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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

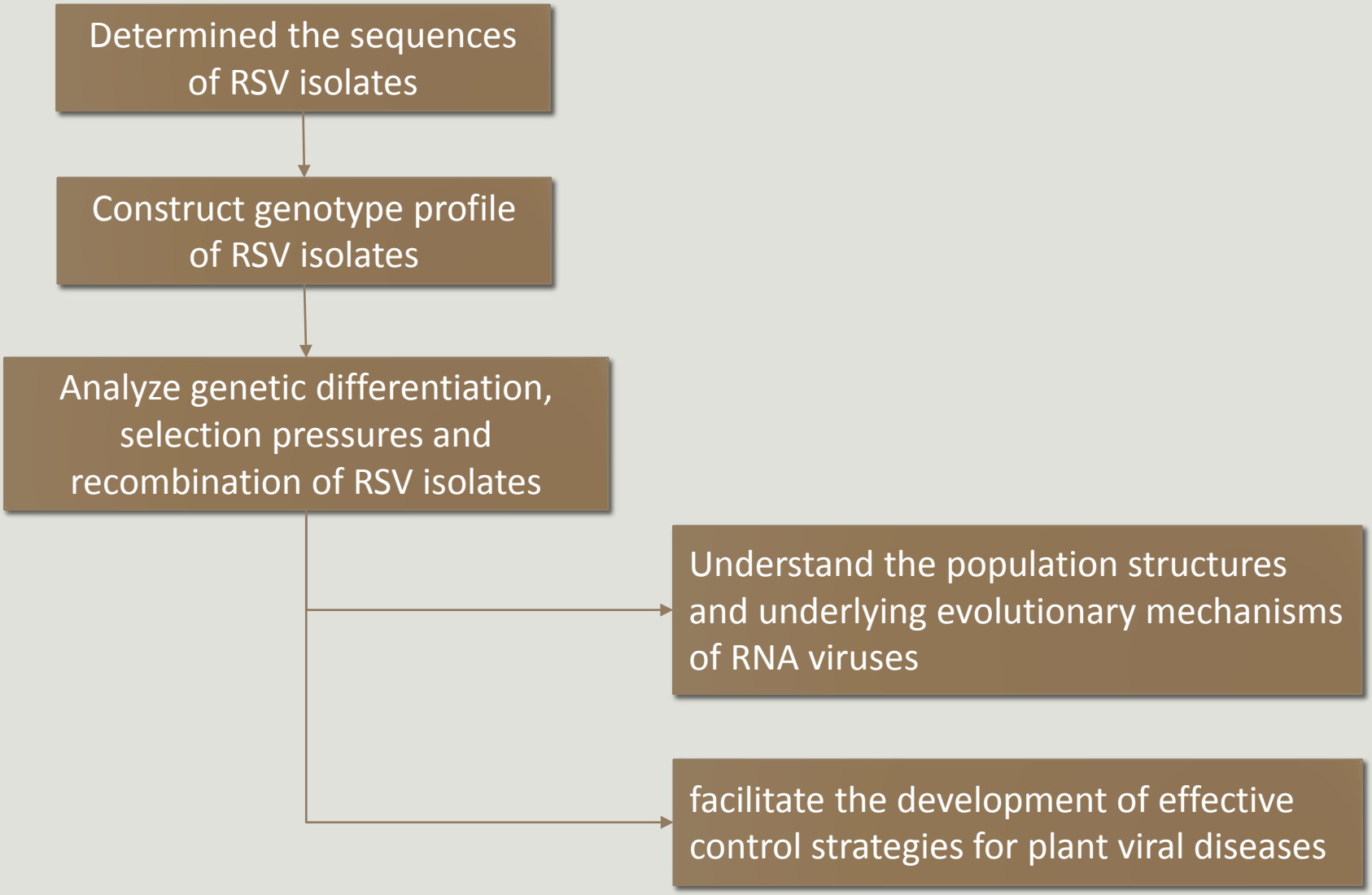
关键词：水稻条纹病毒；遗传变异；遗传进化

- 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