Global Population Structure and Molecular Evolutionary Pattern of Iris yellow spot virus

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Abstract

Iris yellow spot virus (IYSV) is an important virus of Allium species. Using the global repository of IYSV nucleoprotein (N) gene sequences available in GenBank (a total of 142), temporal dynamics and geographic diversity of the IYSV isolates were investigated to gain better insights into the evolutionary forces influencing genetic population structure of IYSV. Based on in silico Restriction Fragment Length Polymorphism (RFLP), N gene sequences showed a 79:55 distribution of known IYSV isolates into two major genotypes, IYSV Netherlands (IYSVNL; 55.63%) and IYSV Brazil (IYSVBR; 38.73%). A little over five percent of the isolates fell in neither group [IYSV other (IYSVOther; 5.63%)]. Phylogenetic tree largely corresponded to the RFLP pattern, and the IYSV genotypes clustered into IYSVNL and IYSVBR genotypes. Based on genetic diversity studies, IYSVNL and IYSVBR genotypes are under purifying selection and population expansion, whereas IYSVOther showed decreasing population size and hence appear to be under balancing selection. Nucleotide diversity comparisons indicated IYSVNL to be least differentiated from IYSVBR, compared to IYSVOther. Two recombinants were detected among all the N gene sequences that were analyzed. The marginal likelihood mean substitution rate was 5.08x10⁻⁵ subs/site/year and 95% highest posterior density (HPD) substitution rate between 5.11x10⁻⁵ – 5.06x10⁻⁵. The substitution rate identified for IYSV N gene is similar to other plant RNA viruses.

BACKGROUND

Tospoviruses are negative sense/ambisense RNA viruses vectored by thrips.

Iris yellow spot orthotospovirus (IYSV) causes economic losses in Allium spp

The virus was discovered in 80’s in Southern Idaho, beginning in 2002 the virus spread to almost all onion producing regions in the US.

The objective of the study was to understand the genetic diversity of the virus based on its nucleocapsid (N) gene.

METHODOLOGY

The complete N gene sequences of 142 IYSV isolates available in GenBank were used to determine the evolutionary pattern.

In silico restriction fragment length polymorphism (RFLP) analysis was performed to group the virus isolates.

Pervasive selection pressure analysis was performed using Datamonkey software (1) to understand the diversity based on occurrence of mutations between the genotypes.

Recombination events were identified using the Recombination Detection Program (2) and the Recombination Analysis Tool to understand whether recombination governs the diversity in the genotypes.

Bayesian phylogenetic analysis was performed using BEAST v2.4.6 to estimate the evolutionary rate.

RESULTS

Based on RFLP, IYSV N gene sequences are divided into IYSVNL, IYSVBR and IYSVOther.

Among IYSVNL and IYSVBR, genotypes, BR genotype is more diverse.

Rate of nucleotide substitution is similar to other plant RNA viruses.

There is a relative correlation between the genotype and its geographic incidence.

REFERENCES


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