DAIRY CATTLE GENETICS AND BREEDING:
A SUMMARY OF SYMPOSIUM 6a

Genética y Mejora del Ganado Vacuno Lechero:
un Resumen de la 6a Symposia

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The introduction to this symposium in 1974 (DE VUYST, 31) stated that "The great diversity of the submitted papers shows that selection for dairy production is very complex." The situation has not changed in eight years. Papers submitted in 1982 included descriptions of applied breeding programs, theoretical derivations, breed modification programs, genetic markers, cytogenetic studies, polymorphisms and computer simulation studies.

Black and White cattle from Lowland Germany and The Netherlands were taken to North America in the Nineteenth Century. Due to different selection goals, the North American cattle (Holsteins) diverged from the European cattle (Friesians) over the past 100 years. The comparative performance of Holsteins and Friesians has become the subject of several European research projects, and the rate at which native Black and White genes may be replaced by Holstein genes concerns some workers. COLLEAU et al (1) estimated that 50 to 80% of the genes in the French Friesian breed will be Holstein genes by 1997. ORDOÑEZ (2) reported that in 1979, 58% of the Friesian inseminations in Spain were from North American bulls.

The effects of performance testing and selection programs may be evaluated by estimating genetic trends. DANELL and ERIKSSON (3) used mixed model techniques and estimates of sire predicted difference to estimate genetic change in two Swedish breeds. CICOGNA et al (4) estimated differences in genetic trend associated with use of Italian and non-Italian bulls. DOHY et al (30) presented plans for and feasibility of establishing a Red and White Holstein-Friesian nucleus population with high production merit. GURNANI and NAGARCENKAR (5) reported negative trends in first lactation milk yield in a closed herd of Tharparkar cattle where male selection was based on dam's milk yield and conformation and female selection was based on growth, reproductive performance, body conformation and milk production.

The progeny test has been accepted as a necessary part of maximization of genetic change accomplished through selection of males. ALENDA et al (32) showed that the progeny test was of little value in maximizing genetic progress for weight gain in beef cattle. However, ALENDA and CARBONELL (6)
applied the same analytical procedure to dairy cattle and confirmed that the progeny test is essential because milk production is expressed only in the female. SINGH and GURNANI (7) derived positive correlations relating own performance, dam's performance and paternal half-sibs' performance to actual lifetime production of Tharparkar cows.

Estimates of variance and covariance components provide the basis for our methods of estimating heritabilities and genetic correlations. These parameters, in turn, provide the basis for designing selection programs and predicting genetic progress. HAGGER et al (8) compared four methods of estimating components in three sets of data. Heritabilities of milk yield ranged from .27 to .37. The F1 sire population had lower heritabilities for fat % and protein % than the purebred sire population. Based on standard errors of sire components, the Minimum Norm Quadratic Unbiased Estimation (MINQUE) method appeared to be slightly superior to the Henderson 3 method of estimating variance components.

GUPTA and GURNANI (9) reported that economic weights can vary up to 30% without influencing accuracy of a selection index. Age at first calving and first lactation milk yield estimated lifetime milk yield with 72% accuracy ($R^2 = .51$).

KORVER (10) compared Dutch Friesians with Holstein-Dutch Friesian crossbreds and compared a high concentrate diet with a high forage diet in a 2 x 2 factorial arrangement of treatments. The interaction between breed type and diet was a non-significant source of variation for milk yield, energy intake and body weight change. Though there was no interaction at Wageningen, these results cannot be extrapolated to include locations with drastically different climatic conditions.

The possibility of practicing selection to modify performance in traits other than yield traits is suggested in several papers. SHOOK et al (11) estimated heritability of somatic cell count to be as high as 0.30 (based on four measures per lactation) and between lactation repeatability to be approximately 0.55. These values support the conclusion that we can reduce somatic cell count through selection and suggest the possibility of reducing clinical mastitis through selection.

CLAUS et al (12) found that, in spite of low heritability, sire ranking based on female fertility traits of first 100 daughters was correlated .71 to .82 with ranking based on first 200 daughters. Since these two means represent a part-whole relationship, this implies that the correlation between first 100 and second 100 daughters is between zero and .34. Stayability or longevity was reported to be greatly affected by fertility and production level by BERGMANN and SIECK (13). Stayability of sire progeny groups was positively correlated with sire's breeding value for milk yield. PATEL and PAREKH (14) reported the genetic parameters for ages at first heat, conception and calving in crossbred herds.
Difficult calving (dystocia) is of economic importance because of lost calves, added labor requirements and occasional death of the cow. GAILLARD and CHAVAZ (15) concluded that we can improve calving performance by culling sires based on progeny test results. However, the changes will not be as great as expected due to antagonism between direct and maternal effects. ZARNECKI (16) reported higher heritabilities for direct (calf) effects than for maternal (dam) effects on calving difficulty.

McCLINTOCK (17) reported that heritabilities of calving interval and days dry and genetic correlations of these traits with lactation yield were modified by using data restricted to a range of 160 days (herd mean ± 80 days) calving interval (95% of records included). Relationships of lactation yield with casein yield and casein percentage were reported by HAYES et al (18). Twinning frequency in daughter groups was not significantly correlated with thyroid activity of the sire (STANDAL and SOLBU, 19).

Extension of partial records is of concern when analyzing dairy records. REISER and HAUSMANN (20) compared four methods and concluded that the most satisfactory method was linear regression of lactation yield on mean or total test-day yield.

