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Genetic parameters for survival rate and harvest weight in *Litopenaeus vannamei* in commercial ponds in Ecuador using genomic relationships

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Introduction

Ecuador has become one of the leading producers and exporters of *Litopenaeus vannamei* worldwide, with production exceeding 1.4 million tons in 2025 and projected to increase in 2026 (CNA, 2026; FAO, 2026).

The profitability of shrimp farming depends on survival and the weight per animal, variables affected by the presence of infectious diseases, which is the most common cause of economic losses in the industry (Huang *et al.,* 2025). Combatting disease is difficult due to high transmission rates, wide geographic distribution, and lack of effective treatment (Gitterle *et al.,* 2005a, 2005b; Huang *et al.,* 2012; Lillehammer *et al.,* 2020). In this context, genetic selection for resistance to major pathogens appears to be an effective preventive strategy, especially when the consequences of disease are high, and there are no alternatives for rapid and low-cost outbreak control (Castillo-Juárez *et al.,* 2015; Lillehammer *et al.,* 2020; Nirea *et al.,* 2025).

The design of genetic evaluation systems for resistance under real-world production conditions has several advantages over challenge-based assays, which, although they have qualities related to standardization and control of factors associated with mortality, may not adequately reflect actual production conditions (Caballero-Zamora *et al.,* 2015). The estimation of genetic parameters such as heritability (h^2) and genetic correlations (r_g) between body weight and survival at the field level provides a starting point for optimizing selection programs and maximizing genetic progress. Previous studies have reported h^2 between 0.09 and 0.24 for body weight in the presence of disease (Gitterle *et al.,* 2005a; Caballero-Zamora *et al.,* 2015), with generally low figures (0.03–0.07) observed for survival against White Spot Syndrome Virus (WSSV), including challenges. This makes using selection to improve resistance difficult (Gitterle *et al.,* 2005a, 2005b). In turn, the r_g between growth and resistance can range from negative (-0.64) to 0 (Gitterle *et al.,* 2005b; Caballero-Zamora *et al.,* 2015).

The objective of this study was to estimate genetic parameters for survival and body weight at harvest under commercial grow-out conditions for the fifth generation of selection in a breeding population of *L. vannamei* from the Genomar /La Chamecita company in the province of Santa Elena, Ecuador, using genomic information from a commercial SNP array, in order to design genetic selection programs including disease resistance, adapted to local production systems.

Materials & Methods

Data and Population. Phenotypic information was obtained from 524 animals for survival and 5,918 for body weight at harvest (g). Data for each trait were obtained from two separate subsets of animals. Each subset comprised animals from two contemporary groups (GS1 and GS2), from the large commercial ponds in the Taura parish of the province of Guayas. These contemporary groups were obtained from four days of artificial insemination each in March 2025.

Study design. Six hapas (2.5 m long x 1.40 m wide x 1 m high) were used for each trial group inside the individual ponds for monitoring and recording of survival data. Individual survival data consisted of survival time (T25, T50, T75, and T100) and binary survival (S25, S50, S75, and S100), with cut-offs at 25, 50, 75, and 100% survival within each contemporary group. We used these cutoff criteria to examine differences in the estimated parameters. Survival was monitored by observing the hapas twice daily (8:00 am and 8:00 pm). At the same time, pleopod samples were collected from moribund and dead animals for genotyping. Binary survival was recorded at the end of the trials, coinciding with the harvest dates, at which time live animals were euthanized and pleopod samples obtained. The total duration of trials in the GS1 and GS2 groups was 522 and 377 hours, respectively. In the GS1 group, a density of 14 animals per m^2 was used, while the GS2 group had two densities: three hapas with 9 animals/m^2 and three hapas with 23 animals/m^2. The body weights at harvest of the 5,918 animals in the two ponds were obtained at 45 (GS1) and 29 (GS2) days in the fattening stage, respectively. DNA samples were collected from all measured animals. Genotypes were obtained from a commercial 50K SNP array for shrimp from the Center for Aquaculture Technologies (CAT). Marker files were processed using Plink and ASRgenomics.

Statistical analysis The genomic relationship matrix was constructed following the VanRaden method using 6,441 animals and 36,672 SNPs after quality control with ASRgenomics. The initial number of SNP was 50,811. Quality control parameters included removing markers with a minor allele frequency (MAF) below 0.05 and marker call rate below 0.20, as well as individuals with a call rate below 0.50 and markers with heterozygosity greater than 0.95. Univariate and bivariate mixed linear models were used for the estimation of variance components and genetic parameters using ASReml-R software with a genomic BLUP (GBLUP) approach. The fixed effects considered in the models for body weight at harvest were sex and pond. For survival traits, the fixed effect was contemporary group-hapa. In both cases animal and residue were included as random effects.

Results

Table 1 presents descriptive statistics for body weight and survival by contemporary group.

Table 1. Descriptive statistics of the population studied by trait and contemporary group.

Contemporary	Weight (g)			Survival	
group	N	Mean	SD	N	%
GS1	2,384	24.86	3.70	298	21.1
GS2	3,534	20.19	2.76	226	29.2

GS1 = Contemporary Group 1, GS2 = Contemporary Group 2, SD = Standard Deviation.

Figure 1 shows the monitoring times of GS1 and GS2 for survival, which were 522 and 377 hours, with final survival rates of 21.1 and 29.2%, respectively.

