AFLP-BASED GENETIC MAP OF BRINE SHRIMP *ARTEMIA FRANCISCANA*

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Brine shrimps of the genus *Artemia* are small planktonic crustaceans found in about 500 natural salt lakes and salterns around the world (Lavens & Sorgeloos, 1996). *Artemia* is the most common live food in aquaculture activities, specifically for larval growth of >85% of the marine species reared in aquaculture (Kavim *et al.*, 2010). The aquaculture industry is the fastest growing food industry today.

Artemia has many features of interest for genomic research:
Artemia has a short life cycle (2-4 weeks). Levels of genetic variability for *Artemia* are among the highest within crustaceans (Abatzopoulos *et al.*, 2002; Bossier *et al.*, 2004). *Artemia* species are extremophiles, genes underlying these extreme phenotypes might be of utmost interest (Clegg, 2005; Robbins *et al.*, 2010). *Artemia* species are used as a model for the metabolism of crustaceans, biodiversity studies, toxicity testing, for *Vibrio* resistance in shrimps and for the interactions between sexual and parthenogenetic populations.

So far, only the mtDNA of *Artemia* has been sequenced completely and no *Artemia* linkage maps are currently available (Valverde *et al.*, 1994). *Artemia* linkage maps would provide basic information for further linkage studies on *Artemia* and other crustaceans, and construction of the maps is a first step towards creating genetic breeding programs. The development of genetic linkage maps is the base of mapping of quantitative trait loci (QTLs) and for marker-assisted selection (MAS). Genetic linkage maps have been reported for many aquaculture species.

A genetic map of the *Artemia franciscana* genome is being constructed with AFLP markers, using a F1 mapping population derived from a cross between two heterozygous strains (San Francisco Bay male x Vinh Chau female) (Vos *et al.*, 1995; Vuylsteke *et al.*, 2007). The phenotypic sex of each individual from the 113 heterozygous F1 offspring has been determined. With 42 primer combinations, we have found around 500 markers, of which two thirds are AFLP markers, segregating 1:1 (BC markers), the rest of the AFLP markers segregate 1:2:1 (F2 markers). Among the BC markers, 13 female markers co-segregate with sex. Based on AFLP markers co-segregating with sex, the genomic region containing the sex locus (or loci) will be identified. All found markers are being used for constructing a genetic map with the software package Joinmap 4 (Kyazma). Published *A. franciscana* SNPs will be put on the completed genetic map.

References

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