SELECTION RESPONSE UNDER ALTERNATIVE MATING DESIGNS IN FISH

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SUMMARY

The objective of this study, was to compare response to selection under mating schemes utilising the reproductive characteristics of fish. The response of a single trait to selection using nested, factorial, partly factorial, and gynogenetic mating designs were compared by stochastic simulation. For each design, a limited number of tanks were available to rear family groups in the absence and presence of tank and maternal effects. The gynogenetic design always resulted in significantly higher responses to selection, varying between 8% and 39% higher responses relative to nested designs. However gynogenetic designs also resulted in higher rates of inbreeding. The partly factorial design always resulted in higher selection response than the nested design. Factorial designs results in higher selection responses, compared to the nested design, in cases where parentage is known. These results highlight the potential to establish mating designs for fish that utilise available tanks more efficiently than nested designs, resulting in higher response to selection.

Keywords: factorial mating, gynogenesis, inbreeding, simulation

INTRODUCTION

Fish are characterised by a high fecundity in both males and females, as well as in vitro fertilization, and the availability of new genetic technologies (eg. gynogenesis, Purdom 1983). However, they are also characterised by the inability to mark individual fish at an early age, making separate rearing of families nessecary. Thus the number of families that can be reared, is a limiting factor in most fish breeding schemes. Nested mating designs are traditionally used in selective breeding schemes for fish, however nested designs do not exploit the reproductive characteristics of fish. These characteristics enable the establishment of other mating designs, which allow available tanks to be more efficiently utilised than in nested designs and result in larger response to selection. Three such designs are the factorial, partly factorial, and gynogenetic mating designs described by Berg & Henryon (1998). These authors demonstrated that there was always at least one of these mating designs which resulted in more accurate and precise estimates of the genetic parameters than the nested design. Engstrom et al (1996) found a larger response to selection with factorial mating compared to single-pair matings. These results suggest that alternative mating designs can result in larger responses to selection.

In this study, the response of a single trait to selection using nested, factorial, partly factorial, and gynogenetic mating designs were compared by stochastic simulation. For each design, a limited number of tanks were available to rear family groups in the absence and presence of tank and maternal effects. Tank effects can arise under production conditions by rearing groups in separate tanks, while maternal effects can arise from variation among dams in the endogenous contributions

made to their eggs during öogenesis. The objective was to establish under which conditions response to selection obtained from factorial, partly factorial, and gynogenic designs is larger than the response obtained from nested designs.

MATERIALS AND METHODS

Nested, factorial, partly factorial, and gynogenetic mating designs were simulated when 50 tanks were available to rear identified groups of fish, with 10 individuals reared in each tank (ie. a total of 500 offspring per generation). The designs were defined as:

- Nested (25 sires, 50 dams): 25 sires were each mated with two dams, and each of the 50 full-sib families were reared in a separate tank.
- Factorial (25 sires, 25 dams): 25 sires were each mated with a batch of eggs randomly sampled from a pool of eggs from 25 dams. Each of the 25 paternal families were divided into two groups, and each group was reared in a separate tank.
- Partly factorial (25 sires, 25 dams): 25 sires were each mated with two dams and, in turn, 25 dams were each mated with two sires. Specifically, sire 1 was mated with dams 1 and 2, sire 2 was mated with dams 2 and 3, and so on. The final sire, sire 25, was mated with dams 1 and 25. The 50 full-sib families were each reared in a separate tank.
- Gynogenetic (25 dams): 25 mitotic gynogenetic families were established from 25 dams. Each family was divided into two groups, and each group was reared in a separate tank. One tank of fish from each family was assumed to be hormonally sex-reversed to males, and gynogenetic generations were alternated with outbred generations where mating followed the factorial mating design.

In the gynogenetic design, mitotic gynogenesis involves the irradiation of sperm from each sire, during which the DNA is destroyed (Purdom; 1983, Thorgaard; 1992, Quillet 1994). Fertilisation results in a haploid embryo, and diploidy is restored by temperature or pressure shock. Should diploidy be restored in the first mitotic division, the offspring are homozygous with a random allele fixed at each locus. As a result, the genetic variance is twice the genetic variance in outbred populations. The variance between groups is equal to the genetic variance, whereas the variance within groups is equal to the genetic plus environmental variances.

Individual observations were simulated as the sum of a genotypic value, tank effect, maternal effect, and a residual environmental effect, where genotypes were simulated by sampling gametes from the parent(s), assuming an infinitesimal genetic model. All effects were assumed to be independent and normally distributed.

Selection of individuals in each generation was on a selection index. For the nested design, the index included an individuals own record, and those of its fullsibs and paternal halfsibs. For the partly factorial design, the index included an individuals own record, and those of its fullsibs and paternal, and maternal halfsibs. Maternal parentage was assumed unknown in the factorial design, and the index included an individuals own record, and those of its paternal fullsibs. For the gynogenetic design, an individuals own record and those of its maternal "fullsibs" were included in the index during the gynogenetic generations. During the non-inbred generations the index followed that of the factorial design.

Simulations were carried out assuming the following standard parameters: phenotypic variance = 1, heritability = 0.1, tank effect= 0, maternal effect=0, and 50 tanks with 10 offspring per tank. Simulations were also carried out when each of these parameter was, in turn, changed to the following alternate values: h2=0.4, tank effect=0.1, maternal effect=0.1, 50 offspring per tank, and 250 tanks (ie. five times as many family groups). All breeding schemes were simulated for 10 generations and in 100 replicates.