Univariate analyses for cumulative survival time and binary survival converged. The h^2 for T25 and S25 were low (0.04±0.05, 0.07±0.06, respectively), with high standard errors, in accordance with the number of phenotypes analyzed. The h^2 of T50-T100 were close to zero as were those for S50-S100, possibly as a result of the high mortalities impacting these parameters. In this way, from the bivariate analysis between weight and T25 and weight and S25, an h^2 for body weight of 0.16±0.02 was found (Table 2). The parameters for T25 and S25 were similar to those observed in the univariate analyses. Estimated genetic correlations between body weight and T25 (-0.12±0.31) and between body weight and S25 (0.01±0.26) were not statistically different from zero.

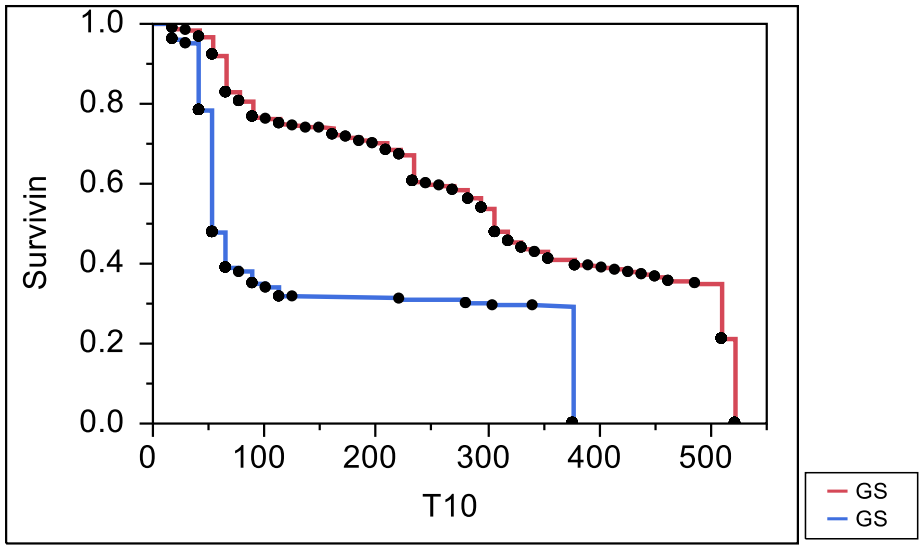

Figure 1. Survival curves (in hours) by contemporary group.

Table 2. Genetic parameters (± standard error) for body weight (g), T25 (hours) and S25 of the bivariate analysis.

Trait	σ^2_A	σ^2_R	h^2	r_g
Weight	1.62±0.21	8.27±0.18	0.16±0.02	-0.12±0.31
T25[1]	112.07±131.64	3,262.15±233.87	0.03±0.04	
Weight	1.62±0.21	8.27±0.18	0.16±0.02	-0.01±0.26
S25[2]	0.0047±0.0042	0.07±0.0057	0.06±0.05	

σ^2_A = Additive genetic variance, σ^2_R = Residual variance, h^2 = heritability and r_g = genetic correlation.

[1] Survival time with a cut-off at 25% survival.

[2] Binary survival with a 25% cut-off survival over time.

Discussion

The genetic parameters estimated in this study, with moderate heritability for body weight (0.16) and low h^2 for survival time (T25) (0.03) and binary survival (S25) (0.06) measured in commercial ponds, are consistent with the results observed in genetic improvement programs of *L. vannamei*, where growth traits tend to show greater additive genetic variation than survival components under adverse sanitary conditions (Gitterle *et al.*, 2005a, 2005b; Martínez-Soler *et al.,* 2024). Estimates of heritabilities for T25 and S25 and r_g between weight and the survival traits were imprecise, with high standard errors due to the relatively small number of observations for survival traits. In studies related to resistance to viruses such as WSSV under commercial production conditions (Caballero-Zamora *et al.,* 2015) and in controlled challenge environments (Gitterle *et al.,* 2005b), moderate genetic antagonisms have been found. Low h^2 of survival and resistance is a common pattern in aquatic species due to the biological complexity of the trait and environmental influences, highlighting the need for multiple trait selection and genomic approaches to capture small but relevant additive effects (Lillehammer *et al.,* 2020; Nirea *et al.,* 2025). As the h^2 of survival in commercial ponds is expected to be small, possibly less than 0.10 (Caballero-Zamora *et al.,* 2015), it is difficult to achieve statistical significance with a relatively small number of individuals. The differences found based on the definition of survival time and binary survival for different cut-offs per quartile of mortality may produce different estimates. Therefore, in this type of study, it is appropriate to analyze

survival time and survival with different cut-offs. In this case, the 25% cut-off resulted in an h^2 value greater than zero. The survival values obtained were lower than those typically reported in commercial ponds in Ecuador during considerably longer growing periods, indicating probable white spot disease, as it is well-established that this is the most prevalent disease in this region and was confirmed in two samples by histopathology. Although it is possible that the estimated genetic variation was low due to high mortality in the period studied and strong environmental adaptation/management effects, several analyses converged, indicating that trials with a larger data set and better conditions may allow for better estimation of genetic (co)variances among shrimp for survival and harvest weight under real-world production conditions.

Conclusions

Despite the lack of statistical significance of estimates for survival, these results suggest low genetic variation for survival under the conditions of this particular study. As it is necessary to have simultaneous advances in growth and resistance in shrimp breeding programs in commercial ponds, further efforts to conduct this type of trial under real-world production conditions using genomic information are warranted. In the future, some changes to the characteristics of the trial, such as density inside the happas and longer adaptation periods compared to those used in this study may be considered.

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