

Transcriptome sequencing of *Verticillium dahliae* from a cotton farm reveals positive correlation between virulence and tolerance of sugar-induced hyperosmosis

Verticillium dahliae causes disease symptoms in its host plants; however, due to its rapid variability, *V. dahliae* is difficult to control.

METHODS

To analyze the reason for this pathogenic differentiation, 22 *V. dahliae* strains with different virulence were isolated from a cotton farm. The genetic diversity of cotton varieties make cotton cultivars have different *Verticillium* wilt resistance, so the Xinluzao 7 (susceptible to *V. dahliae*), Zhongmian 35 (tolerant), and Xinluzao 33 (resistant) were used to investigate the pathogenicity of the strains in a greenhouse.



RESULTS

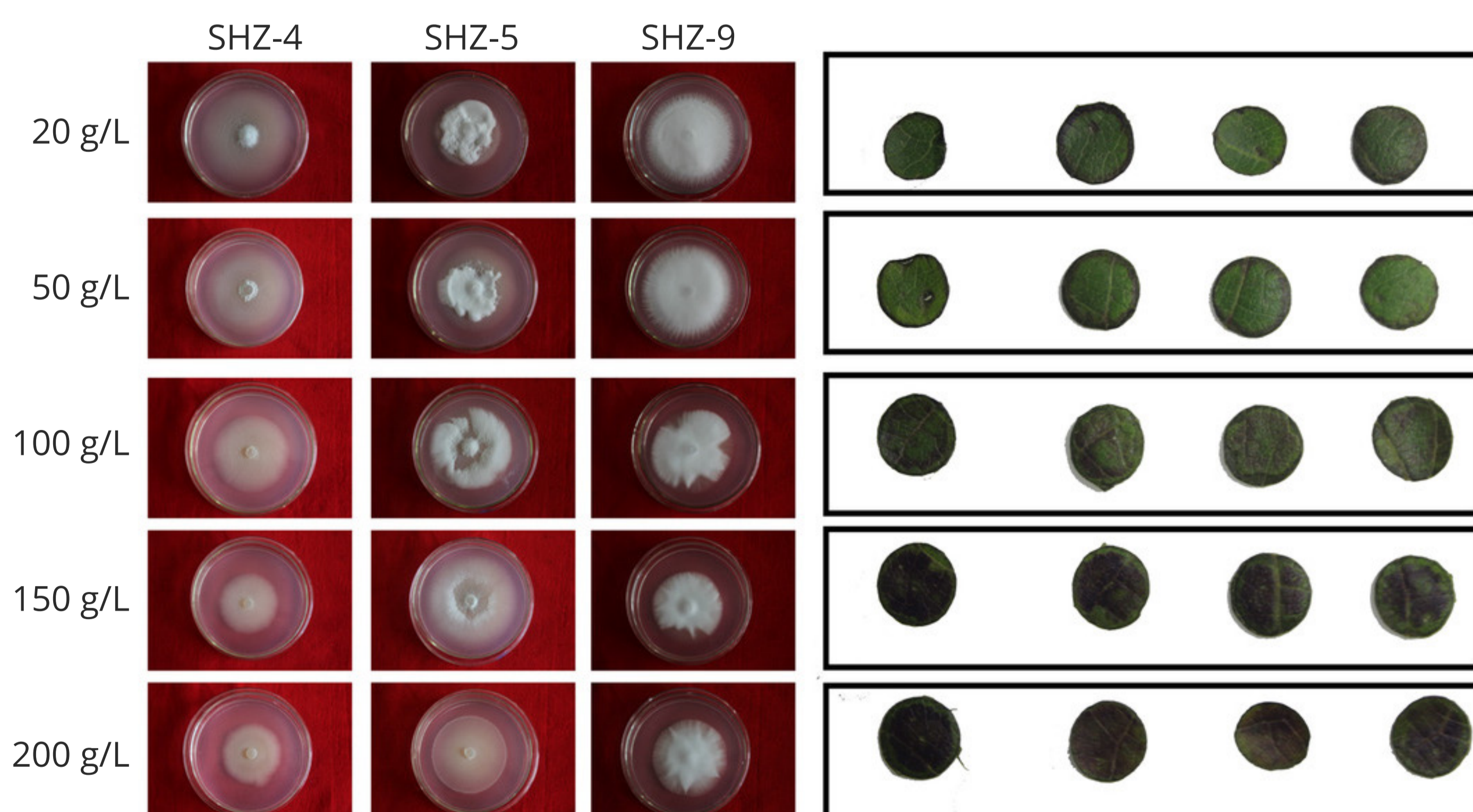
Vegetative compatibility groups (VCGs) assays, Internal Transcribed Spacer (ITS) PCR, and pathogenicity analysis showed that SHZ-4, SHZ-5, and SHZ-9 had close kinship and significantly different pathogenicity. Transcriptome sequencing of the three strains identified 19 of 146 unigenes in SHZ-4_vs_SHZ-5, SHZ-5_vs_SHZ-9, and SHZ-4_vs_SHZ-9. In these unigenes, three proteinase and four polysaccharide degrading hydrolases were found to be associated with the pathogenicity.

However, due to a number of differentially expressed genes in the transport, these unigenes not only played a role in nutrition absorption but might also contribute to the resistance of sugar-induced hyperosmosis. Moreover, the tolerance ability was positively related to the pathogenicity of *V. dahliae*.

Identification of *V. dahliae* strains and cotton leaves that are resistant to sugar-induced hyperosmosis

A The sugar-induced-hyperosmotic resistances of three *V. dahliae* isolates

B The cotton leaf resistance to sugar-induced-hyperosmosis



CONCLUSION

This resistance to sugar-induced hyperosmosis might help *V. dahliae* to access the nutrition of the host. The pathogenicity of *V. dahliae* correlated with the resistance of sugar-induced hyperosmosis, which provides clues for the cultivation of *V. dahliae* resistant varieties.