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Fatty acid synthase 2 contributes to diapause preparation in a beetle by regulating lipid accumulation and stress tolerance genes expression

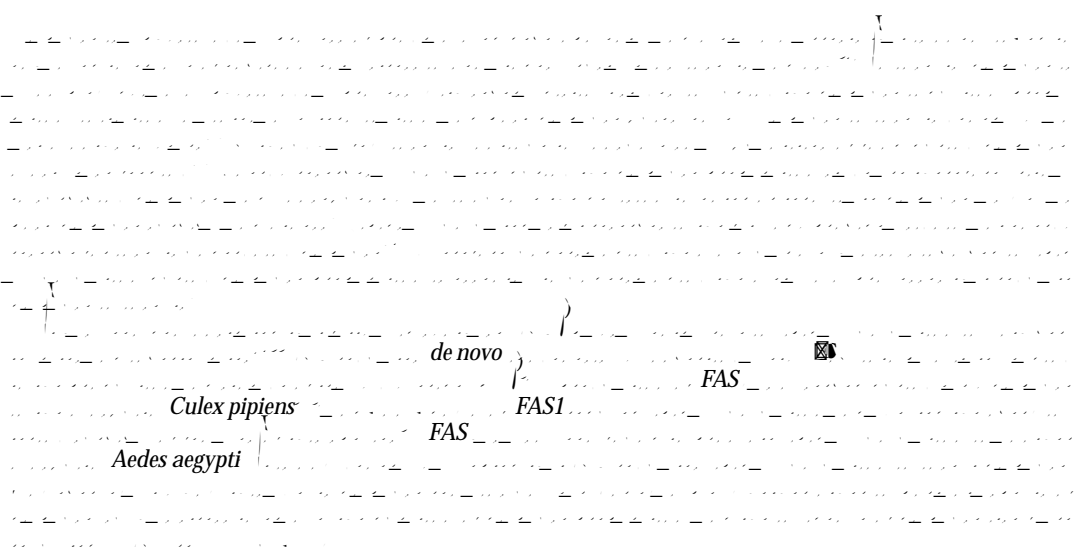
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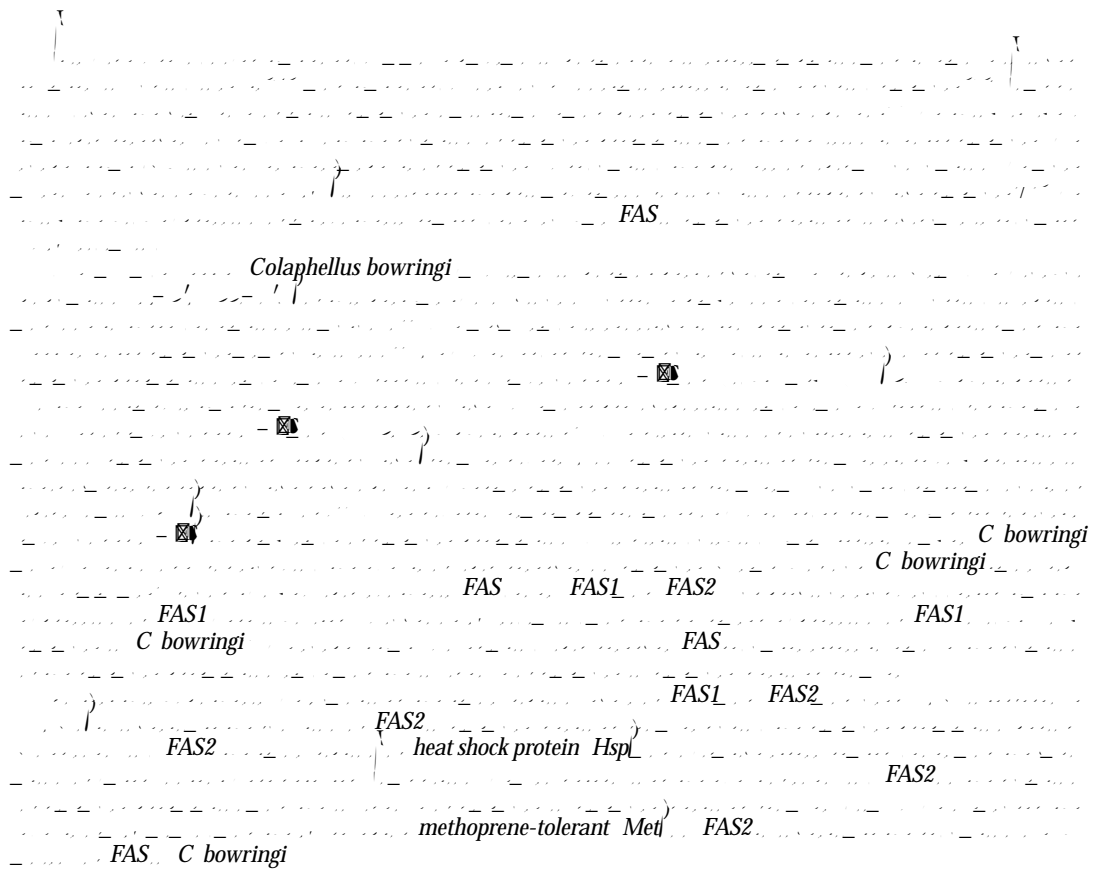
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Diapause, also known as dormancy, is a state of arrested development that allows insects to survive unfavorable environmental conditions. Diapause-destined insects store large amounts of fat when preparing for diapause. However, the extent to which these accumulated fat reserves influence diapause remains unclear. To address this question, we investigated the function of *fatty acid synthase* (*FAS*), which plays a central role in lipid synthesis, in stress tolerance, the duration of diapause preparation, and whether insects enter diapause or not. In diapause-destined adult female cabbage beetles, *Colaphellus bowringi*, *FAS2* was more highly expressed than *FAS1* at the peak stage of diapause preparation. *FAS2* knockdown suppressed lipid accumulation and subsequently affected stress tolerance genes expression and water content. However, silencing *FAS2* had no significant effects on the duration of diapause preparation or the incidence of diapause. *FAS2* transcription was suppressed by juvenile hormone (JH) and the JH receptor *methoprene-tolerant* (*Met*). These results suggest that the absence of JH-Met induces *FAS2* expression, thereby promoting lipid storage in diapause-destined female beetles. These results demonstrate that fat reserves regulate stress tolerance genes expression and water content, but have no significant effect on the duration of diapause preparation or the incidence of diapause.

