COMPARING BREEDING SCHEMES USING INDIVIDUAL PHENOTYPIC VALUES AND BLUP BREEDING VALUES AS SELECTION CRITERIA.

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SUMMARY
Results from simulation using Best Linear Unbiased Prediction (BLUP) as the method of breeding evaluation when selecting, are presented for different heritabilities and population sizes. This method is compared with selection based on individual phenotypic values (mass selection). For heritabilities greater then 0.10, BLUP selection is inferior to phenotypic selection. The reasons for this are discussed, and it is concluded that with the given constrains, the higher selection intensity obtained with phenotypic selection, overrules the higher selection accuracy obtained with BLUP selection.

INTRODUCTION
The long term selection goal for any selection program should be sustainable genetic gain for the traits defined in the breeding goal. This is achieved by keeping control of the inbreeding (see e.g. Caballero *et al.* 1996). In recent years, different methods have been proposed to reduce rates of inbreeding in breeding schemes for livestocks while keeping genetic gain at the same level (see e.g. Meuwissen 1997). Many of the problems and solution strategies relevant for these species are, however, not applicable for aquatic species due to the high fecundity in these species compared to traditional livestocks. Moreover, in aquatic species still other testing design can be performed using the advantage of external fertilisation in most aquatic species (e.g. maternal hierarchical and factorial mating systems). Thus, research especially directed towards fish have been carried out (e.g. Mckay *et al.* 1990; Mckay and Mcmillan, 1991).

In the works of Bentsen and Gjerde (1994) and Gjerde *et al.* (1996), results from simulating and optimising individual phenotypic selection (mass selection) were shown. In the present study, results from selection using Best Linear Unbiased Prediction (BLUP) as the method of breeding evaluation will be shown, and the results will be compared to those obtained with individual phenotypic selection.

METHODS
Artificial selection was practised in a trait controlled by an infinitesimal additive model of gene effects with initial heritability h^2. In generation 0, genotypic values and individual environmental deviations were assumed to be normally distributed with mean zero and variance h^2 and $1-h^2$, respectively. The selection criterion was the individual phenotypic performance or the estimated breeding values using animal model BLUP evaluation. Selection was directional and by truncation. The total number of offspring born per

generation (N) and the number of selected males (n_s) and females (n_d) were constant over generations. For a fixed value N and a fixed mating ratio (nested: one sire with two dams), the value of n_s was optimised as described later. The simulated selection experiment was run for 15 generations, i.e. 14 generations of selection. Each experiment was replicated 20 times and the results presented are averages over replicates.

Parameters studied. Twelve different values of total number of individual born per generation (N), ranging from 300 to 9600 were studied. Three different values of the initial heritability were considered (h^2 = 0.1, 0.2 and 0.4). The rate of inbreeding per generation, ΔF, was restricted at 1 %, which is equivalent to an effective population size, N_e , of 50.

Optimising. The rates (per generation) of genetic gain and inbreeding considered, were averages for the last ten generations of selection. For a given set of values for N and h^2, the optimum design was found iteratively. Optimisation was for the number of sires selected. This parameter, n_s , was varied until the rate of inbreeding per generation converged within ± 0.0005, at the pre-set inbreeding level.

During the simulation, the genetic gain was recorded, and different breeding schemes were compared by partitioning the genetic gain according to the equation:
$$\Delta G = i \ \sigma_G \ r_{GI}$$
where i is the selection intensity, calculated as $\Delta G/\sigma_I$, where σ_I is the standard deviation of the index; σ_G is the true genetic standard deviation; and r_{GI} is the selection accuracy, calculated as σ_I / σ_G.

RESULTS AND DISCUSSION
Figure 1 show the genetic gain per generation with phenotypic and BLUP selection for different populations sizes and different heritabilities. It is noteworthy that phenotypic selection outdo BLUP selection, at least for heritabilities higher than 10 %. This trend is expected, since a higher heritability implies that more genetic information is to be detected on basis of the individual itself.

When increasing the population size over 2-4000, there is diminishing return of genetic gain. This is most pronounced for the lowest heritabilities.

