

Functional evolution of *Pseudofabraea citricarpa* as an adaptation to climate change

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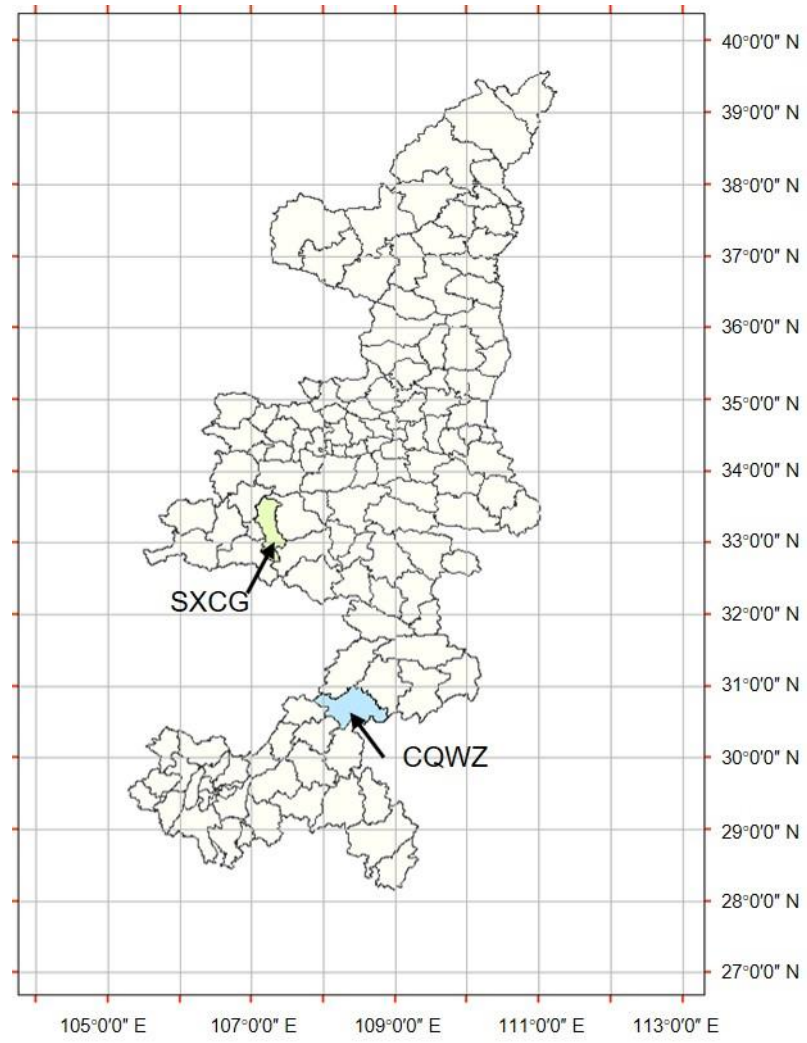
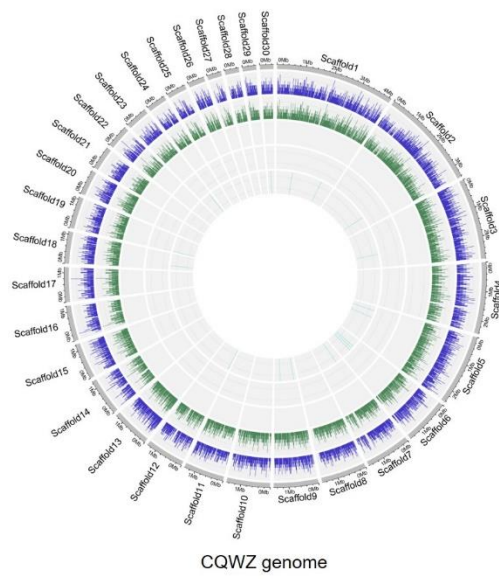
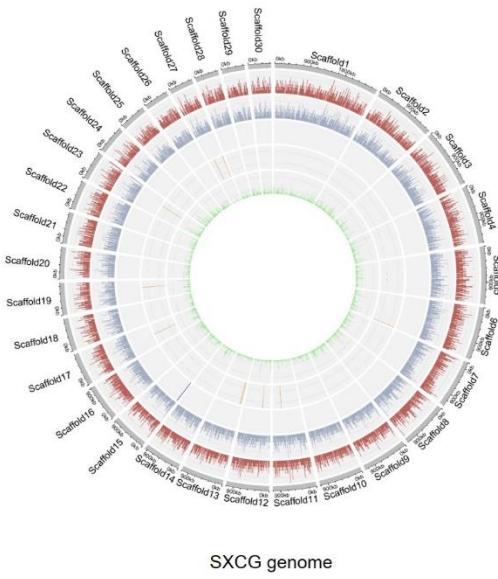


Figure S1. Geographical location of *Pseudofabreaa citricarpa* sampling.



