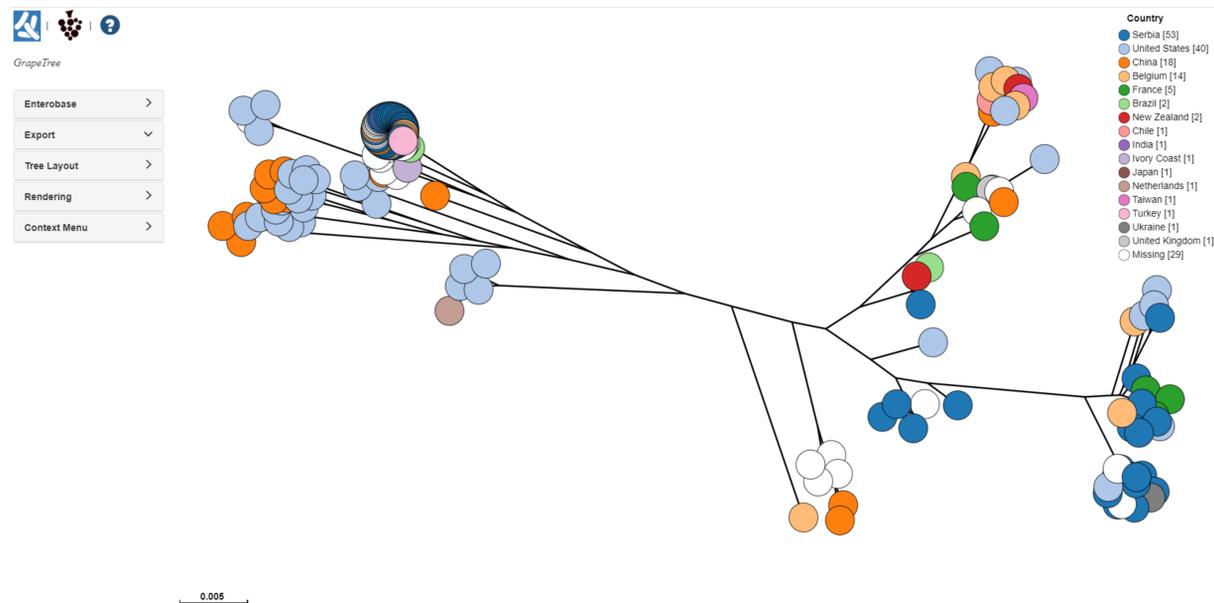


PhytoBacExplorer: A Phylogenomic Resource for the Phytobacterial Community



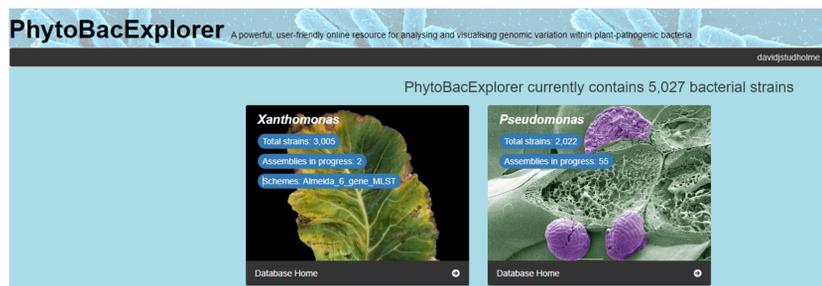
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 1: University of Warwick and 2: University of Exeter

<https://phytobacexplorer.warwick.ac.uk/enterobase@warwick.ac.uk>



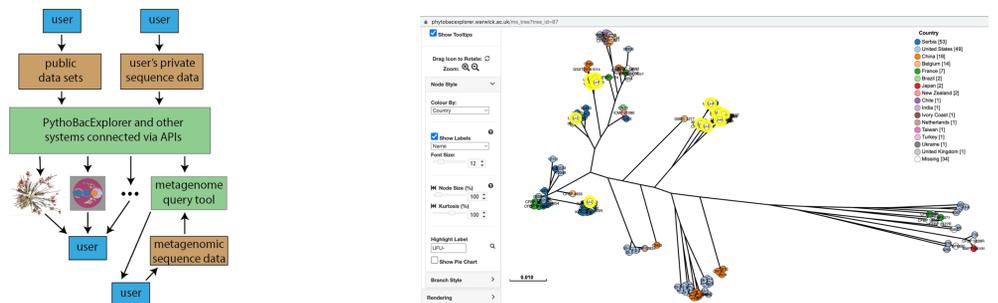
What is PhytoBacExplorer?

