

Testing of Inter-chromosomal LD in a half-sib family of cattle

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Introduction

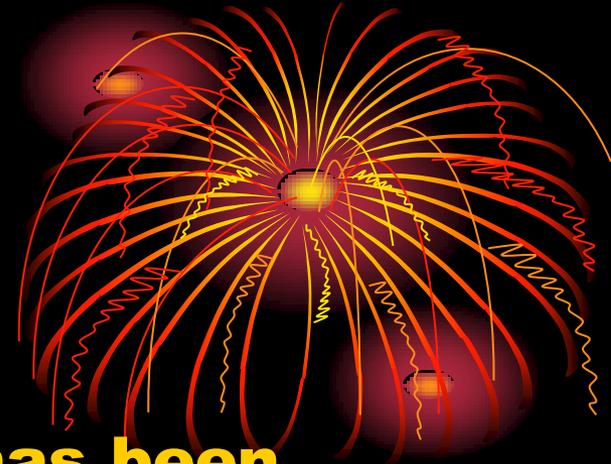
Extent of intrachromosomal LD has been widely investigated in cattle

Very little work has been done investigating interchromosomal LD patterns

Selection (natural or artificial) may result in association of alleles in different chromosomes.



Interchromosomal LD



Introduction

The use of SNP's arrays for testing interchromosomal LD may result in many millions of tests.



DIFFICULT TO IDENTIFY INTERCHROMOSOMAL LD !

Objective



- 1- Strategies to search for interchromosomal LD using dense SNPs arrays.**
- 2.- Test for Interchromosomal LD in a half-sib family of beef cattle.**

Methods

Maximum Likelihood Methods for half-sib families have been proposed

(Gomez-Raya, 2012; Genetics: 191:195).

Sire might be:

- a) double homozygote (direct haplotype counts)**
- b) homo-heterozygote (E.M. algorithm)**
- c) double heterozygote (E.M. algorithm)**

It requires knowledge of recombination fraction.

Strategy for testing interchromosomal LD

- 1) LRT (likelihood ratio test) was not used due to the large number of LD tests.
 - 2) Strategy:
 - a) Average r^2 for all pairs of SNPs per chromosome pair.
 - b) Percentage of LD tests with $r^2 > 0.70$ per chromosome pair.
 - c) **Search for clusters of markers in LD**
(groups of linked markers that are in LD with other group of markers in another chromosome).
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The half-sib cattle family was at the Gund ranch in Nevada (USA)

- 36 calves
- Paternity tested using 25 microsatellites
- Illumina 50k Beadchip (MAF of 0.10 or more)



RESULTS

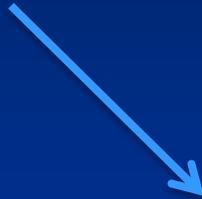


LD tests according to sires's genotype

Homo-Hetero		
Double homo		90,145,142
Double hetero		62,414,196
Total of LD tests		152,559,338

