

QTLs on Chromosome One Associated with Bacterial Leaf Spot Response in *Beta vulgaris*



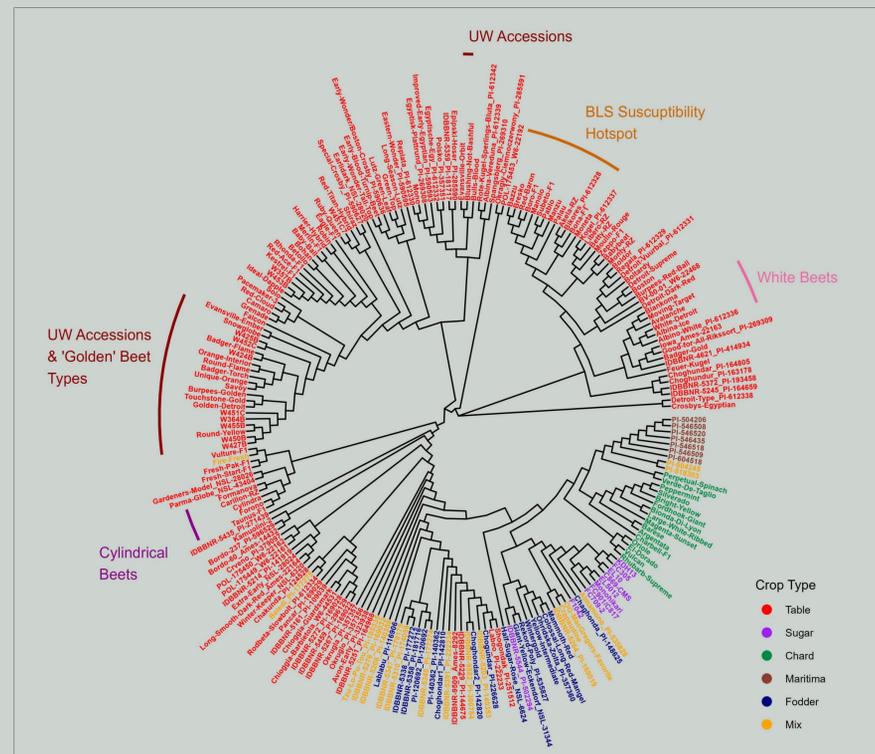
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219 individuals in the Wisconsin Beta Diversity Panel, including table beet, sugar beet, fodder beet, Swiss Chard, and *Beta maritima*

Bacterial Leaf Spot (BLS): an emerging foliar disease affecting beet and chard, caused by *Pseudomonas syringae* pv. *aptata*

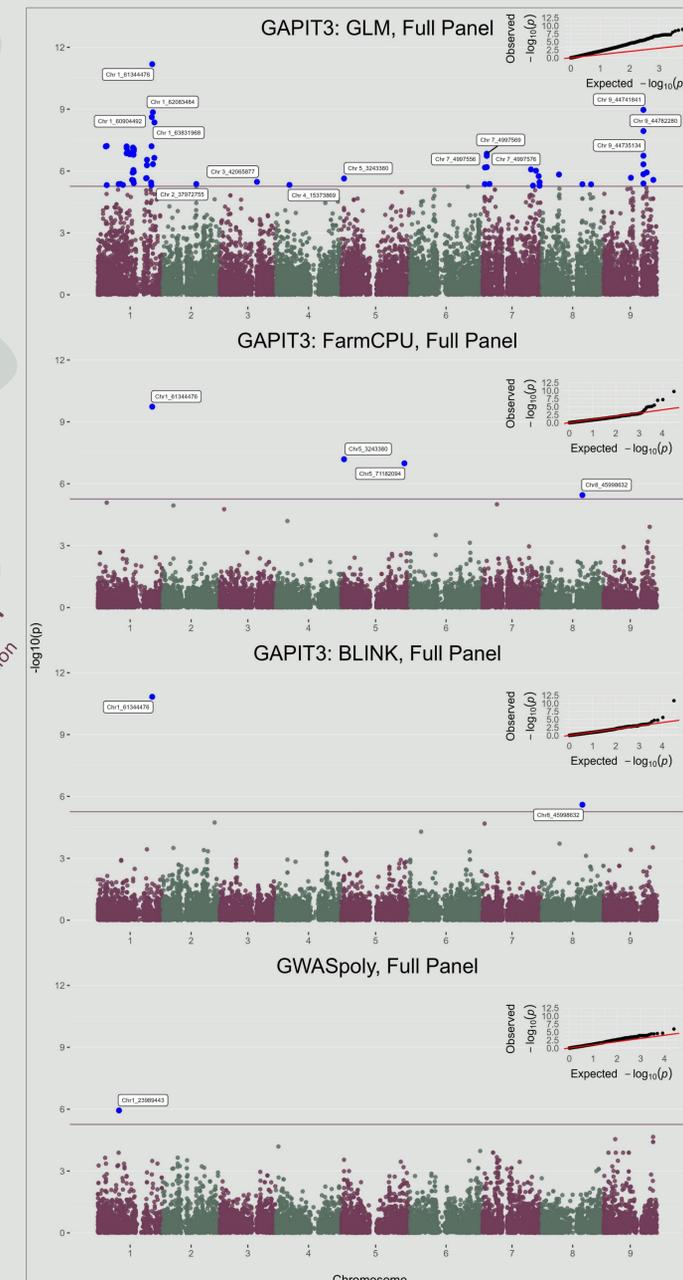
All accessions were screened in the greenhouse over two years. Plants were inoculated and screened for percentage of diseased leaf area 7 days post inoculation

15,813 SNP markers utilized for genotypic and association analysis for the full WBDP



Cladogram of the Wisconsin Beta Diversity Panel subset used in this study (n=219).

