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Detection of Quantitative Trait Loci Influencing Conformation Traits and Calving Ease in Holstein-Friesian Cattle

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ABSTRACT

An extension of our previous genome scan of a North American Holstein-Friesian population was conducted to identify quantitative trait loci (QTL) affecting conformation traits. Resource families consisted of 1404 sons of 10 elite sires. Genome coverage was estimated to be 2713.5 cM (90%) for 406 markers using a granddaughter design. Regression interval mapping was used to detect QTL affecting 22 conformation traits, including body, udder, feet and legs, and dairy conformation as well as calving ease. Analysis of the families jointly identified 41 chromosome-wise significant QTL influencing conformation traits and 3 significant QTL influencing calving ease on 20 chromosomes. The false discovery rate method was used to account for multiple testing and 3/4 of the suggestive and 5/6 of significant QTL should be real effects. Fourteen of the 44 QTL were significant at the genome-wise level. Comparison of these results with other published reports identifies common QTL affecting conformation traits. Regions on 10 chromosomes appear to affect multiple traits, including conformation, milk production, and somatic cell score, within these particular US Holstein families. Additional work is needed to determine the precise locations of the QTL and select positional candidate genes influencing these traits.
(**Key words:** genome scan, dairy, conformation, quantitative trait loci)

Abbreviation key: BD = body depth, **BTA** = *Bos taurus* chromosome, **DBDR** = Dairy Bull DNA Repository, **FA** = foot angle, **FTP** = front teat placement, **FUA** = fore udder attachment; **RA** = rump angle, **RUH** = rear udder height, **TL** = teat length, **UD** = udder depth.

INTRODUCTION

During the last 10 yr, numerous studies from around the world have concentrated on identifying QTL affecting economically important traits in various breeds of dairy cattle. Although the experimental designs, analysis methods, and significance thresholds have varied from study to study, several common QTL affecting milk production traits were detected (Georges et al., 1995; Ron et al., 1998, 2004; Zhang et al., 1998; Heyen et al., 1999; Ashwell et al., 2001; Klungland et al., 2001; Nadesalingam et al., 2001; Boichard et al., 2003). Many fine-mapping studies have commenced (Arranz et al., 1998; Kühn et al., 1999; Ron et al., 2001), and recently, candidate genes underlying 2 of these QTL have been identified (Grisart et al., 2002; Blott et al., 2003). How these discoveries will impact future dairy production has yet to be determined.

Recent studies have focused on detection of QTL affecting conformation and functional traits (Spelman et al., 1999; Schrooten et al., 2000; Boichard et al., 2003; Hiendleder et al., 2003). Although the benefits of identifying QTL for conformation traits are less obvious, significant genetic correlations between them and production and health traits have been found. Examples include stature and production (Short and Lawlor, 1992), feet and leg scores and longevity (Klassen et al., 1992; Dekkers et al., 1994; Vollema and Groen, 1996), conformation and calving interval (Dadati et al., 1986), udder type and SCS (Rogers and Hargrove, 1993; Rogers et al., 1991, 1995), and dairy form and metabolic disease (Rogers et al., 1999). Indeed, most breeding programs include nonproduction traits because of these genetic correlations or because they have a direct impact on the animal's merit. Several of the linear conformation traits such as dairy form, foot angle, and udder depth are useful predictors of an animal's lifetime net merit and longevity in the herd (Vollema et al., 2000). Therefore, detection of QTL affecting these traits may lead to selection for improved conformation and improve-

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Table 1. Number of sons genotyped and those that have conformation and calving ease trait records in each grandsire family.

Family	Genotyped	Conformation traits[1]	Feet and leg score	Calving ease
1	241	228	149	237
2	223	222	222	223
3	178	160	54	178
4	150	141	30	150
5	150	131	84	147
6	113	113	110	113
7	86	84	72	86
8	101	77	46	98
9	92	87	59	92
12	70	59	15	69
Total	1404	1302	841	1393

[1]Excluding feet and leg score.

ment for traits such as production, longevity, mastitis resistance, and reproduction.