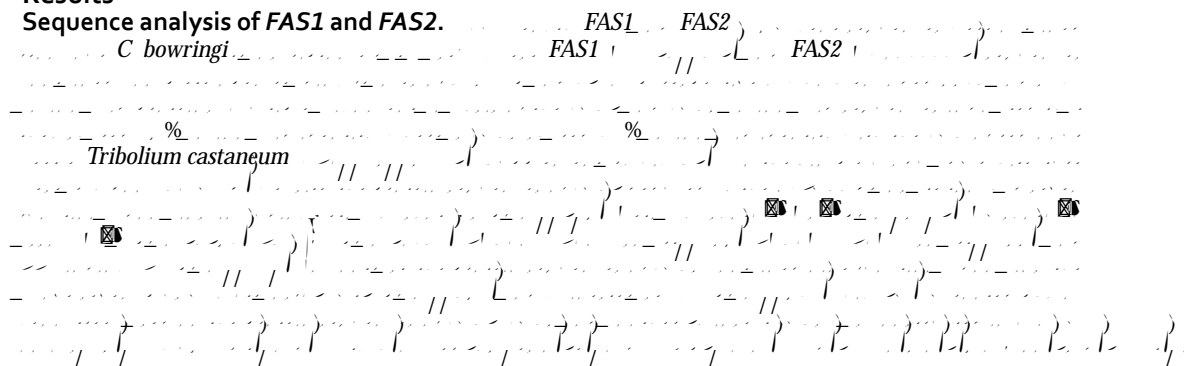


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Results

Sequence analysis of FAS1 and FAS2.