Results

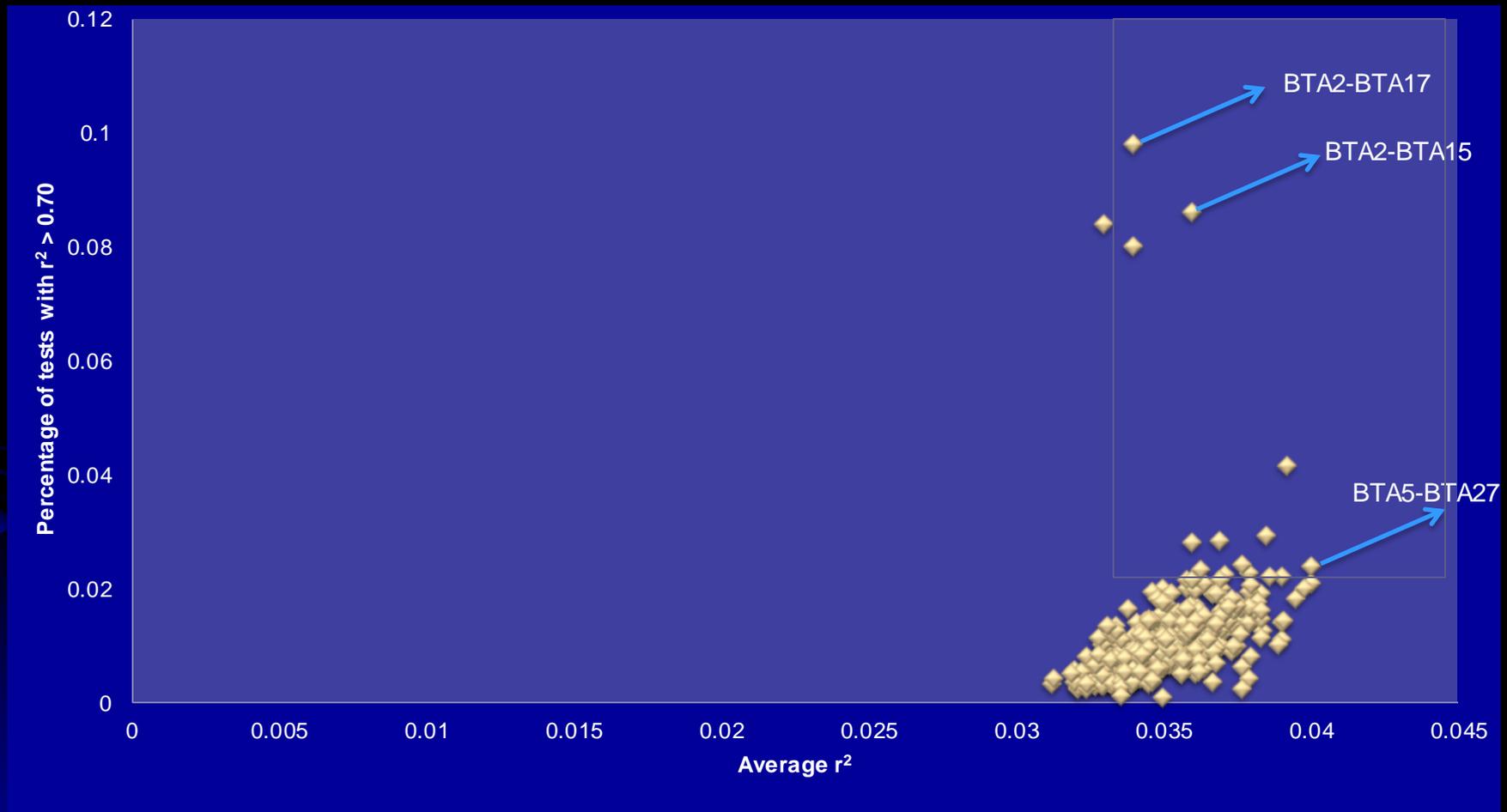
LD for sire with double heterozygote markers were not used.



Recombination fraction and LD can not be jointly estimated in half-sibs and suspicion of possible misplaced SNPs.



