



Mate selection allows changing the genetic variability of the progeny while optimizing genetic response and controlling inbreeding

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ABSTRACT

This study aims to compare results obtained by mate selection accounting for different components in the objective function (OF), including functions related to genetic variability of the future progeny, using Nile tilapia and coho salmon real datasets. A total of 8782 Nile tilapias (NP) from five generations and 79,144 coho salmon (CS) from eight generations were used to optimize different OF accounting for coancestry of parents, expected genetic merit, inbreeding and components associated to genetic variability of the progeny. The candidates for selection were the superior animals of the last generation, corresponding to 281 males for NP population and 328 males for CS population, to be mated with 179 and 440 superior females, respectively. Candidate males were allowed to be mated with a maximum of four females. Different functions related to genetic variability of the progeny were tested in the mate selection and we observed that it was possible to increase the genetic variability or produce more uniform progeny, for both species studied. In addition, some OFs also allowed increasing the number of outstanding superior progeny. The tested OF were effective in optimizing the genetic gain and keeping the coancestry and inbreeding at controlled rates, while reducing or increasing the genetic variability of progeny, depending on the purpose of production.

1. Introduction

Maintenance of genetic variation within a breeding program is essential for long-term sustainable genetic improvement of fish (Kause et al. 2014). However, selection of breeders from a small number of families and high selection intensity could reduce the genetic variability of the population, increase rates of inbreeding and reduce the genetic progress (Gjedrem, 2005). In contrast, the maintenance of genetic variability required in a breeding nucleus contradicts the practical aims of commercial producers. In tilapia production, for instance, commercial farmers are usually awarded for selling fish within the preferred weight range determined by the market (Khaw et al. 2016). Growth uniformity is preferable at commercial level since it allows to deliver more uniform product, harvest a larger proportion of the population at market size, and reduce the need of size grading and multiple harvests (Gilmour et al. 2005; Janhunen et al. 2012a, 2012b). Furthermore, more uniform growth may also reduce competitive interactions

between animals, which contributes to reduce feed monopolization and dominant behavior, and thus improve well-being of fish (Baras and Jobling 2002).

The increasing demand from consumers and commercial farmers for uniformity of production is one of the driving forces for animal breeders to emphasize more this criterion in the selection process (Sae-Lim et al. 2012). Some studies quantified the genetic variation for uniformity in fish and concluded that it is possible to increase uniformity of production by selective breeding in Nile tilapia (Khaw et al. 2016; Marjanovic et al. 2016; Moreno et al. 2012; Omasaki et al. 2017) and in salmonids (Jakobsen et al. 1987; Sae-Lim et al. 2017, 2015, 2012). In addition, different strategies can be used to reduce variability in aquaculture species, such as the use of mono-sex fish (Beardmore et al. 2001), grading the fishes at several stages during the grow-out phase (King et al. 2006) and performing planned mating (Hohenboken 1985).

Genetic variability of progeny could also be accounted for by mate selection (Piyasatian and Kinghorn 2003). When mate selection is used,

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the selection and mate allocation decisions are performed simultaneously by the optimization of an objective function (OF) considering different components (Shepherd and Kinghorn 1999; Kinghorn 2011). Based on optimum contribution selection (OCS) theory, the elementary components to be included in the OF are the expected genetic merit of the progeny and the coancestry among selected parents (Meuwissen 1997; Woolliams and Thompson 1994). The optimization of the OF accounting for these two components allows a higher long-term genetic response than truncation selection, under the same rate of inbreeding (Sonesson and Meuwissen 2000; Woolliams et al. 2015).

Components related to genetic variability could also be accommodated in the OF (Piyasatian and Kinghorn 2003), aiming to increase or reduce the genetic variability of the future progeny according to the interest. This is of great importance to both selection nuclei and multipliers due to the arguments described previously. The supposed benefit of using this strategy, under a mate selection approach, is that the relevant components to be considered in a breeding program could be optimized simultaneously, decreasing the chance of finding a sub-optimal solution by performing selection and mating decisions independently. It is unclear, however, in which extend accounting for genetic variability of the progeny would affect the other components to be optimized such as genetic gain and coancestry.

In the present study, we compared the results of mate selection using different OF in real Nile tilapia and coho salmon datasets, aiming to investigate if mate selection would allow shaping the genetic variability of the future progeny while optimizing genetic response and controlling inbreeding or, more specifically, to contrast the results of different OF accounting (explicitly) or not for the genetic variability of the progeny.

