

## A Plea for Tabulated Descriptions, Keys and Illustrations

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Taxonomists are wed to techniques that probably date back to Linnaean times: paragraphic descriptions, dichotomous keys, and all structures of one species illustrated on the same plate. I think it is time to reexamine these methods to determine whether they ever served their original purpose and whether other methods are more appropriate to modern systematics and computer technology.

### Descriptions

Paragraphic descriptions certainly make describing easy. One can start at the front end of the organism and conveniently describe continuously to the tail end. This technique allows the luxury of very detailed description especially of difficult shapes and color patterns. On the other hand, what taxonomy has to offer biology is the comparison of well-analyzed characters, and it might be argued that except for numerically extreme characteristics an isolated description is impossible to use. For the user, the paragraphic description makes comparison very cumbersome, and, in the case of the study of many species, almost impossible. Furthermore, the paragraphic method often makes it difficult for the author to be consistent in the description of the same character—by the time the 15th species of a genus is being described, one often cannot remember precisely how the eyeball was described for the sixth species, and an otherwise similar eyeball may be inadvertently described in slightly different words. Such variation may be fine for writing style, but is disastrous for comparison.

The vast majority of paragraphic descriptions include without distinction, unique and derived conditions along with primitive ones, and sometimes higher category characters as well. To sort these out the reader is required to thumb through many pages of descriptions and wade through the paragraphs. Distinctions among these types of characters may not be the function of a description, but if such distinctions are made elsewhere (as in character analyses or diagnoses), then there is much overlap and wasted verbiage. If the distinctions are made in diagnoses, there is the possibility of comparison with the wrong species if the postulated relationships are incorrect. When this happens, the user can only go through all the descriptions to work out new comparisons.

All these problems are easily solved with tabulation of characters, a technique which adds, in my opinion, only minor additional complications. Comparison and consistency is almost automatic both for the writer and the reader. One can differentiate unique, derived and primitive conditions at a glance and this can be made even easier with the use of different fonts (also possible in paragraphic descriptions it must be admitted). The problem of mistaken relationships in diagnoses is avoided entirely because the reader can locate other possible

relationships and similarities readily. One great advantage of a table is flexibility in arranging the sequence of characters for a variety of purposes; and the user can quickly locate characters, no matter what their arrangement, because of the ease of finding the different columns. In paragraphic descriptions one is almost rigidly limited to a head to tail sequence; imagine the difficulty in finding characters buried in a paragraph if another arrangement is used.

Perhaps the greatest advantage to the use of tables is the ease with which they lend themselves to computerization. Identification and analysis of relationships are, after all, matters of searching through a data base, something a computer can often do far more efficiently than our minds can. Because all conditions of each character are displayed at once in a table, they can be readily coded. Such codes can be added to the table making evaluation easy, problems readily apparent, and corrections simple.

### Keys

Keys are also hoary remnants of early days in taxonomy. For well differentiated taxa and for those readers very familiar with groups, keys may be convenient. However the very technique of constructing keys limits their utility. Technically, perhaps the best keys are those that utilize the unique characters of each of the taxa included. This kind of key must of necessity have only one couplet less than the total number of taxa, making it cumbersome to use for any more than a few taxa. To alleviate this problem, characters common to successively smaller groups of species are usually utilized. Unfortunately, the search for this type of character, that are also the least variable, often leads to the use of obscure features that are hard to use. The attempt to shorten a key by using these characteristics in common often leads to completely artificial arrangement of taxa. With such an artificial arrangement a single mistake made in running a specimen through the key even in the last couplet often results in an identification of a species unrelated to the true one. For the same reason an undescribed species not in the key is difficult to place unless it is very similar to a taxon in the key in all of its key characters. And even if a new species has all of the key characters of one in the key, the relationship may still be quite wrong. Furthermore, if the user is unable to make a decision in a particular couplet, the only way to proceed is to run the specimen down each of the two alternative pathways from that couplet and to compare the diagnoses of each of the final taxa—an impossibly cumbersome method in all but the shortest of keys. Finally, the user has no way to identify or retrieve his own errors except by laboriously comparing every feature with the description.