

CHROMOSOME LOCATIONS OF *RTE-3_LVa* NON-LTR RETROTRANSPOSON FROM THE FIRST SPECIFIC PATHOGEN-FREE (SPF) *Penaeus vannamei* PRODUCED IN THE UNITED STATES – A POTENTIAL SEX MARKER FOR SHRIMP

Acacia Alcivar-Warren, Jianbo Yuan, Gober Asuncion, Marcos De Donato, Hectorina Rodulfo* and Miriam Alcivar-Arteaga

The Shrimp Epigenome (ShrimpENCODE) Project
Environmental Genomics Inc., P. O. Box 196, Southborough, MA 01772 USA, and
Fundación para la Conservación de la Biodiversidad (FUCOBI), Quito, Ecuador
environmentalgenomics.warren@gmail.com

Infectious hypodermal and hematopoietic necrosis virus (IHHNV), now called *Decapod penstylhamaparvovirus 1*, is one of the major viral pathogens of penaeid shrimps. Infection with this virus resulted in severe mortalities of up to 90% in *Penaeus stylirostris*. It is less virulent in *P. vannamei* and *P. monodon* and does not typically cause mortality; but it can result in runt deformity syndrome (slow growth). A Type-A non-infectious endogenous IHHNV related sequence (DQ228358, 4,655bp; Tang & Ligthner 2006) was previously identified in the genome of *P. monodon* from Madagascar and demonstrated integrated into an RTE-like non-LTR retrotransposon. The shrimp containing DQ228358 do not cause infection in laboratory infection studies. The 3'-flanking sequence of the integrated IHHNV, nucleotides 3262-4655 of DQ228358, shows 98% identity to nucleotides 1531-2924 of a *P. monodon* repeat family *RTE-2_PMon* (3,656-bp) which shares 85% sequence identity along the whole length with *RTE-3_LVa* non-LTR retrotransposon (3,654-bp; www.girinst.org).

RTE-3_LVa was characterized from a pilot genome sequence (total length of ~470 Mb) from the first SPF *P. vannamei* produced by the breeding program of the U.S. Marine Shrimp Farming Program (USMSFP) maintained in Kona and Oahu, Hawaii, USA. Thirteen microsatellites isolated from ovary of SPF *P. vannamei* are homologous to *RTE-3_LVa*, two located onto the sex linkage group 4 (LG4, *ShrimpMap2*) of SPF *P. vannamei*. Homology searches using the whole genome sequences databases in Genbank revealed that *RTE-3_LVa* has many copies in various scaffolds of *P. vannamei* breed Kehai No.1 assembly including in LG18 associated with sex differentiation. PCR amplification using DNA from adult SPF *P. vannamei* and primers from two microsatellites similar to *RTE-3_LVa* showed sex-specific bands, suggesting that *RTE-3_LVa* is a potential sex marker for shrimp. To be confirmed in cultured and wild shrimp.

RTE-3_LVa is also present in various chromosomes of other penaeid species like *P. monodon* from Thailand. Considering the variability in genome sizes of current penaeids assemblies [*P. monodon* from China and Vietnam (~1.4-~1.6 Gb), *P. chinensis* from China (~1.6 Gb), *P. indicus* from India (~1.6 Gb), *P. japonicus* from China and Japan (~1.7 Gb)], which are smaller than the expected ~2.87 Gb genome size of SPF *P. vannamei* from a breeding company in Florida, USA, a new, continuous, whole reference genome sequence is urgently needed from the founding parents of the SPF *P. vannamei* breeding program of the USMSFP and wild *P. vannamei* to study organization and evolution of integrated viruses like IHHNV, expression of *RTE-3_LVa*, and mechanisms of sex determination and differentiation.