METHODS

Discovery of novel RNA viruses from the fall and beet armyworms

Gene of interest (GOI) · Hairpin construct · VIGS Vector · Infectious clone of FAW virus

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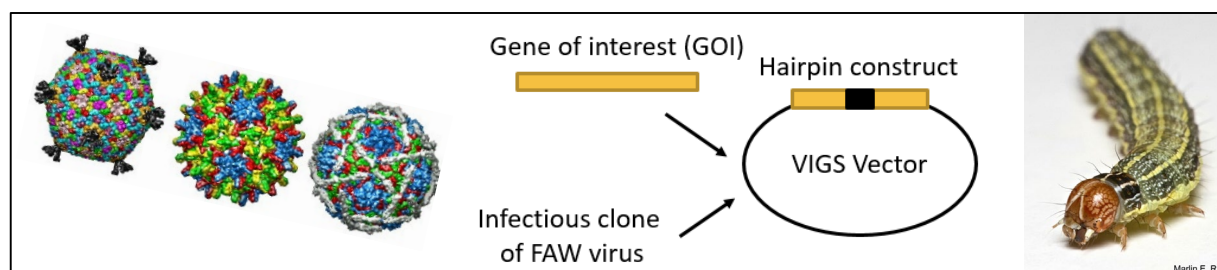
DESCRIPTION

The fall armyworm (FAW), *Spodoptera frugiperda*, and the beet armyworm (BAW), *Spodoptera exigua* are pests of significant economic impact on agriculture with an expanding global presence. These species are polyphagous, and feed on multiple crops in the Americas, in Africa and elsewhere. Resistance has been noted in these species against both classical chemical insecticides and Bt toxins. Increased understanding of the biology of FAW and BAW is essential for development of novel management strategies.

The goal of this project was to identify RNA viruses in laboratory colonies and in field caught samples of FAW and BAW. The identification of small RNA viruses that infect *Spodoptera* spp. may allow for the development of virus-induced gene silencing (VIGS) vectors. These vectors could be used for functional analysis of *Spodoptera* genes toward increased understanding of the biology of these pestiferous species.

HOW THIS IS DIFFERENT THAN RELATED RESEARCH

Prior to the start of this project, relatively little was known about RNA viruses in these insects: one rhabdovirus had been isolated from *S. frugiperda* cell lines, and two iflaviruses had been identified from *S. exigua*. Identification of additional RNA viruses may provide leads for development of VIGS vectors for increased understanding of FAW and BAW biology and gene function.

MEMBER BENEFITS

- Knowledge of virus diversity and distribution within field and laboratory populations of FAW and BAW.

- Identification of a novel candidate virus for development of a VIGS vector for functional analysis of FAW and BAW genes.

- Increased understanding of the biology of FAW and BAW based on use of the resulting VIGS vector.

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