Letters

Progenote or Protogenote?

Questions of scientific terminology have no theoretical significance. They may, however, become significant for the practical task of avoiding confusions. We point out here three recent terminological proposals (*1–3*) and argue against them.

The issue is connected with the work of Carl Woese and his collaborators. He developed in the late 1960s a universal biochemical basis for systematics, including the systematics of microorganisms to which earlier taxonomical methods had been applied without success. Theoretical considerations led him to choose ribosomal RNA as the most sensitive universal evolutionary clock which, he conjectured, would reach back even to organisms with a rudimentary translation machinery. It took 10 years of pioneering experiments to test both his theory and his taxonomic method. The result is now history—the establishment of a universal tree of life (*4, 5*). This great work of discovery and the new problems raised by it justified fully the introduction of two new cytological terms, "progenote" and "genote" (*5, 6*), for organisms with either a rudimentary or a modern translation machinery; and also of a phylogenetic term, "universal ancestors," for organisms below and including the deepest branching. The clear distinction between phylogenetic and cytological terms helped Woese formulate one of the most fascinating and fundamental open problems of biology: Did the progenote-genote transition occur in the stem of the universal ancestors or perhaps at the deepest node itself (if the deepest branching is a node), or only in the three primary branches (*6*)? Answers to this question would presuppose a solution to the wide open problem of the origin and evolution of biochemical isolation against lateral gene transfer. (Incidentally, after these results were achieved, the new names "eucarya," "archaea," and the old name "bacteria" were proposed for the three highest ranking taxons by Woese, Kandler, and Wheelis (*7*); a suggestion that should help one to avoid in the future the somewhat precipitate conclusion that eubacteria and archaebacteria are closely related.)

We think it is important that great achievements should be protected against terminological confusion. In this context we plead for the rejection of the following three linguistic proposals.

1) The recent proposal (*1*) of the term "breakthrough organism" as a synonym for the cytological term "progenote" should be rejected. No justification has been offered for this change.

2) The more recent misuse [for example, (*2*)] of the term "progenote" as a replacement for the phylogenetic term "universal ancestor" should be avoided, since it arose from a mistaken reading.

3) The most recent proposal (*3*) of the new name "protogenote" as a phylogenetic name for the most recent universal ancestor should be rejected because of its confusing similarity with the cytological name "progenote"; and also because it would create the illusion that the problem of the origin of biochemical isolation has been solved, which unfortunately is not the case.

We all may at times be seduced by the tempting ease of introducing new words. But then, we should always respect the forbidding difficulties facing those who toil to establish new facts. As the founders of the Royal Society of London put it in 1663: *"Nullius in verba"*—there is nothing in words. It is facts we seek.

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Hair Analysis

We agree with statements quoted in the recent article "Hairy problems for new drug-testing method" by Constance Holden (News & Comment, 7 Sept., p. 1099) to the effect that insufficient data exist for hair drug analysis to be used for preemployment or mass screening procedures. However, we have found that in clinical treatment and research capacities, testing of hair for the presence of drugs and metabolites is a valuable tool for correlating long-term drug abuse with biological parameters and use histories. Using commercial radioimmunoassays, we screened hair from men for metabolic products of cocaine [benzoylecgonine (BE)] and heroin (morphine). A good correlation existed between the levels of BE and modification of a variety of immunological markers: natural killer cell activity, distribution of T cell subsets, and cytokine release. Only a few hair samples in our study contained detectable levels of morphine, although the majority (67%) were positive for BE. Hair analysis allowed us to assess drug use for 1 to 12 weeks after the last incidence and to validate verbal reports of drug use. However, urinalysis allowed us to identify only 37% of subjects as cocaine users and did not adequately support verbal histories. It therefore appears that hair analysis could be used to check contested urinalyses.

We also found that the uptake of both BE and morphine into the hair of mice injected with cocaine and morphine was directly proportional to the dose administered. Infection of these animals with a retrovirus, LP-BM5, which causes an acquired immuno deficiency disease in mice, almost doubled the amounts of BE and morphine in hair. Hair analysis has been used clinically to determine whether mothers have used drugs by detecting whether metabolites are present in fetal hair (*1*). Hair testing has been used successfully to detect the use or concentrations of many drugs of abuse as well as trace elements (*2*). Although all the parameters that could affect hair analysis for drugs of abuse have not been established, we believe the work performed so far supports the use of hair analysis in clinical and research studies to determine long-term drug exposure. Hair analysis could contribute to the elucidation of immune deficiency and other biological changes associated with drug abuse by making possible better assessment of long-term use patterns.

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The Diaper Dilemma

Any editor, even Daniel E. Koshland, Jr., who writes an editorial such as "The Dirty Air Act" (28 Sept., p. 1481) threatens the underpinning of the American family and should be hung out to dry.

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