



GENETIC VARIATION BETWEEN FARMED AND WILD POPULATIONS OF PACIFIC WHITE SHRIMP (*Litopenaeus vannamei*) USING MICROSATELLITE LOCI.



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Introduction

Breeding programs, in the long term, reduce the genetic variation, due to the reduction of the effective population size (N_e). It is therefore recommended to monitor the genetic variation of the population across time. In aquaculture, there are studies in different species using microsatellites that evaluate the genetic variability on cultured populations across generations (Norris et al., 1999; Lind et al., 2009). Based on these studies it has been possible to detect differences between populations using allele diversity indexes, but they have not shown evidences of differences while comparing the expected heterozygosity (H_e) between populations. A factor that very probably affected the power for testing differences in H_e in these studies was the number of microsatellites used. In most studies only 2 to 12 loci were used. The aim of this study was to compare the genetic variability of shrimps in two generations of a cultured population of *P. vannamei* under genetic selection for growth and a wild shrimp population sampled from the Mexican Pacific Ocean, using 26 microsatellite loci data.

Materials and Methods

We used 77 shrimp samples from 208 families from generation 2005 (G05), 73 shrimp samples from 208 families from generation 2007 (G07) from a farmed population, selected for growth and 54 shrimp samples from wild organisms (WILD). All the samples were genotyped for 26 polymorphic microsatellite loci using multiplex PCR.

The expected heterozygosity (H_e), observed heterozygosity (H_o), number of alleles corrected by rarefaction (A_c), number of unique alleles corrected by rarefaction (A_u) and effective alleles number (A_e) were obtained for all populations, besides the fixation index F_{st} and its analogue R_{st} . In addition the effective population size (N_e) were obtained for populations G05 and WILD.

Results

Statistically significant differences ($P < 0.05$) were found between WILD compared to G05 and G07 populations for H_e , A_c , A_u and A_e , but not between the two later. The effective population size for WILD was significantly larger (271) than population G05 (142), indicating that the main reason of the differences observed in all the studied variability measures between cultured and wild populations are the differences in population sizes.

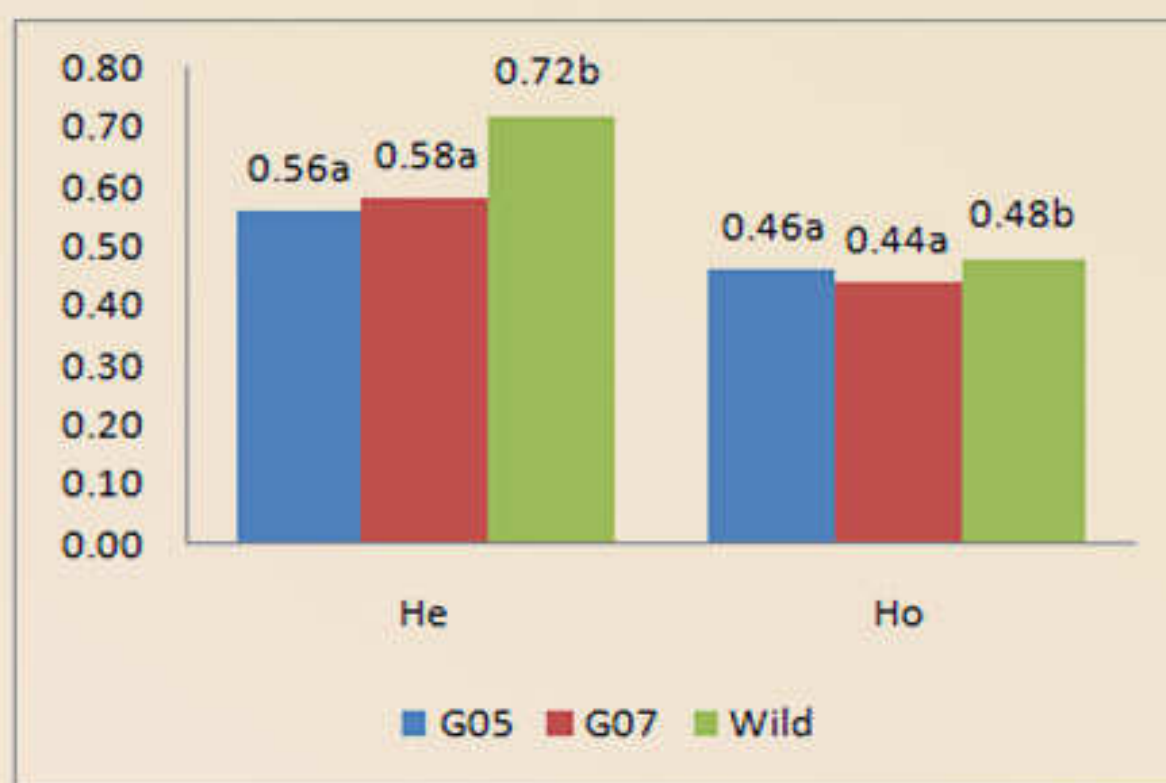


Figure 1. Expected heterozygosity (H_e) and Observed heterozygosity (H_o) values. Different letters indicates statistical differences ($p < 0.01$).

