

Influence of Relatedness in a Pedigree Design on Estimates of IBD Probabilities



NEWSHAM
Choice Genetics

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Background and Objective

- Estimates of IBD probability are key to QTL mapping for (co)variance component method.
- Inbred families could be advantageous for QTL mapping due to reduced genetic variation and higher IBD sharing.
- Demonstrate influence of relatedness within pedigree on IBD probability estimates for practical QTL mapping

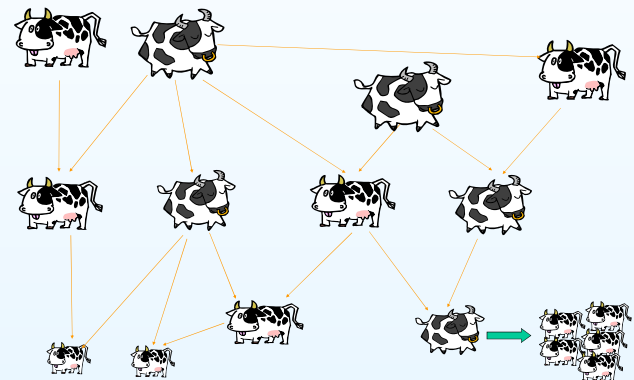
Material and Methods

Data simulation:

- 4 generations with 7 sire families originating from 2 great grandsires (GGS).
- Family structures distinguished by inbreeding coefficient.
- Marked chromosomal segment of 55 cM, one QTL at 41.5 cM. 11 markers, varying simulation parameters.
- PEDSIM simulation method (Schelling et al., 1998).

Calculation and Comparison of IBD- probabilities:

- Calculation of IBD using a deterministic approach (Vukasinovic & Martinez, 2002);
- Rapid recursive algorithm (Pong Wong et al., 2001) that combines general pedigree method and method for estimating IBD between sibs.



Simplified scheme of a pedigree with extremely strong inbreeding

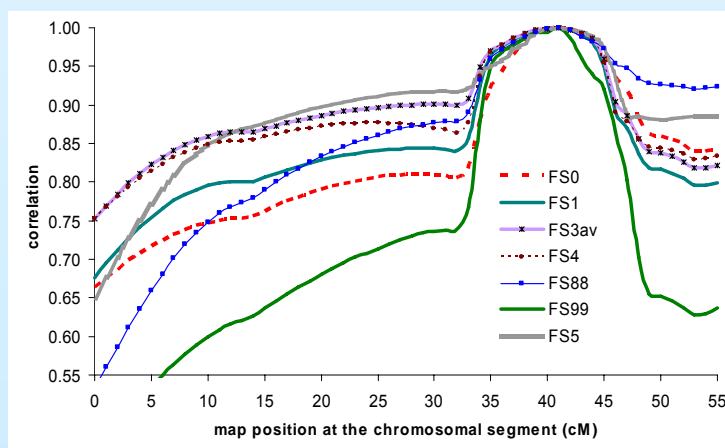
Results

Average IBD- sharing in different family structures (FS)

	FS0	FS1	FS3	FS5	FS88	FS99
overall F_x	0	<0.001	<0.01	0.02	0.01	0.28
highest F_x	0	0.125	0.25	0.38	0.38	0.43
GGS1	0.06	0.11	0.11	0.14	0.15	0.32
GGS2	0.03	0.06	0.04	0.16	0.08	0.14

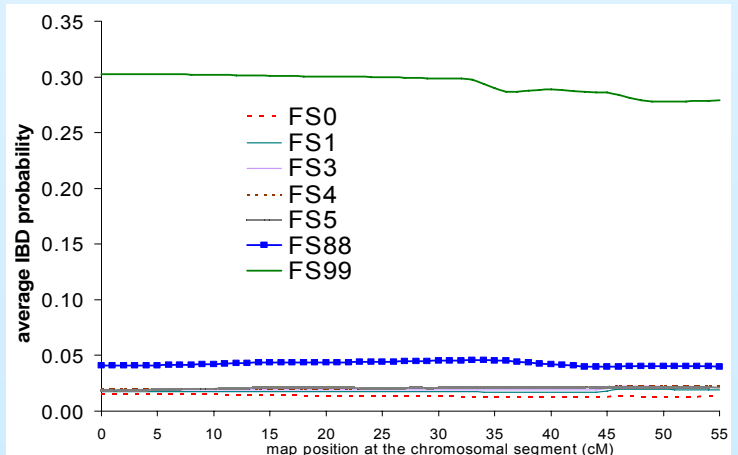
Parameters of IBD probability depend on inbreeding level and on the overall relatedness within the pedigree

- Average IBD sharing of great grand sires GGS1 and GGS2 and their final offspring also increases with inbreeding level.
- FS5, being a pedigree with relatively high inbred sires, does not result in superior IBD parameters, because of isolated sub-families.



Correlation profiles of IBD probabilities at the current map position and at the true QTL position

- Steepest profiles in strongly inbred pedigrees (FS99), i.e. better conditions for QTL detection.
- Isolation of pedigrees yields flat profiles (FS5).



Average IBD probability for different family structures (FS)

- Differences in average IBD probability (incl. SD) increase with increasing inbreeding level.
- "Gaps in the profile" are better to detect in inbred pedigrees.

Conclusion

- Involving inbred sires into calculation of IBD-probabilities facilitates to infer the parental phases of the offspring haplotypes.
- Inclusion of already existing inbred animals in a QTL mapping panel in dairy cattle could be beneficial.