(Some thoughts) ON WITHIN-FAMILY GENOMIC SELECTION IN AQUACULTURE BREEDING PROGRAMMES

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Genomic selection is a method that:

- estimates the association of a large numbers of genetic markers in one part of the population (siblings of the selection candidates, for example) with phenotypes (training)

- and uses these estimates to predict genetic values of other part of the population (testing)

Within family genomic selection is a method that:

- It captures the within-family genetic component, which cannot be estimated for traits that cannot otherwise be measured on the candidates themselves

- It can also be a cost-efficient means of genomic evaluation of selection candidates, because it could require lower marker density

1) Can genomic selection work in a panmictic population in linkage equilibrium?

Yes, because there is always linkage disequilibrium within families

Individual AB/ab → *gametes* →

AB ½ (1-c)
Ab ½c
aB ½ c
ab ½ (1-c)

D=fr(AB)*fr(ab)-fr(Ab)*fr(aB)= + ¼ (1-2c)

c = freq. recombination

Individual Ab/aB → *gametes* →

Ab ½ (1-c)
AB ½c
ab ½c
aB ½ (1-c)

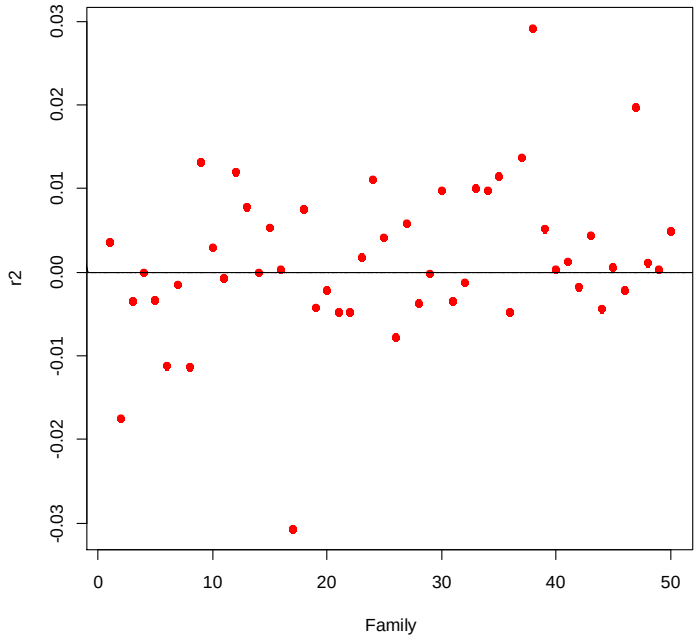
D=fr(AB)*fr(ab)-fr(Ab)*fr(aB)= - ¼ (1-2c)

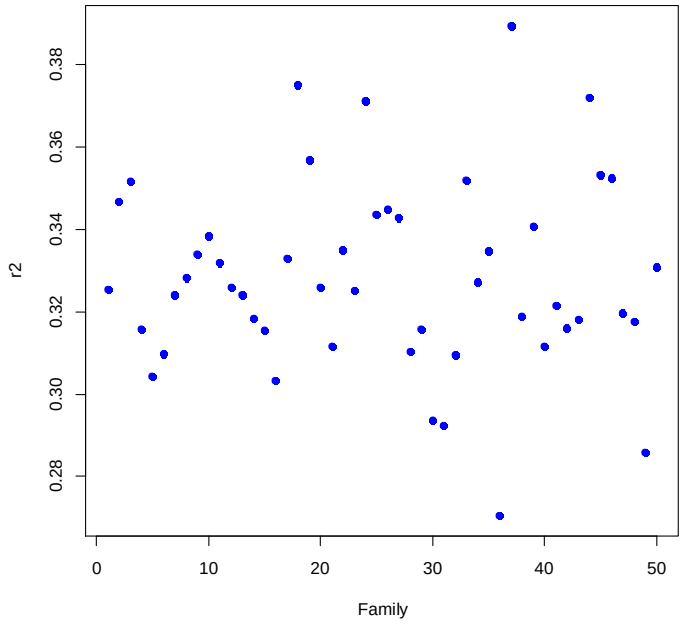
Although this disequilibrium has different sign in different families and therefore the global linkage disequilibrium is zero

1 chromosome of 1 Morgan (200 loci, c=0.005): 50 families of 200 full-sibs (parents in linkage equilibrium, gene frequencies=0.5)

$r^2=D^2/p_Ap_ap_Bp_b$

Between consecutive loci	D	r^2
Intrafamily LD	0.0015	0.3283





	D	r^2
Population LD	0.0009	0.0053

1 chromosome of 1 Morgan (200 loci, r=0.005): 50 families of 200 full-sibs (parents in linkage equilibrium)

