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

A thesis presented in partial fulfilment of the requirements for the degree of Masters of Science in Genetics at Massey University, Palmerston North, New Zealand.

Jennifer Marie Anderson
2002
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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# Table of Contents

Abstract............................................................................................................... ii

Acknowledgements.......................................................................................... iii

Table of Contents.............................................................................................. iv

List of Tables....................................................................................................... vii

List of Figures....................................................................................................... viii

List of Abbreviations.......................................................................................... ix

Chapter 1 Introduction....................................................................................... 1

1.1 Longevity in Dairy cattle............................................................................ 1

1.1.1 Longevity in Dairy cattle......................................................................... 1

1.1.2 Reasons for disposal................................................................................ 2

1.1.3 Calculating Breeding Values.................................................................... 3

1.1.4 Economic Importance of Longevity......................................................... 5

1.2 Identifying Chromosome regions influencing longevity.............................. 6

1.2.1 Genetic tools........................................................................................... 6

1.2.2 QTL Studies........................................................................................... 8

1.2.3 Experimental Design.............................................................................. 10

1.2.4 QTL studies on BTA 23......................................................................... 12

1.3: The Bovine MHC....................................................................................... 13

1.3.1 Overview of the Role of the MHC......................................................... 13

1.3.2 MHC genes .......................................................................................... 15

1.3.3 The structure of the MHC molecules.................................................... 18
Aim of this study.................................................. 23

Chapter 2: Material and Methods.................................. 24
2.1 Materials.......................................................... 24
2.2 Methods.......................................................... 26
   2.2.1 DNA Collection.............................................. 26
   2.2.2 Phenotype Data.............................................. 27
   2.2.3 Polymerase Chain Reaction (PCR)......................... 28
   2.2.4 Troubleshooting for PCR.................................... 29
   2.2.5 Electrophoresis of PCR products........................... 29
   2.2.6 Quantification Gels.......................................... 30
   2.2.7 PCR Purification............................................. 30
   2.2.8 Microsatellite Analysis...................................... 30
   2.2.9 Primer Sets used for Microsatellite Analysis............. 31
   2.2.10 MHC primers............................................... 32
   2.2.11 Cloning...................................................... 32
   2.2.12 Plasmid Preparation........................................ 33
   2.2.13 Restriction Endonuclease Digest........................... 33

Chapter 3: Microsatellites on BTA23................................ 34
3.1 Introduction...................................................... 34
3.2 Identifying microsatellites...................................... 35
3.3 Screening the Grandsires......................................... 37
3.4 Microsatellite Analysis......................................... 39
3.5 Single Marker Analysis......................................... 41
3.6 Interval Mapping................................................ 42
3.7 Threshold Levels................................................. 43
3.8 Grandson Analysis............................................... 45
3.9 Information content............................................. 47
3.10 Conclusions

Chapter 4: Fate Data Analysis
4.1 Introduction
4.2 Data set
4.3 Age Affect on Fate
  4.3.1 Age at death
  4.3.2 Onset of variation
4.4 Fate data analysis
4.5 Independent Fate analysis
4.6 Discussion

Chapter 5: Candidate Gene Analysis
5.1 Introduction
5.2 Comparative Map analysis
5.3 OMIM study
5.4 Candidate genes from the MHC
  5.4.1 Amplification of candidate genes
  5.4.2 Grandsire Analysis
  5.4.3 Allele Identification
  5.4.4 Restriction Digests
  5.4.5 Analysis of the DRB3 in the sons of grandsire 9065
  5.4.6 Analysis in the Grandsons
5.5 Conclusions

Chapter 6: Discussion
6.1 Fate Data
6.2 MHC allele variation
List of Tables

Table 2.1 Microsatellite Primers. 31
Table 2.2 Unlabeled Primers used for MHC Gene Amplification 32
Table 3.1 Calculation of probabilities. 41
Table 4.1 Average Ages. 55
Table 4.2 Explanation of fate groups 57
Table 4.3 Culling factors effects. 59
List of Figures

