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Genetic parameters of economically important traits recorded at a given age in striped catfish (*Pangasianodon hypophthalmus*)

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ABSTRACT

The objective of this study was to estimate heritabilities of and genetic and phenotypic correlations between several body size and carcass quality traits in striped catfish (*Pangasianodon hypophthalmus*), when recorded at about the same age. Predicted data were obtained for fillet weight, fillet yield and fillet fat based on a prediction equation. Partial factorial and nested mating designs were used, respectively, to generate the G2 and G3 generations, with 162 and 156 full-sib families (from 95 sires and 97 dams, and 93 sires and 156 dams in the two generations, respectively). The data-set in the G2 generation consisted of 2767 records (2567 records for predicted fillet weight and predicted fillet yield, as 200 records were used to construct the prediction equations), while 5640 records (body weight and standard length) were available in the G3 generation. Model validation by model fitting (for random effects) and predictive ability (for fixed effects) concluded the statistical model used to analyse the data; that should contain random effects of additive genetic and common environment, and fixed covariates of number of days from spawning till tagging and number of days from tagging till first harvest, respectively. A univariate animal model was used to estimate variance components, while a bivariate model was used to estimate genetic correlations. Moderate heritability estimates were obtained for body weight (0.21–0.34) and fillet weight (0.19–0.22), while low heritability estimates were found for fillet yield (0.03–0.05), intestinal fat (0.04), predicted fillet fat percentage (0.04) and fillet colour (0.04). Of predicted traits, only that for fillet weight showed a heritability with the potential of utilising the information on the selection candidate itself ($h^2 = 0.10$). As most of the variation of fillet weight is explained by the variation in body weight and the two traits are highly genetically correlated (0.95–0.96), this allows for efficient indirect selection for fillet weight through direct selection for body weight. Fillet weight (and body weight) had a moderate positive genetic correlation with fillet fat and was almost uncorrelated with fillet colour, while the two latter traits were also genetically uncorrelated. Thus, selection for fillet weight and/or body weight is expected to increase the fillet fat percentage indirectly. With a goal of keeping the fat percentage of the fillets unchanged, both traits groups need to be considered simultaneously in the breeding program.

1. Introduction

Striped catfish is the most important freshwater aquaculture species in Vietnam. Approximately 90,000 tons were produced in 2000, and production has increased dramatically, to approximately 1.2 million tons in 2007 (Dung, 2008a). A total of 90% of the production is fillets (Tung, 2009), exported to 127 countries worldwide (Dung, 2008b). According to Globefish (2009) the exported and processed production was 633,000 tons in 2008, with a value of 1.4 million US$. To meet future requirements in the market, the producers, processors and exporters are, besides growth rate, becoming increasingly aware of the importance of quality traits, especially fillet yield, fillet fat and fillet colour.

In Vietnam, the breeding program to improve economically important traits in striped catfish by selection was started at the Southern National Breeding Centre for Freshwater Aquaculture (NBCEFAS), under the Research Institute for Aquaculture No.2 (RIA2) in 2001. The base population parents of the first year-class in 2001 (G1) were from wild stocks, while in G1 selection was on the phenotype for body weight. In G2 (year-class 2005) one also selected for fillet yield, by combining individual information on body weight and family information for yield. Inclusion of fillet yield as a second trait was motivated by the assumed high economic importance of this character. Actually, fillet yield has by some been regarded as an important trait for improvement of fish production efficiency (Bosworth et al., 1998, 2001; Cibert et al., 1999; Flick et al., 1990; Kause et al., 2002).

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Later, the risk that selection for growth can result in unfavourable correlated responses in body fat (e.g. Powell et al., 2008) and fillet colour, led to also monitor these traits in the breeding program.

In fish, genetic studies of body weight, when recorded at a given age, are relatively abundant, while fewer studies report results for fillet weight, fillet yield and quality traits, like fillet fat and fillet colour. Generally, the published estimates of heritability of body weight are moderate in size over species (reviewed by Gjedrem, 1997, 2000; Navarro et al., 2009b; Nguyen et al., 2007; Vandeputte, 2003). For fillet weight, moderate heritability estimates have also been reported for tilapia (Nguyen et al., 2010; Rutten et al., 2004), gilthead sea bream (Navarro et al., 2009a), rainbow trout (Kause et al., 2002, 2007), Atlantic salmon (Powell et al., 2008) and coho salmon (Neira et al., 2004). For fillet yield, low to moderate heritability estimates have been obtained for common carp (Kocour et al., 2007), tilapia (Rutten et al., 2005), gilthead sea bream (Navarro et al., 2009a), rainbow trout (Elvingson, 1992; Gjerde and Gjedrem, 1984; Kause et al., 2002, 2007; Quillet et al., 2005), Atlantic salmon (Gjerde and Gjedrem, 1984; Powell et al., 2008) and coho salmon (Neira et al., 2004). For fat percentage in the fillet, considerable heritability estimates have been obtained both in rainbow trout (Gjerde and Schaeffer, 1989; Kause et al., 2002; Sang, 2004) and in Atlantic salmon (Powell et al., 2008; Quinton et al., 2005; Rye and Gjerde, 1996), however much lower in common carp (Vandeputte, 2003), coho salmon (Iwamoto et al., 1990; Neira et al., 2004) and Arctic char (Elvingson and Nilsson, 1992). Finally, for meat and fillet colour (assessed by human eye or by various devices), the heritability estimates vary over a wide range (Elvingson and Nilsson, 1992; Gjerde and Gjedrem, 1984; Gjerde and Schaeffer, 1989; Iwamoto et al., 1990; Kause et al., 2002; Powell et al., 2008; Quinton et al., 2005; Rye and Gjerde, 1996; Sang, 2004).

