HotCross - A Decision Support Aid for Crossbreeding of Beef Cattle in Tropical and Subtropical Environments

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Summary
A primary objective of the Northern Quantitative Genetics project of the Meat Quality CRC is to develop decision support software (DSS) to aid cattle breeders to combine selection and crossbreeding to make educated decisions about crossing systems for a wide array of potential markets. This paper describes the concept and use of DSS (HotCross) to achieve these goals. HotCross is used to predict differences between genotypes in production and quality traits for the environment in which production occurs. Predicted performance of genotypes is adjusted for four environmental stresses: heat, ticks, worms, and nutrition. The option exists for users to input their own environmental stress levels (if known), or rely on default data from the region of northern Australia where the cattle are weaned, grown-out, or finished. The user supplies information on current environment, current performance information, and current genotypes. HotCross has the flexibility to model many diverse crossbreeding systems.

Keywords: Crossbreeding, decision support software, beef cattle, tropics

Introduction
Given the diversity of production environments, management systems, and marketing scenarios within which beef is produced in Australia, least-cost producers will increasingly use crossbreeding as a management strategy. This is especially true in the northern tropical areas of Australia, where a balance must be struck between reducing age and increasing weight at turn-off; increasing rates of reproduction, pre- and postweaning survival; improving carcass and eating quality; and maintaining high levels of adaptation to heat, poor nutrition, tick, and worm stresses.

However, despite the enormous amount of research which has been carried out comparing breeds and crosses, there is no convenient way for a tropical cattle breeder to compare the expected performance of different breeds and crosses in his/her environment. Given the long generation interval in cattle, the development of decision support aids to provide predictive models for crossbreeding programs is worthwhile. In a tropical setting it is important that predictions be adjusted for various stresses operating in the environment in which the animals are produced. The objective of this paper is to describe the development of a decision support tool to help producers make more educated decisions about crossbreeding programs.
PROGRAM DEVELOPMENT

Customer requirements. The software is being developed as part of the Northern Quantitative Genetics (Crossbreeding) Project of the Genetics Sub-program of the Co-operative Research Centre for the Cattle and Beef Industry (Meat Quality). The final product must meet the following prerequisites:

- comprehensive and accurate yet easy to use;
- allows the user to nominate the region where the cattle were produced or grown;
- allows the user to choose from a wide variety of breeds;
- predicts genotype x environment interactions which are known to affect the ranking of breeds in tropical and sub-tropical environments;
- allows the user to input information (i.e., EBV) on specific sires;
- allows economic comparisons among the various crossbreeding systems designed.

For design purposes, an animal's life cycle is partitioned into three phases - breeding (pre-weaning), growing, and finishing. This was done because an animal might be with his/her dam to weaning on one property, grown out on another property, and finished on yet another property (or feedlot).

Programming language. Microsoft Visual Basic was chosen as the platform for programming because of the ubiquitous nature of the Windows operating environment. The software will run under Windows 3.x and 95, and NT 3.x and 4.0. We do not foresee development of other platforms.

User inputs. The user is required to provide information on the region where the cattle are grazed (e.g., Brigalow, Black Speargrass, etc.) and the base level of nutrition (e.g., unimproved pasture, improved pasture, crops, feedlot). This is done for each phase. The user is also required to identify the current genotype of the cow herd. A default value is provided by the software for the performance of the genotype in the environment specified but the user can change this if desired. This genotype and its performance then becomes the basis to which other genotypes are compared. Once the base genotype has been identified, the user can predict and compare various crossing systems.

