Visanu Boonyawiwat 2009: Traditional and Molecular Epidemiology to Determine Risk Factors for Outbreaks of Shrimp White Spot Disease in Thailand. Doctor of Philosophy (Agricultural Biotechnology), Major Field: Agricultural Biotechnology, Interdisciplinary Graduate Program. Thesis Advisor: Professor Timothy William Flegel, Ph.D. 126 pages.

White spot disease (WSD) is a viral disease that causes acutely fatal and massive losses in most commercially cultivated marine shrimp species. A longitudinal retrospective study of the risk factors for WSD outbreaks was investigated based on management practices and environmental variables of a semi-closed farming system. Altogether 384 pond records of 8 continuous production cycles of a 70-pond farm from January 1998 to January 2002 were analyzed using multivariable logistic regression analysis and generalized estimating equations (GEE). WSD outbreak ponds were defined as those where shrimp gave a positive result for WSSV infection using a 1-step PCR method. The average time of shrimp culture in outbreak ponds was 80 days. While the average days of culture in normal ponds was 124 days. Forty-three percent of the ponds had WSD outbreaks throughout the study period. Season was the strongest factor that affected WSD outbreaks. Stocking shrimp during the rainy-winter season (June 16–December 31) dramatically increased the risk of disease (OR = 7.58). On the other hand, pond preparation durations longer than 17 days reduced the risk of WSD outbreaks (OR = 0.33).

A high value of the transmission coefficient (*ß)* in the rainy-winter season was found in the dynamic epidemiology study. It indicated that season is very important for epidemic outbreaks of WSD. Fluctuations in water salinity and low temperature probably had synergistic effects on the osmoregulation capacity of shrimp, increasing susceptibility to infection.

The number of tandem repeats in ORF94 and ORF125 VNTRs were highly variable among various Thai-WSSV isolates. When the 2 markers were used together, 18 WSSV genotypes were found out of 216 possible genotypes.

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