The Characterisation of a Longevity QTL in the New Zealand Holstein Friesian Population

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Abstract

A large scale genome scan analysis to identify QTL relevant to commercial dairy cattle in New Zealand was undertaken using 7 large grandsire families. From this experiment a QTL site situated on bovine chromosome 23 (BTA23) for longevity was identified. The present study investigated this QTL in the subsequent generations.

The addition of more markers to the region under question and the addition of grandsons to the analysis helped support the evidence that a QTL for longevity was indeed present within the region. However a more precise location was not identified. Although this is not helpful for marker assisted selection it will not affect the candidate gene search until the bovine genome sequence is available. This is due to the large inversion event within the BTA23 which means the target region in a comparative map search with HSA6 must still include the entire chromosome.

Analysis of the granddaughters within these families confirmed a link between the speculative QTL site and variation in herd life but could not identify a cause for this variation at a phenotypic level despite a data set of over 800,000 animals. This result indicates that the variation in longevity is most likely the product of a variation in disease resistance at a sub clinical level. As ill health would impact on all production traits, animals affected would be removed for a variety of reasons. Because the only check of health in dairy cattle is their ability to be productive and remain in the herd it is impossible to identify these problems unless animals die from them.

The MHC gene cluster lies within QTL identified and was the prime candidate for linked genes. Analysis of the DRB3 region in the two grandsire families showed a similar genotype in both grandsires. Genotype 1201/090_ was common to both grandsires. Further analysis of the DRB3 by restriction endonuclease digest in the sons and grandsons showed that allele 1201 or alleles similar to 1201 were common in the population whilst alleles 090_ were not seen as often. Variation in phenotype for the 090_ allele suggested a more complex model than a simple inferior/superior allele relationship.

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AI	Artificial Insemination
B cells	Bone lymphocyte cells
BoLA	Bovine Leukocyte Antigen
bp	Base pairs
BTA	Bos Taurus
BV	Breeding Value
cM	Centi Morgan
COMPASS	Comparative Map Analysis of similar sequences
DFM	Days from First Mating
DNA	Deoxyribonucleic acid
ER	Endoplasmic Reticulum
EST	Expressed sequence Tag
FISH	Fluorescent *in situ* Hybridization
HAS	Homo sapiens
HLA	Human Leukocyte Antigen
LB	Luria Broth
LIC	Livestock Improvement Corporation
MARC	Meat Animal Research Centre
MAS	Marker Assisted Selection
Mb	Mega bases
MHC	Major histocompatibility complex
ML	Maximum Likelihood
OMIA	Online Mendalian Inheritance in Animals
OMIM	Online Mendelian Inheritance in Man
QTL	Quantitative Trait Locus
RFLP	Restriction Fragment Length Polymorphism
SNP	Single Nucleotide Polymorphism
SSCP	Single Stranded Conformational Polymorphisim

T cells	Thymus cells
TAP	Transporter for Antigen processing Protein
TCR	T cell receptor