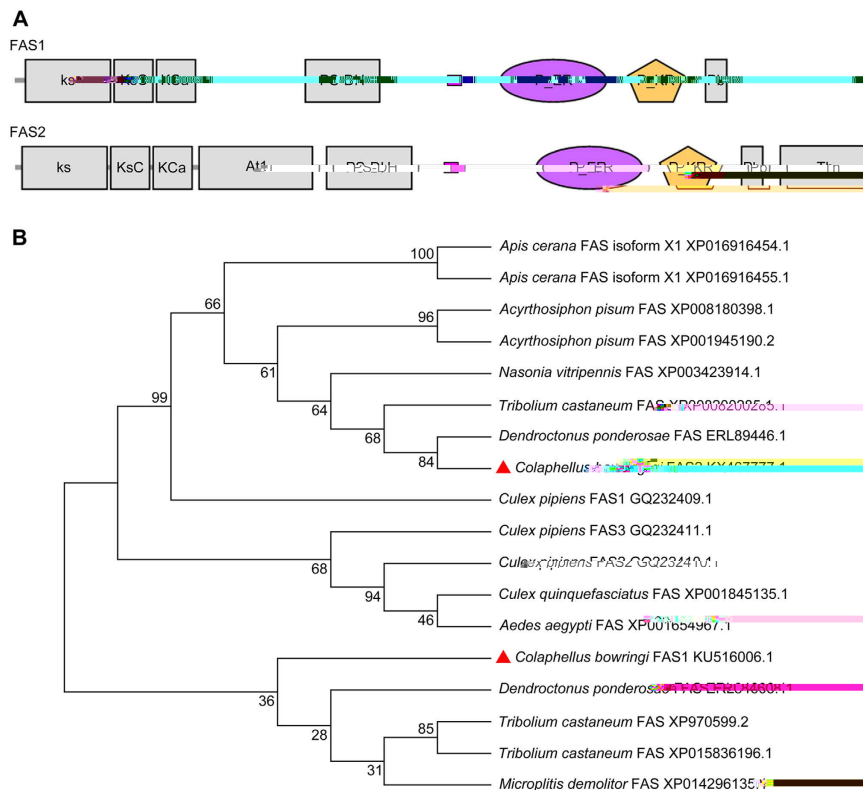
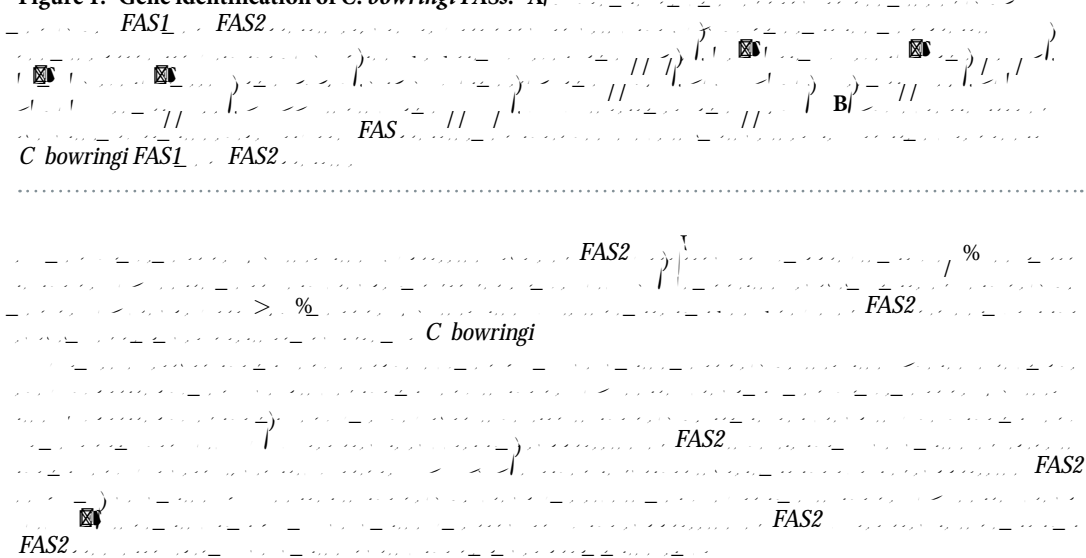
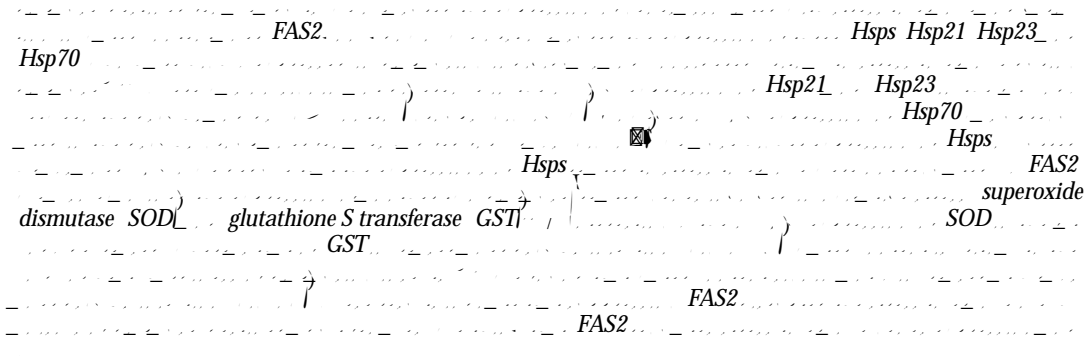


