

WAGYU X LIMOUSIN CROSSBREEDING PROGRAM AT FLYING T RANCH WILL AID IN GENE MAPPING PROJECT

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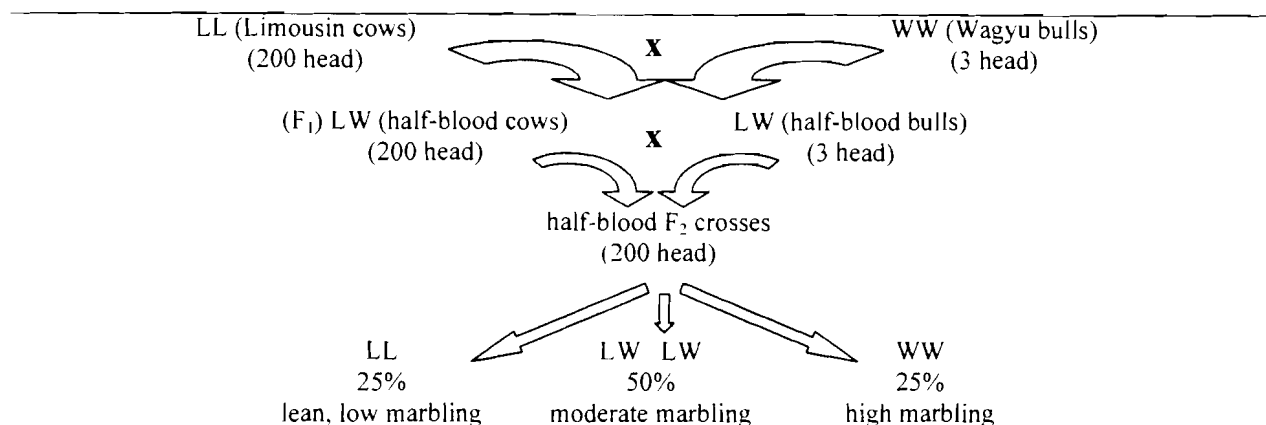
INTRODUCTION

Gene technology has advanced to a degree where it will one day be used as a common production tool for scientists and livestock producers. Washington State University scientists have proposed one major project associated with the Flying T Ranch applying gene technology to cattle. (1) This project concerns gene mapping and involves developing three reference families from 200 Limousin cows crossed with three Wagyu bulls. The resulting half-blood (F_1) females will be bred to supply (F_2) calves used in a gene mapping project of economic quantitative traits such as tenderness, marbling, muscling, feed efficiency, puberty and docility. The identification of specific segments of DNA associated with these traits will be used to more efficiently and quickly identify animals with superior genetic potential.

The Flying T Ranch and equipment were donated to the Department of Animal Sciences at Washington State University by Max and Thelma Baxter in January 1996 (value: 1.8 million dollars). Two hundred Limousin cows on the Flying T have $\frac{1}{2}$ blood Wagyu calves at their sides which will be used to start the gene mapping project. These cows are presently owned by Max and Thelma Baxter, but will be donated to Washington State University when the Department can take over the operation costs of the ranch. The strategy for developing a population of animals for gene mapping requires crossing two breeds which are extremely different in the trait that is being mapped. For example, Limousin are very lean with little marbling, whereas Wagyu are the highest marbling breed.

The half-blood Wagyu x Limousin cows resulting from the original breeding will be bred back to a half-blood Wagyu x Limousin $\frac{1}{2}$ sib bulls. This cross results in a half-blood animal whose genes may randomly segregate either toward the Wagyu or Limousin ancestry as shown by the following scheme (Figure 1).

Figure 1. Scheme of Breeding Program for Mapping Project.



Marbling is not controlled by genes at a single locus, but by genes at several loci. However, as an example, the genes at one of these loci will segregate by chance, so that 25% will be like Wagyu, 25% like Limousin and 50% halfway between. It is important to breed back to the half Wagyu half limousin bulls so that the background genes (other genetic material) will be as similar as possible for all animals being evaluated.

