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Southern Insect Management Research Unit

The Southern Insect Management Research Unit (SIMRU), operating under the Agricultural Research Service of the Department of Agriculture, conducts research dealing with the biology of plant pests in the southern United States in an attempt to find new ways to control the populations of said pests. One particular SIMRU researcher, Dr. O.P. Perera, is an entomologist studying the molecular biology behind *Lygus lineolaris*, also known as the tarnished plant bug and one of the most serious plant pests in North America. As an employee under the Student Temporary Employee Program (STEP), I had the opportunity to witness the work of Dr. Perera and his supervisees first-hand. I learned various protocols and techniques, such as nucleic acid extraction, polymerase chain reaction, and gel electrophoresis, which are currently being employed to further agricultural research.

Using collected *L. lineolaris* insects, it is possible to extract RNA or DNA from either a specific part of the insect or the insect in its entirety. These nucleic acid samples can be utilized in various ways. For example, in his 2011 article published in the Journal of Invertebrate Biology, Dr. Perera explains how he confirms the presence of the RNA virus LyLV-1 in *L. lineolaris* using RNA samples extracted from tarnished plant bugs. He amplified these samples using polymerase chain reaction (PCR), a repetitive process of heating and cooling that

multiplies the amount of genetic material in each sample using primers and enzymes. The primers used are designed to target and selectively amplify a specific area along the RNA strand. Since each primer is designed to target a specific region, certain primers were used to confirm the existence of the LyLV-1 virus, while others were used to verify the occurrence of viral replication. Afterwards, to test whether or not the area of interest is amplified, agarose gel electrophoresis is performed on the samples. The amounts of bases composing the amplified region can be estimated by observing how far the sample travels through the gel. Amplified

samples are then sent to the Agricultural Research Service's Genetics and Bioinformatics Research Unit for sequencing.

Bioinformatics technology can list the exact arrangement of bases in an RNA sample. Then, modeling tools examine this base sequence to decipher what proteins or enzymes can be translated from the RNA strand's coding region. Using these tools to attain the full genome sequence, it is possible to know the complete biochemical composition of the LyLV-1 virus. The genetic coding is then compared with other single-strand RNA viruses to note any similarities, which ultimately play a role in how the virus is taxonomically classified.

The discovery of this insect-infecting virus paves the way for new research. Although the LyLV-1 virus usually does not affect its host, it serves as a potential biological control agent. Past experiments have shown that a pathogen's ability to overcome the immune system of a host may be boosted by introducing another agent. Combining the LyLV-1 virus with another naturally occurring agent, such as an entomopathogenic fungus or bacterial strain, could form an alternative method of reducing the population of *L. lineolaris* in crucial agricultural areas.

References Perera, O.P., et al. The complete

genome sequence of a single-stranded RNA virus from the

tarnished plant bug, *Lygus lineolaris* (Palisot de Beauvois). J. Invertebr. Pathol. (2011),

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