



FIG. 2. (A and B) Equally parsimonious minimum-length trees obtained with the NC.MORPH data set and (C, D, E, and F) the NC.ALLO data set. All internal branches shown here are of nonzero length.

consensus trees are rather poorly resolved; as with the consensus phenogram, there is no resolution of species relationships within the *pulchella* group or (in half of the cases) the *fulgens* group. Half of the strict consensus trees do not even support monophyly of the *pulchella* group.

The consensus index values for these trees ($CI_C = 0.20$ to 0.33 ; $CI_R = 0.07$ to 0.26) encompass the single values obtained with the consensus phenogram, and they fall within the range of CI_C and CI_R values reported by Rohlf et al. (1983:154) for 12 pairs of data sets. The Adams-2 consensus trees between rival cladograms also show about the same level of resolution as the equivalent consensus tree between rival phenograms ($CI_C = 0.60$, $CI_R = 0.47$ to 0.62 ; Fig.

4). The present results provide no indication that cladistic classifications of the New Caledonian *Rhytidoponera* are more stable than phenetic classifications.

Since Adams-2 consensus trees depict both congruent subsets and *intersections* of subsets among rival trees (Adams, 1972), it is not surprising to find in the present instance that they are more fully resolved than the strict consensus trees (which contain only congruent subsets). The increased resolution may be partly illusory, at least from the point of view of recovering monophyletic groups. The additional information depicted in Adams-2 consensus trees is often in the form of sets not present in either of the rival trees (Rohlf, 1982). This is illustrated in Figure 4C and