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Genetic parameters and accuracy of selection for resistance to White Spot Syndrome Virus (WSSV) in *Penaeus (Litopenaeus) vannamei* using different statistical models

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Abstract

Genetic parameters for resistance to White Spot Syndrome Virus (WSSV) in the shrimp species *Penaeus vannamei* were estimated by using five different statistical models to analyze challenge test data. Data were recorded on the offspring of 338 full-sib families experimentally infected with WSSV, corresponding to four consecutive generations. Both the linear model (LBM) and the threshold model (TBM) defined disease resistance based on whether or not the animal was alive when the population reached 50% total mortality. The Cox (CM) and the Weibull (WM) proportional hazard frailty models were based on time until death (days post infection) and took censored observations into account. Finally, the linear repeatability model (LRM), considered test-day survival and censoring; where for every animal a binary record was defined for each test day up till the day of death (0 if still alive or 1 if dies, at the specific day). LBM and TBM measured the probability of surviving, whereas the CM, WM and LRM measured the risk of dying. Heritability estimates ranged from 0.01 (CM and LRM) to 0.21 (WM). The rank correlations between full-sib estimated breeding values (EBVs) from the LBM and TBM was close to 1, but lower between EBVs of these two models and the other models (ranging from −0.82 to −0.89). We attempted to predict the accuracy of selection that would be obtained with each model by calculating Pearson correlation coefficients between the full-sib EBVs estimated with data from different tanks. The highest accuracy of selection was found in the CM (0.79) followed by the WB and LRM (0.77 and 0.75 respectively). However the WM did not model properly the mortality pattern of the test population. Lowest correlations were found in the LBM and TBM (both 0.67). Based on these results we suggest selection programs for white spot resistance should be based on EBVs using models taking time to death into account with proper model of the mortality pattern of the test population (CM and LRM), rather than the models that define survival as a binary trait at 50% mortality (LBM and TBM).

Keywords: Shrimps; *Penaeus (Litopenaeus) vannamei*; WSSV resistance; Genetic selection; Heritability; Survival analysis

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1. Introduction

Shrimp viral diseases continue to be the major threat for the shrimp industry worldwide and among them White Spot Syndrome Virus (WSSV) has had the most harmful impact on the cultured shrimp *Penaeus (Litopenaeus) vannamei* in the western hemisphere. On the Colombian Pacific coast the introduction of White Spot Syndrome Virus (WSSV) in 1999 reduced the average yield from 1800 to less than 300 kg/ha/cycle. As the only applicable on-farm strategy to deal with the virus, farmers reduced production time (from 110 to 40–60 days) combined with lowered stocking densities (from 18 to 5 animals/m^2). However, when disease outbreaks occur, overall pond survival is still below 20%. In this scenario, selective breeding is one of the few alternative means of long-term disease control (Bedier et al., 1998; Roch, 1999; Bachere, 2000). This strategy requires that *P. vannamei* express additive genetic variation for resistance to the disease in question. In a previous study we estimated the additive genetic variance and breeding values for WSSV resistance and harvest weight in two lines using a bivariate linear model (Gitterle et al., 2005a); WSSV resistance in experimental challenge tests was defined as a binary trait (0 = dead, 1 = alive) and evaluated at 50% overall mortality. The estimated heritability in both lines was low (0.03 ± 0.01 and 0.07 ± 0.04, respectively). With linear models, the binary nature of the trait is ignored in the analysis. Threshold models (Gianola and Foulley, 1983; Harville and Mee, 1984) are an alternative which account for the categorical nature of the phenotype by modeling an underlying normal distribution with truncation points (threshold) that determine the categories into which the observed phenotypes fall. However both linear and threshold models ignore the information from time until death (or censoring if animals are still alive at the end of the tests). Survival analysis does use this information, and takes censoring of records into account (as a proportion of animals usually survives the testing period). The most recommended model for analyzing such data is the proportional hazard (PH) model (Cox, 1972; Kalbfleisch and Prentice, 1980). These models give an expression of the hazard (of dying) at time t for an animal with a given specification of a set of explanatory variables (Kleinbaum, 1996). Furthermore, the PH models can be extended to include time dependent covariates and random (genetic) effects (in so-called frailty models) (Ducrocq and Casella, 1996).

A third approach in handling survival data is by dividing the testing period into several shorter periods (e.g., days) and then define survival within each period as a binary trait. Survival at different time periods may be regarded as repeated measures of the same trait (Meuwissen et al., 2002; Ødegård et al., submitted for publication). As with PH models, the linear repeatability model may utilize information from the entire lifespan of the animals, and should therefore make better use of the information contained in the data compared with ordinary linear binary models.

The aim of this study was to apply threshold, proportional hazard and repeatability models to WSSV challenge test data in order to estimate additive genetic variance and breeding values for WSSV resistance in *P. vannamei*, and then to compare the accuracy of these predictions with those of the linear model applied in a previous study (Gitterle et al., 2005a).

2. Material and methods

2.1. Genetic material and production of full-sib families

The data were recorded from the on-going breeding program initiated by CENIACUA (Centro de Investigaciones para la Acuicultura en Colombia) in collaboration with AKVAFORSK (Institute of Aquaculture Research AS, Norway) in 1997. Families from five consecutive generations (family batches) were experimentally challenged to WSSV in single, duplicate or triplicate tanks (Table 1). In total 338 full-sib families representing 142 paternal and 18 maternal half-sib families were evaluated. For detailed information about the Colombian breeding program see Gitterle et al. (2005b).

The production procedures and rearing of individual families until tagging were as described by Gitterle et al. (2005b). In short, families in each batch were produced using a nested mating design, with females nested within males (full-sibs and paternal half-sib), and on a few occasions with males nested within females (full-sibs and maternal half sibs) (Table 1). The families were reared separately in net