Figure 1. Gene identification of *C. bowringi* FASs. A)



Silencing FAS2 regulated stress tolerance genes expression and water content in diapause-destined adult females.



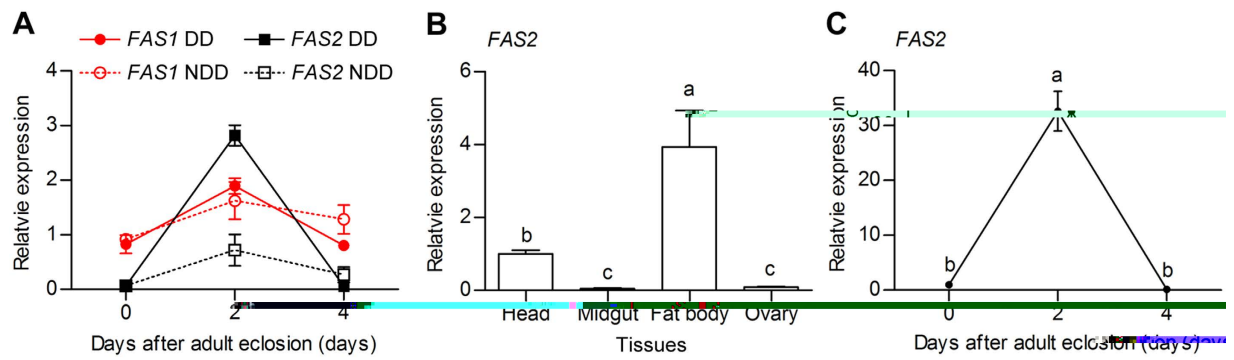


Figure 2. Expression of FAS genes in adult female *C. bowringi*. A) FAS1, FAS2, FAS1, FAS2, *C. bowringi*. B) FAS1, FAS2, *C. bowringi*. C) FAS1, FAS2, *C. bowringi*. $P < 0.05$.

