

## FUNCTIONALLY SIGNIFICANT POLYMORPHISMS IN TUNICATE XENOBIOTIC RECEPTOR GENES

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The vertebrate xenobiotic receptor, pregnane-X- receptor (PXR), is a ligand activated nuclear receptor that regulates multiple detoxification genes. Vertebrate PXR orthologues display considerable inter-taxa variation in ligand binding domain (LBD) sequences suggesting adaptive evolution to enhance the binding of xenobiotics typically encountered by the corresponding organism. Tunicates occupy an intriguing evolutionary position, with adult tunicates being both marine filter-feeders and members of the phylum Chordata. Genomes of the solitary tunicate *Ciona intestinalis* and the colonial tunicate *Botryllus schlosseri* both encode at least two PXR orthologues, designated PXR/VDR $\alpha$  and  $\beta$ . Using PCR, PXR/VDR $\alpha$  and  $\beta$  transcripts were detected throughout the *C. intestinalis* branchial sac, gut, and ovaries. We examined three tunicate PXR/VDR LBD coding sequences for intra-species allelic variation. PXR/VDR LBD coding sequences were amplified from *C. intestinalis* (*Ci*, dissected gut, n = 30) and *Botryllus schlosseri* (*Bs*, complete colonies, n = 30) and the PCR products were sequenced using Illumina MiSeq. Single nucleotide polymorphisms (SNPs) were common in all three amplicons with a mean of 2.6 SNPs / 100 bp. The majority of the SNPs found were synonymous (*Ci*PXR/VDR $\alpha$  86%; *Ci*PXR/VDR $\beta$  70 % and *Bs*PXR/VDR $\alpha$  87%) while sliding window calculations of dN/dS ratios found no evidence of positive selection. Single base deletion (i.e. frameshift) containing allelic variants were found in both the *Ci*PXR/VDR $\alpha$  and  $\beta$  genes - corresponding to predicted proteins having a DNA-binding domain but lacking a LBD. We suggest that the persistence of such frameshift mutations may reflect constitutive detoxification gene expression conferring a selective advantage in some contexts.

## COTESIA FLAVIPES IS ATTRACTED TO A SESQUITERPENE EMITTED BY SUGARCANE IN RESPONSE TO SUGARCANE BORER INFESTATION

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The sugarcane borer, *Diatraea saccharalis*, is a key pest of sugarcane in the Americas. Plants often release a blend of volatile organic compounds (VOCs) in response to damage by herbivorous insects that may serve as location cues to their natural enemies. In trying to elucidate the defense mechanisms of sugarcane response to herbivory by *D. saccharalis*, we have performed herbivore damage assays either by infesting 40-45-day old sugarcane plants with sugarcane borer larvae and treating mechanically wounded plants with oral secretion of *D. saccharalis*. The VOCs were collected and bioassays were performed in a four-arm olfactometer by using adult females of *Cotesia flavipes*, a wasp successfully used in biological control programs in sugarcane fields. Gas chromatography/mass spectrometry analysis revealed a main compound differentially emitted by infested-plants, which was identified as (*E*)- $\beta$ -caryophyllene both by comparison with a mass spectrum standard library and by co-injection with an authentic (*E*)- $\beta$ -caryophyllene standard. In the olfactometer bioassays, the wasps were significantly more attracted to both VOCs from infested plants and non-infested plants containing the (*E*)- $\beta$ -caryophyllene standard in comparison to VOCs from non-infested plants. Interestingly, this sesquiterpene has been previously demonstrated to be emitted by maize leaves and roots in response to attack by herbivores and to act as a signal to attract natural enemies of maize herbivores. These results will pave the way for increasing the efficiency of the *C. flavipes* as a biological control, developing new biological control strategies and might be used as a foundation for the development of sugarcane borer resistant cultivars.