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Heritability estimates for growth in the tropical abalone *Haliotis asinina* using microsatellites to assign parentage

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Abstract

The tropical abalone *Haliotis asinina* is a wild-caught and cultured species throughout the Indo-Pacific as well as being an emerging model species for the study of haliotids. *H. asinina* has the fastest recorded natural growth rate of any abalone and reaches sexual maturity within one year. As such, it is a suitable abalone species for selective breeding for commercially important traits such as rapid growth. Estimating the amount of variation in size that is attributable to heritable genetic differences can assist the development of such a selective breeding program. Here we estimated heritability for growth-related traits at 12 months of age by creating a single cohort of 84 families in a full-factorial mating design consisting of 14 sires and 6 dams. Of 500 progeny sampled, 465 were successfully assigned to their parents based on shared alleles at 5 polymorphic microsatellite loci. Using an animal model, heritability estimates were 0.48±0.15 for shell length, 0.38±0.13 for shell width and 0.36±0.13 for weight. Genetic correlations were >0.98 between shell parameters and weight, indicating that breeding for weight gains could be successfully achieved by selecting for shell length.

Keywords: Gastropod; Abalone; *Haliotis asinina*; Selective breeding; Microsatellite DNA; Growth

1. Introduction

Abalone are marine molluscs that are highly valued for their edible foot muscle. Over the past decade, aquaculture of abalone has become widespread throughout the world, partially in response to over-exploitation of most wild fisheries (Gordon and Cook, 2004). While global supply has not met demand in the past, a massive recent expansion in availability of cultured abalone, particularly in Taiwan and China, has more than compensated for the decrease in wild catches (Gordon and Cook, 2004). Increasing growth rate of abalone through selective breeding is becoming important in terms of viability of the industry and is a priority for growers (Viana, 2002).

The tropical abalone *Haliotis asinina* is found throughout the Indo-Pacific region and is economically important both as a cultured and wild harvested resource (Singhagraiwan and Doi, 1993; Jarayabhand and Paphavasit, 1996; Capinpin et al., 1998; Gallardo and Salayo, 2003). Although *H. asinina* has a high proportion of edible meat and fast growth rate relative to other abalone, it is not yet commercially exploited in Australia. The aim

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of this study is to provide more information about the potential of *H. asinina* in aquaculture and as a candidate for a selective breeding program.

Current practices for spawning *H. asinina* in Australia involve allowing wild-caught broodstock to synchronously spawn approximately every 14 days over a 6 month spawning season (Counihan et al., 2001). This natural spawning pattern allows for specific and large-scale crosses between individual broodstock. While spawning in domesticated stock does not appear to be synchronous (Capinpin et al., 1998), targeted crosses can be undertaken by rearing conditioned broodstock together. *H. asinina* is a fecund abalone species, producing up to 2 million eggs fortnightly. It reaches sexual maturity within one year, as opposed to 3 or 4 years in most temperate species. These attributes, together with the availability of microsatellite DNA markers for genotyping (Selvamani et al., 2000; 2001), make *H. asinina* highly amenable to selective breeding research.

The environment under which tropical abalone are typically cultured is different to, and less variable than, that in the wild (e.g. no predators, more food). From a genetic perspective, the 'optimal' combinations of alleles for survival and growth in culture are unlikely to be fixed in wild populations. This could provide the basis for significant improvement of valuable traits upon domestication (Doyle, 1983). Selective breeding aims to optimise improvements in commercially desirable traits, while avoiding the negative effects of inbreeding and correlated selection response in undesirable traits.

The estimation of genetic parameters (heritabilities and genetic correlations) is important for making decisions regarding design and implementation of selective breeding programs (Mgaya, 2000). In most studies of this kind, heritability is calculated by comparing families grown in separate tanks. The infrastructure and maintenance required to conduct such experiments is expensive (Herbinger et al., 1995; de Leon et al., 1998). This can restrict the number of families in an experiment and hence limit the conclusions that can be drawn from it. An alternative is to pool individuals from different families and raise them together in a single tank, using genetic markers to determine parentage. This greatly reduces cost of rearing, although the cost of genotyping can also become a constraint. A common environment creates a more realistic commercial situation where families compete against each other, and allows for a better scrutiny of the genetic effects underlying a trait by reducing the confounding effects of environment (Herbinger et al., 1999, Dupont-Nivet et al., 2002; Vandeputte et al., 2004). Using a full-factorial design, genetic parameters can be accurately estimated, allowing the separation of additive, dominance and maternal components of variation (Vandeputte et al., 2001).

Despite the proven track record of selective breeding as a method of increasing profit for farmers in agriculture, global research into aquaculture breeding programs has been slow (Lymbery et al., 2000; Gjedrem, 2002; Mair, 2002). Only a small number of studies have reported heritability of growth rate in haliotids (Hara and Kikuchi, 1992; Kawahara et al., 1997; Jonasson et al., 1999; Mgaya, 2000). All suggested that a selective breeding program will increase growth rate. The most comprehensive of these studies reported heritability in *H. rufescens* of 0.34 at 24 months (Jonasson et al., 1999). Two studies have measured actual response to selection of between 10 and 21% per generation (Hara and Kikuchi, 1992; Kawahara et al., 1997). The work presented here estimates heritability for *H. asinina* at 12 months age, using microsatellites to assign parentage from a single tank which housed 84 families.

2. Materials and methods

2.1. Experimental design

To test variation in growth performance between families, a full-factorial mating design was implemented. Our design followed Vandeputte et al. (2004), but employed fewer parents (14 sires and 6 dams). Using this design, variation between sires and dams can be evaluated whilst accounting for interaction and dam effects. A design with more sires than dams is usually most informative, with an optimal number of dams estimated at only two for maximum statistical power (Dupont-Nivet et al., 2002). In this study six dams were used to prevent interaction effects from masking heritable genetic differences between progeny.

2.2. Spawning

Wild broodstock were collected from Heron Island, Queensland and maintained at the Bribie Island Aquaculture Research Centre, where they were individually tagged and housed in a flow-through seawater system and fed to satiation with the red algae *Gracillaria edulis*. Eggs and sperm were procured (as described in Jebreen et al., 2000; Counihan et al., 2001) from 14 males and 6 females from one synchronous natural spawning event in February, 2003. A suspension of eggs from each female was divided into 14 equal portions and fertilised separately by sperm from each of the 14 males, before being rinsed and pooled together for larval culturing. All initial fertilisations were performed within a one minute time frame, before increasing the concentration of sperm to ensure that no viable eggs remained unfertilised. Samples were taken to count fertilisation success before mixing occurred.