Figure 1.1  Marker and QTL relationship  9
Figure 1.2  Experimental designs for QTL identification  10
Figure 1.3  Role of the MHC presentation molecules  15
Figure 1.4  Comparative map of BTA23 and HSA6  17
Figure 1.5  Structure of the MHC I and II binding molecules  19
Figure 2.1  Sire Families  26
Figure 3.1  BTA23 microsatellites used in Grandsire families.  36
Figure 3.2  GeneScan run of new markers in grandsire 9065 and 4189  38
Figure 3.3  Calculating the probability of recombination  39
Figure 3.4  Regression Analysis in Sons of 9065.  44
Figure 3.5  Analysis of suspected QTL site in families of sire 140 and 279  46
Figure 3.6  Information Content for 3 sire families used in study  48
Figure 4.1  Origin of granddaughters used in analysis.  52
Figure 4.2  Age at removal.  55
Figure 4.3  Percentage of granddaughters removed for each fate.  57
Figure 4.4  Onset of leading culling factors  59
Figure 5.1  Polymorphic fragment of MHC gene.  67
Figure 5.2  Restriction Map of alleles 09_ and 1201.  70
Figure 5.3  Digest of PCR for Grandsons.  71
Figure 6.1  Possible models explaining phenotype results  79
## List of Abbreviations

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>AI</td>
<td>Artificial Insemination</td>
</tr>
<tr>
<td>B cells</td>
<td>Bone lymphocyte cells</td>
</tr>
<tr>
<td>BoLA</td>
<td>Bovine Leukocyte Antigen</td>
</tr>
<tr>
<td>bp</td>
<td>Base pairs</td>
</tr>
<tr>
<td>BTA</td>
<td>Bos Taurus</td>
</tr>
<tr>
<td>BV</td>
<td>Breeding Value</td>
</tr>
<tr>
<td>cM</td>
<td>Centi Morgan</td>
</tr>
<tr>
<td>COMPASS</td>
<td>Comparative Map Analysis of similar sequences</td>
</tr>
<tr>
<td>DFM</td>
<td>Days from First Mating</td>
</tr>
<tr>
<td>DNA</td>
<td>Deoxyribonucleic acid</td>
</tr>
<tr>
<td>ER</td>
<td>Endoplasmic Reticulum</td>
</tr>
<tr>
<td>EST</td>
<td>Expressed sequence Tag</td>
</tr>
<tr>
<td>FISH</td>
<td>Fluorescent <em>in situ</em> Hybridization</td>
</tr>
<tr>
<td>HAS</td>
<td>Homo sapiens</td>
</tr>
<tr>
<td>HLA</td>
<td>Human Leukocyte Antigen</td>
</tr>
<tr>
<td>LB</td>
<td>Luria Broth</td>
</tr>
<tr>
<td>LIC</td>
<td>Livestock Improvement Corporation</td>
</tr>
<tr>
<td>MARC</td>
<td>Meat Animal Research Centre</td>
</tr>
<tr>
<td>MAS</td>
<td>Marker Assisted Selection</td>
</tr>
<tr>
<td>Mb</td>
<td>Mega bases</td>
</tr>
<tr>
<td>MHC</td>
<td>Major histocompatibility complex</td>
</tr>
<tr>
<td>ML</td>
<td>Maximum Likelihood</td>
</tr>
<tr>
<td>OMIA</td>
<td>Online Mendelian Inheritance in Animals</td>
</tr>
<tr>
<td>OMIM</td>
<td>Online Mendelian Inheritance in Man</td>
</tr>
<tr>
<td>QTL</td>
<td>Quantitative Trait Locus</td>
</tr>
<tr>
<td>RFLP</td>
<td>Restriction Fragment Length Polymorphism</td>
</tr>
<tr>
<td>SNP</td>
<td>Single Nucleotide Polymorphism</td>
</tr>
<tr>
<td>SSCP</td>
<td>Single Stranded Conformational Polymorphism</td>
</tr>
<tr>
<td>Term</td>
<td>Description</td>
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<tr>
<td>----------</td>
<td>--------------------------------------------------</td>
</tr>
<tr>
<td>T cells</td>
<td>Thymus cells</td>
</tr>
<tr>
<td>TAP</td>
<td>Transporter for Antigen processing Protein</td>
</tr>
<tr>
<td>TCR</td>
<td>T cell receptor</td>
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