Phylogeny

Computer Analysis

A cladistic analysis of Neotropical *Rhagovelia* at the species-group level was performed using the program PAUP 3.0s (Swofford, 1990). This program generates phylogenies using the principle of maximum parsimony and eliminates trees that are identical due to branches of 0 length. The initial ingroup taxa for the PAUP analysis were 17 groups of Neotropical *Rhagovelia* species considered to be monophyletic based on evaluation of the characters discussed in the previous section on character analysis. All of the species within any given group shared common character states for all of the characters in the character-state matrix (see *Appendix 4*). The ingroup was also initially constrained to include the genus *Tetraripis*, which was considered by Andersen (1982) to belong in the subfamily Rhagoveliinae. The trees were rooted via the outgroup method, with the outgroup consisting of the Neotropical veliine genera *Paravelia*, *Stridulivelia*, and *Veloidea*, which were considered to form a monophyletic sister group to the combined ingroup taxa. After initial analyses consistently clustered *Tetraripis* with the outgroup taxa it was removed from the ingroup and treated as a fourth member of the outgroup (see further discussion below).

The characters used in the final phylogenetic analysis were a subset of those discussed in the previous section on character analysis and are listed in Appendix 3. An initial set of heuristic analyses using the computer program