THE IDENTIFICATION OF QUANTITATIVE TRAIT LOCI INFLUENCING MILK PRODUCTION AND HEALTH TRAITS IN DAIRY CATTLE

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♦ Chromosomal regions containing genes with large effects on milk production traits have been identified.

♦ Genetically superior animals within specific pedigrees can now be selected on the basis of genetic markers as well as breeding values.

INTRODUCTION

Economically important traits in dairy cattle such as milk, fat and protein yields and disease resistance are polygenic traits (i.e., influenced by many genes). The identification of these genes, termed quantitative trait loci (QTL), or closely linked genetic markers would allow genetic selection on the basis of both an individual's breeding values and on genotype using "marker-assisted" breeding programs. In the future, molecular identification of QTL may be used to develop pharmacological and transgenic approaches to enhance production or disease resistance.

MATERIAL AND METHODS

The Dairy Bull DNA Repository (DBDR) is a large collection of semen established in 1992 as a DNA resource for the mapping of QTL. One-thousand-seventy-six bulls belonging to 8 Holstein-Friesian cattle families were selected for QTL detection using a granddaughter design. In the granddaughter design, a sire and a number of his sons are genotyped for many genetic markers. For each marker the sons are then sorted into two groups according to the marker allele the son inherited from his sire. Breeding values calculated from the production records of sons daughters (i.e., granddaughters of the sire) are then compared between the two groups of sons. A statistically significant difference between groups of sons indicates a gene influencing the trait is genetically linked to the marker. One-hundred-seventy-four genetic markers were selected to efficiently search for QTL on 29 cattle chromosomes (sex chromosomes were not included). Trait data was obtained from the November 1997 US National Holstein Evaluation and included each bulls' daughter yield deviation (DYD) for seven traits; milk, fat and protein yield, fat and protein percentage, somatic cell concentration, and productive herd life.
RESULTS AND DISCUSSION

The bovine genome was scanned for QTLs affecting health and performance traits in 8 half-sib families. Markers with highly significant associations for milk production traits were detected on chromosomes 3 ($P = 10^{-5}$) and 14 ($P = 10^{-14}$). The QTL on chromosome 14 affected fat yield, whereas the QTL on chromosome 3 affected milk and fat yield. Sons that inherited $BTA14-A$ allele 2 from sire 4 have an average DYD of 8.6 kg fat greater than their half-sibs (Figure 1) yet have no significant difference in milk production. Sons that inherited $BTA3-C$ allele 1 from sire 1 had an average DYD of 112 kg milk yield (Figure 1) greater than their half-sibs which inherited allele 2. Additional putative QTL for milk production traits were detected on chromosomes 1, 2, 3, 5, 7 and 14 ($P < .01$). Markers associated with somatic cell score, an indicator trait for mastitis resistance, were located on chromosomes 5, 7, 22 and 23 ($P < .005$). A putative QTL for length of productive herd life was found on chromosome 21. It must be noted that due to the large number of analyses in this study false associations may be detected due to chance. Therefore, studies confirming the location of these QTLs are necessary.

Markers with trait associations are candidates for marker-assisted selection among descendants of the 8 DBDR sires. Genetic progress as well as profit could be increased if producers select those sons and daughters that inherit marker alleles associated with increased production or resistance to mastitis. As more of the genes contributing to the genetic variance of economically important traits are revealed, producers and AI companies will have a powerful tool for the efficient selection of the next generation of dairy cattle.

**Figure 1.** Trait distribution plots for sons inheriting alternative alleles at a marker locus from

**A. Fat Yield association with $BTA14-A$**

$\Delta = 8.6$ kg

**B. Milk Yield association with $BTA3-C$**

$\Delta = 112$ kg