When comparing the two selection methods in the first figure, one have to be aware of the difference in breeding designs (Table 1). The number of fullsib families needed to keep the inbreeding constrains, are much higher with BLUP selection than with phenotypic selection. This is so because BLUP evaluation tends to give fullsibs similar breeding values and also cluster together animals related to each other (see e.g. Verrier *et al*. 1993). The constrains applied in this simulation, thus force the number of fullsib groups up, in order to keep the number of fullsibs per family, and consequently the inbreeding, down.
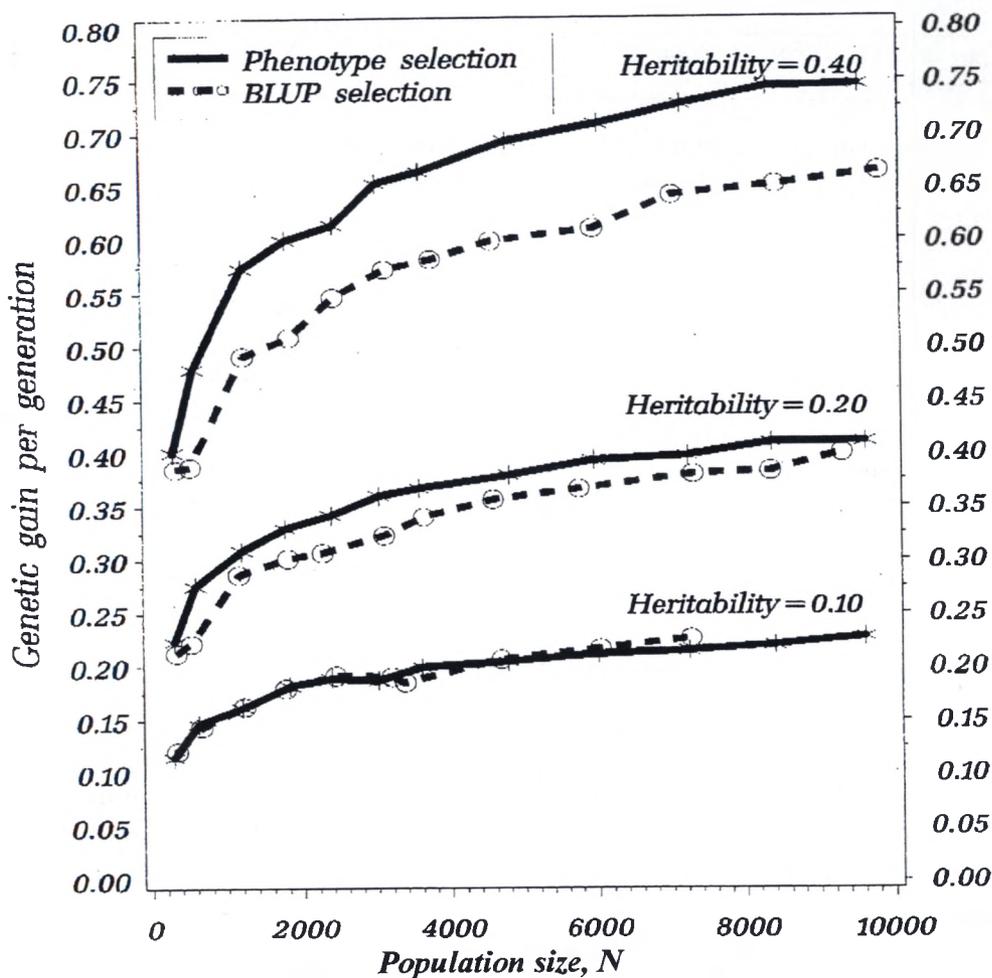
Figure 1. Genetic gain per generation for different population sizes, heritabilities and selection criterion. $\Delta F = 1\ \%$.

Table 1 show the design parameters for the population size of 1200 for both selection methods. The number of families needed, and consequently also the number per family, are very different for the two selection methods.

Table 1. Examples of optimum breeding schemes. $N = 1200$, $h^2 = 0.40$

Selection criteria	Breeding scheme		Rel. gen. gain/gen.
	# of fam.	# per fam.	
Individual phenotypic selection	34	68	100
Individual BLUP selection	103	6	85

Table 1 also show that the relative genetic gain achieved with individual phenotypic and BLUP selection. To reveal the underlying reasons for the difference, the genetic gain was split into selection intensity, selection accuracy and genetic SD (Table 2).

Table 2. Actual and relative figures for selection intensity, selection accuracy and genetic SD with individual phenotypic and BLUP selection. $N = 1200$, $h^2 = 0.40$

	Selection intensity	Selection accuracy	Genetic SD	Genetic gain
Individual phenotypic selection				
- **actual** figure	1.90	0.568	0.535	0.57
- **relative** figure	100	100	100	100
Individual BLUP selection				
- **actual** figure	1.15	0.757	0.563	0.49
- **relative** figure	60	133	105	85

The higher selection intensity obtained with individual phenotypic selection, overrules the higher selection accuracy obtained with individual BLUP selection. The genetic SD should be similar for the two methods, given the restrictions applied in the simulation.

BLUP selection will, however, probably outdo phenotypic selection for multi trait selection, and the strategy for BLUP selection may be improved by selecting individuals less related to those already selected.

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