A PROBLEM OF MISSING LINKS AT THE ULTIMATE PRIMARY STAGE OF EVOLUTION

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Often evolutionary theory has been criticized on the basis of missing links, but in rather imprecise manner. Research in molecular biology results in quantitative contradictions of chemical and genetic theories. A rationale for replacement mutations is now under serious strain due to detection of complete absence of intermediate forms of two alleles, i.e., missing links. Again ambiguity of evolutionary hypotheses is exposed in as much as such theories lack predictive value and thus are not truly scientific.

The concept of missing links is one of the oldest criticisms of evolutionary theory. In the past the criticism has perhaps been overused, with the result that those who wish to evade this issue have been able to ignore it or dismiss it because it is not presented in a rigorous scientific manner.

However, the validity of the criticism has not been successfully challenged, and is recognized by at least some evolutionists. A recent report[1] of missing links on the most fundamental, biochemical level of evolution recalls the criticism in a form which leads to an apparent contradiction of chemical and genetic theories concerning mutational mechanisms of evolution. Moreover, at this level the question of missing links can be stated in exact quantitative form.

The elegant studies of Neurath and his collaborators on the structural details of bovine carboxypeptidase A have demonstrated two different types of heterogeneity in the highly purified enzyme protein. The first type, with which we are not concerned here, is called the activation form, which arises due to cleavage of the zymogen precursor at different sites, yielding products which differ in the length of the polypeptide chain.[2] The other type of heterogeneity, allotypic forms, is a heritable trait which follows Mendelian genetics[3], and the two alleles, which occur in approximately equal amounts, bear upon the question of missing links.

The Val and Leu forms, as the allotypes are designated, differ at three positions in the single linear polypeptides chain of the carboxypeptidase A molecule. The different amine acids which occur at these positions in the two forms are shown in Table I. The salient point of the observation, from an evolutionary point of view, is the critical fact that these replacements are linked; that is, each molecule possesses either all three amino acids of the Val set, or all three amino acids of the Leu set. There is no evidence for the existence of molecules which possess different mixtures of the replacement acids at the three sites.

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Evidence Involves Protein Biosynthesis

The significance of this finding can be comprehended only with reference to evidence from molecular biology concerning the biosynthesis of proteins and the chemical basis for mutations. Present knowledge of these processes indicates that every amino acid in a protein molecule is ultimately specified by a sequence of three nucleotide bases in chromosomal DNA. The genetic code is now known, i.e., the amino acid specified by each triplet of bases has been determined.

A replacement mutation such as those observed here is a chemical event which alters one base in the DNA so that the resulting new triplet specifies a different amino acid at that particular position. Thus the proximal result of a replacement mutation is the replacement of a single amino acid in a particular position in a particular protein by another amino acid. The ultimate result may be death of the organism due to loss or alteration of some critical functions of the protein.

Although the code has some redundancy, not all amino acids can replace each other as the result of a single mutation; i.e. two or even all three bases of some triplets must be modified for certain amino acid replacements to occur. All three of the differences in the carboxypeptidase A allotypes, however, are single-mutation replacements.

Note that the current rationale accounts for one amino acid replacement at a time. Evolutionary theory presupposes that if the protein which has a single amino acid replaced (forming a new allele) confers some advantage upon the organism in which it occurs, it will eventually replace the original allele. Subsequent mutations could then eventually lead to alleles which differ from the original protein at additional sites, if they each conferred some further advantage.

There is no reason to doubt the validity of this process, since it seems to fit with observed facts and admirably explains minor variations within a species, although complete replacement of an allele might be obtainable only under severely selective breeding, as is done with domesticated animals.

Table I

Allotype	Position		
	179	228	305
Val	isoleucine	alanine	valine
Leu	valine	glutamate	leucine

Required Intermediate Forms Absent

However, when this process is applied to the observed alleles of carboxypeptidase A, the question of intermediate forms immediately arises. The two alleles differ at three sites, and according to this rationale a minimum of two intermediate forms must have occurred. One of these intermediate forms would be changed at only one site, and the other at two sites, Additional intermediates would be required if conversion were not direct, but involved an entirely different amino acid at any or all of the sites. However, the required intermediates have been definitively shown to be absent by recent work by Neurath.

Neurath and his colleagues have suggested in 1969 several alternative explanations for the evolutionary origin of the alleles, acknowledging that none of them adequately account for the two missing intermediates. For instance, they are forced to postulate that the three (or more) mutations occurred essentially simultaneously early in the supposed evolutionary development of the species. This postulate implies that after that original burst of mutational activity, no further alterations occurred even though the bovine species was supposedly evolving further by incorporating many other mutations.

The postulate further requires that there are absolutely no functional differences in the two alleles, so that there would be no population pressure for selection of one over the other. Both of these possibilities are extremely unlikely. Other attempted evolutionary interpretations of the observed absences of intermediate forms are sufficiently criticized by the authors themselves.

The discomfiture of evolutionary theory at this fundamental level by precise, experimentally verifiable facts appears to this author to be devastatingly complete. As stated earlier, "microevolution" or variability at this level appears not to conflict with Biblical creationism, since limited changes are observed within a species, so the finding of missing links of this class was unexpected. The full significance of the observation may await further studies to determine whether it is a common occurrence. At any rate a new evolutionary "explanation" of the observation will no doubt be forthcoming, for past experience has demonstrated that evolutionary hypotheses can be made sufficiently imprecise to explain any conceivable situation, no matter how implausible. The ambiguity of such theories robs them of any predictive value and thereby renders them unfit to be classified as truly scientific

References

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[2]Sampath Kumar, K. S. V., J. B. Clegg, and K. A. Walsh. 1964. The N-terminal sequence of bovine carboxypeptidase A and its relation to zymogen activation, *Biochemistry,* 3:1728-32.

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