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Overview of the Meeting

This special issue contains ten articles resulting from a small workshop—"The Aminoacyl-tRNA Synthetases and the Evolution of the Genetic Code"—that was held in Berkeley, California, on July 17–20, 1994. The meeting was arranged by Hyman Hartman under the auspices of the Institute for Advanced Studies in Biology. Funding was generously provided by the Norris Foundation. Approximately 20 scientists from North America and Europe were in attendance. The principal focus was on the recent revelation that the aminoacyl-tRNA synthetases fall into two apparently unrelated groups of ten. The subject was addressed from the diverse viewpoints of genetic coding, three-dimensional X-ray structures, and amino acid sequence comparisons. The nagging question was: is there any connection between the nature of the genetic code and the allocation of the enzymes into the two groups? Put more extremely, was the evolution of the enzymes coincident with the evolution of the code? In the end, the majority view was that the aminoacyl-tRNA synthetases are after-the-fact concoctions that must have displaced earlier decoding systems. Certainly primitive protein coding systems had to begin without the assistance of coded proteins. Several of the articles in this issue address the point. For example, Nicholas and McClain conducted a statistical analysis of all known tRNA sequences in which they searched for any correlation of any nucleotide(s) that could be predictive of synthetase class membership. They found none and concluded that either none ever existed or they have been irretrievably lost during the course of evolution. Discussion also centered on why there were two equally represented classes and whether this was coincidence or reflected some natural advantage. As for the history of gene duplications in the two families, it was obvious that some are easy to chronicle, but the deeper phylogenies are proving more difficult to unravel. Thus, in the case of the class II enzymes, the relationships of the Thr, Ser, and Pro enzymes, on the one hand, and the Asp, Asn, and Lys, on the other, are quite obvious, but the relationship of the Gly, Ala, Phe, and His enzymes remains a matter of dispute. Similarly, in class I, the Val-Ile-Leu-Met cluster has been apparent for several years, as have the Tyr-Trp and Glu-Gln pairs. But the deeper phylogeny of all ten enzymes, including Cys and Arg, is not firmly resolved.

Participants were treated to a veritable panorama of X-ray structures illustrating the mechanism of action of the class II enzymes. These studies, reported by Härtlein and Cusack, underscored the fundamentally different chemistry employed by these enzymes compared with the previously studied class I. Like the class I enzymes, catalysis is more or less limited to one domain and the binding of tRNAs to another, the latter differing remarkably among the different subclasses.

The small size of the group and the general informality contributed to friendly but intense discussion. The participants, several of whom had traveled long distances for the sole purpose of this meeting, were uniform in their agreement that the gathering was extremely informative and worthwhile. We hope readers will find the articles to be equally valuable.

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Guest Editors