Average r^2 versus % of tests $r^2 > 0.70$



RESULTS FOR EACH CHROMOSMAL PAIR

Possible LD between

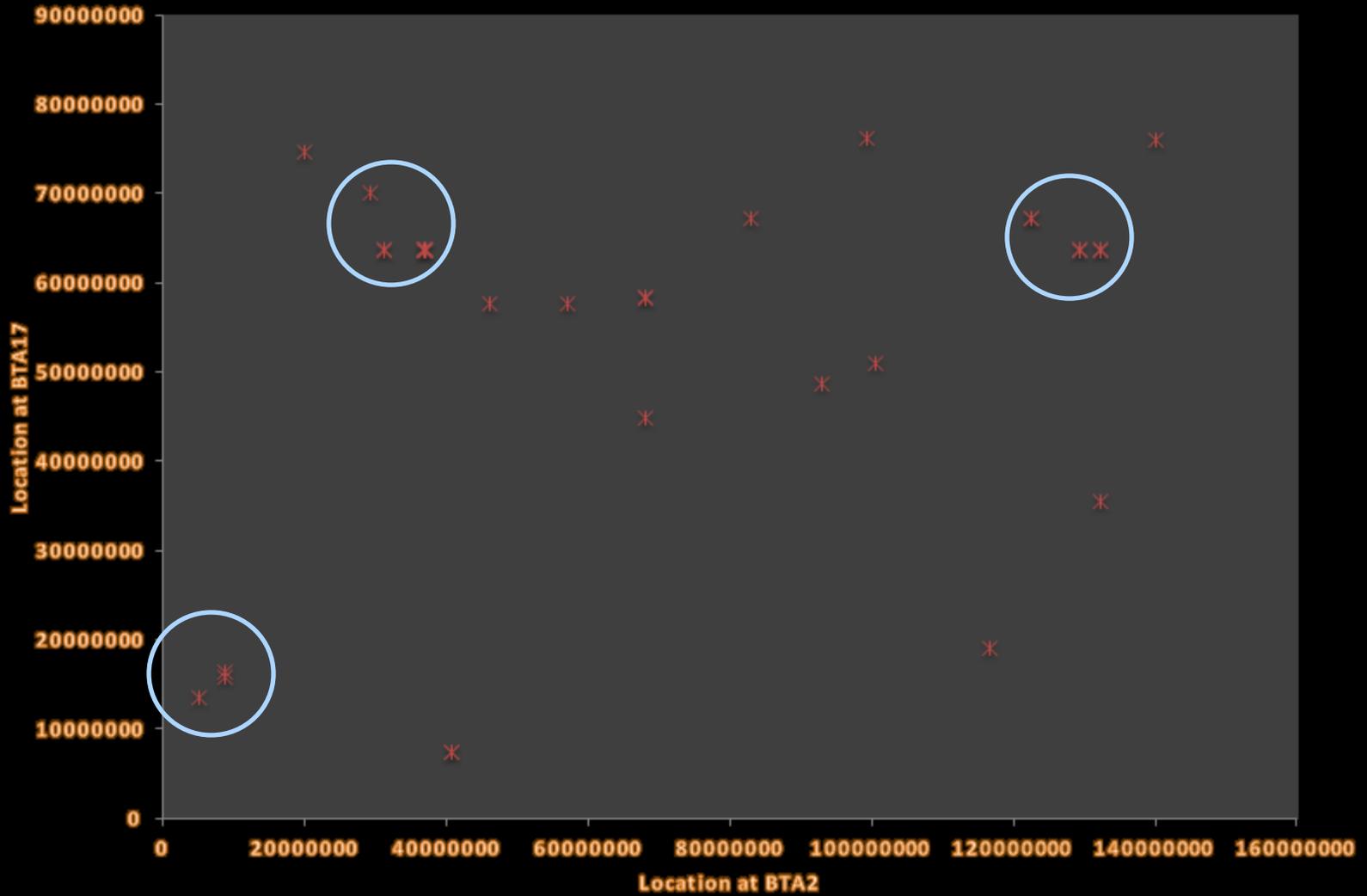
BTA2 and BTA17

BTA2 and BTA15

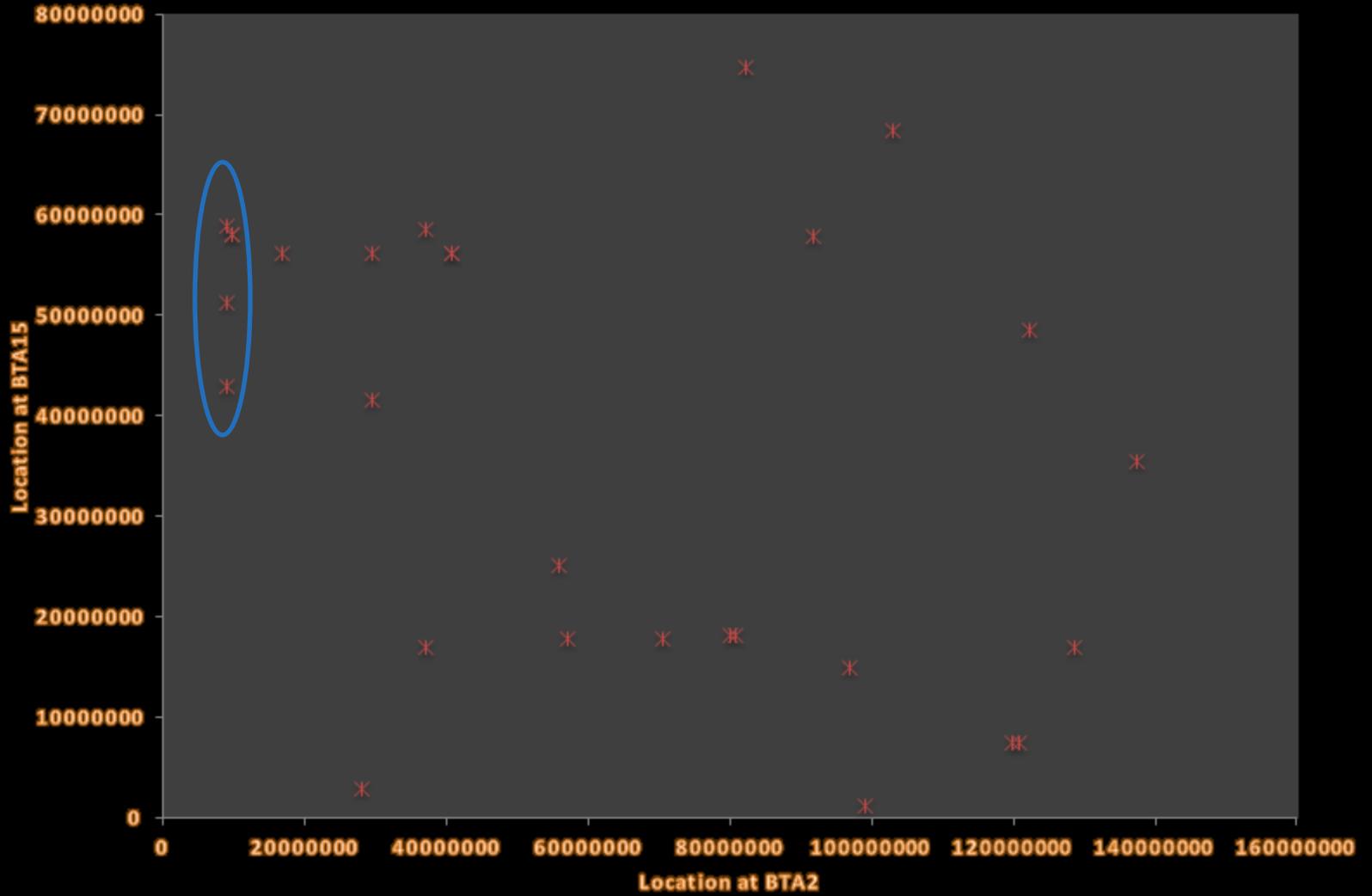