Crossbreeding systems are not widely used in dairy herds in temperate regions. However, crossbreeding has been extensively investigated in tropical regions. Crossing breeds from temperate regions with native cattle has generally indicated that milk yield is maximized at 50 to 75% non-native breeding. RAO and TANEJA (21) reported maximal yield at 50% Holstein breeding in a Holstein-Sahiwal project. The same authors (22) also reported minimal age at first calving at 50% Holstein. However, the 62% and 75% levels of Holstein breeding were near the same age at first calving. MADALENA et al (23) reported similar results for Holstein-Guzera crosses in Brazil.

HICKMAN (24) has described a very different crossbreeding system which is used in Bhutan. The unique point of this report is the use of Bos frontalis (Mithun) bulls which promote extremely high solids content in the milk. The possible use of Mithun to produce synthetic breeds offers an exciting new possibility in dairy cattle breeding.

SITORUS (25) reported that altitude and imported sires both influenced performance of Friesian cattle in Indonesia. CAMACHO et al (26) described a computer simulation program which estimates efficiency of dairy herds in the tropics.

SHANKER et al (27) reported only minor relationships between albumin polymorphisms and economic traits in dairy cattle. Frequencies of haemoglobin polymorphisms were reported by SHANKER and BHATIA (28).
Heterozygosity for Robertsonian translocation was reported for five of 200 bulls karyotyped in Romania by CIUPERCESCU (29). He discussed the possible consequences of using such bulls through artificial insemination.

Based on the papers submitted for this symposium, there is little doubt that selection programs emphasizing increased milk yield will continue to be the foundation of programs for genetic improvement of dairy cattle. In order to make those programs more effective, it will be necessary that we improve the accuracy of estimating both genetic parameters and breeding values of individual animals. The development of optimal testing and selection programs should be concerned with the proportion of the national herd mated to young sires and proven sires. The development and description of optimal combinations of ages and rates of culling cows to maximize genetic change should be addressed more completely than in the past.

It has been proposed many times that each set of environmental conditions can be associated with an optimal genetic combination. Research designed to test this hypothesis has generally resulted in the conclusion that variance associated with G by E interactions is small. The interaction has been important only when either the genetic differences (i.e. Bos Indicus vs Bos Taurus) or the environmental differences were large. The nature and magnitude of such interactions should be more definitely defined. The Holstein or Friesian is not the most superior genotype in exceptionally hot environments. Development of synthetic breeds or new local races of cattle based on both native and non-native breeds is being investigated in several countries.

Total economic value or profitability of the cow depends on several traits. Information on mastitis susceptibility, milk composition, reproduction, longevity, dystocia and other traits influencing profitability can be used to formulate indices of economic merit. Such information is also of value in developing computerized models of management systems.

Work is being continued on more simply inherited traits such as polymorphisms and blood antigens. Cytogenetic investigations have the potential of helping explain the expression of certain physiological phenomena such as reduced male fertility in hot weather.

There were no papers submitted for this session concerning the genetic implications of ovum splitting, embryo transplant or recombinant DNA. Between now and the Third World Congress on Genetics Applied to Livestock Production, one or more of these areas may well become an economically feasible means of improving cattle. If we are to remain abreast of the most efficient means of genetic improvement of livestock, we must begin to consider how these techniques will influence selection intensities, progeny tests, genetic parameters, etc. I sincerely hope that the subject matter of papers submitted for the Third Congress is even more diverse than that presented for the Second Congress.
SUMMARY

The subject matter represented in 30 papers accepted for oral and poster presentation was extremely diverse. Holstein diffusion in Friesian cattle populations of Europe, estimation of genetic trends, importance of the progeny test and methods of estimating variance components all contribute to our knowledge of changes through selection. Selection programs for somatic cell count, fertility and calving difficulty were shown to be capable of producing genetic change in those traits. Information on traits such as casein content of milk, thyroid activity, polymorphisms and translocations was presented. Crossbreeding studies from India and Brazil indicated that maximum yield occurs when proportions of Holstein and native breeds are both near 50%. The possibility of using Bos frontalis bulls in development of synthetic breeds was suggested in one paper.

RESUMEN

El presente tópico está representado por 30 trabajos, aceptados para su presentación ya sea oral o en posters y es extremadamente diverso.

Difusión del ganado Holstein en poblaciones de ganado Friesian en Europa, estimación de la tendencia genética, importancia de las pruebas de progenie y métodos para la estimación de los componentes de varianza, todos ellos contribuyen a nuestro conocimiento para cambios a través de la selección. Selección para el conteo de células somáticas, fertilidad y dificultad al parto, son posibles basados en los trabajos presentados.

Información de las características tales como: caseína contenido en la leche, actividad de la glándula Tiroides, polimorfismo y translocaciones, son también presentados. Estudios de cruzamiento en la India y Brasil indican que la máxima productividad ocurre cuando la proporción de ganado Holstein con las razas nativas es cerca del 50%. Asimismo, se sugiere en un trabajo la Posibilidad del uso de toros Bos frontalis en el desarrollo de razas sintéticas.
2. Calcedo Ordoñez, V.
5. Gurnani, M. and R. Nagarcenkar.
7. Singh, N. and M. Gurnani.
10. Korver, S.
16. Zarnecki, A.
17. McClintock, A. E.
22. Rao, V. P. and V. K. Taneja.
24. Hickman, C. G.
25. Sitorus, P.
29. Ciupercescu, D. D.