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Genetic variability and evolution of rice stripe virus

水稻条纹病毒的遗传变异和进化

Key words: Rice stripe virus, Genetic variability, Genetic evolution

关键词: 水稻条纹病毒; 遗传变异; 遗传进化

- RNA viruses have high mutation rates, which lead to changes of virus host range, disease symptoms, and emergence of new viruses in nature. Analyzing these variations will help us to facilitate the development of effective control strategies for plant viral diseases.
- In this study, the sequences of 6 RSV were determined. The genetic diversity and population structure of the 6 RSV isolates and other isolates with full sequences deposited in GenBank were analyzed.
- All RSV isolates, except isolate CX, could be divided into two subtypes, and isolate CX may be the result of recombination of isolates from two subtypes. Two potential recombination events were detected in RNA4 of isolate CX.
- RSV isolates in Yunnan Province were genetically differentiated from other parts of China, Japan, and Korea and showed infrequent gene flow. All the genes of RSV were under strong negative selection.

Determined the sequences
of RSV isolates

Construct genotype profile
of RSV isolates

Analyze genetic differentiation,
selection pressures and
recombination of RSV isolates

Understand the population structures
and underlying evolutionary mechanisms
of RNA viruses

facilitate the development of effective
control strategies for plant viral diseases

