

The tree comprised solely of these significant subsets can be considered to represent the 95% confidence limits of the *estimate* of the phylogeny.

W. A. E. Day (pers. comm.) has suggested that one way to avoid random selection of a tree when several shortest trees appear in a trial, would be to score each subset according to the number of minimum-length trees in which it appears in the trial. Thus if a given subset appears in three of five shortest trees in a trial, it would be scored as appearing 0.6 times in that trial. Although this procedure was not used in the present study (because I could not be certain that all the shortest trees had been found with 24 different input orders), it would be a useful improvement in future applications of this method.

#### RESULTS

NC.MORPH and NC.ALLO generated phenograms which were similar in overall structure and which preserved the informal species-groups (Fig. 1). At the same time, clusterings *within* the two largest species groups were quite disparate, with the result that the strict consensus tree (Fig. 1C) is rather poorly resolved ( $CI_C = 0.27$ ,  $CI_R = 0.24$ ), although no less than consensus trees reported for other taxa and data sets (e.g., Rohlf et al., 1983:table 3). The Adams-2 consensus tree has substantially higher consensus indices ( $CI_C = 0.67$ ,  $CI_R = 0.51$ ), primarily as a result of increased resolution within the *pulchella* group (Fig. 1D).

Both data sets generated several equally parsimonious minimum-length trees. Two minimum-length trees (length 61) were obtained with NC.MORPH, and four minimum-length trees (length 89) with NC.ALLO (Fig. 2). (James Archie kindly ran the two data sets on David Swofford's PAUP program; several additional but no shorter minimum-length trees were found.) The differences between some of the alternative trees are not trivial (compare Fig. 2C and F). In most of the trees the informal species groups form discrete subsets. For all of the above resolutions, trees containing internal branch lengths

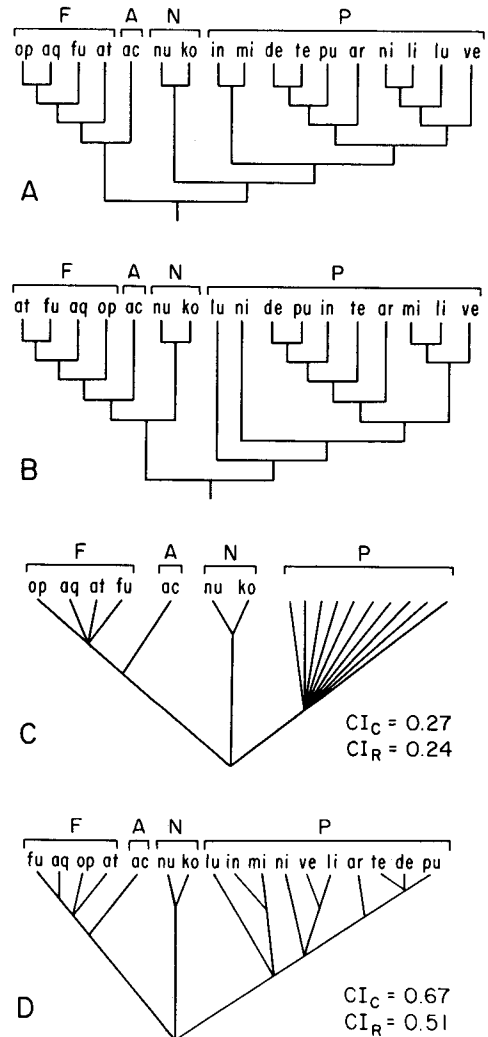


FIG. 1. UPGMA phenograms generated by (A) NC.MORPH and (B) NC.ALLO, as well as (C) strict consensus tree and (D) Adams-2 consensus tree of the two. Species are indicated by the first two letters of the specific epithet.

of zero were not included. If such trees are permitted the number of equally parsimonious trees is much larger; for example the two NC.MORPH trees can be decomposed into 36 fully bifurcating trees, all of length 61.

Strict consensus trees were calculated for all eight possible pairs of the rival cladograms; four different consensus trees were found (Fig. 3), each occurring twice. The