

Quantitative Studies on Major Workers of the Ant Genus *Dorylus* (Hymenoptera: Formicidae: Dorylinae)

WILLIAM H. GOTWALD, JR.² AND DAVID BARR³

ABSTRACT

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Quantitative studies of the major workers of the Old World army ant genus *Dorylus* were undertaken to elucidate the underlying taxonomic structure of the morphological data gathered. This taxonomic structure was then compared to the existing 6 subgenera in which the species of *Dorylus* are currently classified. Although the status of the subgenera *Dichthadia* and *Typhlopone* remains unclear, the subgenera *Alaopone* and *Rhogmus* are deserving of continued individual status. Members of the subgenera *Dorylus* and *Anomma* form a single, diverse, but continuous taxon with species of the *emeryi* group connecting the morphological extremes. A formal taxonomic decision regarding the status of the 6 subgenera is not offered, but future decisions must recognize that these quantitative studies yield only 4 integral species clusters among major workers of *Dorylus* species: these correspond to the subgenera *Rhogmus*, *Alaopone*, *Typhlopone*, and *Dorylus* (s.s.).

Old World army ants of the genera *Dorylus* and *Aenictus* comprise the subfamily Dorylinae, while the New World species of "true army ants" belong to the subfamily Ecitoninae (Snelling 1980). This arrangement constitutes a recent change in taxonomic status for the army ants, since the traditional view placed both groups in a single subfamily. The change reflects the conviction that the New and Old World species are separately derived and that army ant behavior patterns and morphologies were arrived at convergently at least twice. It is possible that even *Dorylus* and *Aenictus* arose from different ancestors and only recently became sympatric over parts of their ranges (Gotwald and Kupiec 1975; Gotwald 1980).

The Ecitoninae were revised by Borgmeier (1953, 1955), and his revision is likely to remain relevant for years to come. The Indo-Australian species of *Dorylus* and *Aenictus* were revised by Wilson (1964), and thus of those army ants once regarded as a monophyletic group, only the African forms of *Dorylus* and *Aenictus* remain to be revised. One of us (WHG) is currently involved in such a revision, and the research reported here is part of the revisionary study.

Species of *Dorylus* are grouped into 6 subgenera (*Alaopone*, *Anomma*, *Dichthadia*, *Dorylus*, *Rhogmus*, and *Typhlopone*) that have been defined by relatively distinctive states of few characters (Fig. 1). These groupings, however, are not without their complications, the most vexing of which centers on the relationship of *Dorylus* (s.s.) to *Anomma*. Within *Anomma* is a series of species, referred to as the *emeryi* group, that appears transitional between the 2 subgenera. Obviously, the status of the subgenera must be reviewed within the context of the generic revision, and adjustments made to reflect accurately the broader taxonomic and phylogenetic conclusions.

With these points in mind, a quantitative study of the major workers of *Dorylus* was undertaken. Although the genus *Dorylus* as presently constituted may contain 40 or more species, only 24 are known from the major

workers. Because the nomenclature for African *Dorylus* has still not been determined decisively, species included in this study are referred to by number only. Correspondence with named species will be recorded in the generic revision (Gotwald, unpubl.). The goal of the research was to provide insight into the grouping of *Dorylus* species relative to the present subgeneric designations.

Materials and Methods

A set of 50 characters was chosen to describe each of the 24 species used in the study. The character set included metric, meristic, and ordered multi-state characters as well as several standard myrmecological indices. The exemplar method (Sneath and Sokal 1973: 183) of characterizing species by a selected specimen of the major worker (relatively rare in collections) for each species was used. One complete analysis was done of the full 50-character data set. A subset of 33 characters was chosen from the 1st to include only metric and meristic characters, and exclude the ordered multi-state characters. A separate analysis of the reduced, 33-character data set was performed to estimate the influence of size which dominates these characters and has influenced earlier taxonomic decisions on this group of species. To eliminate the overwhelming influence of size common to many phenetic studies (Wood 1979), all metric characters were transformed to ratios of pro-femur length, and the transformed data then served as the basis for a third complete set of analyses. Those characters (Appendix 1) retained in the reduced set are marked with an asterisk and those converted to ratios with a dagger. The complete 50-character raw data set of scores for the 24 species of this study is available from either author upon request.

Data for all analyses were first standardized by expressing each score as a deviation from the mean in standard deviation units. The standardized data set was then used to calculate average taxonomic distance from each species to every other species and the product-moment correlation coefficients between all species. Clustering on both of these similarity measures was then performed using the unweighted pair-group method on averages (UPGMA) which has been shown by a number

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² Dept. of Biology, Utica College of Syracuse Univ., Utica, NY 13502.

³ Dept. of Entomology, Royal Ontario Museum, Toronto, Ontario, Canada M5S 2C6 and Dept. of Zoology, Univ. of Toronto.