

Diversity of *Xanthomonas nasturtii*, the cause of black rot of watercress

AUTHOR

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INTRODUCTION

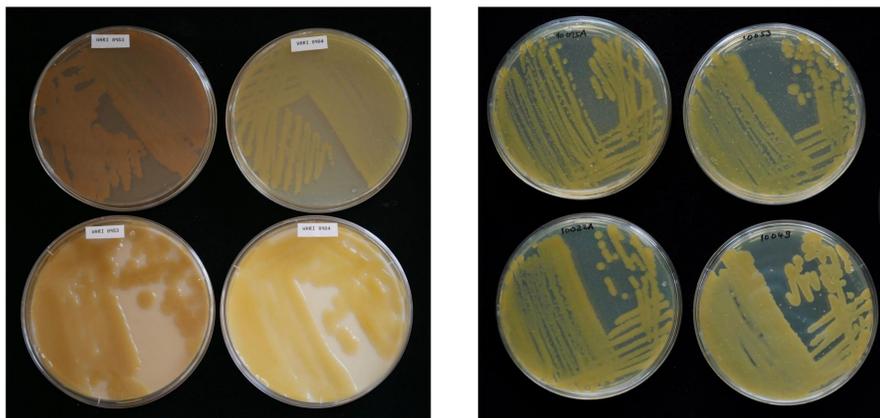
- Watercress (*Nasturtium officinale*; Brassicaceae family) is one of the oldest known leaf vegetables and is a rapidly growing crop that is mainly grown in water beds
- Xanthomonas nasturtii* causes black rot of watercress; symptoms include lesions around the hydathodes, yellowing and wilting of leaves
- The disease was first described in 2017 in samples from Florida (Vicente *et al.*, 2017), but symptoms of this disease had previously been observed in Hawaii and an isolate from 2003, obtained from a Portuguese collection, was also confirmed as *X. nasturtii*; this shows that the disease has probably been associated with watercress production for some decades.



COLLECTION OF ISOLATES

The existing collection of isolates of *X. nasturtii* includes:

- US, Florida (2014) (Vicente *et al.*, 2017) and Hawaii (2017) (Vicente *et al.*, 2023)
- Spain (2018 to 2020) and Portugal (2003, 2021) (Lascelles *et al.*, 2022)



Isolates from Florida (WHRI 8953, darker colour) and Hawaii (WHRI 8984) growing on Kings' B and YDC medium (left image); isolates from Spain (WHRI 10015A and 10053) and Portugal (WHRI 10022A, 10049) growing on Kings' B medium (right image).

PATHOGENICITY TESTING

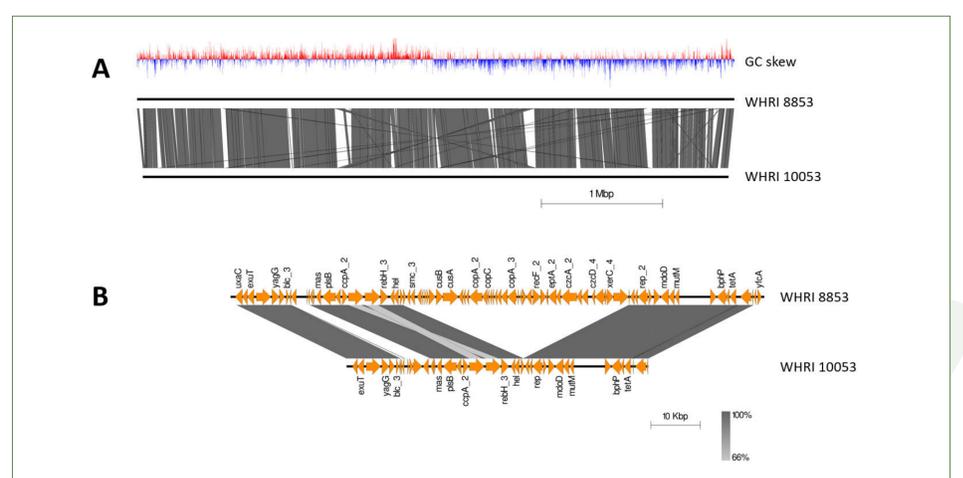
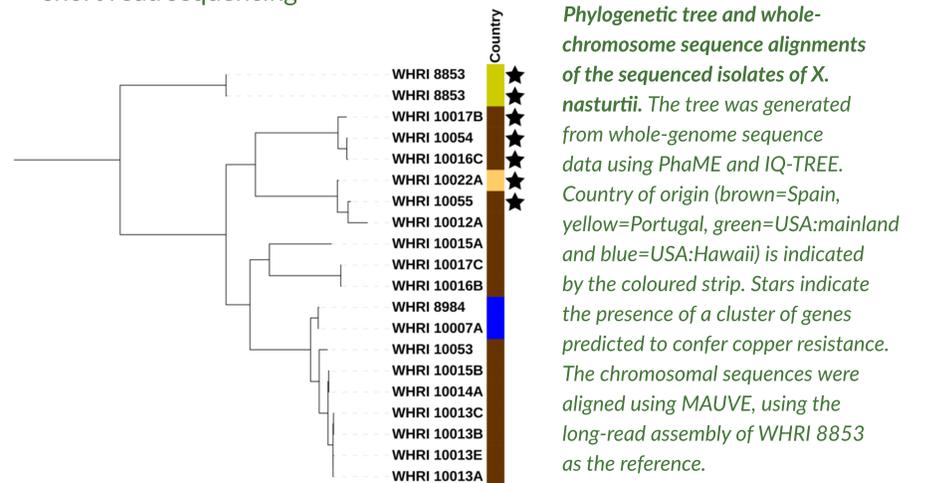
- Testing was performed on three accessions of watercress and Savoy cabbage Wirosa F₁
- Isolates were only pathogenic on watercress; no symptoms were observed on cabbage
- Re-isolations also shown to be pathogenic completing the Koch's postulates



Symptoms of black rot on watercress leaves inoculated with *X. nasturtii* from Hawaii (WHRI 8984) (photographed with a black background and against the light showing the veins)

CHARACTERISATION

- Initial Fatty Acid profiling and *gyrB* partial gene sequencing showed that the isolates belong to the genus *Xanthomonas*
- Whole genome sequencing analyses
 - complete genomes were obtained from long read sequencing for isolates WHRI 8853 = NCPPB 4600 (type strain from Florida) and WHRI 10053 = NCPPB 4622 (from Spain)
 - draft genomes were obtained for all other isolates from Illumina MiSeq short read sequencing



Sequence alignment of the chromosomes of WHRI 8853 and WHRI 10053. Panel A includes the full length of the chromosomes. Panel B is zoomed-in on a genomic region encompassing a cluster of genes predicted to confer copper resistance in WHRI 8853 but absent from WHRI 10053.

CONCLUSIONS

- We have shown that *X. nasturtii* is present in two US states (Florida and Hawaii) and in Europe (Spain and Portugal). Samples from Spain were the most diverse, but also in higher number than other locations
- There is some indication that copper resistance is playing a role in the selection of isolates
- Black rot of watercress is likely to be a seedborne disease; control should involve seed testing to ensure only healthy seeds stocks are used and/or obtaining plants via tissue culture to ensure that they are disease-free.

REFERENCES

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