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### Papaya ring spot virus biotype - P: Phylogenetics and beyond

M.A.R.T.Gunaratna<sup>1</sup> and R.S.Dassanayake<sup>2\*</sup>

<sup>1</sup>Department of Plant Sciences, Faculty of Science, University of Colombo, Colombo 03

<sup>2</sup>Department of Chemistry, Faculty of Science, University of Colombo, Colombo 03

The *Potyvirus*, PRSV biotype-P (PRSV-P) is the single most detrimental virus for papaya worldwide. It differs from its phylogenetic predecessor PRSV biotype-W by its ability to infect papaya. The majority of the pathogen-derived resistance strategies employed against PRSV-P has displayed very limited and localized success. Hence, more potent mechanisms of gene silencing appear to be promising strategies against PRSV-P. High success rates, both regionally and universally, in implementation of novel strategies against PRSV-P, could only be achieved by revealing more information on molecular evolution of PRSV-P. Eventhough phylogenetic reconstructions deliver important insights into virus irradiation, information on the molecular evolution of the genomes is masked. Hence, the objective of the study is to unravel molecular evolution or the prevailing selection pressure on the PRSV-P gene which codes for the viral coat protein.

PAML ver. 4.2 was utilized in analyzing selection pressure on viral coat protein genes from different geographical locations worldwide. The Use of different codon-substitution models and combinations of models with parameter adjustments, verified by previous simulation studies for significant results, illustrated that positively evolving sites in Asian countries are minimal while South American countries such as Brazil, Venezuela and Jamaica demonstrated otherwise. The phylogenetic reconstruction analysis performed using PRSV coat protein gene sequences reconfirmed the incidence of major clusters from the Indian continent, South-East Asia, and America together with Australia. Furthermore, the mixing of the Indian isolate DEL in the American cluster was discovered while the observation of isolate UAS-BLR, as an outgroup branch to the main PRSV cluster, provided an indication of a burgeoning distinct species.

The identification of positive selection signal indicates that a particular entity is not stable but constantly thriving for better adaptation to ensure survival amidst local conditions. The diminished signal of positive selection in highly diverged Asian sequences suggests that the sequences have better adapted to local conditions and stabilized, however the intense signal of positive selection observed among less diverged sequences from American continents demonstrate otherwise. Hence, the results could verify the Asian origin of PRSV and recent occurrence of PRSV in American continents, indicating that the time from the incidence of the virus may be highly correlated with the prevalent stability observed.

**Keywords:** PRSV-P, phylogenetics, molecular evolution, divergence, positive selection