

## **RAD-Seq Data Reveals Evidence of Local Adaptation between Upstream and Downstream Populations of Australian Glass Shrimp**

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**Abstract :** *Paratya australiensis* Kemp (Decapoda: Atyidae) is a widely distributed indigenous freshwater shrimp, highly abundant in eastern Australia. This species has been considered as a model stream organism to study genetics, dispersal, biology, behaviour and evolution in Atyids. *Paratya* has a filter feeding and scavenging habit which plays a significant role in the formation of lotic community structure. It has been shown to reduce periphyton and sediment from hard substrates of coastal streams and hence acts as a strongly-interacting ecosystem macroconsumer. Besides, *Paratya* is one of the major food sources for stream dwelling fishes. *Paratya australiensis* is a cryptic species complex consisting of 9 highly divergent mitochondrial DNA lineages. Among them, one lineage has been observed to favour upstream sites at higher altitudes, with cooler water temperatures. This study aims to identify local adaptation in upstream and downstream populations of this lineage in three streams in the Conondale Range, North-eastern Brisbane, Queensland, Australia. Two populations (up and down stream) from each stream have been chosen to test for local adaptation, and a parallel pattern of adaptation is expected across all streams. Six populations each consisting of 24 individuals were sequenced using the Restriction Site Associated DNA-seq (RAD-seq) technique. Genetic markers (SNPs) were developed using double digest RAD sequencing (ddRAD-seq). These were used for de novo assembly of *Paratya* genome. De novo assembly was done using the STACKs program and produced 56, 344 loci for 47 individuals from one stream. Among these individuals, 39 individuals shared 5819 loci, and these markers are being used to test for local adaptation using Fst outlier tests (Arlequin) and Bayesian analysis (BayeScan) between up and downstream populations. Fst outlier test detected 27 loci likely to be under selection and the Bayesian analysis also detected 27 loci as under selection. Among these 27 loci, 3 loci showed evidence of selection at a significance level using BayeScan program. On the other hand, up and downstream populations are strongly diverged at neutral loci with a Fst =0.37. Similar analysis will be done with all six populations to determine if there is a parallel pattern of adaptation across all streams. Furthermore, multi-locus among population covariance analysis will be done to identify potential markers under selection as well as to compare single locus versus multi-locus approaches for detecting local adaptation. Adaptive genes identified in this study can be used for future studies to design primers and test for adaptation in related crustacean species.

**Keywords :** *Paratya australiensis*, rainforest streams, selection, single nucleotide polymorphism (SNPs)

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