- We are developing PhytoBacExplorer, a new web-based phylogenomics system dedicated to plant-pathogenic bacteria.
- We will provide curation to ensure rich, consistent, and high-quality data and metadata including geographic information, host ranges, and genes underlying pathogenicity.
- PhytoBacExplorer is based on the Enterobase system, which is widely used by the medical bacteriology community.
- It will inherit many useful features from Enterobase, including processing of raw data, identification of the shared "core" genome in a population, identification of the phylogenetic (ancestry) tree based on core genomes, and powerful interactive visualisations.



What will I be able to do, using PhytoBacExplorer?

Users will be able to: **upload** their own sequencing data, **scan metagenomic data** for closest matches, or use the PhytoBacExplorer **without submitting** own data. Data can be submitted **privately** for immediate analysis before publication via existing public repositories.



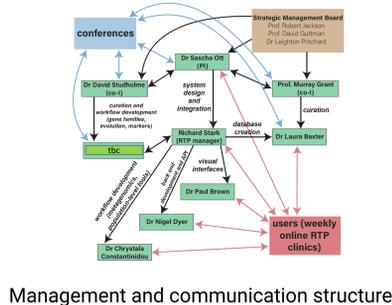
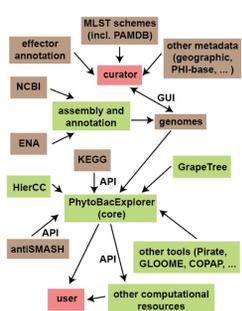
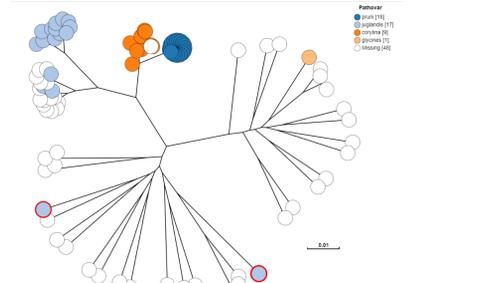
We are still in the first year of a five-year project. New tools are in early stages of development.

Here we uploaded data from newly sequenced strains to find where they fall in the phylogeny of previously sequenced strains.

What is PhytoBacExplorer for?

We are developing PhytoBacExplorer such that ultimately researchers will be able to address questions such as:

- How different is my isolate from the currently known spp. and pathogens?
 - Falls within an existing lineage and taxon or does it represent novel diversity?
- Where is the isolate placed in a phylogenetic tree?
 - What are the most closely related known isolates?
- What is the effector complement? What secretion systems are present?
- What distinguishes a group of related isolates from others in terms of metabolic capabilities, effectors, host range, and geographic distribution?
- Are effectors or other gene families under positive or purifying selection?
- Which gene families co-occur?

Within PhytoBacExplorer, we can edit metadata about sequenced strains.

Here we colour *Xanthomonas arboricola* genomes according to pathovar. Notice how pv. *juglandis* is not monophyletic.

CONCLUSION

- PhytoBacExplorer will be a powerful, user-friendly online resource for analysing and visualising genomic variation within plant-pathogenic bacteria.
- Core functionality and tools are already available. Please try it out and send us feedback!
- You can speak with the PhytoBacExplorer developers at a regular drop-in session via Zoom on most Tuesdays between 9am and 12 noon (UK time): <https://zoom.us/j/8852150277>

FUNDING

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