation between the number of hamuli and the size of the forewing in workers of *A. mellifera* and found it to be remarkably low (0.103),³⁶ although the correlation for left-right wing symmetry approached unity.⁴³ Our findings confirmed low correlations between forewing length and hamuli numbers within species ($0.09 < r < 0.25$), whilst a significantly high correlation was found across species (Table 4, Fig. 2). Finally, Diniz-Filho *et al.* investigated genetic and within-colony environmental components in the number of hamuli in *A. m. scutellata* modified to control for environmental variation.¹⁵ He estimated the heritability for the number of hamuli in the worker progeny of a queen inseminated by 17 drones and calculated heritability to be 0.6768 ± 0.2991 . The within-colony environmental variance component was not significant, hence the heritability values are dependably accurate and identical to those of Oldroyd and Moran.¹⁴

Genetics

Using inbred lines and hybrids of *A. mellifera* that were instrumentally inseminated, Roberts found that heritability for hamuli is high and that there were significant differences among the inbred lines and the hybrids,⁴⁶ results confirmed by others.^{14,15,36,47-49} Subsequently, Lee established that hamuli number was normally distributed, but independent in drones and workers, and that queens had fewer hamuli than their sister workers.³⁶ There was also high variability between different lines in Lee's experiments,³⁶ which indicated a high response to selection. This point was pursued by Goncalves,⁵⁰⁻⁵² Paulino,⁵³ and Petrov,⁴⁴ who developed a directional selection programme for high and low hamuli numbers in two inbred lines of *A. mellifera*. The

inbreeding coefficients of workers and queens, the variance components, coefficient of variance among workers, correlation analysis, and regression of offspring on mid-parents allowed an estimation of heritability. There was a high correlation between the means of mid-parents and offspring of both lines. The symmetry of the parents had no effect on offspring variability in workers, drones or queens. Interestingly, there was also a reduction in the genotypic variance of drones and workers.⁴⁹

While the above results are very telling, two points of interest cannot be determined from them: (1) the natural frequency distribution for hamuli number in a natural population and (2) highly accurate values for heritability (this is because single drone inseminations suffer bias of the effect of dominance variance to covariance in sib worker bees). Oldroyd and Moran developed a method to determine heritability of hamuli numbers in a natural population of *A. mellifera*.¹⁴ Relatedness among workers was estimated as a function of the number of drone matings by the queen, and the relatedness among these drones. Heritability values were obtained by dividing the inter-class correlation for hamuli number by the relatedness among workers within colonies. They estimated the heritability for hamuli number in a natural population of honeybees to be 0.68 ± 0.18 ; using different experimental methods, Diniz-Filho *et al.* calculated heritability for hamuli number to be 0.677 ± 0.29 .¹⁵

Developmental homeostasis

The finding that the correlation for left–right wing symmetry of hamuli was more variable in queens than worker honeybees⁴³ invited the possibility of important developmental effects. Because constancy of a character is a measure of homeostasis, it is necessary to ask whether developmental homeostasis is linked with heterozygosity in haplo-diploid insects? One study on the effects of gene dosage on variability in hamuli number concluded that a higher variance occurs in haploid drones;³⁶ homeostasis of wing symmetry is generally enhanced in haplo-diploid systems such as honeybees.⁵⁴ Recent studies on the genetic basis of wing symmetry in relation to developmental stability showed that the symmetry of distribution of hamuli on the wings of workers of *A. mellifera* did not exhibit any statistical deviation from normality.⁵⁵ Statistically, as the number of hamuli approaches the mean, the greater the probability of symmetry in hamuli numbers in both pairs of wings.¹² However, the genetic component of this system and possible environmental effects require more detailed analysis.

