L. "tubero-interruptus"). Moreover, the alitrunk length in queens (not available for all colonies) was measured.

The relationships between the colonies based on the samples of five workers and the morphological characters mentioned above were analyzed by principal components and after having included the information from the electrophoresis by a discriminant analysis (NORUSIS 1966).

Results

The principal components analysis reveals a high correlation between all morphological characters; the first axis represents 79 %, the second 12 % and hence together 91 % of the variation. This means that the morphological affinities of our 246 samples can be accurately represented by two dimensions (Fig. 2). All four characters are strongly correlated with the first axis and a high value along that axis means dark head, darkened femur, and extensive but weakly demarcated dark area on first gaster tergite. The second axis, being rather closely related to two characters, gives large values to samples with darkened femur and distinct gaster band. Excluding some outliers two clusters are shown, the upper one to the right corresponding to *L. nigriceps* and a large heterogeneous group of which top-left corresponds to *L. unifasciatus*, bottom-left to *L. "tubero-interruptus"* and bottom-right to *L. tuberum*. The three samples between *L. unifasciatus* and *L. nigriceps* have characteristics from both these species.

The variation at the PGI, MDH-1 and PGM loci based on mean allele frequencies for each sample is depicted in Figs. 3–6. As in the morphological variation species seem to be

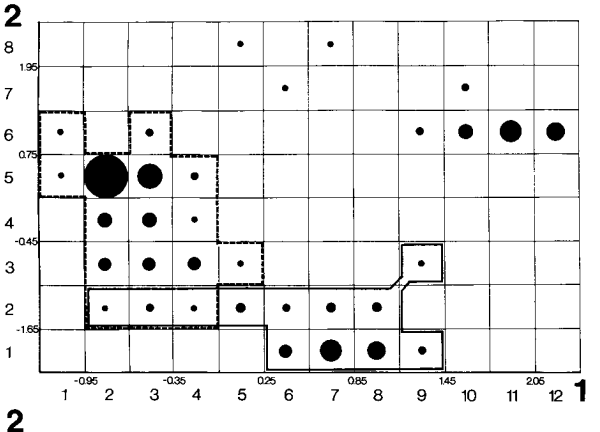

Fig. 2. Principal components analysis of 246 colonies of the *Leptothorax tuberum* group (morphological characters in workers, see text). The two first (1 and 2) axes, representing 91 % of the variation, are shown. The area of the solid circles is approx. proportional to the number of colonies (the smallest = 1 colony, the largest = 82 colonies). The colonies enclosed by the dashed line are analysed in Table 1, and those enclosed by the solid line in Table 2

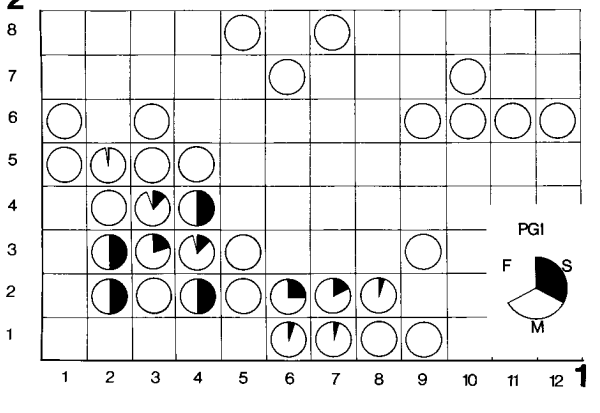

Fig. 3. The variation at the PGI locus (3 alleles) calculated from colony mean allele frequencies (cf. Fig. 2)