Predicting Performance. The performance of alternative breeds or crosses is predicted using two predictive models. First the performance in an environment which doesn't experience stresses typical of the tropics or sub-tropics (poor nutrition, heat, ticks, and worms) is predicted using a classical genetic model. This model contains direct and maternal breed effects and direct and maternal heterosis, estimates of which, based on published reports, are held in a database developed as part of this project (Newman et al. unpublished). Secondly, the decrease in performance caused by stress is predicted based on the stress levels specified by the environment (region and nutrition) and the genotype. At present the genotype's susceptibility to stress is based only on its proportion of Bos indicus or African genes. Currently, prediction of the impact of stress are only made for weight traits. Insufficient data is available to develop accurate adjustment procedures for other traits. Research will continue to enhance this part of the software.
Equations to predict the decrease in growth rate caused by ticks, worms and heat were developed from analyses of 21 published reports. The equations use the tick count, faecal egg count, or rectal temperature to predict decrease in growth rate. To utilise these equations genotype differences in tick count, faecal egg count, and rectal temperature are needed. The effect of temperature is a two step process of first predicting rectal temperature as a function of ambient temperature and genotype and then predicting the reduction in performance associated with elevated rectal temperature. Nutritional stress is currently described as the percentage reduction in performance due to limited foodstuffs for each phase of production.

These results are then used by HotCross in the following sequence. Based on the mating plan input by the user, the non-stress phenotypic performance of the genotype is determined from the breed database and the level of direct and maternal heterosis expected for the cross. Environmental descriptors provided by the user for temperature, ticks and worms are used to determine the stress level for a specific region. Since the effect of ambient temperature on rectal temperature and the effect of parasites are breed specific, those environmental effects must be calculated for each specific genotype. An adjustment in performance due to the amount of environmental stress is then calculated for the genotype and applied to the unstressed performance.

**TASK ANALYSIS**

HotCross is composed of the following screens, or forms:

1. **Environment form** - describes the environment for each of the three life-cycle phases (breeding or pre-weaning, growing, and finishing). Currently the user inputs the region of Queensland where the phase will occur and a nutrition status (unimproved pasture, improved pasture, crop, feedlot). The user also chooses approximate ages for weaning, end of grow-out, and end of finishing (in months). The user has the option to input actual levels of stress (ticks, worms, heat, and nutrition), if known;

2. **Base genotype performance** - This screen is used to select the base genotype (usually the current cow herd), and provides numerical values for performance of the base as well as the performance of chosen straight breeds and crosses. The performance table contains the traits that are presently used in HotCross, partitioned by phase. Performance is predicted in a non-stress environment and after the stress effects have been taken into account. The user can input actual phenotypic performance information if known for the base genotype;

3. **Breeding tree** - allows the user to visually develop crossing systems and study performance on-screen. Crosses are completed by inserting breeds from an available list and identifying sire and dam. Double-clicking with the mouse on the progeny genotype box will provide performance information relative to the chosen base.

4. **Graph form** - allows the user to graph the performance of straight- and crossbred mating performance for the systems generated. Performance for each trait is expressed relative to the base genotype, which can be altered from the breeding tree.

Figure 1 displays the breeding tree of HotCross. The base herd was Brahman. Charolais bulls were joined to Brahman cows, and Angus bulls joined to the F1 females. Brahman bulls were used on the three-way cross females to produce an animal that is 62.5% Brahman, 12.5% Charolais, and
25% Angus. By pressing on the "Insert" button under "Cross" the sire and dam can be chosen arbitrarily. From this screen, environmental information can be changed, the base from which alternative schemes are compared can be changed, as well as adding (and deleting) new breeds and crosses, tabulating or graphing results.

![Figure 1. Example of the breeding tree form from HotCross](image)

**KEY BENEFITS**
The benefits of HotCross include
- accurate prediction of genotypes adjusted for environmental stress;
- the ability to utilise a wide array of genotypes;
- the ability to "simulate" production of a wide variety of crossing systems;
- the ability to calculate the performance of crossbreeding systems generations into the future.

The package will have use for assessing breeding programs in beef production enterprises, for consultants advising beef producers in tropical and sub-tropical areas around the world, and as an educational tool in schools, agricultural colleges, and beef producers, to name a few.

**FUTURE DIRECTIONS**
As of this writing, the alpha-test version has been released to a limited sample of users for trial. A beta version available in June, 1997 will include an economic model to compare alternative schemes, and the ability to utilise Estimated Breeding Values of specific sires into the prediction of crossbred performance. Although currently focused on Queensland, future versions will be relevant for all areas of northern Australia. A fully commercialised version is expected to be available in June, 1998.