

SOME PROPERTIES OF THE MAJOR COMPONENTS OF THE MOUSE GENOME

by G. Cuny, G. Macaya, M. Meunier-Rotival, P. Soriano and G. Bernardi

*Laboratoire de Génétique Moléculaire,
Institut de Recherche en Biologie Moléculaire,
2, Place Jussieu, 75005 Paris*

The technology of *in vitro* recombinant DNA has already achieved a major break-through in the field of the organization of the eukaryotic genome by demonstrating that, contrary to all expectations, eukaryotic genes may contain nucleotide sequences which are not represented in the mRNA transcripts which are translated into proteins. It is quite clear, however, that this new approach may also provide other original insights into the more general problem of genome organization in eukaryotes.

This problem has been mainly studied, so far, by investigating the kinetics of reassociation of DNA. Such an approach has shown that segments of eukaryotic genomes can be classified into different families according to their rate of reassociation; furthermore, it has shown some inter-spersion relationships among DNA segments belonging to different families.

Another experimental approach used in this area has consisted in resolving native DNA fragments by centrifugation in density gradients. Such a method has proven very useful for the separation of « satellite » DNA and of repetitive genes.

More important, density gradient centrifugation has revealed that the bulk of mammalian DNA is formed by three major components, which can be separated from each other. These components comprise : 1) a main component forming 50 to 65 % of total mammalian DNA; in different mammals, this ranges in buoyant density from 1.697 to 1.701 g/ml and can be resolved, in several species, into two sub-components; 2) a component forming 20-25 % of total DNA, and having a buoyant density of 1.704 g/ml; 3) a component forming about 10 % of total DNA and having a buoyant density of 1.708 g/ml. Major components similar to those found in mammalian DNA appear to be present in avian DNA, whereas reptilian, amphibian and fish DNA exhibit a decreasing asymmetry of their CsCl bands; invertebrate DNA show symmetrical CsCl bands. This findings just outlined indicate the existence of phylogenetic differences at the macromolecular level in the organization of eukaryotic genomes, and raise the problem

of the evolutionary origin of the major components of mammalian DNA.

We will report on the organization of nucleotide sequences in the major DNA components of mouse and the localization of certain genes in such components.

KEY-WORDS: Genetic engineering, Eukaryotic genome, Phylogenetics; Note.