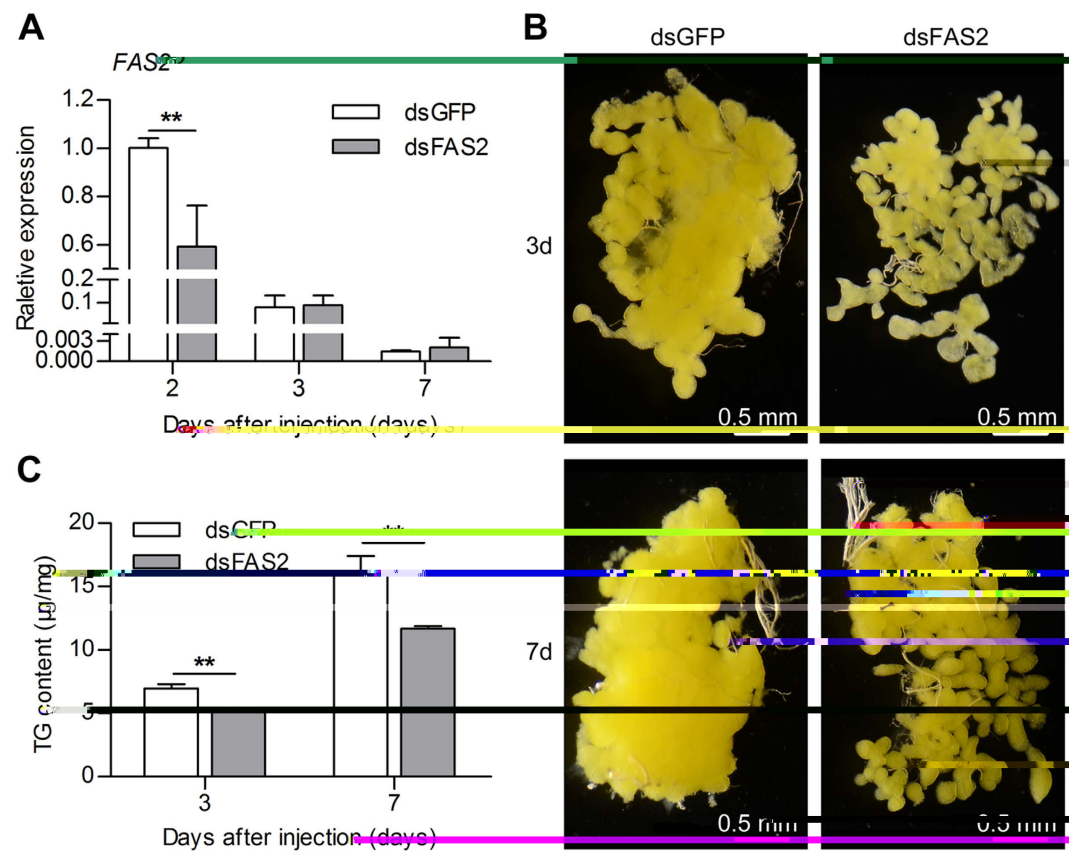


Figure 3. A) FAS2, FAS2, *C. bowringi*. B) FAS2, *C. bowringi*. C) FAS2, *C. bowringi*. $P < 0.05$, t .

