Materials and Methods

Selection of Ingroup Taxa (Table 1)

To test generic limits and estimate relationships of *Sphecosoma* and related genera, we observed 61 of the 89 described species for 12 of the 13 genera associated with *Sphecosoma.* This subset was represented by more than the type specimen and was prepared as described later. Several species are known only from the type specimen, including the monotypic genus *Pseudosphecosoma.* We examined these specimens externally but did not dissect the specimens nor include them in the analyses. For each ingroup species, male–female pairs were chosen from the type locality when possible. Species represented by only one sex were initially included in maximum parsimony (MP) analyses and were placed in genera based on those analyses and genital synapomorphies. For species with large geographic distributions, an additional male–female pair (from a maximally distant locality) was examined to check for geographic variation in characters.

Selection of Outgroup Taxa (Table 1)

To place *Sphecosoma* and related genera within the ctenuchine–euchromiine clades, we examined 39 species of 37 genera to search for potential outgroups. Members of Ctenuchini were included in this survey because recent evidence indicates that tribal definitions are artificial (Simmons and Weller 2001). These included genera and species with narrowed abdomens, producing a hymenopteran-like "metasoma" (e.g., *Phoenicoprocta* Druce, *Chrysocale* Walker). We selected 13 species in seven genera to serve as multiple outgroups, based on male and female genital similarities. These genera were *Calonotos* Hübner, *Chrysocale* Walker, *Horama* Hübner, *Isanthrene* Hübner, *Macrocneme* Hübner, *Metaloba* Hampson, and *Pseudopompilia* Hampson. Specifically, characters found in the *Sphecosoma* generic group, such as multilobed valves and the presence of an accessory bursa, were used as criteria for selecting outgroup taxa (Table 1).