2. Material and methods

2.1. Nile tilapia dataset

The dataset used in this study contained pedigree information and standardized estimated breeding values (sEBV) for harvest weight of 8782 Nile tilapias from five generations (Table 1), provided by PeixeGen Research Group (Universidade Estadual de Maringá, Maringá, PR, Brazil).

The animals evaluated in each generation were produced using natural mating and were obtained from a mate design using two females per male. Inspection of the presence of spawning was done two times per week in the breeding season (from November to February). When the spawning was identified, the sire was removed from the hapa and the dam and the larvae were kept together until the end of breeding season. After that, 100 fingerlings from each family were divided into two equal groups and transferred for nursery structure until the average weight of about 10 g, when 50 animals per family, randomly chosen, were individually identified by passive integrated transponder (PIT) tags, implanted in the visceral cavity. After the identification, the animals were transferred to the grow-out system in cages where they were weighted with approximately 7 months of age.

More details about the origin, family and reproduction structure of

the Nile tilapia population were described by Oliveira et al. (2016) and Yoshida et al. (2017).

2.2. Coho salmon dataset

The coho salmon dataset used in this study contained pedigree information and standardized economic index (sIndex) of 79,144 coho salmon from the even population of AquaChile Breeding Program based at Puerto Montt, Chile, comprising eight generations (Table 2). The sIndex included breeding values for weight at harvest and resistance to *P. salmonis*.

The spawning was induced using hormone and all families were generated within one or two weeks using three to five females per male as mate design. The eggs of each full-sib family were incubated separately, and at eyed stage 2000 eggs of each selected family were moved to individual tanks (400 l each) until they weighted about 5 to 7 g when the animals were identified individually using PIT (Passive Integrated Transponder) tags. Then, 60 to 80 animals per family were transferred into two to three smoltification cages in fresh water conditions. Smoltification occurred naturally at eight months post-spawning and the weight at harvest time (~3 kg) was recorded at 20–21 months of age. More details about this population can be seen at Dufflocq et al. (2016) and Yañez et al. (2014, 2016).

2.3. Objective function

The basic mate selection OF (OF1), used as the standard for comparison with the remaining tested OFs (OF2-OF7), was defined as:

$$OF1 = w_1x'EBV + w_2x'Ax + w_3\bar{F}$$

where, $x'EBV$ is the expected merit of the future progeny; $x'Ax$ is the weighted mean coancestry of selected parents; \bar{F} is the expected average inbreeding coefficient of the future progeny; w_1 to w_3 are the corresponding weighting factors and x is the vector to be optimized of genetic contributions for each candidate (the symbol' denotes a transposed vector). The weights w_1 to w_3 were defined in previous studies, based on their compromise in finding a good balance between genetic response and control of inbreeding, for the Nile tilapia (Yoshida et al. 2017: $w_1 = 1$, $w_2 = -20$ and $w_3 = -1$) and coho salmon population (Yoshida et al. 2016: $w_1 = 1$, $w_2 = -100$ and $w_3 = -1$). This OF is expected to provide the same long-term genetic response and rate of inbreeding as OCS combined with minimum inbreeding mating (Yoshida et al. 2018).

Six alternative OFs (OF2-OF7) were tested including, in addition to the components of OF1, at least one of the following (empirically determined) components related to the genetic variability of the progeny:

Ntop: number of animals in the future progeny with expected genetic merit (mean of parents' EBVs) greater than a certain threshold (3 genetic standard deviations for Nile tilapia and 3.5 for coho salmon), aiming at producing a greater proportion of outstanding (superior) animals;

vEBVt: mean value of sEBV (sIndex) to the cube of future progeny of dams classified as top 50%, favoring the occurrence of positive

Table 1

General information, inbreeding coefficient and standardized estimated breeding value for harvest weight of Nile tilapia, per generation.

Gen	Number				Inbreeding			sEBV ± SD
	Sires	Dams	Families	Progeny	Mean	Min.	Max.	
1	24	33	33	1731	0	0	0	-0.01 ± 1.11
2	40	57	58	1717	0	0	0	0.07 ± 0.55
3	52	79	79	2695	0	0	0	0.39 ± 0.71
4	39	44	50	1127	0.00319	0	0.06300	0.83 ± 1.01
5	29	42	51	1455	0.00016	0	0.00800	0.97 ± 1.28

sEBV, standardized estimated breeding value; SD, standard deviation; Gen, generation; Min, minimum; Max, Maximum; sEBV = EBV/83.036.

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