CQWZ genome



SXCG genome

Figure S2. Genome assembly mapping of *Pseudofabrea citricarpa*.

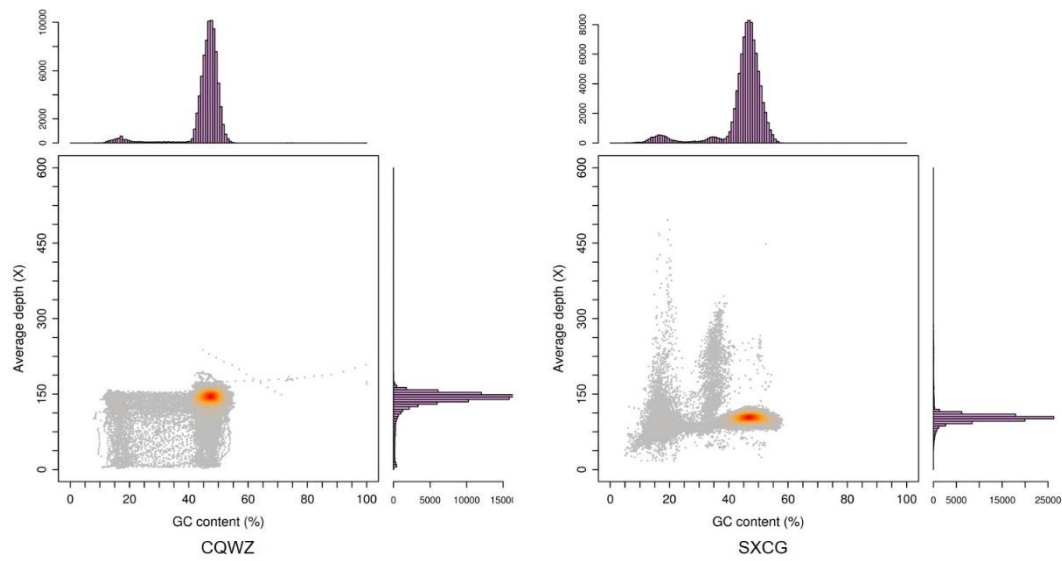


Figure S3. GC depth distribution analysis of *Pseudofabreaa citricarpa*.

The original reads from the PE library were aligned to the assembled sequence using SOAP software to obtain base coverage depth. A window of a chosen size was selected to move along the sequence base by base (or non-repetitive base by base), and the average depth and GC content were calculated for each window. This information was used to generate a GC-depth plot.

