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## RESEARCH REPORTS

Sustainable Aquaculture for a Secure Future

**Title:** Inferring invasion history of red swamp crayfish (*Procambarus clarkii*) in China from mitochondrial control region and nuclear intron sequences

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**Date:** 06 July 2015

Publication Number: AquaFish Research Report 15-346

**Abstract:** AquaFish will not be distributing this publication. Copies may be obtained by writing to the authors.

Identifying the dispersal pathways of an invasive species is useful for adopting the appropriate strategies to prevent and control its spread. However, these processes are exceedingly complex. So, it is necessary to apply new technology and collect representative samples for analysis. This study used Approximate Bayesian Computation (ABC) in combination with traditional genetic tools to examine extensive sample data and historical records to infer the invasion history of the red swamp crayfish, *Procambarus clarkii*, in China. The sequences of the mitochondrial control region and the proPOx intron in the nuclear genome of samples from 37 sites (35 in China and one each in Japan and the USA) were analyzed. The results of combined scenarios testing and historical records revealed a much more complex invasion history in China than previously believed. *P. clarkii* was most likely originally introduced into China from Japan from an unsampled source, and the species then expanded its range primarily into the middle and lower reaches and, to a lesser extent, into the upper reaches of the Changjiang River in China. No transfer was observed from the upper reaches to the middle and lower reaches of the Changjiang River. Human-mediated jump dispersal was an important dispersal pathway for *P. clarkii*. The results provide a better understanding of the evolutionary scenarios involved in the rapid invasion of *P. clarkii* in

**AQUAFISH RESEARCH REPORTS** are published as occasional papers by the Management Entity, AquaFish Innovation Lab, Oregon State University, Corvallis, Oregon 97333-3971 USA. The AquaFish Innovation Lab is supported by the US Agency for International Development under Grant No. EPP-A-00-06-00012-00. See the website at <aquafishcrsp.oregonstate.edu>.

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China.

This abstract was excerpted from the original paper, which was published in the International Journal of Molecular Science (2015). 16: 14623-14639.

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