



Vitis champinii whole genome assembly allows rootstock-specific identification of potential candidate genes for salt and drought tolerance

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INTRODUCTION

Grape production in many regions worldwide is constrained by drought and soil salinisation, as these intensify through climate change.

Vitis champinii cultivars (e.g. Ramsey, Dogridge) are among the most cultivated rootstocks employed to reduce the impact of drought and salinity, with additional features like resistance to nematodes and *phylloxera*.

We produced a whole genome assembly and annotation of *Vitis champinii* that includes allelic variations, and performed precise gene expression analyses for drought and salinity using either the *V. vinifera*^{1,2} or *V. champinii* reference genome.

DISCUSSION AND CONCLUSIONS

Genomic information specific to *Vitis champinii* becomes available with its genome assembly. This includes unique genes, genetic polymorphisms with other *Vitis* species, as well as its own allelic variations.

Compared to the PN40024 genome, the genome assembly of *Vitis champinii* allows a more accurate RNA-Genome matching, which also covers unique genes and heterozygous variants.

Extended gene expression data is therefore achieved, thus uncovering a larger range of genes differentially expressed under water deficit and salinity, with potential relevance to the tolerance against these conditions.

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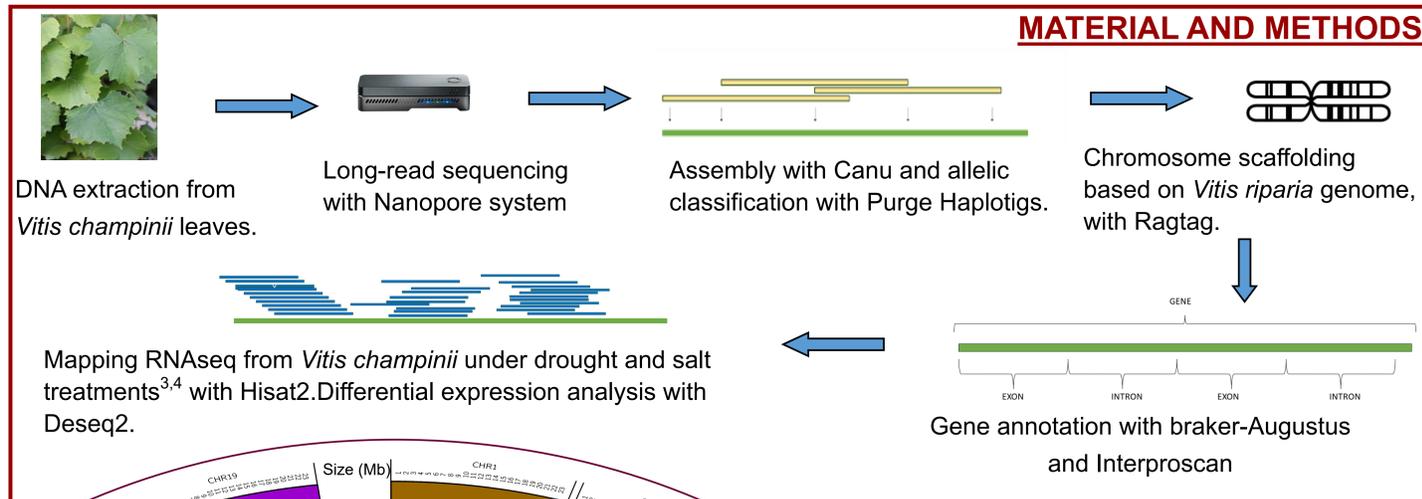
FOR MORE INFORMATION

