Empirical Evaluation Of The Potential Of Walk-back Selection In Breeding Programme For European Whitefish (*Coregonus lavaretus* L.)

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Introduction

Family-based breeding programmes for aquaculture species are traditionally based on separate rearing of full-sib families until individual tagging, and thus demand vast investments and are expensive to run. Common rearing of standardized number of members from each full-sib family would decrease costs of the programme and unify the common environmental effects over the families. In walk-back selection (WBS) fish are reared in a common tank, phenotypically superior fish are genotyped and pedigreed using genetic markers, BLUP breeding values are estimated, and subsequently breeders for the next generation may be selected by optimal contribution (OC) principals (Doyle and Herbinger (1994); Sonesson (2005)). In practice, between-family variation in survival may invalidate the benefits of WBS as a low-cost breeding programme. Another drawback of the WBS method is that selection criteria are restricted only to traits easily measurable from the candidates themselves (Sonesson (2005)). Genotyping, parental assignments and kinship analysis may add the costs of WBS. The purpose of this study was to empirically evaluate the potential of WBS for European whitefish breeding programme.

Material and methods

Data. The data comprised of one year-class of European whitefish (*Coregonus lavaretus* L.) originating from the Finnish national breeding programme maintained together by Finnish Game and Fisheries Institute (FGFRI) and MTT Agrifood Research Finland. The fish were non-selected, second generation progeny of wild fish from the River Kokemäki. Fish were individually tagged with known relationships. Real-life screening of body weight after four growing seasons in freshwater was used as a selection criterion.

Sampling and selection. Original screening order of the fish (N_{tot}=1,143) was maintained and batches of fish (100, 120, 150, 200) were selected for genotyping using mass selection. Thresholds for mass selection (MEAN, MEAN+0.5σ_P, MEAN+1.0σ_P) of breeding candidates were based on known values of the mean (576g) and standard deviation (127g) from the full dataset. For each batch 1) fish above the threshold value were selected for genotyping until

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the size of the batch was fulfilled, 2) breeding values (EBV) were estimated (DMU4, Madsen and Jensen (2008)), and 3) fish were selected as parents by OC principals (EVA, Berg (2004)) requesting 70 full-sib families, as this is the current size of the breeding programme. It was assumed that all mating combinations produced viable progeny. Only two matings per candidate were allowed, as the volume of gametes is restrictive in this size of fish of this species. Evaluation of the WBS method was based on the rate of relationship (Δa), mean EBV of the selected parents (genetic level) and rank order correlation between batch EBV and EBV from the full dataset. Variance components (h^2=0.39±0.08) and EBV for comparisons were obtained from the full dataset, as batch EBV are biased and not suitable for between-scheme comparisons.

Results and discussion

Utilisation of full dataset (corresponds genotyping of all selection candidates) resulted in 101 selected individuals, with mean EBV=113.6 and Δa=0.124. Batch size smaller than 100 fish failed to satisfy either the number of matings requested (N=70) and/or the highest accepted Δa (0.015). Sonesson's (2005) simulation study reported that in breeding schemes with 1,000 candidates, more than one batch of 50 fish was required to meet the accepted inbreeding level. When MEAN+1.0σ_P threshold was used, only batch option N=100 could be fully performed. This resulted in acceptable Δa (0.0140) and mean EBV level comparable with that of full dataset scheme (113.7). Due to the high frequency of immature fish (34%) only 112 fish exceeded the highest threshold. Although the fish selected from this batch were slightly superior to those selected from full dataset (Figure 1), and the fact that genotyping costs would decrease significantly compared to genotyping all individuals, 20% less fish were selected (N=80) causing an increase in Δa. For the rest of the selection schemes, very similar Δa values and number of selected parents were obtained (Table 1).

Table 1: Number (N) of pedigreed candidates, selected parents, and rate of relationship (Δa) with different batch sizes and mass selection thresholds.

Batch size	Mass selection threshold									
	MEAN					MEAN+0.5σ_P				
	N candidates		N selected		Δa	N candidates		N selected		Δa
	♂	♀	♂	♀		♂	♀	♂	♀	
100	57	43	44	40	0.0130	46	54	42	38	0.0134
120	70	50	44	41	0.0131	55	65	43	41	0.0134
150	83	67	42	41	0.0128	67	83	46	44	0.0130
200	113	87	45	42	0.0131	85	115	46	43	0.0129

The efforts of obtaining adequate batch size varied greatly between the threshold values. For threshold MEAN, screening of 58% of the population produced enough candidates for the largest batch size. With similar screening effort 120 fish were obtained if the threshold was increased to MEAN+0.5σ_P. The largest batch size was obtained with MEAN+0.5σ_P threshold when 91% of the population was screened, whereas with MEAN+1.0σ_P threshold 87% of the population needed to be screened for the smallest batch size.

