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Health & Welfare
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Tracing origins, diversity loss in captive shrimp



1 February 2005 Ken Jones, Ph.D. Leland Lai



Genotypes from four wild populations compared to genetic profiles of captive stocks

The implementation of animal breeding programs is enacted through managed inbreeding for selective traits of economic importance. In the process, there will be unintentional diversity loss in the genetic profiles of the broodstock from generation to generation. Such loss can be tracked with the use of microsatellite markers in as little as two generations.

Genetic masking evolves when parent stocks from different populations are crossbred to establish new families. Fast forward several generations, and many programs lose the ability to track data from the parent set representative of the original population.

Specific breeding strategies are required in most captive programs to prevent or minimize genetic loss over multiple generations. The rate of loss for genetic diversity is amplified intentionally when the population is subjected to selection for trait improvement, and unintentionally when there is no breeding strategy for minimizing the loss in captive maintenance of most small breeding populations.

Study setup

The authors conducted studies to determine the extent to which farmed populations of Pacific white shrimp (*Litopenaeus vannamei*) showed loss of genetic diversity relative to their wild founding stocks, and whether the founding stocks could be identified from the genetic makeup of the farmed animals. Research also examined whether genetic markers could be used to identify farmed animals and provide stock protection for breeders who develop specialized lines of animals.

Genotypes from four wild populations were compared to the genetic profiles of captive stocks from Ecuador, Panama, and Mexico. The shrimp from Panama were known to have originated from Panamanian wild stocks. For Ecuador, the captive stocks were several generations removed from their original Panamanian wild stocks. Although of uncertain origin, the captive Mexican stocks reportedly came from Venezuela and were compared to Mexican wild stocks. The diversity of all the captive stocks was compared to that of wild stocks of origin once confirmed by genotype assignment.

Results

All captive stocks showed varying losses of diversity, but could be associated with their originating founding stocks. Table 1 shows the loss of diversity of the farmed animals compared to the wild stocks from four locations.

Table 1. Loss of genetic diversity in farmed *L. vannamei*.

Locus	Wild Stocks					Farmed Stocks			
	WME	WSE	WP	WLMM	Mean	FEPO	FPPO	FMUO	Mean
D28	21	21	22	14	20	15	12	6	11
G27	12	16	14	8	13	11	9	7	9
G131	7	10	6	7	8	5	4	5	5
F706c	14	11	15	8	12	9	9	11	10
D171	24	19	23	9	19	9	8	6	8
D835	10	6	15	6	9	4	9	3	5
F828	14	16	14	13	14	11	11	12	11
G102	6	8	10	7	8	5	8	6	6
G238	17	19	14	12	16	12	13	13	13
G203	27	20	21	17	21	16	11	16	14
Mean alleles	15.2	14.6	15.4	10.1	13.8	13.5	9.4	8.5	10.5
Mean heterozygosity	0.71	0.69	0.72	0.58	0.68	0.62	0.62	0.55	0.60
Mean PIC	0.82	0.79	0.83	0.72	0.79	0.69	0.72	0.67	0.70
P(i)	5.1 x 10 ⁻¹⁶	1.6 x 10 ⁻¹³	1.4 x 10 ⁻¹⁶	1.9 x 10 ⁻¹²		4.8 x 10 ⁻¹¹	7.2 x 10 ⁻¹²	1.1 x 10 ⁻¹⁰	

WME = Wild stock, Manta, Ecuador

WSE = Wild stock, Salinas, Ecuador

WP = Wild stock, Panama

WLMM = Wild stock, Los Mochis, Mexico

FEPO = Farmed Ecuador

FPPO = Farmed Panama, Panama origin

FMUO = Farmed Mexico, unknown origin

The founding stocks of two of the farmed populations (FEPO and FPPO) were known prior to the comparison, while the third (FMU) was not. Loss of diversity was based on the reduction in number of alleles, heterozygosity, polymorphic information content and other factors.

When comparing how captive stocks related genetically to the wild stocks of origin, the association was correct in every pairing, as displayed in Fig. 1. Finally, an assignment test was performed on the sample groups to determine how closely the populations were related (Table 2).

