



Histopathology combined with transcriptome analyses reveals the mechanism of resistance to *Meloidogyne incognita* in *Cucumis metuliferus*

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Background

The root-knot nematode, *Meloidogyne incognita*, is one of the most economically important pest in most cucumber (*Cucumis sativus* L.) growing areas throughout the world. Currently, the use of resistant cultivars is the most effective and environmental friendly nematode management tactic to growers. Up to now, there was no cucumber cultivar with resistance against *M. incognita*. *Cucumis metuliferus*, a relative of cucumber endemic to Africa, is reported to be resistant to *Meloidogyne incognita*. However, early attempts to produce viable interspecific hybrids between *C. metuliferus* and *C. sativus* or *C. melon* have been unsuccessful, and the underlying resistance mechanism also remains unclear.

Objectives

Here we reported that *C. metuliferus* as a model was used to study the resistant interactions between *Cucumis* and *M. incognita*. The research aims were further to evaluate the resistance phenotype in *C. metuliferus* line PI482443 to *M. incognita*, and examine more closely penetration rates and subsequent development of the nematode in selected *Cucumis* species. Moreover, this study for the first time characterized the molecular basis involved in an incompatible PI482443-*M. incognita* interaction and it would provide useful information for further research.

Materials & Methods

The response of resistant *C. metuliferus* line PI482443 following *M. incognita* infection was studied in comparison with susceptible *C. sativus* cv. Jinlv 3. Roots of selected *Cucumis* seedlings were analysed using histological and biochemical techniques. Transcriptome changes of the resistant reaction were investigated by RNA-seq.

Results



Fig. 1 Roots and plants of PI482443 (a-c) and Jinlv No.3 (d-f) at 20, 30, 40 dpi with *M. incognita* respectively.

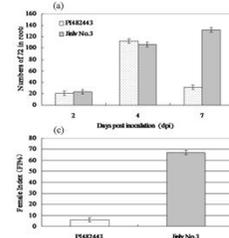


Fig. 2 (a) Number of nematode juveniles penetrating into roots of PI482443 and Jinlv No.3. (b, d) Developmental states of nematode juveniles in roots of two genotypes. (c) Female Index (FI) in roots of two genotypes.

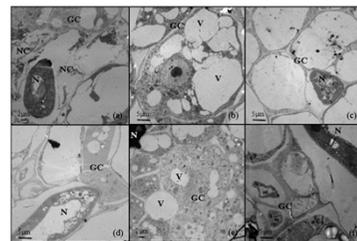


Fig. 4 Longitudinal sections of nematode feeding sites. (a), (b) and (c) are PI482443 root sections and (d), (e) and (f) are Jinlv No.3 root sections at 2, 7 and 14 dpi.

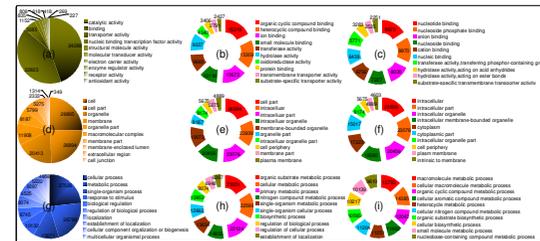


Fig. 5 Top ten most represented GO categories under the "Molecular Function" (a-c), "Cellular Compartment" (d-f) and "Biological Process" (g-i) categories in level 2 (a, d and g), 3 (b, e and h) and 4 (c, f and i).

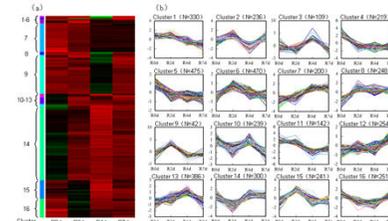


Fig. 6 Schematic representation of gene expression patterns. (a) Heat maps of unigenes with their hierarchical clustering on expression ratios. (b) K-means clustering of unigenes based on expression profiles at the four time points.

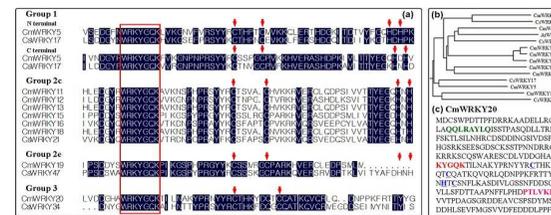


Fig. 7 Classification, system evolution of *CmWRKY* genes and amino acid sequence of *CmWRKY20* in wild *Cucumis metuliferus*.

Conclusion

The resistance in *C. metuliferus* to *M. incognita* was associated with reduced nematode penetration, block of nematode development and HR-mediated cell death. Particularly, transcriptomic analyses of the resistant reaction revealed several most relevant genes that were involved in resistance to the nematode, resulting in the deposition of lignin, toxic compounds synthesis, cell wall reinforcement, suppression of nematode feeding and R protein accumulation. In addition, activation of several transcription factors such as WRKY may induce the expression of *R* genes overcoming the nematode infection. Overall, these results added to the knowledge about the expression of resistance mechanisms induced in *C. metuliferus* by *M. incognita* infection and aided in the identification of potential targets resistant to the pest for cucumber improvement.

Acknowledgements

We acknowledge the Majorbio Bio-Pharm Technology Limited Company (Majorbio, Shanghai, China) for its assistance in original data processing and related bioinformatics analysis. This work was supported by the National Natural Science Foundation of China (Grant No. 31560506).

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