

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 in many laboratories (e.g. BREATHNACH *et al.*, 1977) show that the organisation of genes in higher 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 mRNA 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