Different traits are often genetically correlated. Thus, if the selection program focuses on body weight alone and ignores the potential indirect change in other traits, it may result in unwanted side effects. In aquaculture the experience is that traits that are at acceptable levels at the outset of the program, e.g. fecundity, fillet fat and fillet colour, may change unintentionally and needs thus be continuously monitored (Alderson, 2001). Actually, between body weight and fillet weight, close to unity genetic correlations have been reported in many species; tilapia (0.99, Rutten et al., 2004; 0.96, Nguyen et al., 2010), gilthead sea bream (0.96, Navarro et al., 2009a), rainbow trout (0.93-0.94, Kause et al., 2002, 2007), Atlantic salmon (0.99, Powell et al., 2008) and coho salmon (0.98, Neira et al., 2004). Furthermore, moderate to high positive genetic correlations between body weight and fillet fat percentage have been found in rainbow trout (0.38, Kause et al., 2002; 0.90, Sang, 2004), Atlantic salmon (0.42, Rye and Gjerde, 1996), and coho salmon (0.36, Iwamoto et al., 1990; 0.73, Neira et al., 2004). Similarly, a high positive genetic correlation has been estimated between fillet weight and fillet fat percentage in Atlantic salmon has been estimated (0.82, Powell et al., 2008). For body weight and fillet colour in salmon, low to moderate positive genetic correlations (0.10–0.64) have been reported (reviewed by Gjedrem, 1997; Kause et al., 2002; Sang, 2004; Quinton et al., 2005). The same authors also reported low negative to moderate positive genetic correlations (−0.23–0.61) between fillet fat percentage and fillet colour.

In fish, growth data are known to be affected by common environment of full-sibs (due to the separate rearing from hatching till tagging), potential non-additive (dominance) genetic effects (Pante et al., 2002; Rutten et al., 2005; Rye and Mao, 1998; Winkelman and Peterson, 1994), and possibly maternal effects (Henryon et al., 2002) in addition to additive genetic effects. Thus, this study was founded on the partial factorial (in G2) and nested mating design (in G3), to allow separation of additive genetic and common full-sib effects (Berg and Henryon, 1998; Blanc, 2003; Gjerde, 2005; Henryon et al., 2002).

The overall goal of the present study was to estimate heritabilities of and genetic and phenotypic correlations among several body size and carcass quality traits in striped catfish when recorded at about the same age. In addition, predicted fillet weight, predicted fillet yield and predicted fillet fat percentage were analysed as it would allow information on the selection candidate to be utilised in prediction of breeding values.

2. Materials and methods

2.1. Parental fish, mating, hatching, nursing and individual tagging

2.1.1. The G1 generation

The base population was made up of animals from three different hatcheries in the Mekong Delta, Vietnam; collected over the period 1999–2001 from grow-out farms that reared wild fingerlings caught at several seasons and locations in the Mekong River. In 2001, the base population animals were mated in single pairs within hatchery to produce the 2001 year-class. These fish were not individually tagged, so the parents of the G2 generation (year-class 2005) were selected amongst the G1 animals heaviest for body weight (Table 1).

2.1.2. The G2 generation

In 2005, G2 families were produced in May, the main spawning season. A partial factorial mating design, i.e., one male mated to two females and vice versa, was used to facilitate estimation of effects common to full-sibs (Berg and Henryon, 1998). Full-sib families were produced in four batches over 34 days (Table 1). By stripping 43, 13, 31 and 16 males for the four batches, respectively and mating them to the same number of females (103), in total 206 families were produced. Fertilized eggs were washed to remove sticky layers (otherwise fungus problems will occur), and incubated in separate net-jars in one cement tank. Fertilized eggs usually hatch 22–24 h after fertilization. At this stage, a total of 14 families were considered not to have enough fry and were therefore discarded.

Around 20–25 h post-hatching, approximately three thousand start-fed fry were randomly sampled from each family and reared separately in 1 m^3 fibreglass tanks. Fry were fed with newly-hatched artemia, moina and blood-worms. The water source and water exchange were the same for all rearing tanks. Twenty days from first feeding an average of 300 fry from each full-sib family were randomly sampled and reared separately in $1 \times 1 \times 1$ m^3 net hapas in one earthen pond, to reduce the tank effect common to full-sibs. Fry were fed by blood-worms and standard commercial pellets. The net hapas were cleaned frequently to maintain good water circulation and even out environmental effect among the families. Until the fingerling stage, an additional 30 families were discarded due to no, or only a few, fingerlings that survived.

At the average size and age of 45.9 g and 171 days, respectively, an average of 75 individuals from each full-sib family were randomly sampled and marked by Passive Integrated Transponder tags (PIT-tags, Sokymat, Switzerland) (Table 1). Tagging was done over 47 days in December 2005 and January 2006. Tagged fish from each family were kept for one week in separate hapas to monitor mortality before they were communally stocked in a 2000 m^2 pond at the NBCEFAS - RIA2 and were fed *ad libitum* with commercial pelleted feed, containing 22–28% protein. In total, 12,190 fish were tagged, representing 162 families, from 95 sires and 97 dams (Table 1).

2.1.3. The G3 generation

The G3 families were produced in June and July 2008. This time, a nested mating design was used, i.e. one male mated to two females. Full-sib families were produced in five batches over a total of 28 days (Table 1). In total, 156 full-sib families were produced from 93 sires and 156 dams. Stripping, fertilization, incubation and nursing were done as already described for G2.

In November and December 2008, over 31 days, an average of 51 individuals from each full-sib family were randomly sampled and marked by PIT-tags at average weight and age of 34 grams and 147 days, respectively. Tagged fish from each family were kept one