

International Conference on **Aquaculture & Fisheries** July 20-22, 2015 Brisbane, Australia

Evaluation of germplasm resources and analysis of genetic diversities from the ridgetail white prawn *Exopalaemon carinicauda*

Jitao Li

Chinese Academy of Fishery Sciences, China

The ridgetail, white prawn (*Exopalaemon carinicauda*) is one of the major economic shrimp species, which naturally distributes in the coasts of Yellow Sea and Bohai Sea, China. Due to the multiple merits of fast growth, good reproductive performance and good environmental adaptability, the culture area of *E. carinicauda* has expanded in recent years and contributes to one third of the gross outcome of the polyculture ponds in eastern China. The current cultural pattern depends on wild seedings or parent prawns from the natural sea area, ambiguous genetic background and destabilizing supply heavily influenced the development for culture of *E. carinicauda*. However, few studies on germplasm resources and genetic diversities in *E. carinicauda* have been reported. In the present study, five geographic populations were collected from coastal waters of Bohai and the Yellow Sea since 2011. The regression equation for seven morphological traits to body weight was built using multivariate analysis, the results indicated body length had the most direct impact on weight with path analysis. The results of karyotype analysis showed $2n=56m+8sm+12st+14t=90$. The results of isozyme analysis suggested phylogenetic relationship between populations of Bohai bay and Laizhou bay was close, and followed by populations of Jiaozhou bay and Haizhou bay. The genetic diversity of the population and phylogenetic relationship among Palaemonidae were analyzed based on mitochondrion DNA 16S rRNA, COI sequence and ribosome ITS1 sequence, the results indicated the genetic differentiation coefficient between populations of Xiangshan bay and Laizhou bay was highest, and that was lowest between populations of Laizhou bay and Haizhou bay. A microsatellite-enriched library was constructed using the method of magnetic bead hybridization enrichment and fifty-six polymorphic microsatellite primers were screened, and the genetic diversity of populations was analyzed using twelve polymorphic microsatellite primers, UPGMA clustering tree based on D genetic distance showed that Laizhou Bay stock was more closely related to Xiangshan stock and Haizhou Bay stock was farthest related to Xiangshan stock. In summary, the above results provided basic data for the protection and utilization for germplasm resources of *E. carinicauda*.

lijt@ysfri.ac.cn

The distribution and elimination of Norfloxacin in Chinese white shrimp (*Fenneropenaeus chinensis*) aquaculture system

Zhi-Qiang Chang, Ming Sun, Qian-Qian Zhai and Jian Li

Chinese Academy of Fishery Sciences, China

The Chinese white shrimp *Fenneropenaeus chinensis* is one of the most valuable aquatic shrimp resources in China, distributed mainly in the Bohai Sea and the Yellow Sea. It has also been of great importance to the mariculture industry in China due to the good taste, high commercial value and adaptation to artificial culture conditions. The production used to reach over 200,000 tons in 1989-1992 then devastated significantly by a series of epidemics in the 1990s and early 2000s and maintained around 45,000 tons recently. Antibiotics such as Norfloxacin (NFLX) were occasionally used during shrimp aquaculture to control bacterial infections caused by *Vibrio anguillarum* or other marine pathogens. Therefore, in the study we investigated the distribution and elimination of norfloxacin in *F. chinensis* at different developmental stages and in culture environment as well. First, the mature parent shrimp were exposed to NFLX through medicated water bath at 4 and 10 mg/L for 2 to 5d respectively. NFLX concentration increased in both the parent and their eggs with the increase of time and concentration of drug exposure and the highest level of NFLX residues were detected in the ovary of parent shrimp. Then the drug residues in the larvae at different developmental stages were further examined. The elimination half-lives of NFLX in *Nauplius* exposed to NFLX at 4 and 10 mg/L for 24 hours were 45.36 and 49.85 hours respectively and 31.68 and 33.13 hours in zoea, 42.24 and 47.28 hours in Mysis larvae and 24.48 and 30.96 hour in post larvae. Finally, NFLX concentration in shrimp, water and sediment were also examined after drug administration with 2 different ways, medicated bath and feed. NFLX residues were mostly found in sediments and the elimination half-lives of NFLX in the muscle of shrimp exposed to drug by medicated bath and feed were 40.19 and 31.01 hours respectively.

changzq@ysfri.ac.cn