length on the premise that this was an equally good indicator of overall size. The second strategy was to delete species 2 from the study and then analyse both the raw data and the data with metric characters transformed to ratios of profemur length for the thirteen-species set. The full character set is listed in the appendix, and those characters transformed to ratios are marked with an asterisk as noted. A complete set of raw scores for the thirty-seven-character data on each of fourteen species is available from any of the authors upon request.

Data for each of the full analyses described above were first standardized to deviations from the character mean in standard deviation units. The standardized data set was then used to calculate average taxonomic distance from each species to every other species, and also the product–moment correlation coefficients between all species. The unweighted pair-group method on averages (UPGMA) was used on both of these similarity measures to cluster species, and the results of clustering were plotted in the form of standard phenograms.

Standardized data also served as the basis for ordination procedures used to obtain a continuous view of species relationships, free of the arbitrary boundaries imposed by clustering techniques. Principal components analysis (PCA) was used to array the species of the study in three-dimensional attribute (A) space. Non-metric multidimensional scaling (MDS) on average taxonomic distances was also carried out, because its results are generally less affected by distortions which are inherent in PCA ordination. The MDS ordination was subsequently rotated to alignment with the major axes of variation established by PCA. A minimum spanning tree based on average taxonomic distances served as an objective check on the apparent clusters produced by the MDS analysis and to assist in visualizing any remaining distortion. The MDS results were plotted as three-dimensional diagrams so that similarity of relationships could be more readily assessed visually. All procedures are discussed by Sneath & Sokal (1973).

Computations were carried out on the IBM System 370/3033 computer at the University of Toronto. Clustering and ordination procedures were performed with the NTSYS 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.

Because synonymic details of the pending *Dorylus* revision have yet to be finalized, species included in this study are referred to only by number. Species numbers and the subgenera to which they belong are as follows: *Anomma* 1, 2, 3, 5 and 7; *Alaopone* 8 and 9; *Dorylus* (s.s.) 6, 10, 11, 12 and 13; *Rhogmus* 4; and *Typhlopone* 14.

Results

In this third study in the series, we have continued to use multivariate statistical procedures in the exploratory mode, as a tool for visualizing the inherent taxonomic structure in our data. Our goal here has been only to elucidate the relative phenetic affinities of the *Dorylus* species examined.

Gotwald & Barr (1980) discussed previously the reasons for believing that transformation of metric characters to ratios of a general size indicator provides the most reliable estimates of phenetic relationships. In addition, it was found in this study that analyses carried out on the thirteen-species set using profemur length to correct for size differences were the most reliable. That conclusion can be drawn from the following observations. In all analyses of the fourteen-species data set, species 1, 2 and 3 clustered tightly together, suggesting that species 2 is so similar to 1 and 3 that its phenetic position can always be inferred from the position of the other two. Moreover, analyses performed on the raw data for fourteen species are almost identical to those for the thirteen-species raw data set (with the exception only of the appearance of species 2 itself). Conversely, a comparison of the results from the thirteen-species set transformed first on profemur length and then on mesofemur length, showed many more differences than would be expected if both are equivalent indicators of overall size. Finally, restricting the conclusions of this study to analyses based on profemur transformations only is more clearly in keeping with our goal of maintaining consistency with previous work.