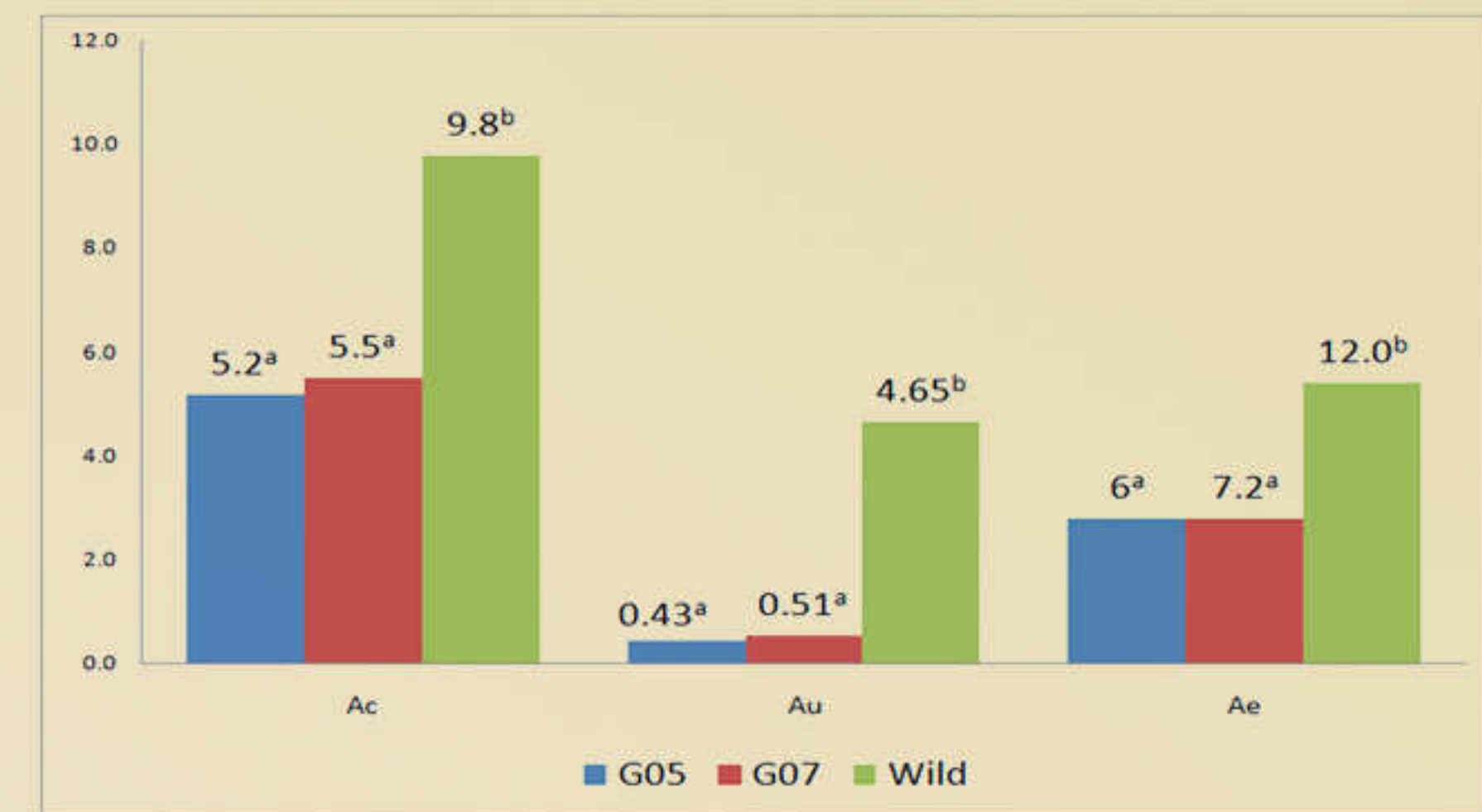


Figure 3. Allelic diversity indexes. A_c : Alleles number corrected by rarefaction; A_u : Unique alleles number corrected by rarefaction; A_e : Effective alleles number. Different letters indicates statistical differences ($p < 0.01$).

The results for F_{st} indicate that all the populations were significantly different from each other, being G05 and G07 those which displayed smaller divergence compared to WILD. These results were consistent with the R_{st} values which showed the same tendency ($P < 0.05$).

The dendrogram (Figure 2) shows that the cultured populations were grouped together and clearly separated from the wild population, indicating a clear differentiation between both cultured populations and the wild one.