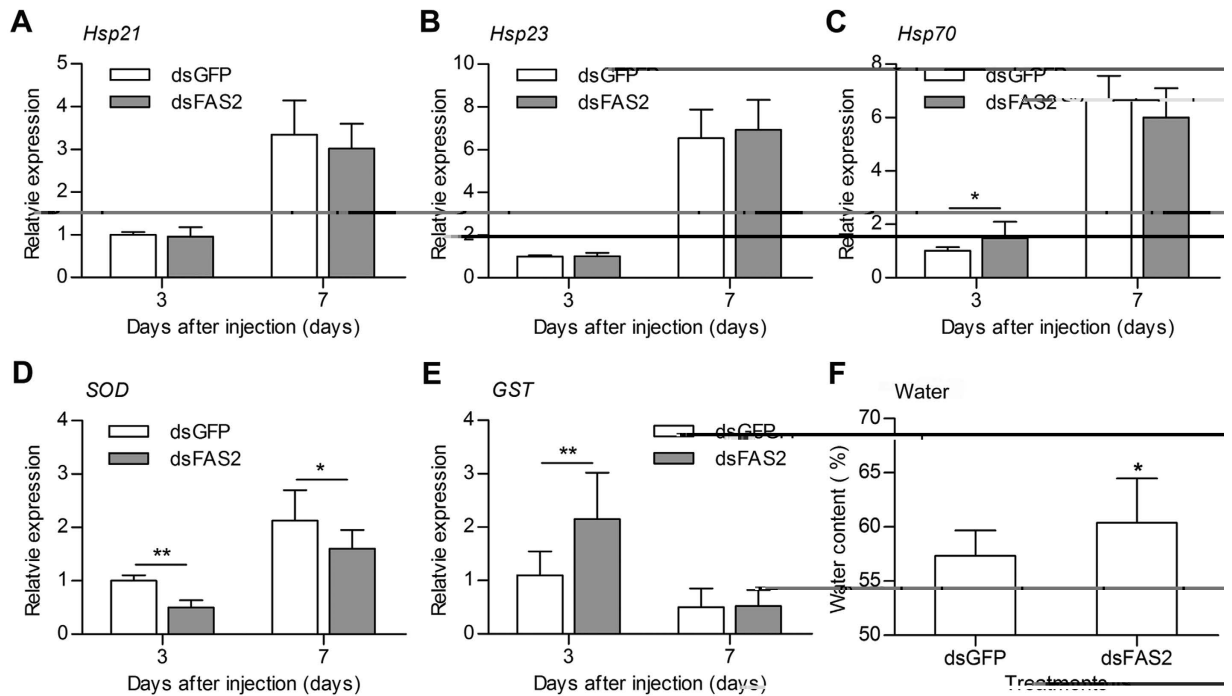


Figure 4. Relative expression of *Hsp21* (A), *Hsp23* (B), *Hsp70* (C), *SOD* (D), and *GST* (E) in *C. bowringi* at 3 and 7 days after injection. Water content (%) is shown in (F). Error bars represent standard deviation. Statistical significance is indicated by asterisks: * $P < 0.05$, ** $P < 0.01$.

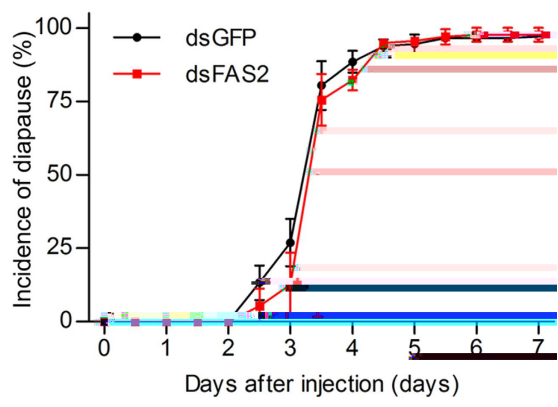
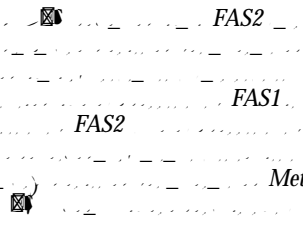


