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Heritability for body weight at harvest size in the Pacific white shrimp, *Penaeus* (*Litopenaeus*) *vannamei*, from a multi-environment experiment using univariate and multivariate animal models

Héctor Castillo-Juárez [a,*], Juan Carlos Quintana Casares [b], Gabriel Campos-Montes [c], Cesáreo Cabrera Villela [b], Alfonso Martínez Ortega [b], Hugo Horacio Montaldo [c]

[a] *Departamento de Producción Agrícola y Animal, Universidad Autónoma Metropolitana, Unidad Xochimilco, Calzada del Hueso 1100, Coyoacán, D.F. C.P. 04960, México*
[b] *Maricultura del Pacífico S.A. de C.V. Pesqueira 502, Local 5, Colonia Centro, Mazatlán, Sinaloa, C.P. 82040, México*
[c] *Departamento de Genética y Bioestadística, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Circuito Exterior, Ciudad Universitaria, Coyoacán, D.F. C.P. 04510, México*

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Abstract

To estimate family BLUP breeding values and the heritability of body weight at harvest size (BW) in the Pacific white shrimp, *Penaeus* (*Litopenaeus*) *vannamei*, an experiment was conduced using information from two farm units of a Mexican hatchery and two shrimp population densities at each location. Data consisted of 12,658 shrimps that were siblings from 48 sires and 77 dams with a nested dam–sire structure. Shrimps were individually weighed at an average age of 130 days post-hatching. BW phenotypic mean (S.D.) was 18.2 (2.4) g, with values ranging from 8.4 to 30.0 g. Data were analyzed using univariate and multivariate models that considered BW within location by density pond environment as a different trait and included or not a common full-sib effect (*c*). The multivariate animal model included fixed effects of days from hatching and sex. For univariate models that included *c* effects, BW heritability (S.E.) estimates ranged from 0.24 (0.14) to 0.35 (0.18) across environments (heritability was zero in one environment). For multivariate models (excluding the environment with zero heritability) the heritabilities increased and ranged from 0.37 (0.06) to 0.45 (0.09). Standard errors of heritabilities and *c* effects were both drastically reduced in the multivariate analysis. Pairwise genetic correlations between environments were from 0.80 (0.08) to 0.86 (0.04). These differences may be indicative of genotype–environment interaction for BW at 130 days post-hatching. Statistical problems found to separate *c* from additive genetic effects both in univariate models were reduced using multivariate models. Correlation between family raw phenotypic means and family BV means from the multivariate analysis was 0.93 indicating a rather low risk of miss selecting superior families if BLUP solutions were neglected using replicated environment data. It is also concluded that use of incorrect statistical models or unreplicated data may lead to biased or inaccurate estimates of genetic parameters in shrimp breeding programs.

Keywords: Shrimp breeding; Pacific white shrimp; *Penaeus* (*Litopenaeus*) *vannamei*; BLUP; Family selection; REML; Multivariate animal models

* Corresponding author. Tel.: +52 55 5617 4126; fax: +52 55 5483 7230.
E-mail address: hcjuarez@correo.xoc.uam.mx (H. Castillo-Juárez).

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1. Introduction

The development and application of selective breeding programs is becoming an increasingly important strategy for increasing the economic efficiency of farmed shrimp (Argue et al., 2002; Pérez-Rostro and Ibarra, 2003b; Gitterle et al., 2005a,b). Until recently, most breeding programs in the aquaculture industry were based on ad-hoc methodologies based on mixtures of individual and family raw data, mainly because individual identification was not feasible and mixing families in performance tests was not possible. However, methods for tagging individuals are now available (e.g., Arce et al., 2003) permitting mixed model techniques, commonly used for years in farm animals, to be applied in fish and shrimp breeding programs (Bolívar and Newkirk, 2002; Gall and Bakar, 2002; Gitterle et al., 2005a,b). Mixed models are very flexible and can be used for unbiased estimation of genetic parameters and breeding values under a range of different situations. Most of the published genetic parameters and mean family breeding values in shrimp farms have been estimated using simple regression (Hetzel et al., 2000) and ANOVA procedures (Benzie et al., 1997; Argue et al., 2002). Mixed model analysis has also been recently used; one with a large data set coming from commercial conditions (Gitterle et al., 2005a) and another using a smaller data set from experimental conditions (Pérez-Rostro and Ibarra, 2003a).