The results presented herein represent the second phase of a genome scan of a US Holstein population for QTL influencing production, health, reproduction, and conformation traits. Results of a scan for QTL affecting production traits, SCS, and daughter pregnancy rate were previously reported (Ashwell et al., 2004). Putative QTL exceeding chromosome-wise suggestive and significant thresholds for conformation traits and calving ease are presented.

MATERIALS AND METHODS

Resource Populations and Description of Phenotypic Data

Ten large half-sib families from the Dairy Bull DNA Repository (**DBDR**; Da et al., 1994) consisting of 1414 bulls were selected for QTL detection using the granddaughter design. The DBDR family sizes ranged from 70 to 241 progeny-tested sons that were genotyped, but family size was generally smaller due to missing conformation phenotypes (Table 1). The Holstein Association, USA (1999) provided the conformation trait data (May 2003 release) and the Animal Improvement Programs Laboratory of USDA-ARS provided the calving ease data (February 2002 release). Four groups of type traits with available composite indexes were used: udder, body form, feet and legs, and dairy capacity. The individual traits for each composite index are as follows: the udder group, consisting of fore udder attachment (**FUA**), rear udder height (**RUH**), rear udder width, udder depth (**UD**), udder cleft, front teat placement (**FTP**), and teat length (**TL**); the body form group, consisting of stature, body depth (**BD**), rump angle (**RA**), and thurl width; the feet and legs group, consisting of feet and leg score, rear legs-side view, rear legs-rear view, and foot angle (**FA**); and the dairy capacity group, consisting of dairy form and strength. The standardized PTA for the 17 linear conformation traits and composite indices and the PTA for an overall type composite and direct maternal effects for calving ease (percent difficult births) were analyzed.

Genotyping

Genotyping methods and genome coverage for the 406 typed markers are summarized in Ashwell et al. (2004). Briefly, microsatellite markers were selected at approximately 20-cM intervals from published bovine maps (Barendse et al., 1994, 1997; Bishop et al., 1994; Ma et al., 1996; Kappes et al., 1997). Genome coverage was estimated to be 2713.5 cM (90%), assuming a 3000-cM genome. The average marker interval was 7.4 cM.

Statistical Methods

Similar to the analysis procedures in Ashwell et al. (2004), data were analyzed using a regression approach described by Haley and Knott (1992). The web-based version of the method (QTL Express; Seaton et al., 2002; http://qtl.cap.ed.ac.uk) was used to detect QTL within and across the families. Analysis was conducted at 1-cM intervals along each chromosome. The reliability of each bull's standardized PTA was used as the weight variable in the analysis to give increased value to bulls with higher accuracies. Bootstrapping using 1000 resamples was used to calculate the 95% QTL position confidence intervals. Chromosome-wise significance thresholds were calculated from the *F*-statistics using permutation testing as described by Churchill and Doerge (1994). One thousand permutations were completed to determine the critical threshold values. Chromosome-wise thresholds were calculated for all chromosome-trait combinations (Table 2). Suggestive ($P < 0.05$) and significant ($P < 0.01$) chromosome-wise *F*-value thresholds for the different traits were used to identify putative QTL and are summarized in Table 2.

The QTL Express method will calculate genome-wise threshold values using permutation testing, but is limited to a total of 345 individuals on 29 chromosomes (total must be ≤10,000). Therefore, an alternative method based on Spelman et al. (1999) was used to determine which QTL were significant at the genome-wise level. In this calculation, *F*-statistics generated by QTL Express were converted to *P*-values using the SAS PROBF function (SAS Institute, 2005). The genome-wise *P*-value (P_{genome}) for each chromosome-wise significant QTL was calculated using $P_{genome} = 1 - (1 - P_{chr})^n$, where P_{chr} is the chromosome-wise *P*-value and n is the total number of chromosomes (n = 29).

To account for multiple testing, due to both multiple traits and markers, the false discovery rate (Benjamini