Regulation of the pheromone biosynthetic pathway in the Indian meal moth

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Abstract

The circadian regulation by Pheromone-Biosynthesis-Activating-Neuropeptide (PBAN) of the main diene pheromone component of *Plodia interpunctella*, (Z,E)-9,12-tetradecadienyl acetate (Z9,E12-14:Ac) has been demonstrated (Rafaeli and Gileadi, 1995). In *P. interpunctella*, nine different desaturase encoding transcripts have been isolated (Knipple et al., 2002) as potential desaturase genes but their functionality has not been demonstrated. Here we combine the use of labeled precursors with enzyme inhibitors to decipher the rate-limiting step that is regulated in the biosynthetic pathway (Choi et al., 2003). Incorporation of label from the 13C sodium acetate precursor is activated by PBAN, whereas no stimulatory action is observed in the incorporation of the precursors: 13C malonyl coenzyme A; hexadecanoic 16,16,16-2H3 or tetradecanoic 14,14,14-2H3 acids. The Acetyl Coenzyme A Carboxylase (ACCase) inhibitor, tralkoxydim, inhibits the PBAN-stimulation of incorporation of stable isotope. These results (Tsfadia et al., 2008) provide irrefutable support for the hypothesis that PBAN affects the synthesis of malonyl coenzyme A from acetate by the action of ACCase in the pheromone glands of this moth species. The study showed that *P. interpunctella* utilizes hexadecanoic acid, and to a lesser extent tetradecanoic acid, for the biosynthesis of Z9,E12-14:Ac with the involvement of mainly D11 desaturase, chain shortening, followed by D12 desaturase. Nine different female specific desaturase encoding transcripts are detected by specific primers using PCR but only two desaturase genes need to be functional to produce the diene pheromone component. Relative gene expression (Real Time Quantitative PCR, RT-qPCR) of these gene transcripts in the pheromone glands showed high expression levels in only two genes accession numbers: AF482923 and AF482924). The other seven genes are at least 105 fold lower or undetectable. Future characterization of full gene sequences of the two highly expressed genes and appropriate functional expression studies will define the functional genes.

References

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