Genetic parameter estimates for growth and non-growth traits and comparison of growth performance in sea cages vs land tanks for yellowtail kingfish *Seriola lalandi*

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ARTICLE INFO

ABSTRACT

The aquaculture of yellowtail kingfish *Seriola lalandi*, is now expanding worldwide. Production is conducted in two very different types of commercial facilities: predominately in sea cages in Australia, Mexico, Chile and Hawaii; and in indoor facilities in Europe. With expansion, there is concordant commercial interest to develop genetically improved stocks for production. However, there is a great paucity of genetic information about this species. Knowledge gaps include accurate genetic parameter estimates (i.e., from large sample sizes) that are essential to develop accurate and efficient selection indices. Specifically we require accurate information on non-growth traits (such as parasite load and deformities) and their correlations with growth traits (body weight and fork length), and information on any genotype by environment (G × E) interactions between the two major growing systems to determine whether a single or multiple selection programs are required. Here we address all these fundamental genetic knowledge gaps and provide, for the first time: relatively accurate genetic parameter estimates based on approximately 1400 genotyped and phenotyped animals; and preliminary tests for G × E interactions between growth in sea cages vs land tanks. The heritability estimates were moderate and significant (0.42 ± 0.10) for growth traits, whereas heritability estimates for non-growth traits were low (0.01–0.06). The genetic correlation between body weight and fork length was positive and close to one (0.98); in contrast, the correlation between growth traits with occurrence of fluke and deformity were not significant. The genetic correlations for growth traits between two culture environments were high (0.92–0.97); they were however, associated with large standard errors. In summary, the new set of genetic parameters obtained from this study provide accurate information that is essential to develop genetically improved stocks of yellowtail kingfish for commercial production.

1. Introduction

Yellowtail kingfish *Seriola lalandi* is a marine pelagic species belonging to Order Perciformes, Family Carangidae. It is widely distributed throughout the warm-temperate Atlantic and Pacific oceans and found in waters around Australia, New Zealand, Japan, South and East China seas, Mediterranean Sea and the Pacific coast of America, from Canada to Chile (Dyer and Westneat, 2010; Eschmeyer and Herald, 1983; Nakada, 2008; Nugroho et al., 2001; Smith-Vaniz, 2000). Yellowtail kingfish is becoming popular in marine aquaculture around the world, in both sea-cage culture as well as in land-based culture facilities (Abbink et al., 2011; Orellana et al., 2014).

However, essential and accurate information required to plan and operate efficient genetic improvement programs for this species is not yet available. Whatmore et al. (2013) presented some estimates of growth traits, but these data were based on too few samples for highly precise estimates that are required to develop efficient selection indices.

Moreover, there are no or but limited estimates for commercial traits other than growth-related traits, nor do we know their genetic correlations with growth traits. One trait of interest in the present study is that of parasitic skin fluke loadings. The monogenean fluke parasite *Benedenia seriolae* is one of the parasite problems in sea-cage kingfish culture; this fluke infects the skin and fins of *Seriola* spp. and feeds on mucus and epithelial cells (Sharp et al., 2004; Tubbs et al., 2005).
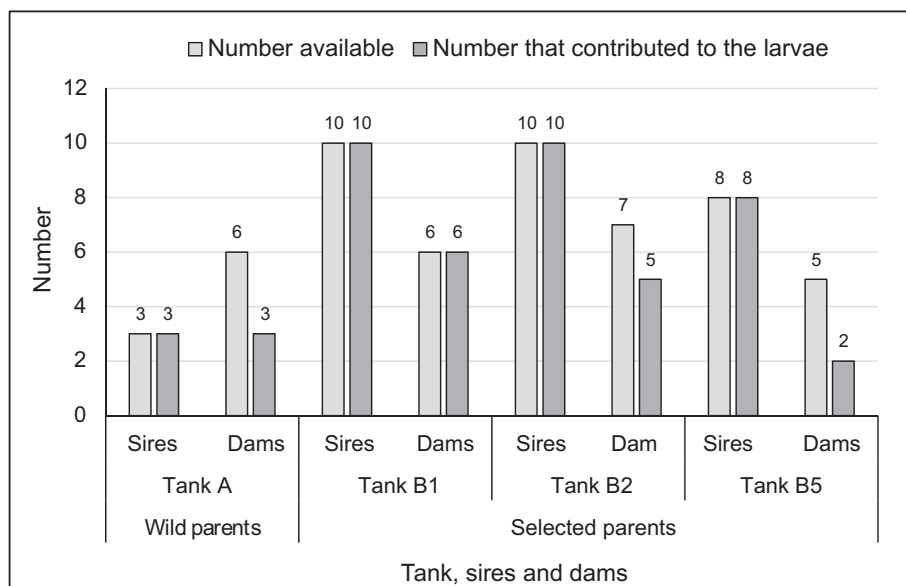
However, there are no heritability estimates for skin fluke levels in kingfish, so it is unknown whether selection for fluke levels will achieve selection response, nor do we know the genetic correlations between fluke infection levels and growth. Another trait, the incidence of deformities, is also a non-growth trait of substantial commercial importance. Nguyen et al. (2016) reported that deformities in kingfish may have some genetic determination, but the data were limited to a relatively small sample size and constrained by the relatively low incidence of deformities and high standard errors; precise information is needed to optimize multi-trait selection indices.

