

Independent Emergence of Pathogenic Lifestyles Uncovered by Comparative Genomics of plant associated *Pantoea* spp.

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Key messages

- *Pantoea* strains, whether phytopathogenic or symbionts, present very similar percentages of Plant Growth Promoting Bacteria (PGPB) traits.
- Phylogenomic analysis of the phytopathogenic and phytobeneficial lifestyles distribution revealed that beneficial traits came first, and that the acquisition of pathogenicity was a recent evolutionary phenomenon that occurred independently in different species of this genus at different times of their evolution.

1. Intro

The *Pantoea* genus includes soil dwelling bacteria capable of colonizing different plant species, establishing pathogenic or beneficial symbiont relationships². Using phylogenomics and comparative genomics³, we investigated the complex evolutionary relationships between plant-related *Pantoea* species, focusing on their ability to either promote plant growth or exhibit phytopathogenic tendencies.

3. Results and discussion

While certain strains within this genus possess inherent genomic capabilities to enhance plant growth, through direct and indirect mechanisms, resulting in a significant positive impact on plant health and productivity; surprisingly such positive genomic traits are shared with other pathogenic *Pantoea* strains (fig. 1).

P. agglomerans GB1 strain is misidentified as *P. ananatis* GB1. *Curtobacterium plantarum* strain, classified as a Gram-positive bacteria, presented a close genetic similarity to the *P. pleuroti* and *P. agglomerans* strains. We suggested that this strain actually belongs to the genus *Pantoea*. We also propose 2 sp. nov. based on genomic data (dDDH < 70%): *Shigella* sp. 1.19 and *Pantoea* sp. AS-PWVM4 (fig. 2, fig. 3).

Based on the phylogenomic analysis, the pathogenic lifestyles of several strains from different *Pantoea* species seem to have appeared recently, compared to original beneficial strains from the remaining species, which leads us to believe that phytopathogenicity has independently emerged multiple times within the *Pantoea* group (fig. 4).

2. Methods

- A dataset of 30 selected strains from the **Plabase platform**⁵. <https://plabase.cs.uni-tuebingen.de/pb/plabase.php>
- Phylogenomics through the 'Type Strain Genome Server' **TYGS**⁴ platform <https://tygs.dsmz.de/> based on dDDH and GC%
- The distribution of genes encoding Plant Growth Promoting Bacteria (PGPB) traits using data from **PlaBa-db**.
- **The origin of pathogenicity and the beneficial lifestyles based on phylogenomics super trees.**

Fig.1 The phylogenetic tree based on 16S rRNA illustrating the evolutionary relationships between the different strains of *Pantoea* in "restricted" mode

