

Comparative gene expression analysis of moulting in Insect and Crustacean lineages

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ABSTRACT

Pancrustacea (crustaceans and hexapods) is the most species-rich clade in the Arthropoda phylum, comprising the majority of animal species on earth. Arthropods such as Insects and crustaceans produce a hard chitinous exoskeleton that they need to shed in a process called moulting. This developmental process is conserved throughout Arthropoda, and yet the molecular processes underlying moulting and how it evolved in different arthropod lineages remain unclear. To examine the gene expression dynamics of moulting across different pancrustacean lineages, we analysed publicly available RNA-seq datasets from pre-moult and post-moult stages of several Crustaceans (*Litopenaeus vannamei*, *Parhyale hawaiiensis*, *Eriocheir sinensis*) and Insects (*Drosophila melanogaster*, *Bactrocera dorsalis*, *Zeugodacus cucurbitae*). Enrichment analysis reveals that differentially expressed genes before and after moulting are related to moulting pathways and structural processes such as chitin-based cuticle development, ecdysteroid metabolic process and chitin binding. Co-expression analysis of moulting across various pancrustacean lineages revealed two major clusters of orthogroups which reflect the transition from pre-moult to post-moult stage. We recovered genes that are likely involved in late-genes pathway such as chitin biosynthesis, which suggests that moulting processes other than the hormonal biosynthetic pathway are also conserved. Examining the specific gene families involved in the late-genes pathway and their evolutionary relationships in different taxa will be important to further elucidate the evolution of moulting in Arthropods.