Population studies and clines

Clinal variation in honeybees was first demonstrated by Alpatov, who measured hamuli frequencies for *A. mellifera* between 50°N and 55°N latitude in central Russia and recorded an increase in the average number of hamuli for worker bees from south to north.⁵⁶ He also detected what is now termed an altitudinal cline in the Caucasus Mountains (Table 1).³¹ It is of historical interest to note that the term 'cline' was first proposed by Huxley to describe geographical variation⁵⁷ on the basis of Alpatov's data. Similar clines have been documented for *A. dorsata*⁵⁸ and *A. cerana* in the sub-Himalayan region^{32–34,59–61} and in central Europe⁶² (cf. Table 1). In this study, no significant correlations were found between altitude and hamuli numbers within species or between species (Table 4). No altitudinal clines were found.

Of equal importance from a population perspective, Kellogg showed that the average coefficient of variability for *A. cerana* differed significantly from *A. mellifera*.¹⁸ This suggests a greater heterogeneity in the natural populations of the native *A. cerana*

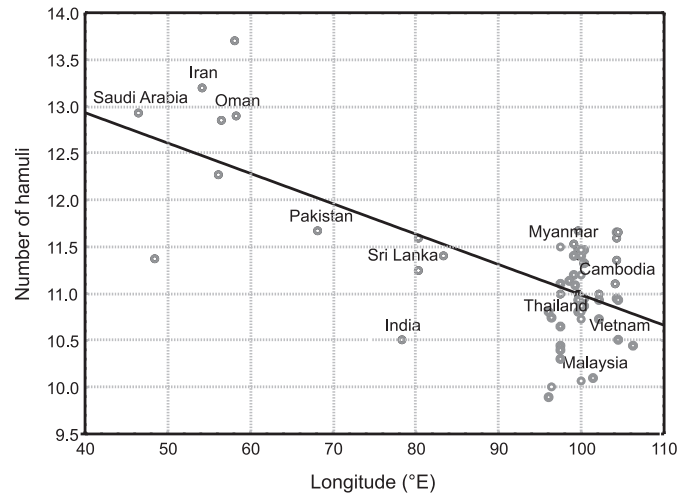


Fig. 3. Longitudinal cline in the number of hamuli in *Apis florea*.

of China against those imported from a smaller European gene pool of *A. mellifera*. Finally, Norkina and Korolev calculated the incidence of discrete phenotypic traits (phenes) that could define two populations within Grey and central Russian bees (both *A. m. caucasica*) because the drones of two groups differed significantly for a spectrum of phenes including hamuli.⁶³ Our analysis of the most complete data sets shows that hamuli numbers exhibit significant longitudinal and latitudinal clines over large distances in *A. florea* and *A. cerana* worker honeybees (*A. florea*: longitude: $r = -0.68$, $P < 0.0001$; latitude: $r = 0.51$, $P < 0.0001$; *A. cerana*: longitude: $r = -0.34$, $P < 0.0001$; latitude: $r = 0.35$, $P < 0.0001$, Fig. 3). The number of hamuli decreases along a sloping cline from 30°34'N in northwestern Iran to 9°20'N in southeastern Vietnam.

Conclusions

The number of hamuli and their linear extent on the edge of the hindwings of honeybees have high heritability values and are readily modified by genetic selection. They differ significantly between the sexes and female castes. They vary among most species of *Apis* as well as in infraspecific categories (workers and queens of *A. m. caucasica* and *A. m. carnica* versus *A. m. ligustica*). The frequency distributions of hamuli and their extent on hindwings significantly vary at the population level and exhibit latitudinal and longitudinal clines over large distances. Likewise, there are geographical oscillations in the occurrence of high and low values for the coefficient of variation that indicate the relative homogeneity or heterogeneity of local populations. These results show that hamuli numbers are useful in the classification of honeybee populations. Whether hamuli would be useful in multivariate analysis depends on the correlation between hamuli numbers and the other characters used. If hamuli numbers are highly correlated with a character that has greater discriminatory power of populations, then hamuli numbers may not be selected in the character suite.

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