High rank order correlations (0.68-0.88) between batch EBV and EBV from the full dataset reflected moderate re-ranking of the selection candidates. The relationship structure of this study was rather weak, as the pedigree goes back only for two generations. More severe re-ranking, i.e. larger batch EBV bias, would be expected with more complicated pedigrees.

The genetic level of selected individuals from different selection schemes in the terms of the mean of the full data EBV is presented in Figure 1. Increasing the mass selection threshold from MEAN to MEAN+$0.5\sigma_P$ improved the genetic quality of the candidates. Difference between batch sizes 150 and 200 in the MEAN+$0.5\sigma_P$ scheme was marginal in genetic terms and would increase genotyping costs. Depending on the costs of the screening efforts and the price of the genotyping, batch sizes 120 or 150 and mass selection threshold of MEAN+$0.5\sigma_P$ showed to be optimal for WBS of the breeding population of European whitefish in this study.
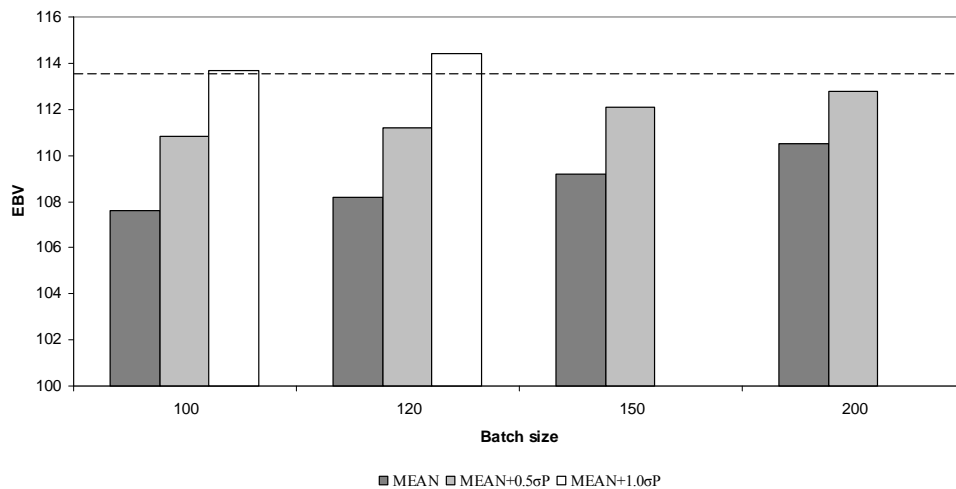

Figure 1: Mean EBV for selected parents from different selection schemes. Horizontal broken line indicates the mean EBV for the selected parents if all candidates were genotyped.

In this study even sex ratio was not required at mass selection. The random sex ratio reduced the success of the smallest selection schemes (not shown), and altered the within-batch selection intensities for the two sexes. Additionally, it was assumed that phenotypic screening of the whole population was not feasible, which is likely to be the case in large breeding nucleus. Consequently, our selection schemes (except those screening majority of the population) are likely to miss some of the phenotypically largest individuals and not fully exploit the mass selection potential of the population.

In practice, large differences in reproductive capacity have been observed in European whitefish, especially in that of females. Egg volume of the fish used in this study varied from 0-200 ml during the family production fall 2009. Additionally, large between-family differences exist in early survival and approximately 20% of the families will fall out before

start-feeding. Both of these practical limitations will complicate the use of WBS for whitefish as they call for a significant increase in the number of selected parents to maintain sustainable number of families in the breeding nucleus.

Identification of the family background of the individuals in a WBS programme is imperative. In this study, known relationships reflect perfect assignment of progeny to their parents and identification of siblings. In real-life WBS the family background and the relatedness of the individuals will be identified by DNA-microsatellite markers, which also can reveal the background relatedness of the parental generation. In order to test the precision and accuracy of the genotype assignments, 46 offspring of known origin were analysed together with their parents for 16 DNA-microsatellite loci (Winkler and Weiss, (2008)). Each individual represented one family, with different parents. In all 29 female and 35 male parents were included in the test. All individuals were assigned correctly to their male and female parent. Program Colony (Wang (2004)), was used for the assignments. Further relatedness analyses will be conducted during 2010.

Conclusion

Utilization of WBS method for body weight with partial screening of the breeding population in a small whitefish population proved to be successful. This gives promise for practical implementation for WBS method as soon as questions related to reproductive differences, between-family differences in survival, and cost and success of the genotyping and parental assignment are further assessed. Only traits easily measurable from the candidates themselves may be selected by WBS. The genetic and economic consequences of simplifying selection criteria on the breeding programme and whitefish aquaculture industry has to be evaluated.

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