Irregular-shaped BLS lesion illustration



Manhattan plots from four GWAS models for an association study of a *Beta vulgaris* diversity panel screened for response to *Pseudomonas syringae* pv. *aptata*. Markers in blue have a $-\log_{10}(p)$ higher than the Bonferroni threshold (purple line). QQ plots for each model are also included. Software used: GAPIT3¹ (BLINK, FarmCPU, GLM) & GWASpoly².

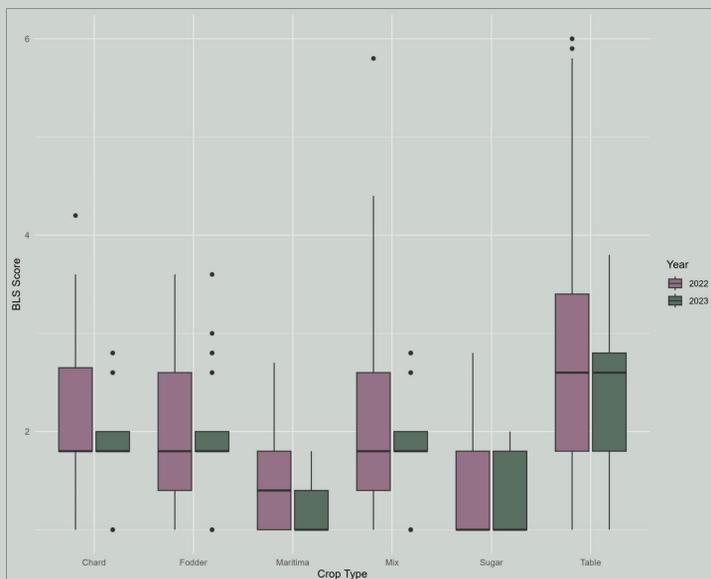


Mapping populations developed after identifying segregating parents from these screens (RxS).

- Touchstone Gold, White Detroit, & Barese chard identified as having low percentage of diseased leaf area ("R").
- Forono, Pablo, Akela, & Charbell F1 identified as having high percentage of diseased leaf area ("S").
- Mapping to be conducted in the F2 and F3 generations.

Acknowledgements

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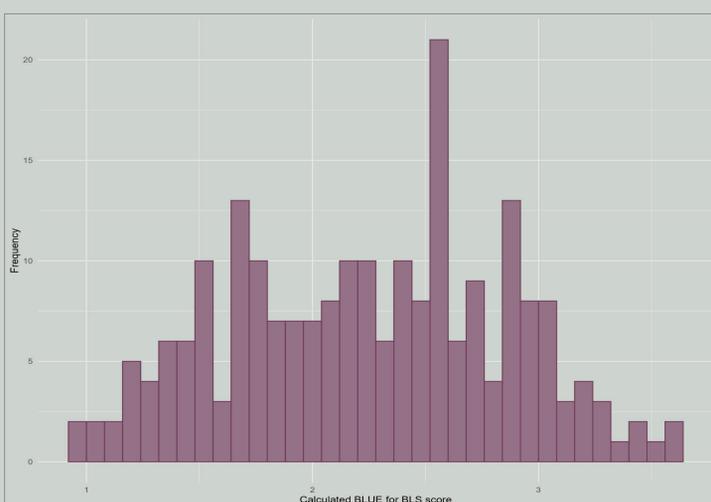


Using a Genome Wide Association Study (GWAS), QTLs were found on **chromosome one** of the *Beta vulgaris* crop complex to be associated with Bacterial Leaf Spot response.

- Large variability in BLS response was found in table beet; better resistance was noted for sugar beet & *Beta maritima*.
- Weak ($r=-0.55$) but significant ($P<0.001$) correlation of leaf color with BLS response was found.
- Candidate genes on chromosome one identified to have direct roles in plant defense response, such as an F-box domain and RNA binding proteins.



Consistent markers on chromosome one may be useful in breeding (Chr1_61344476, Chr1_23989443).



References

- ¹Rosyara, U. R., De Jong, W. S., Douches, D. S., & Endelman, J. B. (2016). Software for Genome-Wide Association Studies in Autopolyploids and Its Application to Potato. *The Plant Genome*, 9(2), plantgenome2015.08.0073. <https://doi.org/10.3835/plantgenome2015.08.0073>
- ²Wang, J., & Zhang, Z. (2021). GAPIT Version 3: Boosting Power and Accuracy for Genomic Association and Prediction. *Genomics, Proteomics & Bioinformatics*, 19(4), 629–640. <https://doi.org/10.1016/j.gpb.2021.08.005>