	D	r^2
Intrafamily	0.0015	0.3283
Population	0.0009	0.0053

Between consecutive loci

If parents are from a F1 between inbreed lines

	D	r^2
Intrafamily	0.2468	0.9799
Population	0.2475	0.9799

If r=0.5

	D	r^2
Intrafamily	0.0001	0.1104
Population	-0.0002	0.0027

2) GBLUP evaluation can be done either independently in each family (Genomic matrix 200x200) or for the whole population (Genomic matrix 10000x10000)

h^2=0.40, 50 families of 200 full-sibs (all phenotyped and genotyped)

Correlation between true and genomic estimated breeding value

Intrafamily GBLUP evaluation

Marker/ chrom	**QTLs/chrom**			
	200	**100**	**20**	**1**
200	0.60	0.57	0.60	0.65
100	0.52	0.59	0.61	0.63
20	0.54	0.54	0.54	0.57
1	0.32	0.33	0.31	0.14

-substancial accuracies even with 20 markers/chrom.

50 families of 200 full-sibs, h2=0.40 (all phenotyped and genotyped)

Correlation between true and genomic estimated breeding value (correlations calculated across the population)

Population GBLUP evaluation

Marker/ chrom	QTLs/chrom			
	200	**100**	**20**	**1**
200	0.42	0.41	0.43	0.45
100	0.33	0.37	0.38	0.39
20	0.16	0.18	0.18	0.18
1	0.01	0.01	0.01	0.01

-lower accuracies

- accuracies decrease by 60% for 20 markers/chrom

Marker / chrom	**QTLs/chrom**			
	200	**100**	**20**	**1**
200	**0.60**	**0.57**	**0.60**	**0.64**
100	**0.52**	**0.59**	**0.61**	**0.63**
20	**0.54**	**0.54**	**0.54**	**0.57**
1	**0.32**	**0.33**	**0.31**	**0.12**

50 families of 200 full-sibs, h2=0.40 (100 training and 100 testing)

Correlation between true and genomic estimated breeding value in the testing set

Intrafamily GBLUP evaluation

Marker/ chrom	**QTLs/chrom**			
	200	**100**	**20**	**1**
200	0.37	0.35	0.37	0.41
100	0.28	0.35	0.36	0.39
20	0.29	0.27	0.28	0.30
1	0.32	0.16	0.16	0.18

- Accuracies with 20 markers/chrom are 80% of those with 200 markers

50 families of 200 full-sibs, h2=0.40 (100 training and 100 testing)

Correlation between true and genomic estimated breeding value in the testing set

Population GBLUP evaluation

Marker/ chrom	QTLs/chrom			
	200	**100**	**20**	**1**
200	0.21	0.18	0.21	0.23
100	0.12	0.16	0.18	0.19
20	0.08	0.09	0.08	0.09
1	0.01	0.00	0.01	0.01

- Accuracies decrease by 60% with 20 markers/chrom

Marker/ chrom	QTLs/chrom			
	200	**100**	**20**	**1**
200	**0.37**	**0.35**	**0.37**	**0.41**
100	**0.28**	**0.35**	**0.36**	**0.39**
20	**0.29**	**0.27**	**0.28**	**0.30**
1	**0.32**	**0.16**	**0.16**	**0.18**

3) Selection response after 10 generations of intrafamily selection with intrafamily evaluation and three mating systems

50 families of 200 full-sibs (all full-sibs phenotyped and genotyped)

Assortative: pairs with similar estimated genomic value

Disassortative: pairs with disimilar estimated genomic value

	Random	**Dissasortative**	**Assortative**
h^2=0.4 c^2=0.0	6.29	6.29	5.86
h^2=0.4 c^2=0.4	7.25	7.33	6.83
h^2=0.1 c^2=0.0	1.57	1.62	1.48
h^2=0.1 c^2=0.4	1.96	1.98	1.65
		+1%	***-8.25%***

50 families of 200 full-sibs (100 full-sibs phenotyped and genotyped and 100 only genotyped)

	Random	**Dissasortative**	**Assortative**
h^2=0.4 c^2=0.0	3.40	3.50	3.21
h^2=0.4 c^2=0.4	4.11	4.33	4.00
h^2=0.1 c^2=0.0	0.76	0.81	0.70
h^2=0.1 c^2=0.4	0.98	0.99	0.79
		+4%	***-5.84%***

Remarks

- In the scenario considered GBLUP evaluation done independently in each family provides sustantial correlation between the true and the genomic value that are maintained with lower number of markers (20)

- Intrafamily genomic selection response is larger with high values of common environment

- There is a small positive effect of dissassortative mating

- There is a substantial negative effect of assortative mating

Future work

- To explore more realistic models of linkage disequilibrium in the base population
- To combine the ’within family genomic selection breeding value’ with a traditional ’between family breeding value’ to obtain accurate total breeding values
- To develop tools to manage the inbreeding at the genomic level

THANKS FOR YOUR ATTENTION

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