III. — Développements actuels en matière de génétique élémentaire

Origin and maintenance of genetic polymorphism

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The current controversy in population genetics concerns the mechanism, by which single-gene polymorphisms are maintained. As the levels of heterozygosity per locus per individual are in vertebrates around 20 p. 100 and in invertebrates over 50 p. 100, it is assumed that most of this polymorphism is adaptively neutral rather than balanced. There are also selective hypotheses that would resolve the paradox of the genetic load.

Selection theory with overlapping generations

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The implications for selection of genetic differences between animals of different ages and between progeny of the same age but from parents of different ages are discussed. Correct definitions of generation length and of selection differential when replacements are selected disproportionately from parental-age subgroups can be made in two ways. Seeking most rapid genetic gain may involve using many young dams despite their poorer maternal ability. Making proper allowances for genetic age effects is similar in principle to making allowance for genetic trend and for parental breeding value in BLUP methods.

Matrix methods of predicting response to selection are illustrated by an example with disproportionate selection from parental-age subgroups. Proper specification of an appropriate control population is essential for evaluation of genetic gains, but if a control population is established from a line previously under selection it may show appreciable fluctuations in mean quite separate from genetic drift, and the final control population mean may be significantly different from the initial mean even in the absence of environmental change. The relative contributions of the control line and the selection line to fluctuations in genetic gain depend on the initial conditions.

A look at the modern picture of the gene

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In comparison with bacteria and other prokaryotes much less is known about gene expression and its control in *higher organisms* with their much more complicated nucleated cells. However, recent discoveries in this field of research have contributed significantly to the development of the picture of the eukaryotic gene (as reviewed by WILLIAMSON, 1977; MARX, 1978; GILBERT, 1978; DOOLITTLE, 1978). These findings from basic genetical studies carried out many laboratories (e.g. BREATHNACH *et al.*, 1977) show that the organisation of genes in higer organisms is not the same as in primitive, prokaryotic organisms.

Thus, the *eukaryotic gene* has been found to be organized so that the structural genes are subdivided into several smaller expressed (coding) regions with larger intragenic regions of DNA inserted between them. These inserted sequences are not found in the final *m*RNA transcript of the gene, i.e. their genetic message is not passed on to the ribosomes where the proteins are synthesized by means of the process of translation The most probable mechanism which has been

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

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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

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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.