



GENETIC PARAMETERS OF BODY WEIGHT AND RESISTANCE TO WHITE SPOT SYNDROME IN PACIFIC WHITE SHRIMP USING GENOMIC INFORMATION

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INTRODUCTION

Resistance to White Spot Syndrome Virus (WSSV) and body weight are important criteria in genetic evaluations in the shrimp industry. The availability of microarrays with thousands of Simple Nucleotides of Polymorphism (SNPs) for *Litopenaeus vannamei* offers the opportunity to obtain better estimates of genetic parameters to consider the genomic information and genealogy available at the same time.

OBJETIVE

Estimate the genetic parameters of White Spot Syndrome Virus resistance and body weight at 120 days of age in *Litopenaeus vannamei* using genomic data.

METHODOLOGY

INFORMATION			
176 families from two cycles of population of Maricultura del Pacifico company			
	Cycle	Phenotypes	Genotypes
2020	Data generated a challenge test to prove the resistance to WSSV	Binary survival (sWSSV) (n=6108)	n=1684
2021	Data are obtained individuals that grown up controlled facilities	Weight at 120 days of age (P120) (n=824)	n=824
Plus Genotypes of 429 parents			
Genotyped			
Genotyped Center for Aquaculture Technologies Chip AquaArray HD (50,811 K) vannamei®		Quality control Call rate 80% MAF<0.05 Hardy-Wainberg equilibrium p< 1 x 10 Exclusion of organisms with call rate <80	
Estimate of genetic parameters to sWSSV and P120 Two approaches, two models			
Model	Data	Fixed effects	Random effects
BLUP	Pedigree	sWSSV: The test vat and weight at challenge test registered P 120: Sex and age	Additive genetic effect, common to full sibs effect and residual
ssGBLUP	Pedigree and genomic		
Analyzed with AiREREMLP90			

RESULTS AND DISCUSSION

The standard error of estimations of heritability with ssGBLUP is reduced for both traits, improving their precisions. The r_G was consistently negative and not significant in either model, as has been observed in other studies between body weight and WSSV resistance indicators.

CONCLUSION

We can conclude that use of pedigree and genomic data at the same time allow better the precision of heritability and genetic correlations.

