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Friesian Jersey crossbred trial: Generating phenotypes for the discovery of quantitative trait loci

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ABSTRACT

A F₂ experiment is being undertaken with New Zealand Friesian and Jersey cattle. The objective of the experiment is to identify the underlying genetic differences between Friesian and Jersey breeds and to exploit the results through marker assisted selection or sale of intellectual property e.g. genotyping tests. Approximately 800 F₂ cows have calved as two-year-olds and completed their first lactation. These cows will be milked and phenotyped up to their fourth lactation. The 5 main categories that the cows are being extensively phenotyped in are; milk characteristics, milk production, reproduction, health and disease, and growth and development. First quantitative trait loci (QTL) results are expected in the second half of 2004 and available for utilisation in the Livestock Improvement breeding scheme in 2005.

Keywords: dairy cattle; quantitative trait loci; crossbred.

INTRODUCTION

Livestock Improvement Corporation (LIC) operates the largest dairy breeding progeny test scheme in New Zealand. The breeding scheme involves testing up to 300 bulls per annum and identifying the elite sires based on their daughters' phenotypic performance. In recent years, LIC has been supplementing the phenotypic data with genotypic information, termed marker assisted selection (MAS), and thus increasing the rate of genetic gain achieved in the breeding scheme. The genotypic information has been sourced from successful experiments that have identified quantitative trait loci (QTL) that affect milk production traits (Spelman *et al.*, 2001a). In two of these instances the polymorphisms that underlie these QTL have been identified (Blott *et al.*, 2003; Grisart *et al.*, 2002).

Traits with low heritability or traits that are expensive to measure, have the most potential to be improved with utilisation of MAS (Smith, 1967). These traits, by their nature, are not routinely collected by commercial dairy farmers to the detail that is required for QTL discovery. Therefore to identify QTL for these traits a herd of cows was established to specifically undertake the detailed measurements.

LIC and the formerly New Zealand Dairy Board (NZDB) commenced the establishment of this herd in 1998, with the sourcing of the sires that generated the experimental herd, now referred to as the Friesian Jersey crossbred herd. ViaLactia BioSciences (a subsidiary of Fonterra) has taken over the NZDB component of the trial and utilises the resources in conjunction with LIC.

EXPERIMENTAL DESIGN

A F₂ experimental design with a half-sib structure was chosen. Friesian and Jersey breeds were used primarily because they differ phenotypically for a number of milk characteristic traits (e.g. soft fat content,

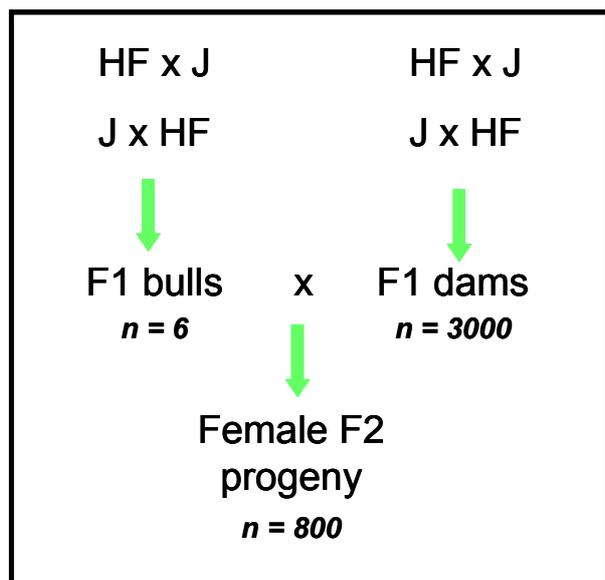
milk fat colour), which were traits of interest at the time of trial inception. In addition to their phenotypic differences, they are the two dominant breeds in the NZ dairy population and a large resource of F₁ crossbred cows exist in the commercial population.

The second option for the experiment was a backcross (F₁ bull mated to Friesian and Jersey cows). However, in general more animals are required for a backcross design to have equivalent power to the F₂ design (Soller *et al.*, 1976).

