Expression analysis of genes potentially involved in sex determination in Diachasmimorpha longicaudata

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Introduction

Although there is information about ecological and behavioral traits of Diachasmimorpha longicaudata (Hymenoptera: Braconidae) little is known about its genetics, metabolic pathways and regulatory systems including the sex determination.

Objectives

• Analyze transcripts differentially expressed between D. longicaudata sexes.
• Characterize genes involved in sex determination cascade.

Results

• RNA seq analysis
Female vs male transcriptome analysis showed 98 transcripts differentially expressed between sexes (Figure 1).
• RT-qPCR validation (adults and immature stages)
Significant (p<0.05) differences in expression levels between sexes for dlfem (isotigs 07202, 06880) and dl fsx (isotig 08230) were found. Adults (Figure 2) and immature stages (Figure 3).

Conclusions

• The differential expression analysis between sexes (RNA seq) and blast searches allowed the identification candidate genes for sex determination: fem and dsx.
• RT-qPCR analysis in immature stages reveals a potential regulation from the regulator fem to the effector dsx in D. longicaudata.