

of authors (Sokal and Rohlf 1962, Sneath 1969) to yield highest correlations with the original similarity matrices. The results of clustering are displayed in the form of standard phenograms.

The standardized data also served as the basis for ordination procedures used to test the consistency of major groupings indicated by the clustering techniques. Principal components analysis (PCA) was used to array the 24 species in three-dimensional attribute (A) space. An ordination producing less distortion from the original distance matrices was produced by the technique of non-metric multi-dimensional scaling (MDS). The MDS ordination was subsequently rotated to alignment with the major axes of variation established by PCA. Areas of distortion of taxonomic relationships between the 24 taxa of the study were identified in both ordination techniques by fitting a minimum spanning tree based on distances or correlations as appropriate. Results were plotted as a three-dimensional diagram so that similarity of relationships could be more readily assessed visually. All procedures are discussed by Sneath and Sokal (1973).

Computations were carried out on the IBM system 370-165 computer at the Univ. of Toronto. Clustering and ordination procedures were performed with the NT-SYS package of programs (Rohlf et al. 1972). Representation of ordinations in three-dimensional perspective was accomplished by the program PHYSETER written by Ralph Gibson at the University of Toronto.

Results

The multivariate procedures used in this study have been employed in an exploratory rather than a confirmatory mode; no significance, therefore, is attached to precise similarity values. Rather, our attempt has been to discover the taxonomic structure inherent in the data and to draw preliminary conclusions as to the phenetic affinities of the *Dorylus* species included.

All phenograms produced by the UPGMA technique were similar, and those illustrated in Fig. 2 and 3 are representative. The UPGMA phenogram (Fig. 2) based upon average taxonomic distances from transformed data shows 6 distinct species clusters that reappear in one form or another in most analyses and resemble the subgeneric classification presently used (see Gotwald 1980) within the genus *Dorylus*. The 3 species of the subgenus *Typhlopone* cluster together and are joined at a lower level of similarity by the single *Dichthadia* species in the study. All species of the subgenus *Rhogmus* also cluster together as do the 5 members of *Dorylus* (s.s.). The 2 *Alaopone* species cluster together and are related at only a relatively low level of similarity to all of the aforementioned groups. Six species of the subgenus *Anomma* cluster together and are related at an extremely low level of similarity to the subgenera clustering with *Dorylus* (s.s.). The major difference between this phenogram and the existing classification is seen in the 3 *Anomma* species (20, 21, and 24) that cluster at a low level of similarity, not with the other 6 *Anomma* species, but with the remaining subgenera within the genus.

In the 2 other distance phenograms not reproduced here, the subgeneric groupings representing *Rhogmus* and *Alaopone* species are relatively well-integrated and

robust. The integrity of other groupings, however, is compromised by anomalous behaviour of several individual species and species groups. The small group of *Anomma* species, 20, 21, and 24, cluster in both instances with the other members of their subgenus, and *Typhlopone* species 2 and 3 are in one instance grouped with the *Anomma* species as well, as is *Dorylus* species 11. Even *Rhogmus* species 6 in one instance clusters more closely with the species of *Dorylus* (s.s.) than with its own group. All the distance phenograms agree with that illustrated in Fig. 2 in the detection of a major dichotomy between those species groups associated with the subgenus *Anomma* and those associated with the subgenus *Dorylus* (s.s.).

The correlation phenograms (e.g., Fig. 3) are also basically consistent with the currently accepted subgeneric classification of the *Dorylus* species in this study. Again, the groupings of *Typhlopone* species, *Rhogmus* species, *Alaopone* species, *Dorylus* (s.s.) species, and *Anomma* species show a high degree of integrity (Fig. 3). The single *Dichthadia* species is most closely related to *Typhlopone*, and *Rhogmus* and *Alaopone* have clustered together. Only *Dorylus* (s.s.) species 11 shows a degree of distinction from the other 4 species in the group. Most *Anomma* species show a relatively close, stepwise, relationship to one another except for the loose cluster of 3 species: 20, 21, and 24.

Only one major variation upon this pattern was seen in the correlation phenograms derived from the raw data of 50- and 33-characters. *Dorylus* (s.s.) species 11 clustered in one case loosely and in a second case more closely with species of the subgenus *Anomma*. When well integrated into the *Anomma* cluster, *Dorylus* species 11 showed greatest affinity with the already distinctive subgroup of species 20, 21, and 24 (33-character data set). All clustering analyses of this type preserved the clear dichotomy between species clustering with *Dorylus* (s.s.) and those species clustering with the subgenus *Anomma*. In all cases the 1st group included the major portion of the subgenera *Typhlopone*, *Rhogmus*, *Alaopone*, and the single *Dichthadia* species.

Ordination procedures in general can produce a more realistic picture of the affinities among included groups of OTU's in a numerical taxonomic study, because they preserve a continuous picture of degrees of similarity between closely related groups. Accordingly, an ordination procedure is not so readily adaptable to providing a classification (nor to matching existing classifications) as are the clustering procedures discussed above. Nevertheless, ordinations provide a healthy perspective on the results of clustering by indicating when clustering subdivisions represent artificial boundaries imposed on the true structure of the data.

Ordination by principal components analysis (PCA) in particular is generally considered to produce more accurate representation of the relationships between major subgroups of included taxa, but to be less reliable in representing the fine structure of phenetic affinities in subgroups (Rohlf 1972). All PCA ordinations computed in this study were fitted with a minimum spanning tree calculated from both distance and correlation matrix data, and all showed major distortions not only in the