Another substantial knowledge gap is whether rankings and magnitudes of genetic differences observed in land facilities are similar to those for fish grown in the less controlled conditions in sea cages; water is filtered in land facilities, whereas at sea pathogens and parasites such as flukes are free to infect fish. Differences in rankings, i.e., genotype by environment (G × E) interactions, may be a real possibility since Nguyen (2016) and Sae-Lim et al. (2015) reported that when the two environments are remarkably different, G × E effects may be significant. Even when rankings are similar and there is little evidence of G × E, there still could be magnitude differences; for example, it has been reported that fish grown under "harsh" environments may fail to show genetic differences (Nguyen, 2016; Ponzoni et al., 2008). Resolution of these knowledge gaps will determine whether it is possible to operate just one selection program for both land and sea facilities, a matter of some importance given that two different production systems operate around the world, yet stock developed in one type of system are being shipped and grown out in another.

Here we address a number of commercially important and outstanding knowledge gaps regarding kingfish genetics: based on approximately 1400 samples, we provide revised, more accurate estimates of weight and length genetic parameters, we provide the first estimates for fluke infection genetic parameters, and we assess, for the first time, the magnitude of G × E effects between rearing in sea cages vs land tanks.

2. Methodology

2.1. Genetic group A broodfish (cohort A)

The parents of cohort A broodfish were part of a group of 40 wild animals collected as large wild mature animals of indeterminate age from the Spencer Gulf (a gulf in South Australia, approximately 200 km west of the city of Adelaide). Cohort A broodfish derived from mass spawning of the wild parents in 2007; they were grown in sea cages until "market size" of 3-4 kg and selected by industry informally on the basis of their visual appearance (well conformed fish without deformity and with an apparent high condition factor); no precise data on weights and lengths were available. When cohort A broodfish were mated, we avoided any crosses with relatives.

2.2. Genetic group B broodfish (cohort B)

Cohort B was similar to A, except: Cohort B broodfish derived from spawning of wild fish (all different individuals from those wild parents of cohort A) in January 2010. The selection procedure for cohort B broodfish was first to sample > 100 random fish and measure the weight and length to estimate cut-off points for the top 10% by weight, and note the minimum length of fish in the top 10%. The average weight estimated from the random samples was 3.07 kg. At harvest, the minimum length was used as a very approximate guide to take fish for actual weighing; fish above the threshold weight were also informally selected to be well conformed (i.e., appearing to have an above-average condition factor, defined following, and free of abnormalities/deformities). These procedures resulted in selecting 5–10% of approximately 1500 animals with an average weight of 3.75 kg (all selected fish were measured for weight and length).

2.3. Genetic group C broodfish (cohort C)

Cohort C was similar to B, except: Cohort C broodfish derived from spawning of wild fish (again, all different from those wild parents of cohorts A and B) in December 2010.

2.4. Genetic group D broodfish (cohort D)

Cohort D broodfish was a new collection of wild fish unrelated to the parents of A, B and C.

2.5. Spawning of broodfish from different genetic groups

Sexually mature broodfish were held in a common tank until chosen for spawning, and then were assigned to spawning tanks (details of the numbers assigned and fish actively participating in spawning are given in Fig. 1). For the present experiment, all the selected broodfish (cohorts A, B, C), though of different ages, were spawned communally on the same day across several tanks to produce the offspring that were