ABSTRACT

An attempt has been made to characterize different PRSV isolates which infects papaya plants were collected from different parts of Tamil Nadu. The isolates were of PRSV-P type strain and the Coat Protein gene (CP) varied in size from 840- 860 bp which encodes 280 - 284 amino acids. Sequence alignment results revealed that the seven sequences obtained from different regions shared a homology of about 90% -95% with each other and homology of about 96% with the already reported Indian isolate and 88-90% with the other country isolates collected from NCBI. KE repeats were observed in the N terminus of the CP coding region from the different isolates found out. Phylogenetic analysis revealed that the isolates identified here placed on the same group and reference isolates were grouped in a different progeny. Our study further helped us to identify conserved regions among the seven isolates and we also constructed an RNAi silencing vector targeting Coat protein gene to challenge the Papaya Ring Spot Virus (PRSV) for our future study