Including dominance effects in genomic selection

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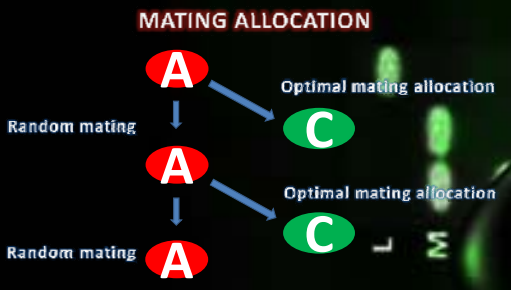
1. HOW TO PROFIT FROM DOMINANCE:

Any methodology that pretends to use non-additive effects:

It must contemplate TWO types of matings:

i. Matings from which the population will be propagated

ii. Matings to obtain commercial animals



2. SIMULATION:

- Population of Ne=100 during 1000 generations;
- The populations was increased up to 500 males and 500 females during 3 generations;
- These 3000 (generation 1001, 1002 and 1003) individuals were genotyped and phenotyped and used as training population to estimate additive and dominance effects of SNPs;
- Generation 1004 was formed from 25 sires and 250 dams of generations 1003 (populations after selection)

Genetic Assumptions:

- 10 chromosomes of 100 cM
- 10.000 loci (9.000 SNP and 1.000 QTLs)
- Both SNPs and QTLs have two alelles
- Mutation rates were 0.0025for SNPs and 0.00005 for QTls (about 8.000 SNP and 80 QTLs were segregating in generetion 1.000)

Genetic Effects:

- Additive and dominance effects sampled from N(0,1)

Residual Effects:

- Residuals were samples from a N(0,1) and rescaled according the desired heritability

Four Strategies of Selection compared:

Phenotypic Selection (PS): 25 sires and 250 dams were selected from 500 males and 500 females based on phenotypic values. Mating at random;

Genomic selection (GS-ND): 25 sires and 250 dams were selected from 500 males and 500 females based on additive effects estimated via Bayes A without including dominance in the model. Mating at random

Genomic selection (GS-D): 25 sires and 250 dams were selected from 500 males and 500 females based on additive effects estimated via Bayes A but including dominance in the model. Mating at random

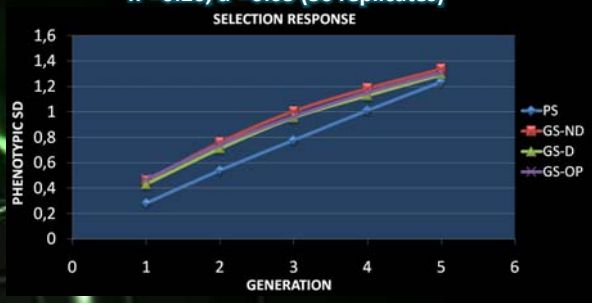
Genomic Selection + Optimal mate allocation (GS-OP): From the 6.250 (25 x 250) possibles matings, we choose the best 250 based on the dominance prediction of the mating using simulated annealing;

3. INCREASE OF RESPONSE (ONE GENERATION, 50 REPLICATES) OF GS-OP VS GS-ND, GS-D AND PS:

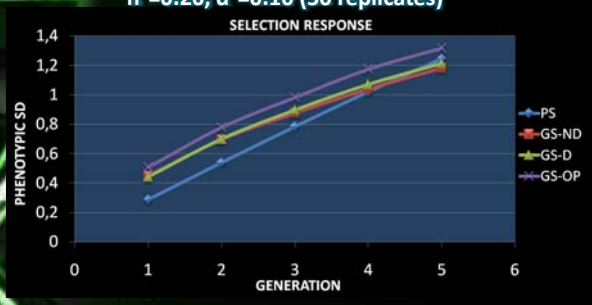
	GS-ND	GS-D	PS
h^2=0.20; d^2=0.05	2.4%	9.3%	66.1%
h^2=0.20; d^2=0.10	13.1%	15.2%	76.4%
h^2=0.40; d^2=0.05	-3.2%	6.1%	30.4%
h^2=0.40; d^2=0.10	5.7%	10.7%	39.8%

4. LONG TERM RESULTS:

h^2=0.20, d^2=0.05 (50 replicates)



h^2=0.20, d^2=0.10 (50 replicates)



h^2=0.40, d^2=0.05 (50 replicates)

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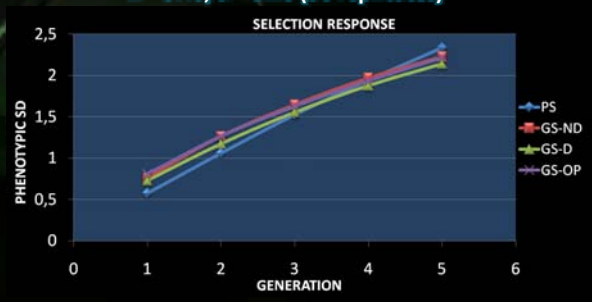

PS= Phenotypic Selection
GS-D= Genomic selection evaluated with dominance
GS-ND=Genomic selection evaluated without dominance
GS-OP= Genomic selection + Optimal mating allocation

5. REMARKS:

The inclusion of dominance effects in the model could deteriorate, in some circomstances, the estimation of additive effects;

The increase of response of GS-OP (Genomic Selection and Optimal Mating) vs. GS (Genomic Selection) could be up 15 % if the amount of dominance variance is substantial;

Advantage of mating allocation disappear after one generation of response;