

FIG. 4. Phenogram produced by UPGMA clustering of average taxonomic distances calculated on the thirteen-queen data set transformed by profemur length. Matrix correlation (cophenetic correlation) $r = 0.846$.

Thus, we will report here the results of analyses carried out on thirteen *Dorylus* queens, with metric characters transformed to ratios of profemur length. The affinities of species 2 will be assumed to be indicated accurately by the affinities of species 1 and 3, on the basis of the fourteen-species analyses not reported here in detail. Most of the species groups recognized in analyses of the transformed data were also present in similar results from the raw data, although inter-group relationships and placement of certain species varied.

Phenograms generated by the UPGMA technique on the thirteen-species set (raw data or profemur transformation) were similar in general features, and those illu-

strated in Figs. 4 and 5, based on the transformed data, are representative. The phenogram based on average taxonomic distances (Fig. 4) shows species 1 and 3 clustering separately from all other species. Within the second species group no compact clusters are seen, but rather a series of sequential linkages between four minor clusters. The identifiable species groups are: (i) species 4, 5 and 7, (ii) species 12 and 13, (iii) species 6 and 11, and (iv) species 9 and 14. These clusters mirror the subgeneric classification presently in use for this genus (Gotwald, 1982) only loosely. The subgenus *Anomma* is split into two distantly associated portions, and species in the subgenus *Dorylus* (s.s.), although occurring in

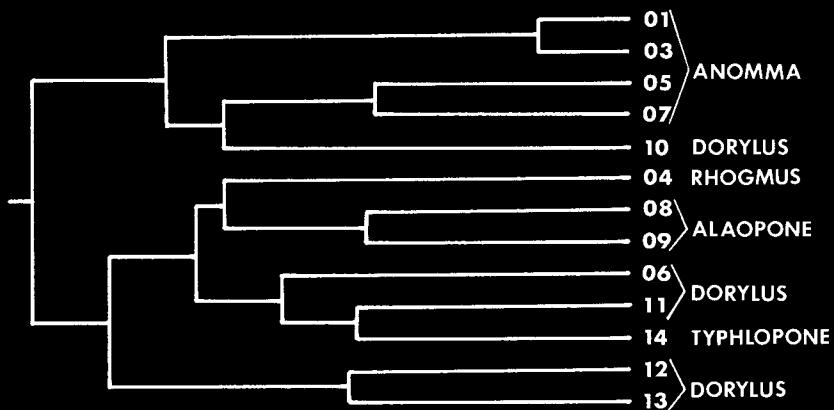


FIG. 5. Phenogram produced by UPGMA clustering of product-moment correlation coefficients calculated on the transformed data. Matrix correlation $r = 0.783$.