

the same area of the phenogram, are only loosely associated. The single *Rhogmus* species is most closely associated with *Dorylus* (s.s.) and part of *Anomma*, but the two *Alaopone* species and the single *Typhlopone* species are well separated from the rest of the genus.

The phenogram based on correlation coefficients (Fig. 5) shows more distinct clusters than that based on distances and displays better correspondence with the existing classification. There are two major clusters, the first consisting of all species of *Anomma* with a single *Dorylus* (s.s.) species clustering with *Anomma* species 5 and 7. The second major cluster consists of widely dispersed *Dorylus* species associated loosely with the included species of *Rhogmus*, *Typhlopone* and *Alaopone*. A subcluster within this second group pairs the two *Alaopone* species and shows the single species of *Rhogmus* most closely associated with them.

In the belief that PCA analyses are somewhat less reliable than those from the MDS procedure, we utilized the former primarily as an aid to establishing the three most significant axes of variation, to determine the relative contribution of different characters to those first three principal component axes and as a seed for the MDS analysis. The first three component axes generated in the PCA procedure accounted for 64.2% of total variation in the transformed data set, a reduction from the 86.4% for the first three component axes in the analysis of raw data.

The explanation for this reduction continues to lie (as described previously by Gotwald & Barr, 1980, and Barr & Gotwald, 1982) in the greatly reduced explanatory value of the first component axis (37.3% v. 67.1%) concordant with its change from being primarily an indicator of size differences to one of shape differences. Explanatory values for the second two axes actually increased for the transformed data.

In the transformed data set, principal component axis I was influenced most heavily (both positive and negative loadings) by characters expressing shape, either transformed lengths (distributed over all three body regions) or standard myrmecological shape indices. Body colour and absolute profemur length also made important contributions. Component axis II accounted for 16.7% of the variation in the data set. Of major significance for separating species in this dimension were relative size of several areas of the thorax, relative width of the first gastral segment, and the shape of the pygidium. Component axis III accounted for only 10.3% of the total variation and was strongly influenced only by the cephalic index, the relative metatibia length and the shape of the hypopygium.

Results of the MDS ordination are graphed in Fig. 6. Species are distributed widely through the attribute space, and few distinct clusters are evident. These are precisely the type of diffuse species relationships which produce the variable species groupings seen in

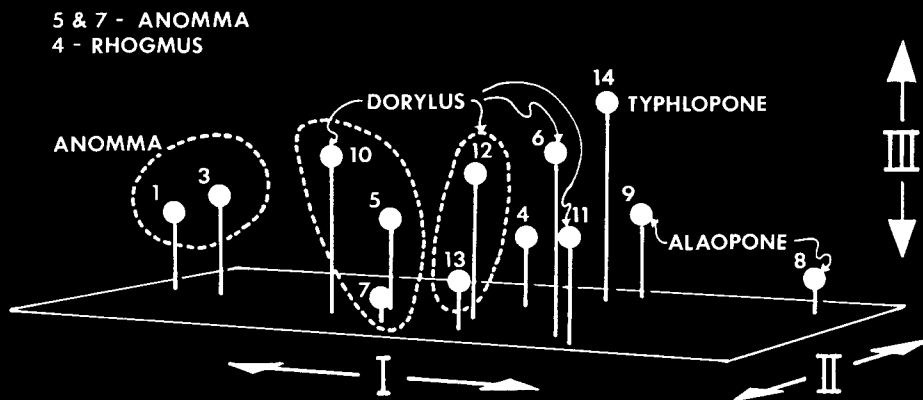


FIG. 6. Non-metric multidimensional scaling ordination of the thirteen *Dorylus* queens in the A space defined by the first three component axes (I, II, III), based on average taxonomic distances calculated on the transformed data (stress = 0.138). Matrix correlation $r = 0.969$.