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PROCEEDINGS OF THE SYMPOSIUM "MACROMOLECULAR IDENTIFICATION AND CLASSIFICATION OF ORGANISMS" (ANTWERP, 1991) :

INTRODUCTION

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In the last years the Royal Botanical Society of Belgium successfully organized several one-day-meetings or mini-symposia in cooperation with other societies. In 1991 the choice of the theme "Macromolecular Identification and Classification of Organisms" made it evident to meet with the Royal Zoological Society of Belgium and the Belgian Biochemical Society. Since the association Young Belgian Researchers tries to promote communication between young researchers and helps them to get access to the information they need, its goal was fully in line with that of the organizers. The Biochemistry Department of the U.I.A. (University of Antwerp) agreed to be the host institute providing the necessary facilities for the organisation of the meeting.

The purposes of the organizers were double : (1) to introduce classical taxonomists into the new methods of molecular classification and identification and (2) to bring together practitioners of the molecular approaches, mainly from Belgium and neighbouring countries and improve mutual contacts and communication.

Whether these goals have fully been reached can only be answered by the participants. At any event, there was great response ; more than 200 participants from Belgium, the Netherlands, France and Germany have attended the program with 9 lectures and 52 poster presentations. They covered a broad diversity of organisms (from bacteria to all major groups of animals and plants) together with a multitude of techniques (from isozymes to DNA sequencing).

The present Proceedings, containing a selection of papers or short articles based on the lectures or posters, and abstracts of most other ones, reflect the scientific content of this Symposium and provide to any reader a first access to different aspects of molecular identification and classification.

Until the first part of the twentieth century, identification and classification, or systematics as a science, used the human sensory capacities to interpret Gestalt and general morphology. This was the basis of all classical surveys of the diversity of fossils and living beings. Since then, the scope of systematic evidence was gradually broadened, and today four levels of taxonomic information are available, as explained in the lecture of GILLIS (page 221, this volume) : (1) the structure of nucleic acids ; (2) the structure of proteins ; (3) the chemical structure of cellular components ; and (4) the phenotype, in the broad sense.

New methods of chemical analysis have allowed to explore the third level of secondary compounds, and chemotaxonomy is flourishing until today. The access to the first and second level of information, namely the macromolecules, was opened owing to the technical progresses in biochemistry and molecular biology. It gives the possibility to decipher the genetic information, directly at the source of all the

variations which may affect the following levels of taxonomic information. Because these levels, particularly the third and fourth ones, result from the interactions of many genetic factors with each other and with the environment, it can be difficult to distinguish true homologies from so-called homoplasies (parallel evolution and reversals). However, complex mechanisms are also acting at the level of the genome and interpretation of macromolecular data may not be straightforward (Nei 1987). As any new area of development, the macromolecular approach has given rise to overoptimistic expectations and overnegative criticisms. More trivially, it also has introduced, once more, a new vocabulary ; this "slang" may complicate communication and act as a barrier if one is not aware of the obstacle. These Proceedings are too limited to address the problem but the reader can consult the books by Hillis & Moritz (1990) and Crawford (1990).

As discussed by Hillis (1987), the molecular and the morphological approaches have their own advantages and limits and "Morphological techniques are applicable to an enormous range of museum and fossil material, and a large portion of the Earth's organisms will continue to be studied primarily or exclusively from morphological information. On the other hand, the potential molecular data set is incredibly extensive and, when fully utilized, should provide a detailed record of the history of life. Studies that combine the two approaches can thereby maximize both information content and usefulness." Only five years later both fossils and museum specimens belong to the study objects of molecular biology.

Hillis also warned that the methods of data analysis should be carefully selected, an aspect sometimes neglected. From the viewpoint of interpretation, we consider it a happy circumstance that "fourth level taxonomy" (systematics mainly based on morphology) is now aligned to macromolecular systematics. In the two doctrines formal analyses use either distance matrix or parsimony methods. These were shortly compared in the lecture of Beintema (p. 159, this volume). The reader is referred to the book of Stuessy (1990) for a magistral discussion and comparison of these two fundamentally differing approaches.

The present Proceedings illustrate the contribution of the macromolecular approach to very different taxonomic problems, from the identification of sibling species to the inference of the evolution of all the living beings. Organisms studied are as diverse as bacteria, protists, fungi, animals and plants. However, the uniting thread going through all the contributions is the search to reconstruct evolutionary processes using the new macromolecular information sources.

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