



[ANIMAL HEALTH & WELFARE \(/ADVOCATE/CATEGORY/ANIMAL-HEALTH-WELFARE/\)](/ADVOCATE/CATEGORY/ANIMAL-HEALTH-WELFARE/)

Genetic variation for resistance to WSS, AHPND in Pacific white shrimp

Friday, 11 September 2015

By Héctor Castillo-Juárez, Ph.D. , Hugo H. Montaldo, Ph.D. , Sonia Soto-Rodríguez, Ph.D. and Juan Carlos Quintana Casares

Trials evaluate complex relationships between hosts and etiological agents

White spot syndrome (WSS) and acute hepatopancreatic necrosis disease (AHPND) have become the main causes of economic loss in shrimp production worldwide. Prevention of these diseases is very difficult to achieve, and efforts to control them have often seen inconsistent results. Moreover, some intensive production systems seem to favor their rapid spread.

In such scenarios, breeding for disease resistance is a viable option to deal with this issue in commercial shrimp culture. Breeding shrimp for disease resistance is worthwhile when there are no other simple, cost-effective control measures, and there are genetic differences for resistance to the pathogen.



Shrimp in the AHPND trial were challenged with *Vibrio parahaemolyticus* in laboratory aquariums.

Experimental trials

The authors conducted a preliminary analysis of data from experimental trials performed in 2014 to evaluate whether there is genetic resistance to WSS and AHPND. The heterogeneous population involved families of Pacific white shrimp, *Litopenaeus vannamei*, from the Mexican Maricultura del Pacífico hatchery line and families from two different Ecuadorian sources, including their crosses.

For the AHPND challenge, 144 families (28 full-sib Ecuadorian, 100 half-sib Mexican and 16 full-sib Ecuadorian x Mexican families) with average individual body weights of about 2g were kept in two replicated aquariums. A bacterial inoculum of AHPND-causing M0904 strain *Vibrio parahaemolyticus* was added directly at a final density of 105 colony-forming units/mL.

For the WSS challenge, six replicated tanks containing all the families with shrimp averaging 4g body weight were orally infected using a dose larger than 107 copies of viral DNA/g. Details on the experimental procedures and complete results will be presented in a scientific journal soon.

Heritability for AHPND resistance was low, below 0.10, while at close to 0.20, that for WSS was moderate. These results indicated that genetically improving resistance to these two diseases is feasible, although genetic progress in the case of AHPND will be slower. Genetic correlation did not indicate any strong antagonism between the resistances to these diseases.

The authors also found significant differences in disease resistance when comparing a high-growth genetic selection line, two low-growth genetic lines from Ecuador and their crosses. Compared to the Mexican line, the Ecuadorian lines were more resistant to both AHPND at 1 g of body weight and WSS at 4 g body weight. However, there was no difference between lines for AHPND resistance at 8 g of body weight.

Analysis of first-generation and parental lines suggested dominant effects for AHPND resistance and recessive effects for WSS resistance. The results suggested there are



L. vannamei families were challenged with white spot syndrome virus in lined laboratory tanks.

differences for disease resistance and body weight between genetic lines and different mechanisms of resistance for each disease. These genetic lines will be the basis for the development of a new disease-resistant, high-growth genetic line.

Genetic evaluation

Heritability is an important element in predicting the expected response to genetic selection. The greater the heritability, the greater the response to selection will be. It is important to remember that genetic change due to selection accumulates in the population across generations, allowing continuous advances even when the heritability for the selected traits is low.

One of the primary challenges in the genetic evaluation of disease resistance is how to generate disease resistance data. In practical terms, disease resistance can be measured as the survival rate of the animals challenged.

For an animal to survive, it needs mechanisms for resisting or being resilient to challenges, or it must be protected artificially from them. The measurement of how animals survive during infection is therefore crucial to being able to select families of animals with a higher degree of genetic resistance.

Most studies are well-designed experimental challenges, but in this type of experiment, some of the natural conditions of the outbreaks may be excluded. Other studies can be performed using data generated from natural disease outbreaks, although these involve many non-controlled variables.

Outbreak or experiment

When the genetic evaluation of families is conducted during natural disease outbreaks, resistance is observed under the actual conditions where the disease occurs. However, it is difficult to predict where disease is going to occur. Moreover, recovering breeding animals from disease-affected commercial ponds is difficult.

This approach can be associated with increased expenses from disease-related losses and the efforts to keep track of the pedigree of the animals from the affected ponds. Moreover, the animals can die or survive during a natural outbreak for reasons unrelated to the targeted disease.

On the other hand, evaluations based on experimental challenges make it possible to standardize a management procedure, which ensures recognition of possible causes of death and maintains pedigree control. Genetic evaluation is therefore more accurate, but the disease conditions may differ widely from those occurring naturally.

Perspectives

The complex relationships between hosts and etiological agents vary among species, animal populations, environments and time periods. These factors are relevant when considering long-term strategies of genetic selection for disease resistance.

The development of breeding programs for disease resistance requires an evaluation of the genetic variation to the diseases being considered and their genetic associations with other important traits, such as growth and overall survival, in order to maximize the profitability of shrimp farms. We must keep in mind, however, that results cannot always be extrapolated to other populations or production conditions.

Authors



HÉCTOR CASTILLO-JUÁREZ, PH.D.

Departamento de Producción Agrícola y Animal

Universidad Autónoma Metropolitana

Unidad Xochimilco

Calzada del Hueso 1100

Col. Villa Quietud, Delegación Coyoacán

04960, Distrito Federal México

mejoracamaron@gmail.com (<mailto:mejoracamaron@gmail.com>)



HUGO H. MONTALDO, PH.D.

Facultad de Medicina Veterinaria y Zootecnia

Universidad Nacional Autónoma de México

Ciudad Universitaria

Distrito Federal México



SONIA SOTO-RODRÍGUEZ, PH.D.

Leobardo Montoya-Rodríguez
Centro de Investigación en Alimentación y Desarrollo
Unidad Mazatlán para la Acuicultura y el Manejo Ambiental
Mazatlán, Sinaloa, México



JUAN CARLOS QUINTANA CASARES

Maricultura del Pacífico, S.A. de C.V.
Mazatlán, Sinaloa, México

Copyright © 2016–2018
Global Aquaculture Alliance