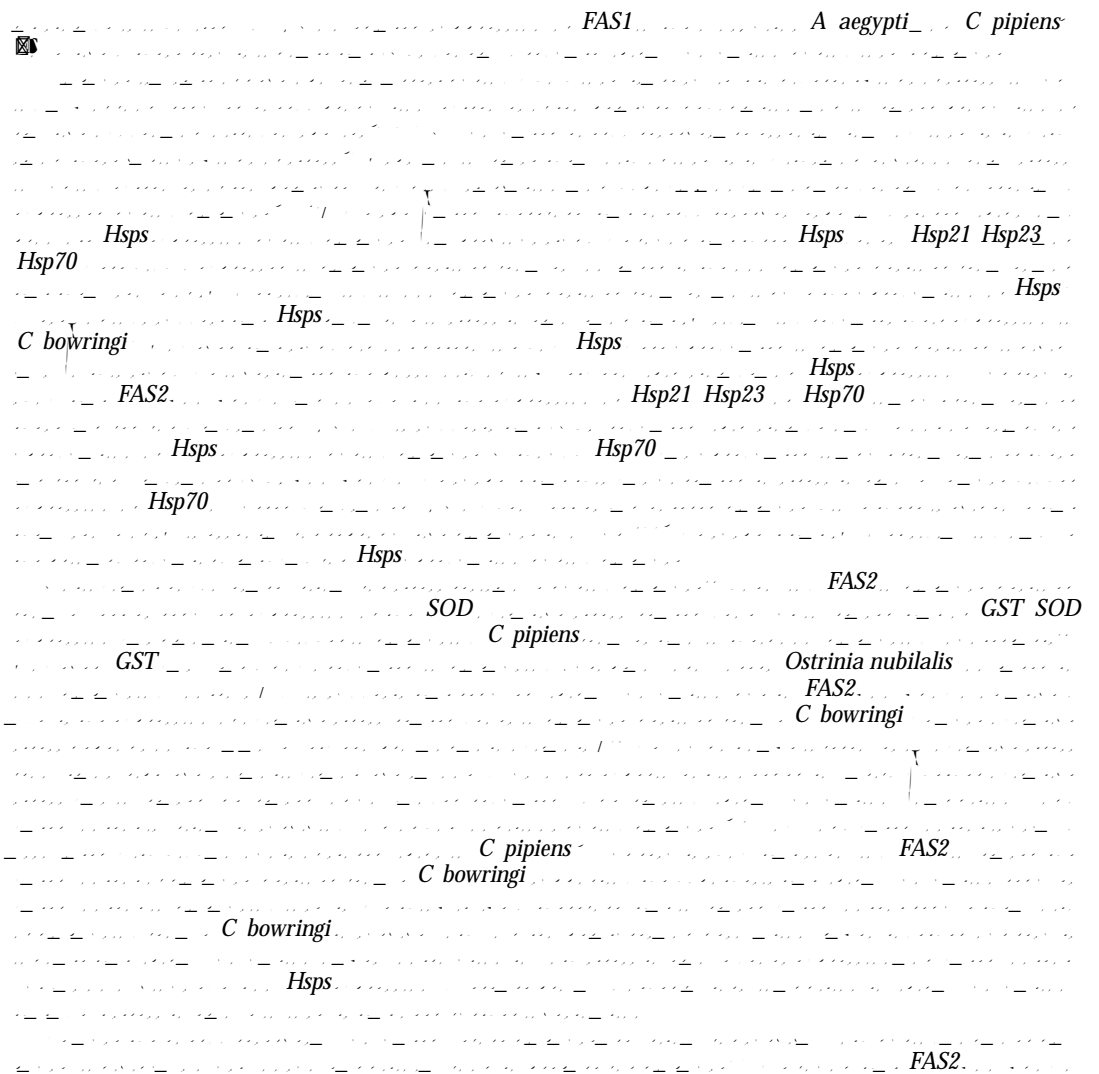
Figure 5. Effects of *FAS2* RNAi on the duration of diapause preparation and incidence of diapause in adult female *C. bowringi*.

Silencing *FAS2* does not significantly affect the duration of diapause preparation, or the incidence of diapause. *C. bowringi*.

Statistical analysis: $\chi^2 = \dots = p = \dots$ (not significant), $t = \dots = p = \dots$ (not significant).

