Comments and Communications

Taxonomic Characteristics for *Amoebae*

In a recent communication by King and Jahn (*Science*, March 19, pp. 293–294) it has been suggested that the names *Amoeba proteus, Chaos carolinensis,* and *Pelomyxa palustris* be used in referring to the well-known species *Amoeba proteus* Leidy, *Pelomyxa carolinensis* Wilson, and *Pelomyxa palustris* Greeff, respectively. The argument is based on the contention that "the type of locomotion of an ameba is one of its principal taxonomic characters."

It is maintained that "*P. palustris* does not ordinarily form pseudopodia, and certainly it does not locomote by means of pseudopodia." Furthermore, it is held that locomotion in *Amoeba proteus* and in *Pelomyxa carolinensis* is the same, for which reason Schaeffer put them into the same genus, *Chaos.*

Facts reported in the literature do not support the contentions of King and Jahn, however. It is known from the work of Mast that "the process of locomotion in *Pelomyxa palustris* is essentially the same as in *Amoeba proteus*" (*Physical. Zool.*, 1934, 7, 470–478). Moreover, Wilber has shown that there are consistent differences in the details of locomotion in *Amoeba proteus* and *Pelomyxa carolinensis* (*Trans. Amer. mic. Soc.*, 1946, **65**, 318–322). If the published facts contradict the premises of these authors, it is obvious that the method of locomotion is not a "valid generic character."

King and Jahn refer to a quotation from a paper by Wilber (*Trans. Amer. mic. Soc.*, 1947, **66**, 99–101) in which it is stated that general differences of form are unsafe taxonomic characters for amebas. They say that in view of Schaeffer's 1926 monograph the stated position is invalid. Moreover, they seem to imply that because one paragraph is questioned by them, the conclusions in the paper (to the effect that *Amoeba proteus* and *Pelomyxa carolinensis* are valid species properly named) are unwarranted. They fail to point out that in the same paper reference is made to the writings of Greeff, Wilson, Lankester, Kudo, and others, all of whom support the contention that the "nuclear condition is of first importance in determining whether a rhizopod is an *Amoeba* or a *Pelomyxa.*"

General shape of amebas and superficial characteristics of locomotion are dangerous to use as taxonomic norms because environmental factors of various sorts exert profound changes in the form of *Amoeba* (see Mast. *J. exp. Zool.*, 1928, 51, 97–120). Such factors do not, however, change the nuclear condition.

Kudo (*J. Morphol.*, 1946, 78, 317–352) has discussed the question of nomenclature for the genus *Pelomyxa* and comes to the conclusion that "it seems reasonable to consider that *P. palustris* and *P. carolinensis* are two valid and distinct species."

In view of the fact that the evidence in the literature does not support the view of King and Jahn, it seems that their breakdown of these controversial rhizopods into three genera is unwarranted. The weight of present evidence indicates that the following are valid species: *Amoeba proteus, Pelomyxa carolinensis, Pelomyxa palustris.*

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The Native Proteins as Polycondensations of Amino Acids

The native proteins are polycondensations of α-amino acids, NH_2—$HC_\alpha R$—$COOH$, about 21 different species and 2 cyclic amino acids being obtained to date. The proteins are of unknown structure, and the question then arises as to the light which organic polycondensations of known structure can throw upon this problem. So far there has been no indication of a stepwise polycondensation resulting in the synthesis of protein. However, just as the structure of the silicates can be resolved without reference to geochemistry, so the structure of proteins can be studied without reference to the anabolic path. The known atomic patterns of minerals (W. L. Bragg. *Atomic patterns of minerals.* Ithaca, N. Y.: Cornell Univ. Press, 1937) indicate how these structures can be formalistically analyzed into certain "monomer" units, in a definite spatial pattern. The study of proteins has a similar objective—the discovery of the spatial patterns in which the amino acid residues are interlocked.

There are a few similarities between organic high polymers in general and proteins in particular. Both comprise large molecules in which many atoms are interlocked by primary valences; in both, secondary valences can affect the formation of particles whose size and shape may vary widely with variations in the experimental conditions. The dissimilarities, however, prove to be more numerous and more significant. (1) High-molecular-weight materials, in general, are not uniform and do not consist of molecules or particles which are chemically identical. The word *macromolecular* focuses attention on this fact. The word *megamolecular* was correspondingly introduced to focus attention on the diametrically different situation in the proteins. (2) Proteins, in general, crystallize—and indeed maintain their existence—only with the aid of foreign molecules or ions, notably water. Furthermore, one and the same protein can crystallize with different water complements (D. Crowfoot. *Chem. Rev.*, 1941, 28, 215). (3) The single category of substance, protein, has already yielded crystals belonging to all the crystal systems. (4) The incidence of high, even cubic, symmetry, among the crystalline proteins, distinguishes them from all other organic materials. (5) Twins and intergrowths are frequently observed. (6) Macromolecular substances do not crystallize with anything approaching the degree of perfection of small molecules. By contrast, X-ray diffraction patterns, indicating a very high degree of regularity, have been obtained from certain proteins in their mother liquor (Crowfoot, *op. cit.*). (7) All the amino acids in proteins have