Using mass and family selection techniques in aquaculture have proven to be effective and some results show an increase of body weight from 9 to 14% in selected shrimp populations compared to wild shrimp in only three generations (Preston et al., 2004). Another study showed that a line selected for growth was 21% larger than the unselected control line after only one generation (Argue et al., 2002).

We conducted a multi-environment experiment with the following objectives: a) to estimate the heritability of body weight at harvest size (BW) in the Pacific white shrimp, *Penaeus* (*Litopenaeus*) *vannamei*, using univariate and multivariate animal models; b) to estimate genetic correlations between environments and c) to estimate correlations of full-sib family best linear unbiased predicted (BLUP) breeding values means for BW with BW family raw phenotypic means.

2. Materials and methods

2.1. Broodstock selection

The study was carried out in two shrimp farm units from a Mexican hatchery, one located in Pozos, Sinaloa, and the other in Guasave, Sinaloa, both in the northwest of Mexico. A large number of the procedures were performed according to the commercial hatchery management practices. By the end of October 2003 the broodstock were selected from two Pozos ponds that had been stocked with post-larvae coming from the 2002 family selection program. These families originally came from a mass selection program that started in 1998 in which wild shrimp from Sinaloa, Mexico, and domesticated shrimp from Venezuela, Colombia, Florida and Ecuador had been incorporated.

Using body weight as the criterion, the top 30% of the females and top 15% of the males were selected. Selected shrimp were individually tagged using numbered rings placed on one ocular peduncle. The broodstock were stocked into maturation tanks at a density of eight shrimp/m^2, with males and females placed in separate tanks. Maturation tank dimensions were 12 × 3 m with a water column of 0.35 m, kept at 28–29 °C, with a salinity of 34 ppt and a daily water exchange rate of 400%. They were fed with commercial pellets containing 35 to 40% protein. After 14 to 21 days to let the shrimp adapt to this new environment, and in order to accelerate the gonad maturation process, unilateral ocular ablation in females was performed.

2.2. Production of families

Mature and ready to spawn female breeders were artificially inseminated using one male for every two females to produce full- and paternal half-sib families. Family origin was considered to avoid mating between sibs. These inseminated females were moved to individual spawning tanks where they spawned after 1 to 4 h. Their eggs were then collected in 10-l tanks, washed with iodine and placed back in the spawning tanks where they hatched with strong aeration conditions after 8–9 h. Originally 108 females and 54 males were used, but they only yielded 101 families. A record for every family included body weight of the male and female, number of obtained eggs and nauplii, as well as the number of nauplii cultured to growth.

2.3. Larvae culture

The larvae culture of every family and the control shrimp from the production area was done in 500-l tanks keeping one family per tank, using the regular procedures from the hatchery including a mixed diet of *Chaetoceros* sp., *Artemia* sp. and commercial larval diets. The initial density was 80 nauplii/l. Post-larvae were reared to the PL-5 stage, then counted to get survival estimates by weighing total biomass and counting the number of post-larvae in one gram. When post-larvae reached the PL-15 stage they were harvested to obtain total biomass, survival and mean weight. Post-larval rearing densities were adjusted to 1 post-larvae/l per tank. Post-larvae were then reared in the same tanks until they were around 1 to 3 g (averaging 2.54 g) and 70 to 90 days post-hatching. This size allowed us to tag them individually.

2.4. Tagging

Shrimp were injected with a colored elastomer tag (Northwest Marine Technology) to identify full-sib families. Two different tags per shrimp were injected using four different