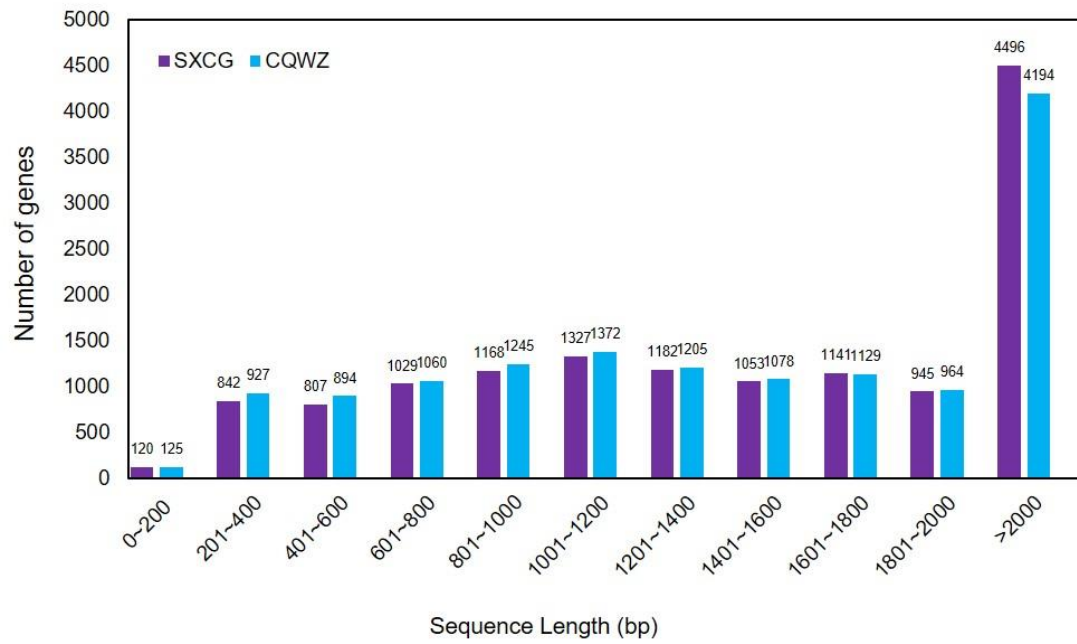


Figure S4. Length of genes encoded in the genome of *Pseudofabreaa citricarpa*.

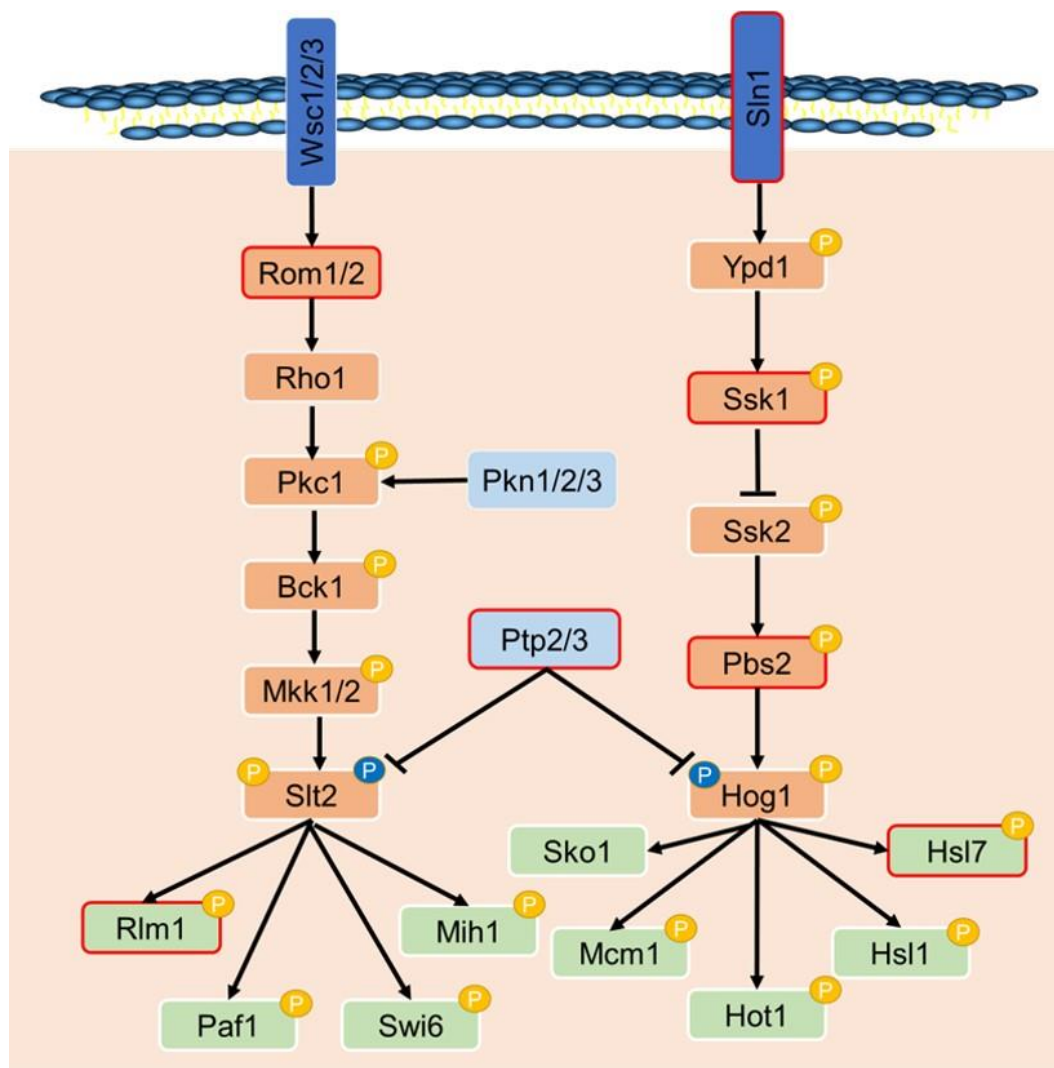


Figure S5. Differences between the two strains in the MAPK pathway. Red boxes indicate amino acid sequence differences.