It was statistically determined that 800 F₂ animals (completing at least one lactation) were required to have a high probability of success of identifying QTL (Spelman *et al.*, 2001b). To generate the 800 F₂ animals, 6 crossbred sires were sourced in 1998. These sires were contract mated to high breeding worth first cross commercial cows in 1999 and 2000 on approximately 400 herds in total. The first cross commercial cows were selected on the basis of pedigree information and the owners of these cows were contracted to mate these cows to the crossbred sires. The resultant F₂ calves were purchased, parentage tested and moved to the experimental farm when they were 4-10 days of age (Figure 1). From this point the animals have been farmed in a common environment and phenotyped for an extensive selection /range of traits.

The F₂ animals were reared and grazed primarily at the AgResearch Tokanui research property. Just prior to their first calving (2002 for cohort 1 and 2003 for cohort 2) the cows were transported to the Whareroa research farm, which is part of the green belt around the Fonterra Whareroa dairy factory in Hawera. The cows are milked on a 60 bale rotary platform and have a number of measurements taken in the double herringbone science facility. To undertake the extensive phenotyping, 4 fulltime science technicians are employed on the farm and supplemented by casual or contracted staff as required.

FIGURE 1: Experimental design for Friesian-Jersey crossbred trial.



The crossbred herd has a breeding worth of 139, which puts it in the top ½ percent of herds in the country. Three hundred and fifty four cohort one cows completed their first lactation in the 2002-03 season with average 270 day corrected production figures of 3056 litres of milk and 122 kg of protein and 164 kg of fat. In the 2003-04 season, 460 cohort 2 cows are near completion of their first lactation. One of the 6 crossbred bulls, Bolts Lancaster, is one of the top 3 sires in the country based on breeding worth. The 6 bulls have an average breeding worth of 155 (Animal Evaluation unit 17th April 2004).

MAIN PHENOTYPES OF INTEREST

Milk production

Daily milk volumes (am and pm) are collected on the research farm. This near continuous collection of milk production data enables the lactation curve of each cow to be modelled. The lactation curves enable different estimates of persistency to be measured and also yields for certain times during lactation. In addition, every fortnight fat, protein, casein, and lactose yield over a 24-hour period are collected.

In New Zealand's dairy industry the number of cows being milked once a day, for an extended period of time, is increasing each year. This trait is being investigated within the trial with the cows undertaking short-term and long-term once a day (OAD) milking regimes. Results from cohort one saw a decrease in milk production of approximately 20% for milk volume and yield for both of the short-term OAD milking periods. There was a high degree of repeatability for animals that decreased milk production by more than 30% under an OAD regime. In addition to OAD milking, the cows were also milked three times a day for a short period. The average increase in milk production was 1.2% over that achieved from twice a day milking. The top tenth percentile had an increase of 13 percent.

Milk characteristics

ViaLactia BioSciences are undertaking an in-depth study of the milk characteristics with Fonterra Marketing and Innovation. These measures revolve around specific aspects of fat, such as the degree of saturation and the proportion of major and minor proteins.

Health and disease

Mastitis is the major target in this category as it is the number one animal health cost on New Zealand dairy farms. The cows are being monitored for somatic cells on a fortnightly basis. Each cow is sampled three times during the lactation for bacteriology counts from each quarter. In addition, when a cow exceeds a defined somatic cell count threshold the cow has a further bacteriology sample taken. All clinical cases are recorded. Morphological aspects of the teat such as teat length, shape and colour, have also been measured.

Further to the routine collection of mastitis occurrence, a mastitis challenge is planned. This will involve the cows being infused with a known pathogen and then being monitored for the next week to identify which cows are able to mount an immune response sufficient to ensure the bacteria do not multiply and the gland does not go clinical (McDougall *et al.*, 2004).

A general immune measure has been undertaken on the cohort 2 animals when they received their 5 in 1 clostridial vaccination. The animals were monitored for the antibody production to two of the antigens in the vaccine (Harcourt *et al.*, 2004). Finally, the animals have also been subjected to a stress challenge, which revolved around the transporting the animals for half an hour when they were 6-10 months of age.

