

Recent Gene Duplications May Promote Rapid Adaptation in the Intramolluscan Stages of Schistosoma mansoni

Gene duplication is a major driver of genome evolution, facilitating functional innovation. In parasitic organisms, duplication may be particularly important, as parasites must continuously adapt to host immune defences in ongoing Red Queen dynamics. *Schistosoma mansoni*, a major human helminth parasite, requires infection of *Biomphalaria* snails as an intermediate host to complete its life cycle. Recent studies have identified duplicated genes that are highly expressed in the tegument during intramolluscan stages, suggesting that gene family expansion may contribute to successful snail infection.

To investigate how gene duplications of different evolutionary ages contribute to distinct life-cycle stages, we analysed stage-specific expression patterns and molecular evolutionary signatures across duplicate classes. We found that recent, species-specific duplications are strongly enriched for expression during snail stages and are particularly overrepresented in tegument-associated transcripts. In contrast, older duplications show broader expression across developmental stages and tissues.

Molecular evolutionary analyses further revealed that recent duplications are significantly enriched for signatures of positive selection. Moreover, snail stage-specific inparalogues exhibit elevated dN/dS ratios relative to other inparalogues, consistent with accelerated protein evolution. Together, these patterns suggest that recently duplicated genes may facilitate host-specific adaptation, potentially through rapid diversification and increased gene dosage during snail infection.

We propose that species-specific gene duplications contribute to adaptation to novel snail hosts and may underlie host compatibility differences among schistosome species. Ongoing functional assays using gene knockdowns aim to directly test the role of these candidates in snail infection success.