WITHIN-FAMILY LINKAGE DISEQUILIBRIUM IN AQUACULTURE POPULATIONS

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Summary

In classical aquaculture breeding programs selection within families cannot be applied for traits that cannot be recorded on the candidates. However, this problem can be overcome if genomic information is available. In particular within-family genomic selection has been proposed for aquaculture programs since large family sizes are available and high levels of within-family linkage disequilibrium (LD) can be attained with a limited number of markers. In this study we have investigated within-family LD under three scenarios: 1) base populations in global linkage equilibrium; 2) base populations with the maximum possible linkage disequilibrium (F1 between two inbred lines) and 3) base populations with an intermediate LD (F20, after twenty generations of random mating from the F1). Populations composed of 50 families were simulated. The genome consisted of 20 chromosomes of 1 Morgan each, with 20, 50, 100, 200, 300 and 400 genes. The genes were biallelic ($p = 0.5$) and evenly distributed across the chromosomes. Within each family 200 full-sibs were genotyped. The table shows the values of LD measured as the square of the correlation coefficient.

No. genes/ch	Pop. equilibrium		F1		F20	
	Population LD	Intrafamily LD	Population LD	Intrafamily LD	Population LD	Intrafamily LD
400	0.0050	0.3310	0.9876	0.9876	0.9442	0.9557
300	0.0050	0.3308	0.9835	0.9835	0.9265	0.9415
200	0.0050	0.3283	0.9754	0.9754	0.8922	0.9139
100	0.0049	0.3231	0.9512	0.9513	0.7955	0.8368
50	0.0048	0.3124	0.9040	0.9042	0.6317	0.7070
20	0.0045	0.2834	0.7714	0.7719	0.3134	0.4712

It can be observed that in the particular situation of aquaculture the intrafamily LD is more important that the global LD. The relevance of these results in the context of intrafamily genomic evaluations is discussed.