

ber of binary and multistate morphological characters utilized as diagnostic features in Ward (1984). These include: (i) metric measurements and indices, which were gap-coded using a conservative a posteriori test of mean differences (Scheffé's test, $\alpha = 0.01$); (ii) qualitative morphological characters involving aspects of shape, sculpture, pilosity, and color; and (iii) three binary characters dealing with nest architecture and foraging. NC.MORPH is given in Appendix II, and details of character coding are provided in Appendix III.

Phenetic and cladistic analyses.—For both data sets, coefficients of average taxonomic distance (Sneath and Sokal, 1973) were calculated between all possible pairs of the 17 taxa, and UPGMA cluster analysis (Sneath and Sokal, 1973) was carried out manually to construct the two phenograms (there were no ties). For cladistic evaluations, the two data sets were also analyzed separately. The MIX program on Joseph Felsenstein's PHYLIP package was used to search for the most parsimonious (minimum-length) trees. Twenty-four different input orders of the 18 taxa were used (the same for both data sets). The trees were rooted at the point where *Rhytidoponera confusa* joined the network.

The trees produced by MIX are fully bifurcating. There were often several alternative, equally parsimonious schemes of character-state change for a minimum-length tree of given (fully bifurcating) topology, and in some cases these alternative schemes affected the number of branches lacking character transformations. When this occurred, I chose the arrangement which minimized the number of branches of zero length. In all cases internal branch lengths of zero were eliminated by substituting multifurcations, before any comparisons were made among trees.

I calculated both strict consensus trees (Sokal and Rohlf, 1981) and Adams-2 consensus trees (Adams, 1972) for all pairs of rival trees. The degree of agreement between the rival trees was assessed by measuring the degree of resolution of the con-

sensus tree, using Colless' (1980) consensus fork index (CI_C), and Rohlf's (1982) consensus index, CI_1 (hereafter referred to as CI_R). A variety of other consensus methods and indices has been proposed (e.g., Mickevich, 1978; Margush and McMorris, 1981; Neumann, 1983; Day and McMorris, 1985; Stinebrickner, 1984), and some of the newer formulations are clearly more appropriate as general methods for assessing agreement among trees. However, the consensus trees and indices used here facilitate comparison of the present results with other recent literature on taxonomic congruence and stability (e.g., Rohlf et al., 1983; Sokal, 1983; Sokal et al., 1984). CI_C and CI_R suffer the disadvantage that, when rival trees are not fully bifurcating, these indices confound congruence among the trees with information content (Sokal et al., 1984). In the present study the rival phenograms were fully bifurcating and the rival cladograms were fully resolved or nearly so (0 to 3 multifurcations, mean 1.2; none more than a trifurcation) so this effect should not obscure the general patterns of congruence.

Assigning cladogram confidence limits.—NC.MORPH and NC.ALLO were combined into a single composite data set with 87 characters (NC.COMP), and a search was made for the minimum-length tree using the MIX program on PHYLIP. The confidence limits of this tree were estimated with a nonparametric method, the "bootstrap" (Efron, 1979), using an approach outlined by Felsenstein (1985): the characters were randomly sampled, *with replacement*, to obtain 87 characters and a minimum-length tree was sought on the basis of this character set. The "Weights" option on MIX was used to weight each character by the number of times it was sampled. The minimum-length tree was the shortest tree (or a random selection of one of several shortest trees) obtained with 24 different input orders of the 18 taxa. This character sampling and tree construction was repeated for 20 trials, and those tree partitions (subsets) which appeared in at least 19 out of 20 trees (95%) were considered significant at the 5% level.