Leafhopper Virus in Texas Glassy-Winged Sharpshooters*

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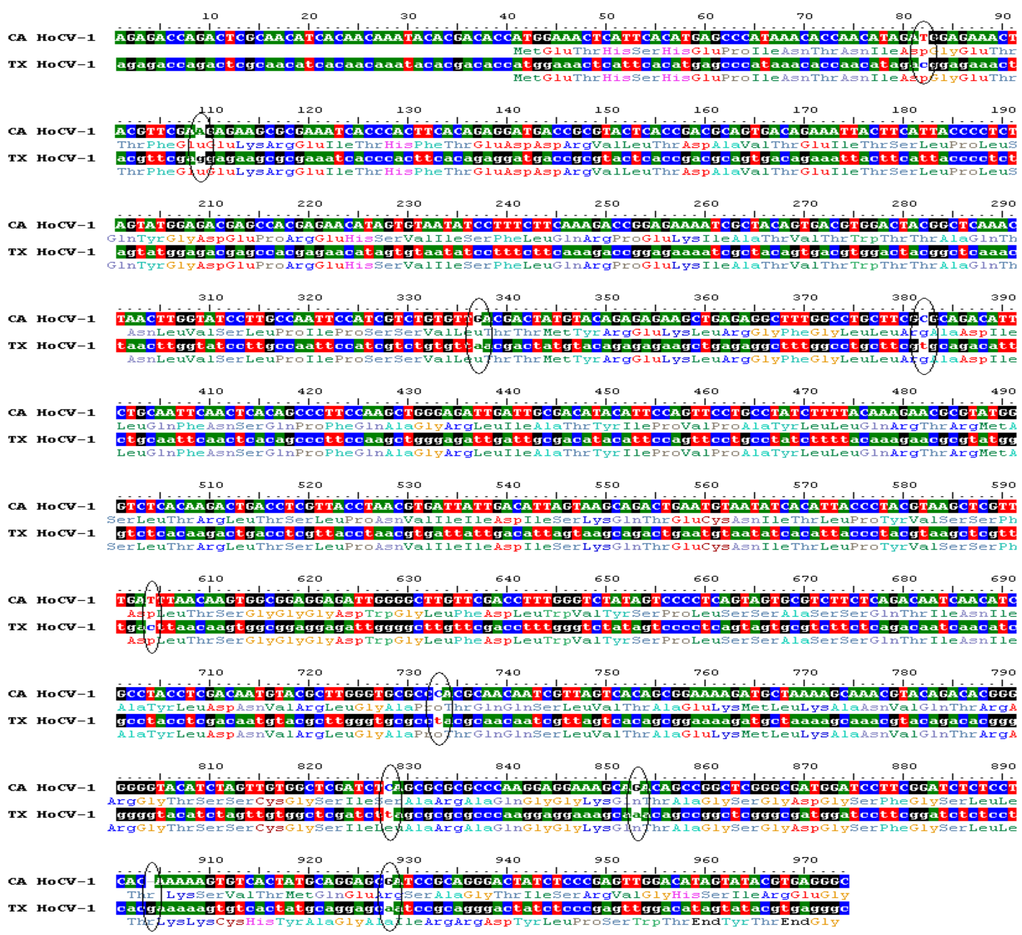
ABSTRACT- Abstract

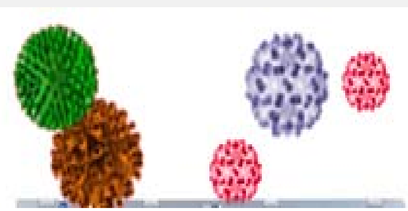
The glassy-winged sharpshooter *Homalodisca vitripennis* is an invasive pest and important vector of *Xylella fastidiosa*, a xylem-limiting bacteria that causes Pierce's Disease in grapes and other woody fruit and tree crops. The primary method of managing the spread of *Xylella* is controlling its insect vector populations. Methods such as chemical control are not target specific and lead to problems such as residue contamination, injury to non-target organisms, and development of insecticide resistance.

Identifying microbial biological agents that can reduce *H. vitripennis* is the goal of one biological control strategy. In this study, we have identified *Homalodisca coagulata virus-1,* in populations of *H. vitripennis* collected in Texas. The virus is a novel virus that harbors pathogenic potential with regard to GWSS. DNA sequencing of the viral capsid protein gene was used to determine genetic variability between Florida *HoCV-1* and Texas HoCV-TX strains. The genetic variability may be related to increased virulence of the Texas strain to leafhoppers.

Introduction

The glassy-winged sharpshooter, *Homalodisca vitripennis* (Hemiptera: Cicadellidae), is the major vector of *Xylella fastidiosa* Wells in the Southern USA (Adlerz 1980; Blua et al., 1999). The plant pathogenic bacterium, *X. fastidiosa*, has caused economic losses to several agricultural industries in North America and is associated with many plant diseases such as Pierce's disease, and oleander leaf scorch. Pierce's disease of grapevine has become a well recognized *Xylella*-related disease; the vector profile is well known and the epidemiology of the disease is well documented (Hopkins et al., 2002). The introduction of *H. vitripennis* into new areas is directly related to increased occurrence of Pierce's disease in vineyards (Perring et al., 2001). Therefore, the management of Pierce's disease depends heavily on the ability to control its vectors, especially *H. vitripennis*.





Results

- *HoCV-1* has been detected in GWSS populations collected in Texas.
- Sequence comparison of the Texas virus strain against the sequenced California strain (Hunnicutt et al., 2006) shows some variation. The percent similarity between the strains is **98.8%.** Supporting within species variation.
- Base pair 828, Cytosine in the California strain, is a Thymine in the consensus strain (*Fig. 1*). This changes the amino acid translation from Serine (polar side chain) into Leucine (nonpolar side chain).
- Due to a Guanine insertion in the consensus strain at base pair 904 (possibly a deletion in the California strain), variation downstream in the amino acid chain was observed (*Fig. 1*).

Discussion

- The presence of variation between the Texas *HoCV-1* sequence and the California *HoCV-1* sequence showed amino acid changes, which may be the beginning of genetic selection in leafhoppers under Texas environmental conditions.
- The Guanine insertion at base pair 904 caused variation in all downstream amino acid translation. This could lead to changes in protein folding and ultimately changes in protein function. Altered protein functions may cause an increase in virulence in the Texas *HoCV-1* strain, making it a more ideal viral bio-control and pest management strategy.

References

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