

THE EFFECT OF MAJOR GENES IN ANIMAL POPULATIONS

Efecto de los genes mayores
en la producción animal

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The purpose of this Roundtable was to present in a condensed form the various problems posed to scientists and to breeders of farm animals by genes with large effect on quantitative traits, illustrating general considerations by the most typical examples of major genes form in species of economic importance.

First Dr R.C. Roberts and C. Smith's paper (from Edinburgh) is a general introduction to the subject, covering a broad range of theoretical and applied aspects in a compact and very clear form for a non-specialist. After recalling that in the past little attention and importance was attributed to genes with large effect in animal breeding, the authors review the various methods which have been suggested for detection of such genes in animal populations. The purely statistical methods, based in some way on analysis of frequency distributions, are not of a high efficiency (although screening of extreme variants should not be neglected), and the safest approach is still that starting from "marker" genes identified by a qualitative effect, preferably if there are some hints on their physio-biochemical implications. A few examples drawn from laboratory species or from plants suggests some directions of research also on large animals. In connection with problems of detection or screening, mention is done of difficulties in incorporating genetic material of foreign and less productive origin into populations with high level of performance. Genetic engineering might be in the future a solution for avoiding introducing undesired genetic material besides the desired gene. Then for exploitation of a gene with large effects in a breeding program, different strategies are to be followed according to particular features of the gene effects at a quantitative level. In the simplest case of within strain selection, using classical selection methods based on the polygenic hypothesis may be sufficient, but in presence of a gene with large effect a gain in efficiency will be obtained by identifying it and taking account of it. It is shown then how genetic parameters are modified when a major gene is segregating in a population. Turning to the ease of fixing or eliminating a specified allele, it is recalled how this depends on its dominance or recessivity. On the other hand another and perhaps more widespread case will be that of a gene with an overall advantage for a heterozygous genotype ; then the optimum procedure will be making different parental populations homozygous for different alleles and crossing them. Finally, the authors stress very strongly on the fact that, before

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deciding to take account of a particular gene in a breeding program, effects associated with all genotypes at the considered locus on all economically important traits must be known with sufficient accuracy, which always represents considerable experimental work.

Dr Buss's (from Pennsylvania) contribution will be centered on examples of deeper insight at the physiological level of major gene effects in domestic birds. The well known works of Dr Buss and his coworkers on genes with an effect at the hormonal level (such as the polydipsic gene) or on transfer proteins (such as a gene causing riboflavin deficiency in the egg) suggest a general and new research approach for detection of such genes and study of their possible impact at the production level.

Dr Hanset (from Belgium) after recalling general ideas concerning problems of population and quantitative genetics in relation with major gene and their use in breeding, chooses a few among the most conspicuous examples to illustrate major gene effects in cattle and pigs. While white heifer disease in cattle shows a case of a deleterious gene with problems of elimination, both double-muscled condition and the Hal locus respectively in cattle and pigs require more elaborate breeding strategies. Dr Hanset discusses them at some length : favoring the gene responsible for the condition, or contrariwise eliminating it in breeds and / or environments where its unfavorable side-effects are too large, or breeding for polygenic modifiers reducing these undesirable effects ; still another way being to use heterozygotes for production. In pigs, the association of a "double-muscled" condition with a syndrome of halothane susceptibility has led to quite interesting developments toward understanding the effects of this mendelian complex at a more physiological level, this being completed by the discovery of close linkage with biochemical markers. Finally, in swine the finding of a recessive gene responsible for resistance to neonatal diarrhoea by absence of cellular receptors for the pathogen is a good example of a mendelian factor for genetic resistance to disease. Its recessivity and the maternal effect superimposed to the effect of the zygote's genotype lead to interpret at the level of population genetics the frequent polymorphism at the corresponding locus. On the other hand, the features of this gene show some similarity with the genes responsible for cellular resistance to tumor viruses in the fowl. Dr Hanset concludes that in specific cases the use of identified genes is able to render breeding programs more rational and more precise. The progress of laboratory techniques gives some hope of discovering now marker genes with effects on quantitative traits in the future.

Dr Ricordeau (from France) mentions a number of genes with important effect on economic traits in sheep and goats. Most concern reproductive traits, such as the gene for polledness in goats, with effects on fertility, and genital malformations in the homozygous genotype. In sheep, a major gene affecting litter size in Booroola ewes is potentially useful. Another area is resistance to disease, with an example

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concerning scrapie in sheep, and various effects associated with haemoglobin type in the same species.

It is clear that a wide range of topics has been covered. A concern is the choice of specific examples, some, like the complex histocompatibility factor in several species, were not treated only for circumstantial reasons. Concerning general problems and conclusions, contributions to the Roundtable show the main points waiting for further discussion. Methods of detection are one of them. Among those based on statistical analysis only, it might be suggested that more studies on ways of screening extreme variants by multivariate methods would be of some use. Another way is looking for new markers : biochemical, serological, pharmacological, etc... May be also genes with effect on specific nutritional requirements should be more investigated ? Then a different but related problem not commented here is conservation of unusual and rare mutants. Problems of transfer of a gene from one population to another could not be discussed at length ; in smaller species like poultry its difficulties are not completely insuperable.

The idea that the effect of a gene on all important economic characters must be known might deserve to be further illustrated by proper examples.

Breeding strategies including individual genes were discussed at some length. In many cases it is likely that genes dealt with will not correspond to the simplest model and that in particular they will affect several traits of economic importance, favorably for some, unfavorably for others. One point to consider further is the ease or difficulty of direct selection on each trait : a single gene will offer interesting perspectives if its favorable effects bear on traits on which direct selection is costly or difficult. If on the other hand the same gene has unfavorable effects on traits more easily amenable to breeding, the optimal strategy may be breeding on polygenic modifiers of the effect of the "major" gene as far as these last traits are concerned. On the other hand, cases are not rare when gene effects depend on the environment, and the best use of the gene may depend on it being limited to the proper environment(s). Finally, problems of "between populations" selection caused by single gene effects should not be ignored.