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Molecular variability and evolution of a natural population of tomato yellow leaf curl virus in Shanghai, China

番茄黄化曲叶病毒自然种群的分子变异和进化研究

Key words: Molecular variability, Tomato yellow leaf curl virus (TYLCV), Geminivirus, Evolution

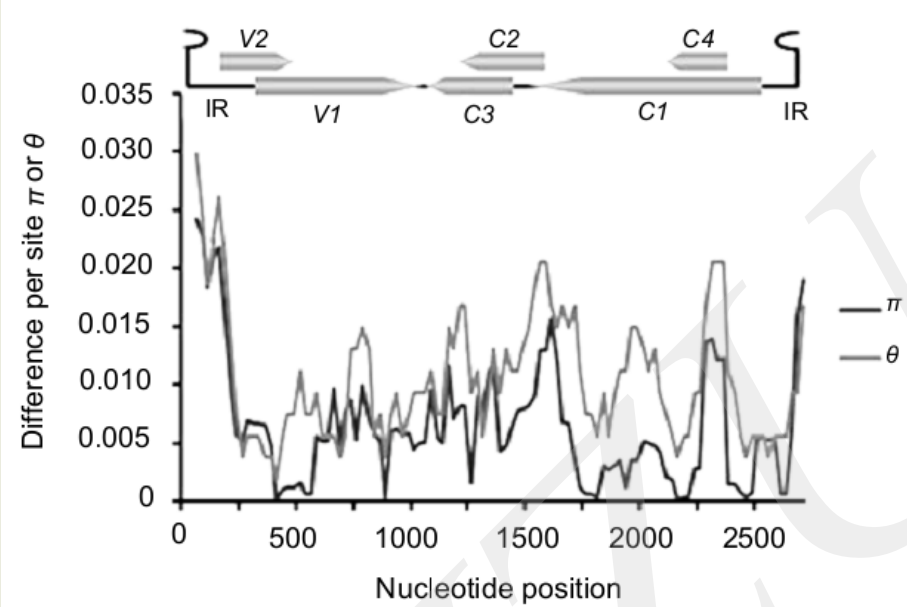
关键词：分子变异；番茄黄化曲叶病毒（TYLCV）；双生病毒；进化

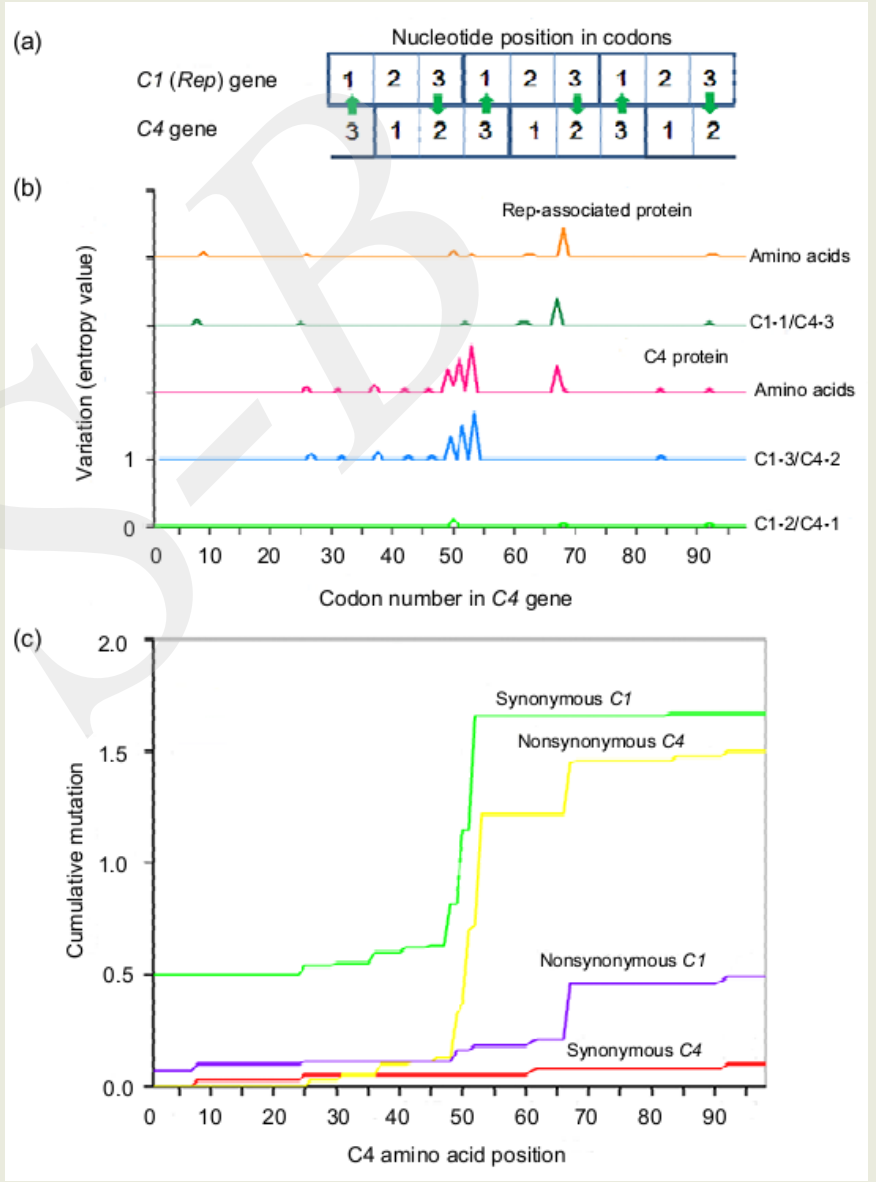
- Tomato yellow leaf curl virus (TYLCV), belonging to the genus *Begomovirus* of the family *Geminiviridae*, is emerging as the most destructive pathogen of tomato plants.

- TYLCV was first reported in Shanghai, China in 2006, and it has since spread rapidly to 13 provinces or autonomous regions of China, which provided a great opportunity to understand the evolution of a plant DNA virus soon after its first introduction to a new area.

- The molecular variability and evolution of TYLCV were monitored in Shanghai from its first upsurge in 2006 until 2010. Full-length genomic sequences of 26 isolates were obtained by rolling circle amplification.

- Sequence analysis showed that the intergenic region was the most variable, and that a mechanism of independent evolution of overlapping regions could apply to the natural population of TYLCV in Shanghai, China.


V2
C2
C4
IR
V1
C3
C1
IR
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0
Difference per site π or θ
0
500
1000
1500
2000
2500
Nucleotide position
π
θ


(a)
Nucleotide position in codons
C1 (Rep) gene
C4 gene
1 2 3 1 2 3 1 2 3
3 1 2 3 1 2 3 1 2
(b)
Rep-associated protein
Amino acids
C1-1/C4-3
C4 protein
Amino acids
C1-3/C4-2
C1-2/C4-1
Variation (entropy value)
1
0
0 10 20 30 40 50 60 70 80 90
Codon number in C4 gene
(c)
2.0
1.5
1.0
0.5
0.0
Cumulative mutation
Synonymous C1
Nonsynonymous C4
Nonsynonymous C1
Synonymous C4
0 10 20 30 40 50 60 70 80 90
C4 amino acid position