proposed to account for this disappearance of the intragenic regions during the process of transcription or shortly afterwards is that both the intragenic and expressed sequences are first transcribed into a precursor *m*RNA (HnRNA). After that the inserts are excised while the released coding regions are spliced to from the final active *m*RNA. Specific enzymes are responsible for this processes.

According to speculations on the possible function of the intragenic sequences the most probable alternative is that they have some control function in the regulation of protein synthesis (MARX, 1978).

The new model of " the gene in pieces " gives rise to some interesting aspects on the *origin of genetic variation.*

First, moderately repetitive sequences within the intragenic regions are supposed to be sites where recombination through crossing-over frequently occurs (GILBERT, 1978). Obviously, such recombinational events would change the base sequences of the intragenic regions of DNA (outside the repetitive sequences) as well as the order between the expressed regions. Thus, these changes within the gene would be comparable with some sort of major mutations. If such within-gene rearrangements are not rare they should be a tremendously rich source of new genetic variation in a heterozygous population. In fact, they could for instance easily explain (1) why selection in such a population can result in strains which after a number of generations transcend the limits of variation in the original population, or (2) why crossing of two different lines after they have reached a selection plateau can give rise to new genetic variation for selection to work on.

The recombinational changes of the intragenic base sequences of DNA would, in accordance with the earlier assumptions, give rise to changes in the rate of protein (enzyme) synthesis by regulation of the rate of transcription while the changes of the order between the expressed regions would generate new combinations of polypeptides coded by these regions.

Consequently, eukaryotes would be able to develop new, complex functions faster than prokaryotes without any need of increasing the rate of mutations in already existing base sequences (DOOLITTLE, 1978).

In animal breeding selection has mainly been focused on increasing the rates of synthesis of various products suitable as food like milk, eggs and meat. It seems therefore natural to assume that these improvements have been brought about by increasing the rates of synthesis of those enzymes which are responsible for catalyzing the reactions involved in the production processes referred to. If this is true, the variation caused by differences among the controlling genes should constitute the main part of the genetic variation exposed to artificial selection.

## IMMUNOGENETICS: A REVIEW AND FUTURE PROSPECTS

B. GAHNE

*Departement of Animal Breeding and Genetics*
*Swedish University of Agricultural Sciences, S-750 07 Uppsala, Sweden*

The following areas of immunogenetics are briefly reviewed: red cell and histocompatibility antigens, immune response genes, general genetic immune responsiveness, allotypes and immunodeficiencies. The emphasis is placed on basic principles and on farm animals. Some applications and future prospects within the field of immunogenetics are also discussed.

## MOLECULAR APPROACH TO QUANTITATIVE INHERITANCE

M. GILLOIS, C. CHEVALET and A. MICALI

*Laboratoire de génétique cellulaire*
*Centre de Recherches de Toulouse, I.N.R.A.,*
*B.P. 12, 31 320 Castanet, Tolosan, France*

Two main ideas are considered: genes do not work independently, but according to one or many ordered sequences as in metabolic pathways; and genes code for sequential molecules whose main property is to enter into stereospecific associations, involved in enzymatic catalysis and in regulation mechanisms. Quantitative effects and interactions of genes are defined as resulting from the dynamical processes attached to biochemical networks. First results about one enzymatic step are quoted, and discussed with respect to their relevance to quantitative inheritance.