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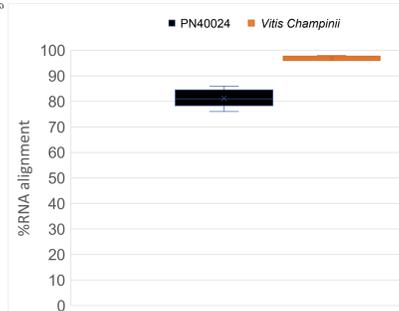
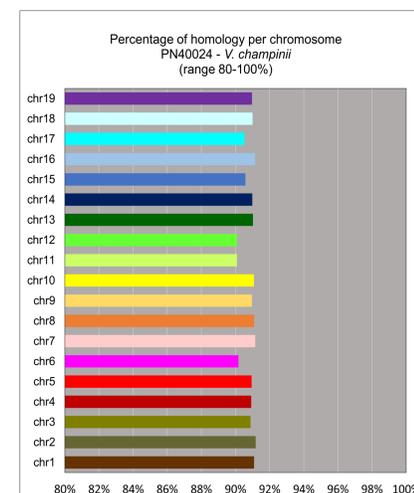
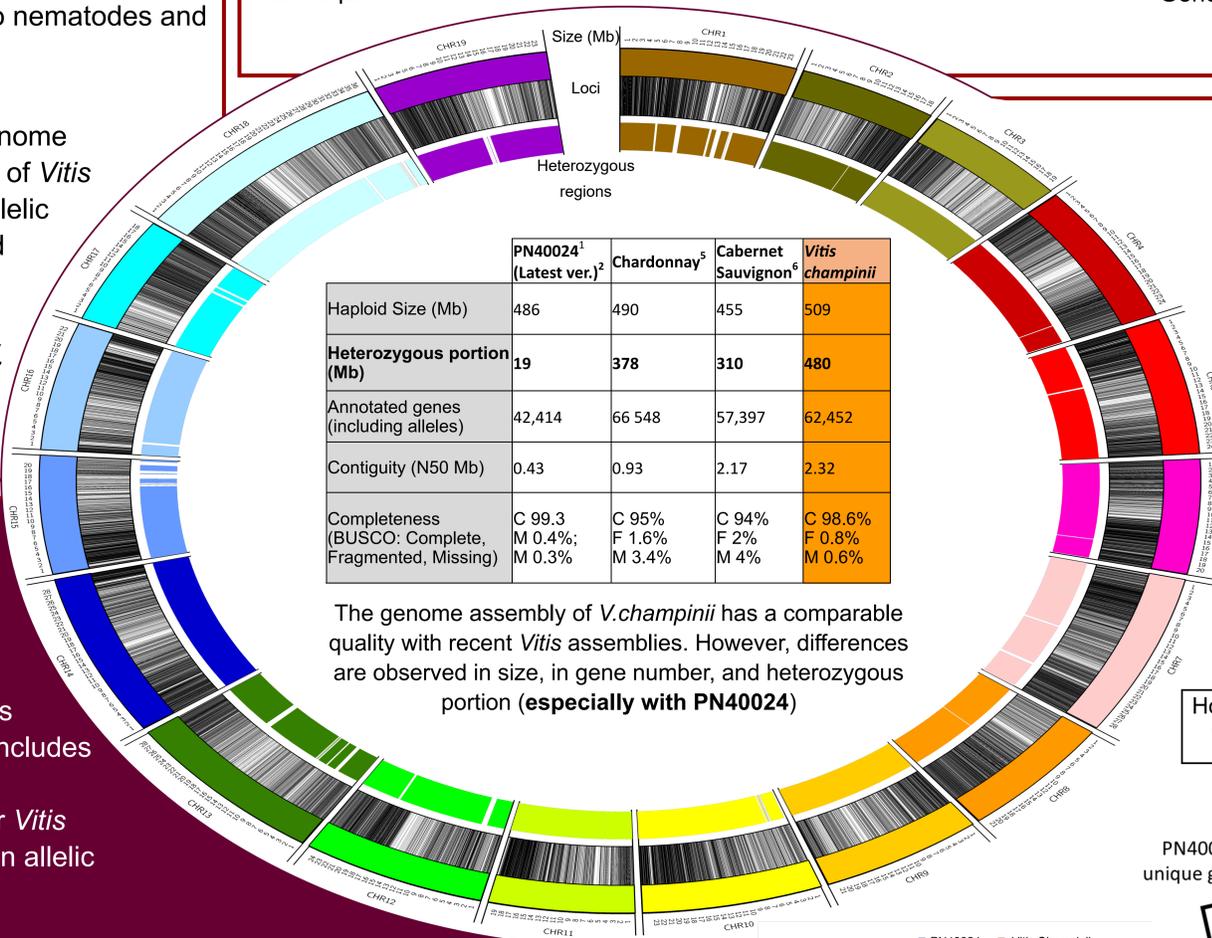


PROJECT PARTNERS

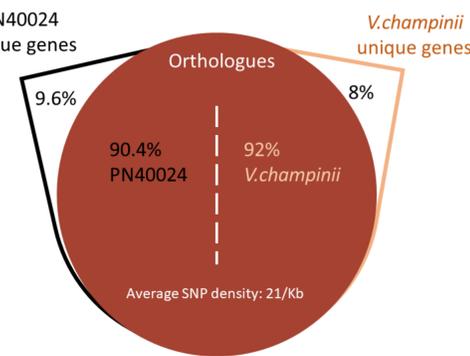


MATERIAL AND METHODS

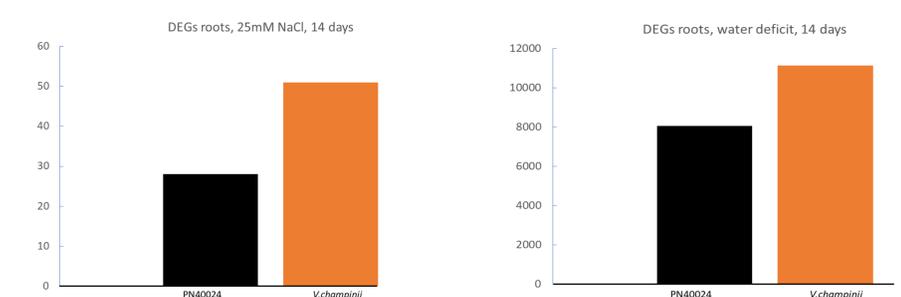
RESULTS



V. champinii RNA mapping rates improve when using its specific genome



Both *V. champinii* and PN40024 possess unique genes with no corresponding ortholog from the other genotype.



On both drought and salt treatments^{3,4}, larger sets of differentially expressed genes are observed in the *V. champinii* specific mapping.