

the relative frequencies (or probabilities with  $\sum p_i = 1$ ) for phenotypes A and B. Table 1 gives a synopsis of all characters with arithmetic mean, borders of 95% probability range, extreme values and discriminatory power on the basis of nest sample means. Arranged in falling order of discriminatory power the best characters are **pn**, **uhl**, **pp**, **pnl** and **uh**, having a non-overlap of 88–94%, while **pe**, **mn** and **bh** are less useful with **d** ranging 47–78%.

	phenotype P	phenotype I	phenotype R	dis. power
uh	0–0.15– <b>1.706</b> –3.5–4.1	2.3–2.4– <b>4.587</b> –6.6–6.7	3.7–4.9– <b>7.148</b> –9.9–10.45	0.8776
bh	0–0– <b>3.080</b> –0.34–0.7	0–0– <b>0.354</b> –0.97–1.38	0–0– <b>0.714</b> –2.3–3.83	0.4729
pn	0.25–0.4– <b>3.539</b> –8.25–11.0	5.0–5.9– <b>10.24</b> –14.6–16.7	11.9–15.3– <b>26.16</b> –39.9–46.9	0.9423
mn	0.70–1.0– <b>3.650</b> –6.80–8.25	2.3–2.6– <b>6.275</b> –9.94–10.8	3.9–5.3– <b>11.90</b> –19.4–22.9	0.7238
pp	6–0.2– <b>3.161</b> –6.90–8.31	4.6–4.7– <b>7.622</b> –10.65–11.5	8.0–9.5– <b>16.01</b> –23.5–28.6	0.9095
pe	0.3–0.8– <b>2.840</b> –5.20–6.30	2.22–2.9– <b>5.286</b> –7.6–8.0	3.21–5.3– <b>8.059</b> –11.5–12.9	0.7764
uhl	14–19– <b>57.6</b> –103–111	81–83– <b>125.5</b> –197–205	131–146– <b>192.7</b> –239–257	0.9110
pnl	5–8– <b>40.8</b> –62–66	52–53– <b>72.5</b> –97–103	76–79– <b>99.6</b> –123–135	0.8934
HW <sub>max</sub>	1643–1686– <b>1831</b> –1998–2089	1658–1697– <b>1883</b> –2075–2220	1643–1770– <b>2001</b> –2193–2249	—

Table 1 Distribution of nest sample means of morphometric data in workers. Sequence of data for each character: lower extreme – lower limit of 95% interval – **arithmetic mean** – upper limit of 95% interval – upper extreme. The discriminatory power (= non-overlap of frequency distributions) was computed as arithmetic mean of the three between-phenotype values. HW<sub>max</sub> is the largest head width in a nest sample.

### 3.2. The influence of body size on pilosity data and comments on confidence of phenotype determinations

Because of the limited computing capacity, I have confined all evaluations in this and the following sections on sample means. Such a reduction to 430 sample means is not expected to produce principally different results than a computation from 5500 individual workers. However, in detail, we may predict systematic deviations since the nest means were computed as arithmetic means in each character whereas tentative regressions with individual values, along a large body size range, frequently resulted in nonlinear functions, particularly in **pht R**.

Table 2 shows the dependency of pilosity data in the five most discriminating characters as function of HW. In general we can state the pilosity to be almost independent from body size in **pht P** and to have a weakly positive correlation in **pht I**. The rather low number of 164 or 70 regressed pairs in **pht P** or **pht I** does not allow to prove a significance where a weak correlation really exists: In a tentative computation with 800 individual workers the reduction of **uhl** with growing HW in **pht P** was found to be highly significant ( $p < 0.001$ ).

In **pht R** we have always a highly significant, positive correlation of pilosity length and number with body size. To have described the size-dependency of the pilosity index **H** and to reach a better phenotype separation, I have defined a size-corrected pilosity index **H<sub>cor</sub>**. Since slopes of regression lines increase the more hairy a phenotype is, it is appropriate to use different correction functions for either **pht P**, **pht I** or **pht R**. For **H < 20.0** the correction was

$$H_{cor} = H - 0.00253 HW + 4.23$$

and for **H ≥ 20.0** the correction was performed as

$$H_{cor} = H - 0.0101 HW + 17.0$$

where **HW** is given in  $\mu\text{m}$ . The slopes of these functions were estimated by regression of **H** against **HW** within the intervals **H** = [11.0, 19.0] and **H** = [20.0, 30.0]. The constants 4.23 and 17.0 were added to give **H<sub>cor</sub>** similar values as **H**.

Fig. 11 shows the frequency distribution of **H<sub>cor</sub>**. Compared to Fig. 1, we have a better separation of **pht I** and **pht R** but no advantage to separate **pht I** and **pht P** indicating that only the correction function for **H ≥ 20.0** gives a sense. The largest **H<sub>cor</sub>** for **pht I** is 23.8 and the smallest for **pht R** is 25.3 making one believe we have a perfect separation. However, we have to expect nest samples where in reality no either or decision is possible. This refers particularly to the rare nests with phenotype mixtures or to those rare nests where a shift from one phenotype to another is just in progress (see section 3.5). The same qualification must be made for distinction between **pht P** and **pht I**. For these reasons,