GENETIC MODELS WITH LABORATORY ANIMALS
Modelos genéticos con animales de laboratorio

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There is a general consensus on the fact that quantitative genetics has drawn off nearly all its possibilities and there is not future for more developments and advances.

Quantitative genetics at the level of mathematical models, assuming allelic frequencies and genetic values known, has been very well and exhaustively developed. Firstly, during its classical period, by Fisher, Sewall Wright, Lush, Lerner, etc., mainly considering that concerning additivity. Afterwards, interaction models were developed; being perhaps the zenith of that period the work of Kempthorne (1957). Other works interesting to note are those of Griffing (1962, 1963) and McNew and Bell (1971,1976), concerning non-additivity in crossbreeding.

Quantitative genetics at the level of real metric traits has developed a positive methodology with statistical tools to predict and interpret selection responses and other phenomena related with practical breeding. But, unfortunately, they are only based on additive gene action, because it is that the only prediction possible when we do not know allelic frequencies nor gene effect values. Everything that is not-additive is included in the "error term" and so, depending on the relative magnitude of those non-additive effects, the prediction, or interpretation, of selection responses should be better or worse. The application of that methodology has been exhaustive in poultry and, in general, very widely used in larger domestic species.

The only methodology developed to take advantage of non-additive genetic action has been that presented by Comstock et al. (1949). That was a nice tool to use overdominance even though we could not predict statistically the possible magnitude of selection response, if any. Out

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RESUMEN

Puesto que en genética cuantitativa, cuando se trata de efectos no additivos, no podemos desarrollar técnicas estadísticas para la interpretación y predicción de las respuestas a la selección y otros fenómenos relacionados con la mejora, la única forma de aprovechar dicha acción génica es el diseñar métodos adecuados que respondan a ella. Aparte de la propuesta de Comstock para la utilización de la sobredominancia, a través de la selección recíproca recurrente, no ha sido diseñada ninguna otra metodología. El uso de animales de laboratorio en mejora genética animal deberá tener en el futuro un papel preponderante en la contrastación de esas metodologías que puedan sugerirse o diseñarse. Por el contratio, creemos ya innecesaria, excepto en casos muy concretos, su uso en comprobaciones de modelos de aditividad que ya han sido contrastados exhaustivamente. Por último, no ocultamos nuestro pesimismo respecto a la inventiva de nuevos métodos para sacar provecho de la varianza no aditiva; pesimismo que contrasta con el relativo optimismo que reflejan las perspectivas ofrecidas, sobre diversas materias, por los autores que participan en esta sesión, y presentadas en sus interesantes contribuciones.

of poultry and laboratory animals very little has been applied or even studied concerning such a methodology. But, even more with larger species attempts to interprete the results of crossbreeding have been very limited.

Therefore, since we do not have appropiate methodology, with statistical tools, to confront the problem of non-additivity, we have necesarily to use alive material. So laboratory organisms could play a more important role to contrast practical methodologies designed to use those non-additive effects.

In my opinion, the use of biological organisms in the laboratory should not continue trying to test the goodness of genetic models, since there are not adequate models on non-additivity, and nearly all is already known about additivity. Only contrasting methodologies seems to promise some possitive results. However, the sad side of that possibility is that after the above mentioned development of Comstock, no other methodology has been proposed to take advantage from, or to use, any kind of non-additive genetic action. In other words, out of the possible utilization of overdominance, no new tool has been developed. Breeding designs to use maternal effects through specialized sire and dam lines, are, I think, very rough.

It is obvious that laboratory animals will continue being used to study other genetic branches concerning with the knowledge of the true function and action of the gene, whose advances perhaps some day in the future could be related to the interpretation of the heredity of metric traits, and so to quantitative genetics. In the meantime, it is worthwhile to note carefully the several outlooks included in the interesting papers presented by the authors participating in this session. Perhaps their perspective be more optimistic than my today thinking; that perspective being in the more balanced middle point between my optimism expressed on my paper at the Ist Congress (Orozco, 1974), which I do not mantain any more, and the somewhat pessimistic concern I an geeling now. I like to think they are true.

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