FAS2 transcript expression is regulated by JH-Met signaling.  *FAS2*
C. bowringi *FAS1*
FAS *FAS2* *Met*
FASs *C. bowringi*

Discussion



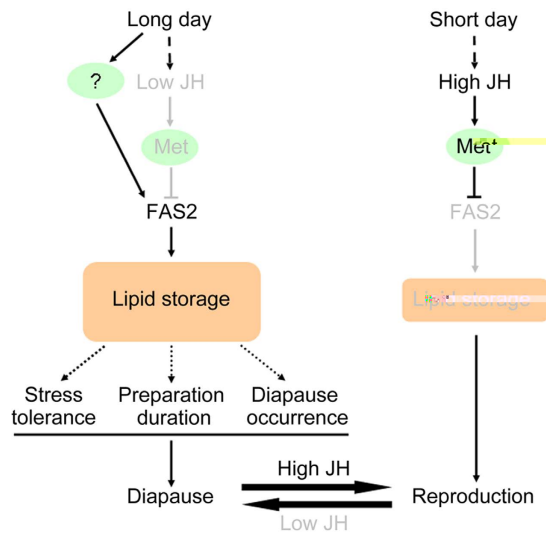


Figure 7. Model of how FAS2 promotes diapause preparation in *C. bowringi*.

Materials and Methods

Insect rearing.

Colaphellus bowringi

cDNA cloning and sequence analysis. *FAS1 FAS2 SOD GST*

C. bowringi

FAS1 Hsp21 Hsp23 Hsp70

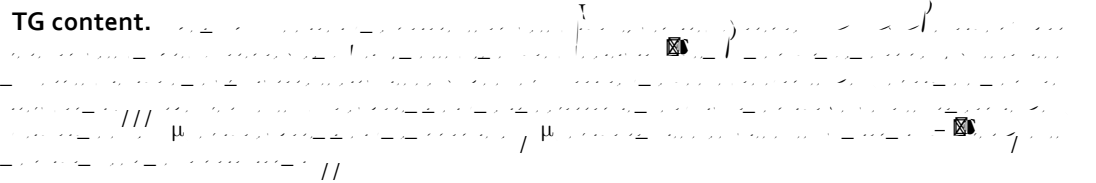
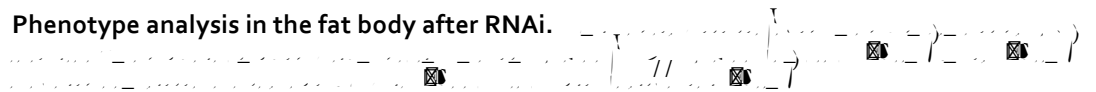
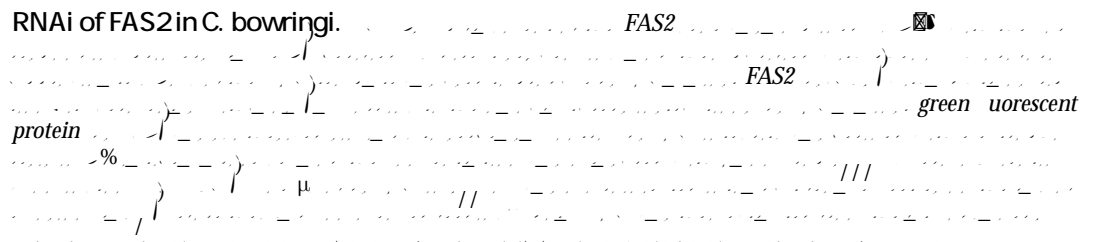
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C. bowringi

FAS2 SOD GST FAS1 Hsp21 Hsp23 Hsp70

Quantitative Real Time PCR (qRT-PCR) for mRNA quantification.

Ribosomal protein L19 RPL19



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Author Contributions

Additional Information

Supplementary information

Competing financial interests:

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