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.*

CHARLES G. WILBER

Fordham University

The Native Proteins as Polycondensations of Amino Acids

The native proteins are polycondensations of α-amino acids, NH_2—HC_aR—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

the same (levo) configuration. By contrast, macromolecular polypeptides recently obtained can incorporate both dextro and levo residues. (8) Proteins, with their tendency to 'denature,' are intrinsically unstable, a characteristic setting them apart from most—possibly all—other substances.

These many differences carry a number of implications. (1) There is a deep-seated antithesis between the structure of organic macromolecules and of protein molecules. A macromolecule, whether it is a chain (with or without branches or cross bonds) or whether it is a 2- or 3-dimensional network, is 'open': it comprises any one of a range of different numbers of monomers, the range being dependent on the method of preparation. Evidently a protein, by contrast, comprises a coherent, integrated spatial pattern of its residues. The growing indications that many proteins are particles and not molecules emphasizes the possibility that proteins may contain relatively few residues per molecule. Thus, with the emergence of insulin as a trimer (J. L. Oncley. *Science*, 1947, **106**, 509) comprising 3 subparticles (which may or may not be molecules), the molecules apparently have a maximum molecular weight of $\sim$ 12,000. Such relatively small molecules would resolve the apparent conflict between the hypothesis of characteristic skeletons for all proteins and the wide variety of 'molecular' weights and shapes. Actually, it is already known in numerous cases that such weights and shapes refer to particles, not to molecules. (2) The characteristics of crystalline proteins mentioned above in (3) and (4) have already been encountered in crystallography—in the silicates and alumino-silicates (Bragg, *op. cit.*). There they are known to be a direct indication of the presence of a major theme, comprising a cubic motif or a motif on a cubic lattice or lattices, accompanied by a minor theme which may or may not be cubic. This permits the interpretation of these protein characteristics on similar lines (D. Wrinch. *Amer. Mineral.*, 1947, 32, 695; 1948, in press). In this event, the major theme would be the interlocked (N—C_a—C) skeletons of the protein molecules; the minor theme, the R-substituents and the foreign molecules or ions. This viewpoint gains support from the fact that many of the hemoglobin twins can then be interpreted, as in the case of inorganic twins (e.g. staurolite, tetrahedrite), as due to the emergence of the major theme. (3) To interlock into skeletons which are cubic or lie on a cubic lattice or lattices, the anorthic (N—C_a—C) units require, in some or all cases, a functionality higher than two. It is suggested that this higher functionality, which distinguishes a protein from a Fischer polypeptide or a cyclic polypeptide (D. Wrinch. *Proc. roy. Soc.*, 1937, **A160**, 59; *Phil. Mag.*, 1938, 25, 705; 1947, 38, 373; *J. Amer. chem. Soc.*, 1941, 63, 330), is effected by means of a labile bond (explaining the intrinsic instability of protein molecules), and that the opening of labile bonds, *i.e.* disjoining of the molecular skeletons, is the real meaning of the so called 'denaturation' of proteins, a phenomenon entirely distinct from dissociation of a particle into subparticles or molecules. (4) To form crystals of so high a degree of regularity, protein molecules must be capable of multipoint associations. Precisely this problem is successfully solved by the large phosphotungstic acid anion by a cubic structure whose enveloping polyhedron apposes its faces to form symmetric intermolecular associations and symmetric associations with symmetric water clusters. The points of similarity between the proteins and the 5- and 29-hydrates of phosphotungstic acid (Wrinch, *op. cit.*) suggest a similar picture for proteins. The occurrence, in 2s and 3s and 6s and 12s of certain amino acids would be expected in protein molecules, though not necessarily in protein particles, if the intermolecular protein associations are also to have symmetry elements. (5) The uniform (levo) character of the amino acids in proteins seems to be the clearest indication of a "surface" structure for protein skeletons, the uniform configuration then permitting the emergence of all Rs. It has recently been shown that this same conclusion, a structure one residue thick, follows from the study of the nature of protein replication (Wrinch, *op. cit.*). It is also supported by the fact that many proteins, diverse in nature, form monolayers on the surface of water with thicknesses of 7–11 A. (6) The nature of the labile bond in protein skeletons remains to be established. A lactim-lactam transformation has been suggested (Wrinch, *op. cit.*). Such a viewpoint affords simple interpretations of recent studies of denaturation and of degradation products of proteins. Taken with (4), the hypothesis that protein structure is, for the most part, an exercise in the interlocking of oligo-peptides presents itself. In the original formulation (Wrinch, *op. cit.*), these comprised cyclic hexapeptides and tetrapeptides. It may now be pointed out that the coherence of the smallest such structure can be maintained with 4 hexapeptides plus 6 tetrapeptides or 8 hexapeptides, yielding a skeleton residue number of 48 and molecular weight slightly below 6,000. These two 48-residue structures suggest that complete cyclic hexapeptides or tetrapeptides or smaller peptides can be incorporated into, or deleted from, protein molecules without disjoining the skeleton, a picture which may be studied in connection with Schoenheimer's original results and with the relations between certain proteins and their precursors. Each 48-residue structure has 24 residues still in the bifunctional form. Here, then, are sites for the insertion of residues or peptides by one terminal only, leaving a free backbone —NH_2, such as have been found for some proteins and/or a free backbone—COOH. In this event some of the residues covered by the chemical analysis of a protein may be functioning as substituents on, rather than as parts of, the molecular skeleton, with the residue number and the skeletal residue number no longer identical. Significance in terms of symmetry elements is only to be expected for the latter. 'Raw edges,' when present, may also be sites for synthesis of nonprotein structures, and there are indications that the close biological relationship between the proteins and the alkaloids and the nucleic acids has its locus at such positions on the molecular skeletons of proteins.

DOROTHY WRINCH

Smith College