All F₂ animals will be fed in the feedlot under a Japanese-type feeding system so each animal has a chance to express their marbling ability. The animals will be slaughtered and carcass data evaluated. The animals will be placed into categories such as high marbling, low marbling and moderate marbling. Various segments of polymorphic DNA segments (called microsatellites) will be evaluated by Applied BioSystems. Linkage Genetics and scientists at Washington State University. The cost and time to map these samples is an extraordinary undertaking. It is important we work with a company with the technical ability of Applied BioSystems. Washington State University will share in patent and royalties of these gene markers. This is a vital research project for the cattle industry and one which will make as much impact on the cattle industry as artificial insemination has over the last 40 years. The Japanese government is also starting on a Limousin x Wagyu cross like our project, but they seem reluctant to work together on these projects.

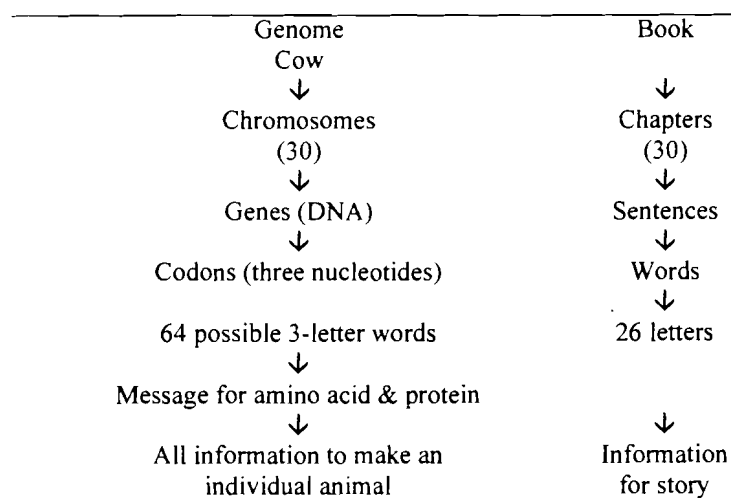
Our goal is to cooperate with other labs, because the sooner we determine markers associated with specific traits, the sooner the industry can use this information to select superior animals. The time-line on this project is to have all the F₂ calves slaughtered by the year 2002. We will

be collecting and processing DNA samples from all the original cattle, the F₁ and F₂ animals each year.

To understand the application of DNA technology we must understand some of the terms and concepts of this science.

The bovine genome can be looked at as an enormous message that is analogous to a book. Just as a book is organized into chapters, paragraphs, sentences, words and letters, the genome is organized into chromosomes, genes, triplet codons and bases. The bovine book (genome) is composed of three billion characters or bases which are organized into thirty chapters or chromosomes. Each chapter is further divided into paragraphs and sentences where a grammatically correct sentence is analogous to a gene that contains information for making a specific protein. The bovine book contains approximately sixty thousand sentences or genes. The book is written in a specific language known as the “genetic code”. What this language communicates depends on how the alphabet of 4 letters (A, G, C and T) are arranged to form the 64 possible 3-letter words known as codons and finally how the words go together to form sentences or genes. This genomic book contains all of the information required for the development and function of a normal individual.

Figure 1. Comparison of bovine genome to a book.



DNA MARKER-ASSISTED SELECTION

At the present time, embryo sexing is being used by commercial companies in the marketing of bovine embryos. This is a DNA probe specific for the sites or DNA on the Y chromosome. Coat color and horned or polled characteristics are traits ABS can evaluate by DNA markers at the present time. In the swine industry, the DNA area associated with Porcine Stress Syndrome (PSS) has been mapped to a linkage group on pig chromosome 6. DNA markers with this area have been successful in selecting against the PSS condition. With the mapping of the bovine genome, traits important to cattle production may be located in which we may be able to evaluate what phenotypic performance will be before birth. These new tools are coming into animal agriculture and will be part of our future breeding programs. They will be as common in the future as birth weights and EPD's are today for evaluating and marketing our cattle. We have used markers to assist in selection of cattle for many years. The most common has been the white face of the Hereford breed. In the future, we will be selecting cattle on markers or genes for specific traits.