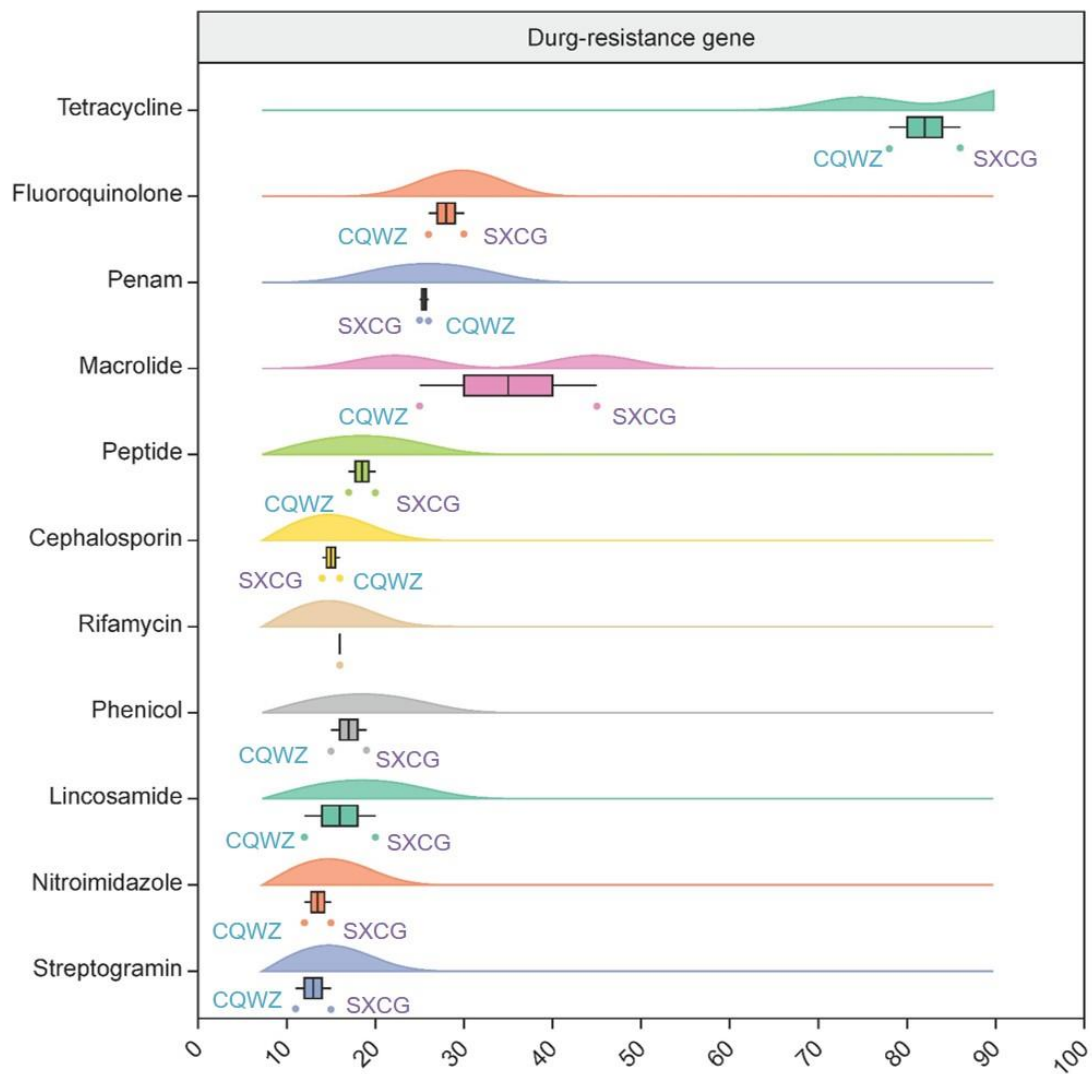


Figure S7. Differences in the number of resistance genes between the SXCG and CQWZ.