Genetic Correlation Between Body Weight At 28 And 130 Days Post-Hatching In The Pacific White Shrimp (*Penaeus (Litopenaeus) vannamei*)

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Introduction

Breeding programs that include multi-stage selection are an option for traits that can be measured at several times in the span life of farm animals. This selection scheme may include an early selection stage consisting on selecting animals based on a trait measured early in life with the idea of improving another trait measured at later stage in life. The efficiency of this process clearly depends on the heritability of the traits involved and their genetic correlations (r_G). Hence, it is crucial to have reliable estimates of these genetic parameters before deciding to integrate multi-stage selection in the breeding programs (Martínez et al., 2006).

There are few studies in shrimp providing estimates of genetic correlations between body weights at different ages. Kenway et al. (2006) reported convergence problems during their analysis and were hence not able to estimate the r_G between body weight at 10 and 16 weeks of age in *Penaeus monodon* suggesting innadequate modeling. Pérez-Rostro e Ibarra (2003) estimated the r_G between body weight at 17 and 29 weekss in *Penaeus (Litopenaeus) vannamei* as 0.56.

The objective of this study was to estimate the genetic correlation between body weight at 28 and 130 days post-hatching in *P. vannamei.*

Material and methods

The study was carried out from may to september 2009 in the Genetic Nucleus of the largest shrimp Mexican hatchery (Maricultura del Pacífico) located in the state of Sinaloa (northwest of Mexico). Three hundred half-sib and full-sib families were produced using artificial insemination (one male per two females). Each family was seeded within 24 hours

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post-hatching in two 200 l replicate tanks at a density of 100 organisms/l. Body weight of 40 organisms per tank was measured at 28 days of age (W28).

Family breeding values (FBV) for W28 were estimated using an animal model. Then, 150 families were selected based on FBV. A total of 23,676 individual W28 records were used for this analysis. Post-larvae were injected with a colored elastomer to identify full-sib selected families. Three different tags per shrimp were injected using 6 different colors and 3 anatomical areas at 2 g of body weight (around 40 days post-hatching). At 2 months of age, 45 shrimp per family were seeded in 3 different pond environments, simulating 3 different commercial rearing conditions, with seeding densities of 10 shrimp/m^2, 30 shrimp/m^2, and 100 shrimp/m^2, respectively. At 130 days post-hatching, all the animals were harvested and individually weighed (W130). The total number of W130 records was 9,369.

(Co)variance components for W28 and W130 were estimated using ASReml (Gilmour et al., 2009). For W28 the model included the fixed effect of area of the green house larvae room, while the effects of animal, common environment of growth tank (replicate), and the residual were considered as random. For W130 the model included the fixed effects of pond, sex, and age at harvesting as a covariate, while the effects of animal, common environment to full-sibs, and the residual as random (Castillo-Juárez et al., 2007). The environmental covariance beteen traits was assumed to be zero.

Phenotypic variance was calculated as the sum of the variance components for each trait in each model and heritability estimates (h^2), the proportion of environment effects common to full-sibs (f^2) and the proportion of the effects common to growth tank (t^2) were estimated as the corresponding proportion of each variance component to the phenotypic variance. The genetic correlation (r_G) was estimated as the ratio between the genetic covariance and the product of the correspondent additive genetic standard deviations.

Results and discussion

Mean (standard deviation) for W28 and W130 were 41.4 mg (22.0) and 14.5 g (2.9), respectively. The correlation between the family phenotypic means between W28 and W130 was 0.26 ($P<0.05$). Heritability estimates were 0.25 ± 0.04 and 0.23 ± 0.07 for W28 and W130, respectively, while t^2 and f^2 were 0.12 ± 0.01 and 0.09 ± 0.03, respectively, and the r_G between W28 and W130 was estimated as 0.80 ± 0.13.

Our genetic correlation estimate was larger than the one observed between body weight at 17 and 29 weeks of age (0.56) by Pérez-Rostro and Ibarra (2003) in a model where these authors neglected the common effects to full-sibs. Based on the discrepancies observed between the family phenotypic correlation between W28 and W130 and its genetic correlation, it would be dangerous to select at early stages based only on the family phenotypic means. The environmental correlation was not estimated since the shrimp measured at W28 and W130 are full-sibs and not the same animals.

Conclusion

There was a positive genetic correlation between body weight at 28 and 130 days post-hatching. Including these two traits in a two-stage selection breeding program in the shrimp industry for *P. vannamei* will lead to a larger genetic gain for body weight at harvesting (W130).

References

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