Conclusion

Due the genetic variability of the two generations of farmed populations (G05 and G07) didn't show differences for H_e and for allelic richness indexes between them, it can be concluded that in the short term (2 selection cycles) the genetic improvement program didn't affect the genetic variation of the population in a significant degree. Nevertheless, F_{st} and R_{st} values between pairs of populations indicate that there can be a small differentiation between populations G05 and G07, differentiation that may be due to selection and/or to genetic drift. Our results also indicate that the introduction of wild shrimps into the cultured population could be beneficial for maintaining or increasing the genetic variability of selected populations of captive *P. vannamei*.

Acknowledgments

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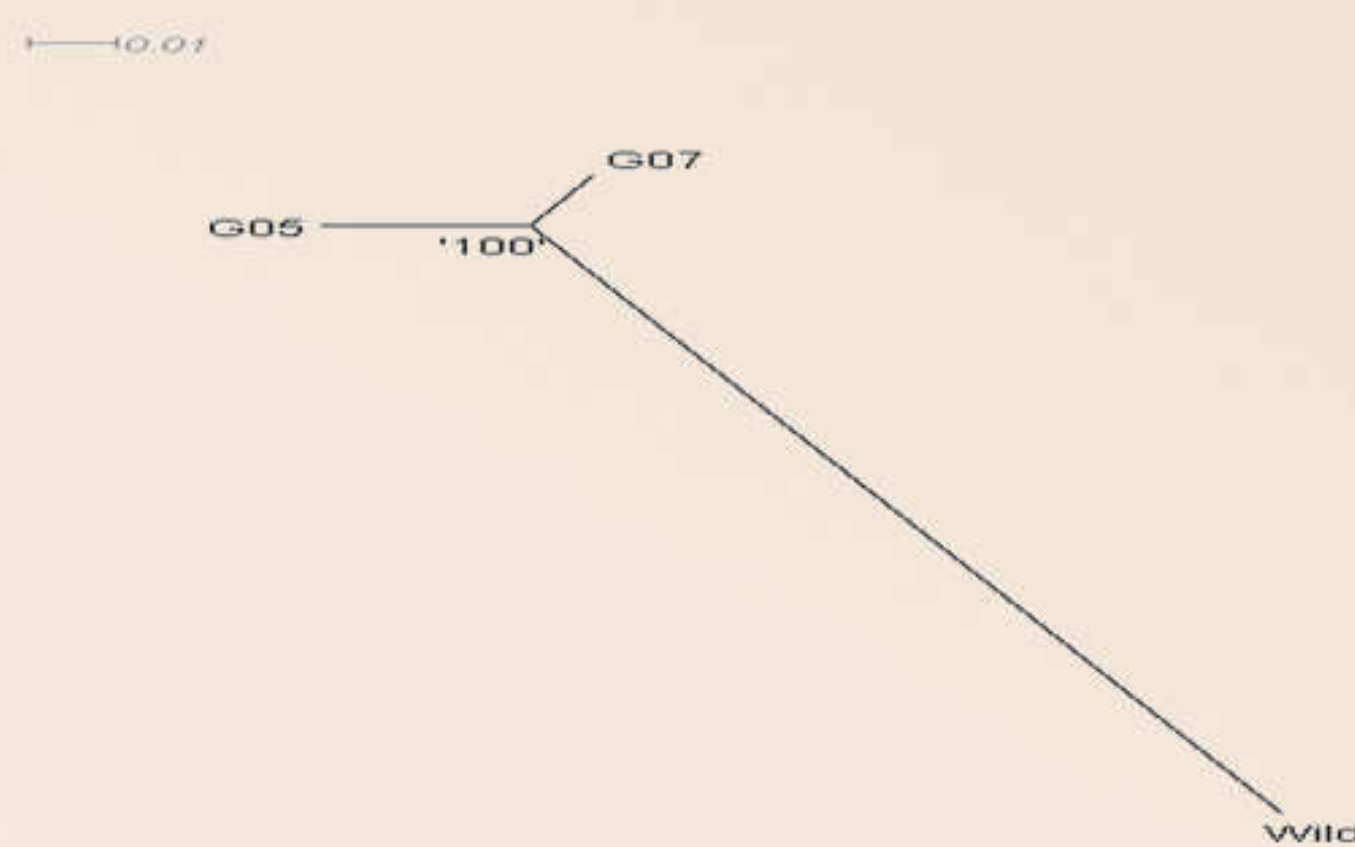


Figure 2. Dendrogram showing the distances between populations G05, G07, and Wild.

Table 1. Paired divergence values between populations (F_{st} below diagonal and R_{st} over diagonal)

	Populations		
	G05	G07	WILD
G05		0.01094*	0.0436*
G07	0.0182*		0.0298*
WILD	0.0857*	0.0800*	

* $p < 0.05$