BTA5 and BTA27



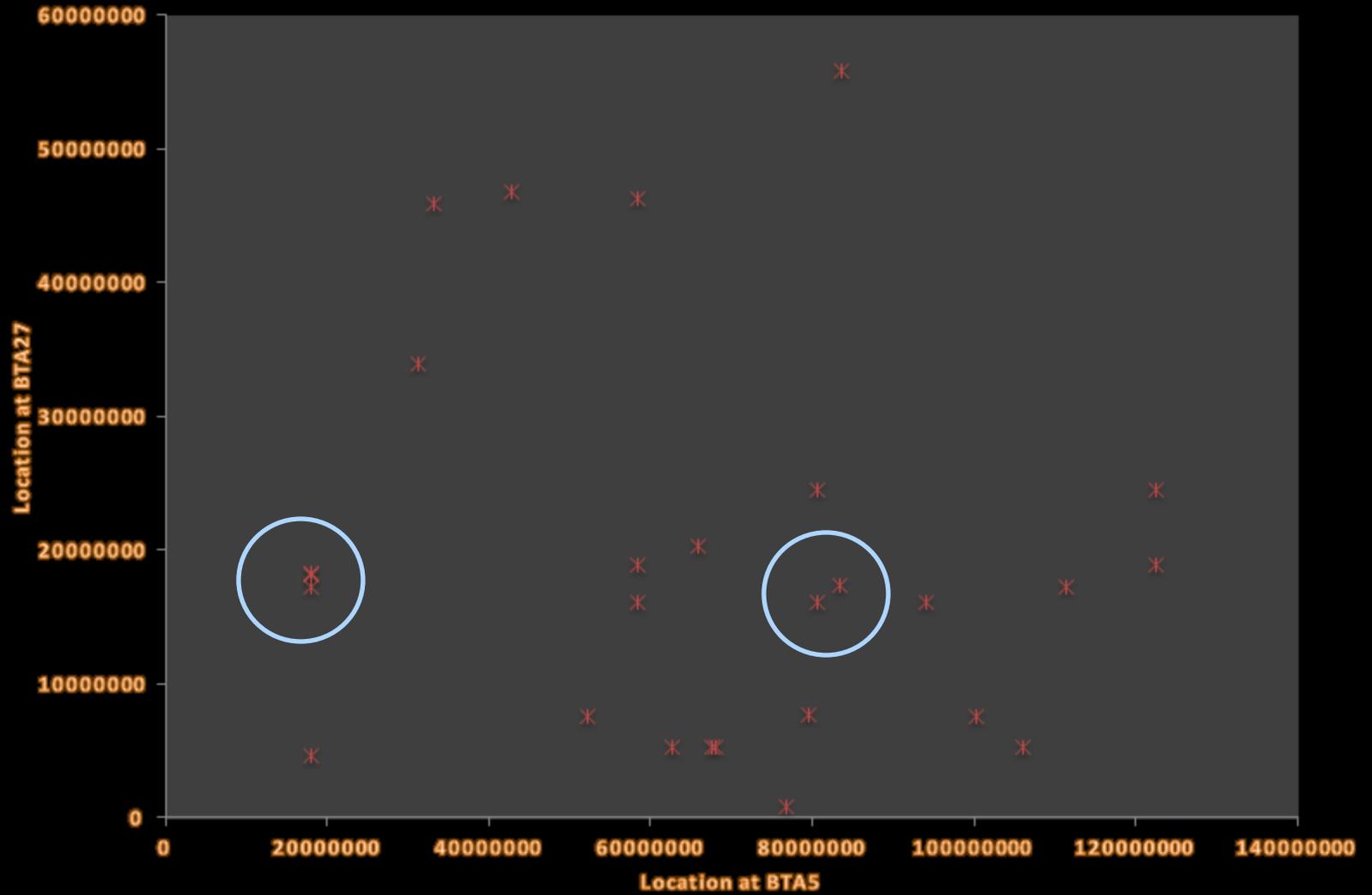
Clustering of LD between BTA2 and BTA17



Clustering of LD between BTA2 and BTA15



Clustering of LD between BTA5 and BTA27



Conclusions

Large number of tests makes difficult to investigate LD between chromosomes.

Possible LD between:

BTA2 and BTA17

BTA2 and BTA15

BTA5 and BTA27

Further testing in regions with high LD using other material is necessary.



THANKS!