

choose *Cerapachys* (Cerapachyinae) as outgroup. If one takes the analysis of Baroni Urbani et al. (1992) as reliable (but see Grimaldi et al. 1997 for an opinion to the contrary), *Cerapachys* is a good choice for an outgroup; it is closely related to Ponerinae without being nested inside this subfamily and it lacks all the specializations found in the army ants. The latter situation makes homology assessment between *Cerapachys* and the ingroup more straightforward. However, as was previously discussed, the method used by Bolton (1990a) casts some doubts about the validity of his decision to revive Cerapachyinae as a group outside Ponerinae and consequently about the choice of terminals by Baroni Urbani et al. (1992).

Myrmecia is a better choice for an outgroup. It is outside the poneroid group (Grimaldi et al. 1997), and therefore does not suffer from all the problematic taxonomic history of that group. Also in comparison with other groups outside the poneroid group it still has many comparable attributes shared with poneroids. It is puzzling then, that Lattke included *Myrmecia* but ignored the result from that analysis. In any case, both outgroups should be analyzed simultaneously in an unconstrained analysis to maximize global parsimony (Farris 1982; Clark & Curran 1986; Nixon & Carpenter 1993).

Aside from the taxon sampling problem, Lattke's study contains some problems regarding the characters used. The problems range from misassignment of states to questionable decisions about character coding. The following sections present a critical reanalysis of Lattke's data, concerning both taxon sampling and character reevaluation.

Methods

Cladistic analysis was performed using the programs Nona (Goloboff 1996) and Winclada (Nixon 1999). Winclada was used to edit the data matrices and as a platform to submit the matrices to Nona. Nona was used for cladogram evaluation by applying the multiple tree search command (mult*) via random addition sequence with tree bisection-reconnection branch swapping and 50 random additions. This was followed by the 'max*' command to perform additional branch swapping. Consensus trees were calculated with Nona ('nel' command) if more than one most parsimonious tree was found. Winclada was then used to visual-

ize trees, to map changes on branches and to edit trees for output purposes. Bremer support values (Bremer 1988) were calculated for the final cladogram (analysis 3, see below) using Nona, setting 'hold' to 4,000 and applying the suboptimal command to keep trees up to six steps longer, then applying the command 'bs' to sort the pool of trees and produce the necessary consensus.

Three different analyses were performed as follows based on modification of Lattke's (1994) data.

1. The original matrix was analyzed with *Cerapachys* and *Myrmecia* included at the same time (16 taxa and 36 characters). *Myrmecia* (as Myrmeciinae) was used to orient the trees in this and all the rest of the analyses for the reasons explained in the previous section.

2. The 16 taxa matrix was revised by reevaluating each character resulting as follows: characters 6 and 24 were deleted because of ambiguous homology assessment (6, the anterior clypeal shape, is extremely variable among the taxa considered which Lattke tried to deal with by creating a five state additive character, but the additivity is not well justified and the character loses all information if treated as nonadditive; 24 describes the relative protrusion of the helcium, but this attribute is continuous across taxa and is difficult to define. Characters 9 and 15 contain states coded as 'variable'. This appears to mean polymorphic and was recoded as such. Character 35 describes the relative curvature of the gaster ventrally as: absent (0), arched on either abdominal segments III or IV (1), and arched on segment IV only (2). The distinction between states 1 and 2 of this character is vague, so these states were merged to describe only the absence (0) or presence of gaster curvature (1). All multistate characters were recoded as nonadditive because of untenable justification to the contrary. All uninformative characters were excluded from the analysis (i. e., 2, 17, 20, 21, 26, 27, 29, 31). The revised matrix contained 16 taxa and 26 informative characters.

3. Three additional taxa were included in the revised matrix. *Nothomyrmecia* Clark (Nothomyrmeciinae) was chosen as an additional outgroup to include another member of the myrmecoid complex (see Fig. 1); *Apomyrma* (Apomyrminae) was included to test its placement outside Ponerinae; and, *Cheliomyrmex* Mayr (Ecitoninae) was included to represent the army ants. The inclusion of these three taxa reduced the number of uninforma-