Phylogeny

A classification and reconstructed phylogeny were prepared using cladistic methods (e.g., Wiley 1981). Analysis of the matrix in Table 1 using the branch and bound option of Hennig 86 (Farris 1988) yielded 14 equally parsimonious phylogenies for *Pipunculus*. Character optimization and tree output were achieved using Clados (Nixon 1992). Table 2 displays the characters used in a phylogenetic analysis of New World *Pipunculus*. One of the possible phylogenies is represented in Fig. 83. Only 2 clades vary among the other equally parsimonious phylogenies, and all of the possible permutations are shown separately in Fig. 84. Two species, *P. apicarinus* and *P. bulbistylus*, are excluded from this phylogenetic analysis; both belong to the *P. campestris* group, but because of inadequate material they could not be scored for several important characters. More specimens of these species are needed.

Choice of Outgroup. A higher phylogeny of the Pipunculidae produced by Rafael and De Meyer (1992) provides the necessary context for delimiting an outgroup for this study. The subfamilial organization provided by Rafael and De Meyer (1992) is probably correct because the subfamilies are supported by several synapomorphies.

The ingroup is a well-supported monophyletic group including *Pipunculus* and *Parapipunculus*, for which the sister group is a clade including the other 18 genera of Pipunculinae (Rafael and De Meyer 1992). Ten of these genera were examined and scored for the characters of interest, and the balance were scored on the basis of published descriptions. Groundplan character states for the entire sister outgroup were then estimated following Maddison et al. (1984), and groundplan states were entered as ancestral states (all coded 0) in the matrix used for the current analysis.

Phylogenetic Relationships. The monophyly of the genus is supported by the following 4 synapomorphies: the presence of dense thoracic and abdominal pilosity (5), streaked pruinosity on the abdomen (15), the absence