

INCORPORATION OF GENETIC CONCEPTS INTO A GENERAL CATTLE PRODUCTION SYSTEMS MODEL

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SUMMARY

The Texas A&M Beef Cattle Production model was expanded to include basic concepts of quantitative genetics. In the original model genetic potentials were specified by growth rate, mature weight and milk production. The progeny inherited these traits from the dam with no contribution from the sire. The model was modified so that the progeny inherited attributes from both the sire and the dam. The incorporation of genetics into the model allowed for the introduction of variation among individuals and from generation to generation. This was achieved by interfacing the original model with stochastic genetic subroutines. A restricted selection index and a function to examine dystocia levels in cows were also included in the model.

INTRODUCTION

The Texas A&M Beef Cattle Production model (TAMU) model (Sanders and Cartwright, 1979a,b) is perhaps the most comprehensive and complex beef production simulation model (Chudleigh and Cezar, 1982). It is a generalized model for simulating beef cattle production under a wide range of management schemes and environments with cattle differing widely in genotypes for size, growth and milk production. Genotypes are specified as production potentials which are reached only if past and present planes of nutrition are adequate. Even though the TAMU Beef Cattle Simulation Model has comprehensive biological components, its treatment of genetics is basic and rudimentary. Genetic production potentials are specified by mature weight, growth rate and milk yield. The calf inherits these attributes from its dam and as a result there is no variation among animals. It is imperative that modeling efforts must incorporate the heterogeneity and complexity that now exists in the animal production industry. The objective of this study was to modify the TAMU model by developing and including genetic variation among animals for growth and milk production traits.

METHODS AND MATERIALS

The Texas A&M Beef Cattle Production model was used as a foundation for this study. The new subroutines added to the model to simulate genetics are largely stochastic because genetic improvement in populations is a stochastic process. Birth weight, yearling weight, mature weight and milk production are the traits simulated to introduce genetic variation. Birth weight, yearling weight, mature weight and milk production are modeled as:

$$Y = \mu + G + E + T$$

where Y is the trait being modeled; μ is the population mean for the trait; G is the breeding value of the animal for the trait; E is the direct environmental effect on the animal; and T is the temporary herd environmental effect common to all animals in that herd and in that year. The individual's breeding value is generated as follows:

$$G_i = 0.5G_s + 0.5G_D + \sigma_G * D * 0.5^{1/2}$$

where G_s is the breeding value of the sire; G_D is the breeding value of the dam; σ_G is the genetic standard deviation for the trait and D is the random multivariate normal deviate $\sim N(0,1)$. A detailed description of the generation of parameters used in the model is given by Dzama (1993). A selection index described by Yamada et al. (1975) Dystocia measured as a calving difficulty score (CDS) was computed by modifying a function developed by Cook et al. (1993) as:

$$CDS = 12.26 - (2.202 * \text{RATIO}) + (0.1069 * \text{RATIO}^2)$$

where $\text{RATIO} = \text{precalving pelvic area/birth weight}$. A mean precalving pelvic area for a particular breed is set for heifers and for cows. Birth weight is adjusted for mature size using the assumption that birth weight is generally equal to one seventeenth of the mature weight.

RESULTS

The model was run until herd structure reached steady state (100 years) and the output was examined for a marked departure from the expected age-class structure. In addition output data was analyzed using SAS (1987) to check if the phenotypic means and genetic parameters for the traits in question had remained unchanged. The model was also run on an IBM 9375 model 60 mini-mainframe computer with a different compiler to check if the random numbers and parameters generated were the same as those generated when running the model on a personal computer. Dzama (1993) illustrated the model using five different selection experiments.

DISCUSSION

The main objective of this study was to modify the TAMU model by including genetic concepts and introduce variation in individual animals. An opportunity for selection of animals with certain desirable characteristics was created. This was accomplished by integrating concepts of quantitative genetics and selection index theory. This was done in such a way that many of the original concepts in the model were left intact. The new model provides a tool for quantifying short and long term selection goals and predicting genetic gains stochastically.

In general terms, the underlying genetic conceptual basis of the model is similar to other genetic models e.g. Tier, (1984) and Middleton, (1982). The major difference is that the genetic modules developed in the current study have been interfaced with a biological model that has been verified and validated. This allows for a great deal of flexibility in terms of simulation of different management strategies, selection and culling goals, and different genotypes and populations. Analysis of data from this model or perhaps interfacing it with an economic or financial model will provide a decision making tool both at farm level and at regional, national or international livestock policy making levels. In its current form, the model would be best suited for the former because use at farm level would require greater simplification and user-friendliness.

Although numerous factors were considered in developing this model, the extent and appropriateness of the results depend on the limitations and validity of assumptions of biological and genetic parameters. The biology of the model was developed about two

decades ago and since then some new concepts have been developed. An obvious area where the biology modules need to be modified is where utilization of fat for energy is assumed to be as metabolically efficient as fat synthesis. The former process is generally considered to be more energetically efficient (W. C. Ellis, personal communication).

Since the model already contains provisions for buying and selling animals and can account for the feed resources an economic component can be easily added to the model. An economic component would allow improvements in the ability of the model to help in decision making both in the short and long term periods. Other future considerations include integration of more traits (e.g. reproduction traits) into the genetic framework already established and stochastically integrating crossbreeding systems. In making the suggested changes and additions one has to be careful not to alter the original objectives of the model. The model might become so big that it loses flexibility and ease of management. One way to further modify the model in future would be to utilize objects oriented programming, a common feature of some of the structured languages like Pascal.

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