

Among the ants (family Formicidae), the maximum normal antennomere counts are 13 in the males, 12 in females (including workers); the maxillary and labial palpi have at most 6 and 4 segments respectively; and 5 is the invariable number of tarsomeres. It can scarcely be coincidence that wasp groups showing many other similarities to the ants also display these basic numbers in their more generalized species. In even the lowest phytophagous Hymenoptera, we find the same "basic" numbers of palpomeres (6 and 4) and tarsomeres (5), although the antennomeres are basically more numerous (and more variable in number). Against a general background of phyletic reduction throughout the order, the "second trochanter" found in many phytophagous and parasitic Hymenoptera (a piece apparently split off from the distal end of the femur, lost again in the higher families of the order) shows up as a "secondary increase" character like that of the extra antennomeres in *Prionus*. The pentamerous tarsal count, on the other hand, is the usual one among Hymenoptera, and no doubt carries back eventually to protoperlarian ancestors.

Meristic characters are not *always* so helpful, and within smaller taxa such as genera and tribes few or none of them may vary enough to give a clear picture of phyletic progression. So it is in the specialized ant genus *Strumigenys*, with over 150 known species (Brown, 1962); one cannot yet say with certainty in this genus which characters (and consequently, which species) are primitive, and which are derivative.

It is nonetheless possible to arrange the species of *Strumigenys* in branching relationship-chains, or "open-ended morphoclines," without making a hard-and-fast decision as to which free end of the chain represents the primitive condition. As evidence gathers, in the form of newly discovered species and closer investigation of the ones already known, it is often possible to "polarize" such a morphocline—that is, to show its probable evolutionary direction(s) and to point out the loose chain-end that is

most likely primitive. Elements of the theory of morphoclines are set forth in an apparently neglected paper by Maslin (1952) in *Systematic Zoology*; this article is sensible reading for any systematist. But even before a happy state of phylogenetic polarity is attained, the open-ended morphocline can be a valuable basis for classifying and thinking about any taxon above the species level, as I have found in working with the aforementioned genus *Strumigenys* and other ant groups.

Possibilities for the Future

It may well be that the reasoning used in constructing a morphocline, taking account of the reduction rule, is a better way to approach classification and phylogeny than the best that numerical taxonomy has to offer. One notes that numerical taxonomy has worked out rather poorly in the mosquito genus *Aedes*, where Rohlf (1963a, b) has not been able to align larval- and adult-based systems in spite of the employment of a large number of characters from both adults and larvae. Furthermore, two different methods of analysis yielded different results for Rohlf, even for the same stages of the same species-field (Barr and Chapman, 1964). One wonders how a reduction-morphocline approach might work on this collection of *Aedes* species; there has been no opportunity to try it yet.

In my opinion, numerical taxonomy's chief virtue has been its need to see the characters systematically and completely compared for all taxonomic units. The best modern form for such a comparison is a matrix in which every taxon is listed against every character used in the study. This form has been used by many taxonomists in past years, especially for the "rough work" of keymaking. It should be developed and consciously used much more widely in systematic work.

Summary

1. Numerical taxonomy is inadequate to deal with systematic situations involving adaptive convergence since these