Reproduction

Extensive phenotyping has been undertaken on each animal to identify reproductive performance over the animal's lifetime. The first fertility measure was to ascertain the onset of puberty. A blood sample was taken from each animal on a fortnightly basis for blood-progesterone ELISA analysis. In addition, physical evidence of the animal being ridden was collected. Large phenotypic variation was observed with 'age of onset of puberty' ranging from 155 days to 470 days, and live weight ranging from 80 kg to 320 kg.

Progesterone measures have been undertaken on a twice-weekly basis for all cows once they have calved until the end of the mating period (Sanders *et al.*, 2004). These measures allow post-partum anoestrus intervals to be calculated, and also the detection of irregular cycle length and early embryonic loss among a number of other traits. Farm staff have also recorded heat observations and all mating records are used in conjunction with the progesterone results to identify cows that cycle but do not exhibit oestrus.

For the cohort 1 animals in their first lactation, the average interval to postpartum onset of luteal activity was 29.7 days (sd=16.8). Pregnancy rates confirmed to within the first three weeks of mating were 70% (Sanders *et al.*, 2004).

Growth and development

The animals have been measured on a fortnightly basis for live weight and condition score until they have entered the milking herd. Also during this period the animals have had their height and girth measured on a monthly basis. Once the animals had calved they had weekly condition scores and live weight measures at least twice a week. In the 2003-04 season an automatic weighing system has ensured that on average over 80% of the animals have two live weights recorded each day. Height and girth measurements are taken on an annual basis once the cows enter the milking herd. The intensive condition score and live weight measures, combined with the milk yield data has enabled accurate estimates of energy balance over the lactation for each cow.

DISCUSSION

The herd of experimental F₂ cows is being phenotyped extensively for a number of traits of which data is not routinely collected on commercial New Zealand dairy farms. The detailed phenotyping process ensures that a greater biological understanding of the animals is gained which will increase the probability of identifying QTL. In addition, a number of challenges have been carried out such as the endocrine challenge, once a day and three times a day milking, stress challenge and a mastitis challenge. The challenges are expected to further accentuate the biological and genetic differences between animals and thus increase the probability of understanding the underlying genetic basis.

The dataset that has been collected to date also offers opportunities for other New Zealand scientists to carry out QTL studies and farm systems research. The Pastoral Greenhouse Gas Research Consortium who collected methane emissions on all of the cohort 1 animals in early 2004 has used this opportunity. This data will be used for QTL studies. Farm systems research could benefit from the data set of nearly 800 cows being followed throughout their life farmed in a common environment with exceptionally detailed data on most aspects of dairy science and husbandry for each cow.

The QTL experiment started in 1998 and will probably continue in some form for all of this decade. The first QTL results are expected this year with the genotyping being completed and all of the animals finishing at least one lactation. The QTL results are unlikely to be directly applicable to the breeding scheme as the QTL regions will cover up to approximately 50% of the identified chromosome. Thus fine mapping will be undertaken by genotyping extra markers on the animals and also utilising progeny from the F₂ animals. The fine mapping will ensure that some QTL will be able to be utilised in the Livestock breeding scheme or through sale of genotyping tests through GeneMark™. The QTL that are found will be a combination of QTL that are fixed in both breeds and those that are still segregating within breed. For the QTL that are fixed for

different alleles in the two breeds there is no potential to apply MAS within the respective breeds. However, with the advent of the KiwiCross™ breed there is the opportunity to utilise the best alleles from each breed and bring them into the KiwiCross™ crossbred bulls. Where the QTL are still segregating within the breeds MAS can occur within breed as well as previously mentioned crossbred scenario.

The results from the Friesian Jersey crossbred trial will result in greater genetic gain in the Livestock Improvement breeding scheme through more accurate selection, and selection of animals at an earlier age. In addition, New Zealand dairy farmers will be able to make selection decisions for traits such as mastitis resistance and fertility that are currently indirectly measured, or inaccurately measured due to the low heritability of the trait. The results can be applied to the Jersey and Holstein-Friesian breeds but will possibly have greater utility in the crossbred population.

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