RESULTS

The gynogenetic design resulted in significantly larger responses to selection and higher levels of inbreeding (Tables 1 and 2). The response obtained from the gynogenetic design was between 8% and 39% larger than the response from the nested design, while the level of inbreeding from the gynogenetic design was between 24% and 186% higher. In the small designs (50 tanks) the superiority of the gynogenetic design was due to a significantly larger response to selection in the gynogenetic generations, and especially in the first gynogenetic generation. In larger populations (250 tanks) the gynogenetic design resulted in significantly higher response throughout the 10 generations. The partly factorial design resulted in 1% to 13% larger response to selection and in 11% to 57% higher levels of inbreeding in generation 10 relative to the nested design.

Table 1. Cumulative response to 10 generations of selection under nested, factorial, partly factorial and gynogenetic mating designs. Mean \pm standard error from 100 replicates in phenotypic standard deviations for standard parameters ($h^2=0.1$, tank effect = 0.0, maternal effect = 0.0, 10 offspring per tank and 50 tanks), and for situations with one of these changed

Change of standard _ parameters	Mating design			. (
	Nested	Factorial	Partly factorial	Gynogenetic	
-	1.68 ± .02	1.63 ± .02	1.85 ± .02	2.12 ± .03	
$h^2=0.4$	$4.90 \pm .03$	$5.21 \pm .03$	$5.28 \pm .03$	$5.73 \ \overline{\pm} \ .03$	
Tank effect = 0.1	$1.45 \pm .02$	$1.40 \pm .02$	$1.58 \pm .02$	$1.88 \pm .03$	
Maternal effect = 0.1	$1.48 \pm .02$	$1.62 \pm .02$	$1.55 \pm .02$	$1.81 \pm .02$	
50 offspring per tank	$2.47 \pm .02$	$2.41 \pm .02$	$2.49 \pm .03$	$2.66 \pm .03$	
250 tanks	1.84 + .01	$1.78 \pm .01$	2.08 + .01	2.56 + .01	

Table 2. Inbreeding coefficients after 10 generations of selection under nested, factorial, partly factorial and gynogenetic mating designs. ($h^2=0.1$, tank effect = 0.0, maternal effect = 0.0, 10 offspring per tank and 50 tanks). Standard error of mean < 0.01

Change of standard parameters	Mating design				
	Nested	Factorial	Partly factorial	Gynogenetic	
-	0,25	0.21	0.37	0.51	
$h^2=0.4$	0.20	0.16	0.28	0.40	
Tank effect = 0.1	0.23	0.23	0.34	0.56	
Maternal effect = 0.1	0.23	0.16	0.32	0.58	
50 offspring per tank	0.59	0.41	0.66	0.73	
250 tanks	0.07	0.05	0.11	0.20	

The factorial design was only significantly better than the nested design with high heritability (0.4) and in the presence of maternal effects. However it resulted in the lowest levels of inbreeding

(Table2) and the lowest variance of response in generation 10 (Table1). In terms of response per unit inbreeding the factorial design was the most efficient in all cases.

Differences between mating designs in genetic variance generally resulted in the same order as inbreeding coefficients in Table 2. In the gynogenetic design, a large increase in genetic variance was observed in inbred generations as expected, but genetic variation in outbred generations was always lower than in the other designs. The factorial design always resulted in the smallest decrease in genetic variance.

The largest differences between mating designs in response to selection occurred when the number of available tanks, and therefore, the number of family groups, was increased from 50 to 250, and the smallest when number of offspring was increased from 10 to 50. The effects of heritability, tank and maternal effects on the relative differences between mating designs were minor, except for the factorial design.

DISCUSSION

Response to selection and rates of inbreeding differed significantly between mating designs. In all cases studied, response to selection was largest in the gynogenetic mating design,. The superiority of the gynogenetic design was due to a significantly larger response to selection in the first gynogenetic generations. Selection response was not significantly different in gynogenetic and partly factorial designs in the last 5 generations in small breeding schemes (50 tanks). Thus, gynogenesis can be advantageous, especially in the early generations of a selection scheme.

In the outbred generation in the gynogenetic design and in all generations in the factorial design, it was assumed that maternal parentage was unknown. However, if the parentage could be established (eg. by DNA-markers), these designs would give a higher response to selection. It was found that selection response in the factorial design with known maternal parentage did not differ significantly from the partly factorial design (1.81 phenotypic standard deviations), but at a significantly lower rate of inbreeding (level of inbreeding in generation 10 of 0.24).

Despite the theoretical superiority gynogenetic design are technically the most difficult design to implement in practice. Mitotic gynogenesis is not widely used across fish species, and gynogenetic individuals have low viability caused by inbreeding depression, and the success of producing gynogenetic fry is low (Purdom 1983; Thorgaard 1992; Quillet 1994).

This study highlights the potential to establish mating designs for fish that utilise available tanks more efficiently than traditional nested designs, resulting in higher responses to selection. These mating designs successfully exploit the reproductive characteristics of fish, namely their high fecundity, in vitro fertilization, and the availability of new genetic technologies.

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