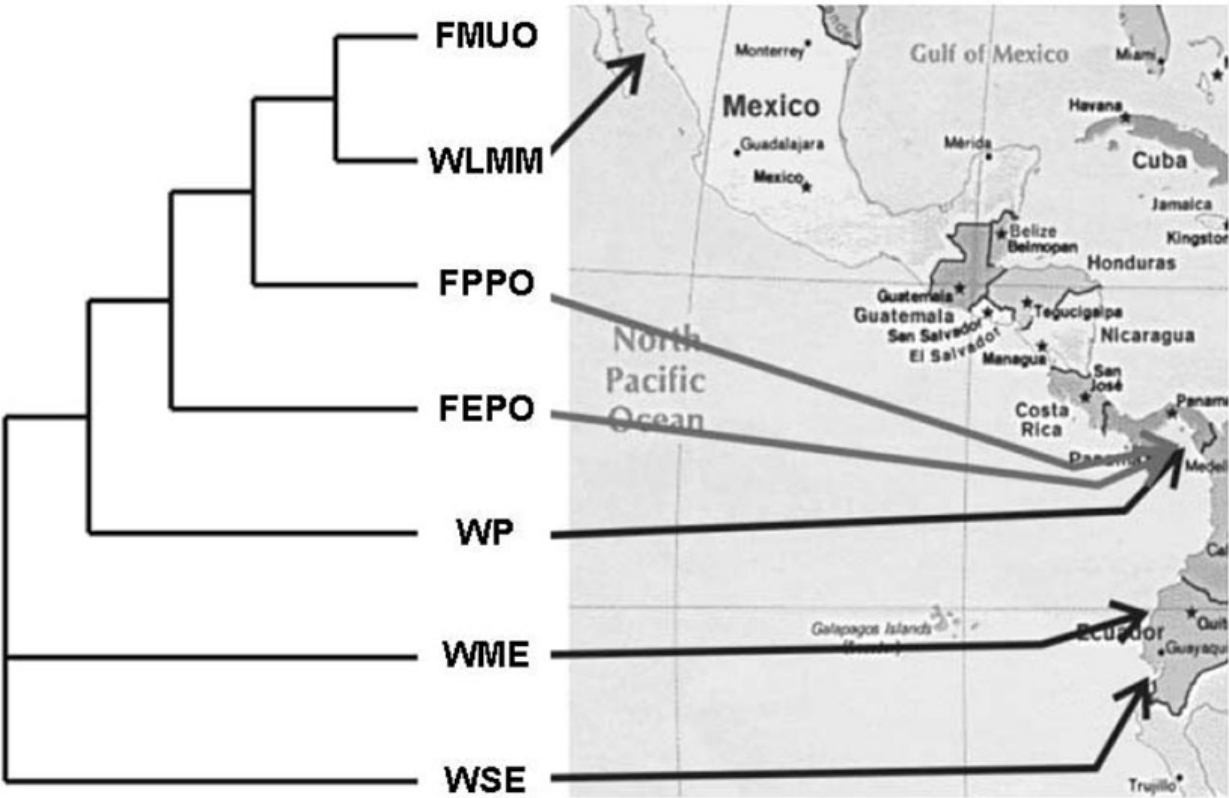


Fig. 1: Comparison of how captive stocks relate genetically to wild stocks of origin.

In all cases, the assignment of sample populations to a reference population based on genotype produced assignments exceeding 50 percent, and above 90 percent in two of the three farmed populations selected. The Mexican farmed sample of unknown origin were still assigned at 85 percent to the unknown category, but 13 percent related more closely to genetic profiles found in wild stocks found in Los Mochis, which is located less than 150 km from the source of the farmed animal samples.

Animals from the same founding wild stocks under different captive maintenance programs showed finite differences for identification purposes. Such differences can be used for “fingerprinting” pedigree and tracked irrespective of where they are farmed.

(Editor's Note: This article was originally published in the February 2005 print edition of the Global Aquaculture Advocate.)

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