Multi-author Reviews

Genetic Code 1990

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Genetic code 1990. Introduction

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I still vividly remember the morning when our microbiology teacher, Urs Leupold, entered the class waving a newspaper with the headline 'Genetic Code cracked'. A furious race between competing laboratories had come to its end, the 'Code Sun' (C. Bresch) had been established. This sun shone, brilliant and immaculate; each amino acid had been assigned its codon(s), and that was that. However, as in real life, slowly, and in exponential order, sunspots began to appear. The classical wobble rules were questioned, and more and more exceptions found, and, with some delay, also accepted. However, these deviations from the wobble rules did not excite the general public, it was rather something for specialists. This situation has now drastically changed. Nowadays we cannot always simply deduce the protein sequence from the sequence of a mature message. Ribosome and tRNA hopping, frameshifting, readthrough, and RNA editing have to be considered. Furthermore, it was discovered that the code was not as universal as originally thought. Some organisms and organelles (e.g. ciliates, mycoplasma, mitochondria, chloroplasts etc.) have some codewords of their own. The field has become more complicated, but at the same time has also regained the original excitement.

At the 1989 tRNA workshop in Vancouver, I asked some friends and colleagues whether they would find it useful to compile an issue on the 'Genetic Code 1990'; they were enthusiastic, and the result is now presented in this multi-author review. I have asked the authors to put more emphasis on a personal view than on complete coverage. Thus, the blame for any omissions should fall on the coordinator of this review and not on the authors.

The accuracy of aminoacylation – ensuring the fidelity of the genetic code

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Summary. The fidelity of protein biosynthesis rests not only on the proper interaction of the messenger RNA codon with the anticodon of the tRNA, but also on the correct attachment of amino acids to their corresponding (cognate) transfer RNA (tRNA) species. This process is catalyzed by the aminoacyl-tRNA synthetases which discriminate with remarkable selectivity amongst many structurally similar tRNAs. The basis for this highly specific recognition of tRNA by these enzymes (also referred to as 'tRNA identity') is currently being elucidated by genetic, biochemical and biophysical techniques. At least two factors are important in determining the accuracy of aminoacylation: a) 'identity elements' in tRNA denote nucleotides in certain positions crucial for protein interactions determining specificity, and b) the occurrence in vivo of competition between synthetases for a particular tRNA which may have ambiguous identity.

Key words. trNA; recognition; identity; aminoacylation; mischarging.

Research is a cyclical process. Fields develop and mature and create unified concepts. Fashion and research then move to other areas. Meanwhile, with the development of new methods the original concepts may be reexamined by novel and more incisive techniques which often give rise to findings which challenge accepted notions. In just such a way, the methods of molecular biology, gene synthesis, and in vitro genetics have rejuvenated the field of protein biosynthesis, where new views on the structure and action of ribosomes[3,37], tRNA function[3,46,51], tRNA identity (see below), and coding for 'new' amino acids (reviewed in this volume) have emerged. The arti-