Use of SNP for marker assisted selection in french dairy cattle

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Description of MAS in France

- Current MAS program
  - Microsatellites markers – low density map :
    - 2-5 markers by QTL (45 markers for 14 QTLs)
    - Usually more than 10 cM between markers
  - Linkage Equilibrium – within family estimation
- Evolutions: towards genomic selection
  - 10000 SNPs or more
  - All chromosomal segments

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Alternative use of SNPs markers

- Use of 600 to 1000 SNPs
  - Lower costs
  - Still a few identified QTLs (± 10 SNPs by QTL)
  - Denser markers maps (all markers within 1-2 cM)
    - Larger informativity
  - Possibility to use linkage disequilibrium

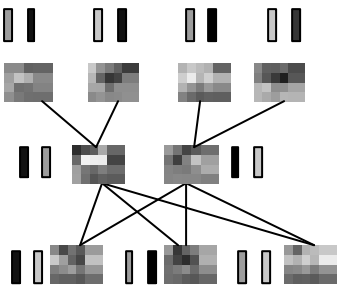
New model

- Use of haplotypes effects (1-2 cM)
- Few haplotypes contribute to haplotypes of young bulls
  - Pedigree with 6 generations from young bulls to ancestors
  - 75 % of the young bulls haplotypes came from 25 founder haplotypes (even less if more generations known)
- High probability for small haplotypes to be transmitted IBD over recent generations

Consequences

- Not necessary to genotype all animals from common founders to young bulls
- Not necessary to compute transmission probabilities
- Fewer effects to estimate (higher precision)
  - Possibly less animals to genotype

Simulation to test precision of estimation of QTL effects



1) Start from 576 candidates
2) Construct pedigree over 4 generations
3) Assign 2 haplotypes to each ancestors (Sampled from real data set to mimic LD)
4) Transmit these haplotypes through the population

→ Repeated for every QTL

Haplotypes for base animals

- Sampled from a real data set
  - 374 SNPs selected on dense SNPs map on BTA3
    - Gautier et al., genetics –accepted
  - 925 genotyped Holstein bulls
  - Regions with 11 SNP within 2 cM
  - Central SNP removed
    - Number of different haplotypes
    - use haplotype to predict central SNP (Hayes et al., 2006)

Description of haplotypes on BTA3

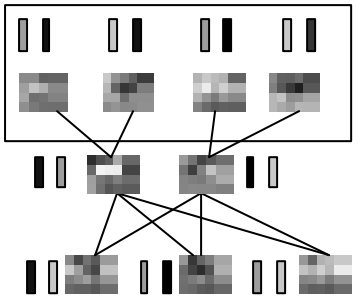
(Hayes et al.,2006) $r^2(h,q) = \sum_{i=1}^{n} \frac{D_i^2}{p_i} / q_1 q_2$

Size of haplotype	Max	1 cM		2cM	
		nb Haplotype	r^2	nb Haplotype	r^2
4	16	9.91	0.63	9.55	0.63
6	64	17.87	0.76	17.45	0.77
8	256	24.25	0.86	24.4	0.86
10	1024	27.35	0.91	28.8	0.91

Simulation of phenotypes

- The central SNP of haplotypes is used as QTL
- Simulation of phenotypes based on polygenic, QTL and residual effects for each animal
- Actual parameters of MAS program are used(h^2, QTL variance, frequencies, etc.)

Evaluation



1) Subset of 2634 animals with known genotypes
   1) 2058 ancestors with records
   2) 576 young animals without records
2) Central SNP is discarded
3) Evaluation with a BLUP model based on IBS haplotypes

Evaluation model

$$\mathbf{y} = \boldsymbol{\mu} + \mathbf{u} + \mathbf{X}'\boldsymbol{ß} + \mathbf{e}$$

y = vector of phenotypes of individuals

μ = vector with the intercept

u = vector of polygenic effects

X = matrix relating animals to haplotypes effects for all QTLs

ß = vector with solutions for random haplotypes effects

e = the residual of the model

Correlations between true and estimated QTL effects

Results obtained for young bulls without records – 100 replications
Fat yield (h^2=0.30)

	QTL1	QTL2	QTL3	QTL4	QTL5
% Var(QTL)	0.05	0.05	0.15	0.05	0.20
MAS in LE	0.557	0.371	0.573	0.384	0.523
4 SNPs Haplotypes	0.536	0.314	0.897	0.485	0.947
10 SNPs Haplotypes	0.714	0.762	0.875	0.673	0.908

Correlations between true and estimated QTL effects

Results obtained for young bulls without records – 100 replications
Fat content (h^2=0.50)

	QTL1	QTL2	QTL3	QTL4
% Var(QTL)	0.05	0.05	0.40	0.10
MAS in LE	0.570	0.413	0.681	0.494
4 SNPs Haplotypes	0.531	0.363	0.933	0.708
10 SNPs Haplotypes	0.708	0.811	0.942	0.773

Conclusions

- With dense SNPs maps, efficiency of MAS is improved:
  - Higher marker informativity
  - Use of linkage disequilibrium
  - More precise estimation of QTL effects
  - Less genotyped animals are required

Acknowledgments

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