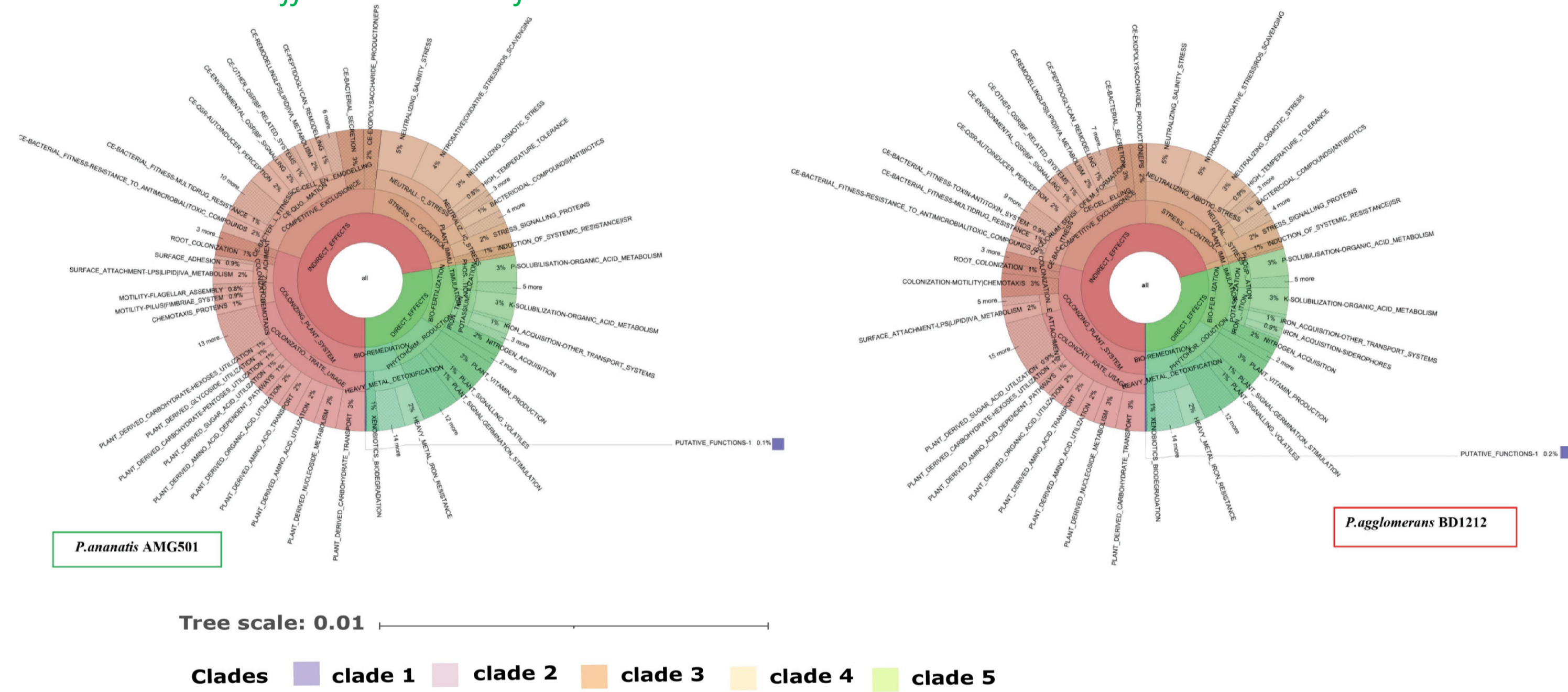


Fig.2

Restricted phylogenomic tree of *Pantoea* spp. by the GBDP approach

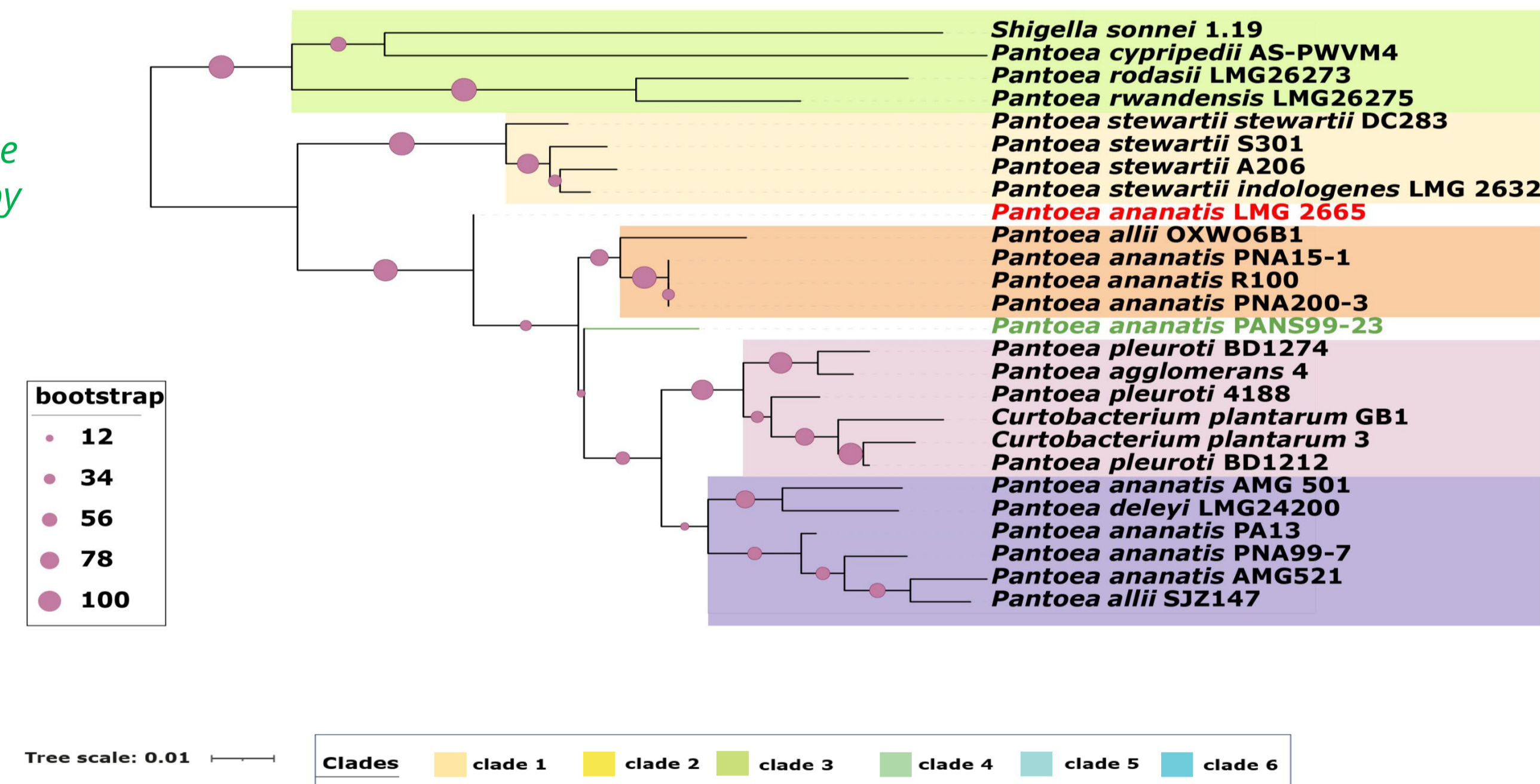


Fig.2

Extended phylogenomic tree of *Pantoea* spp. by the GBDP approach

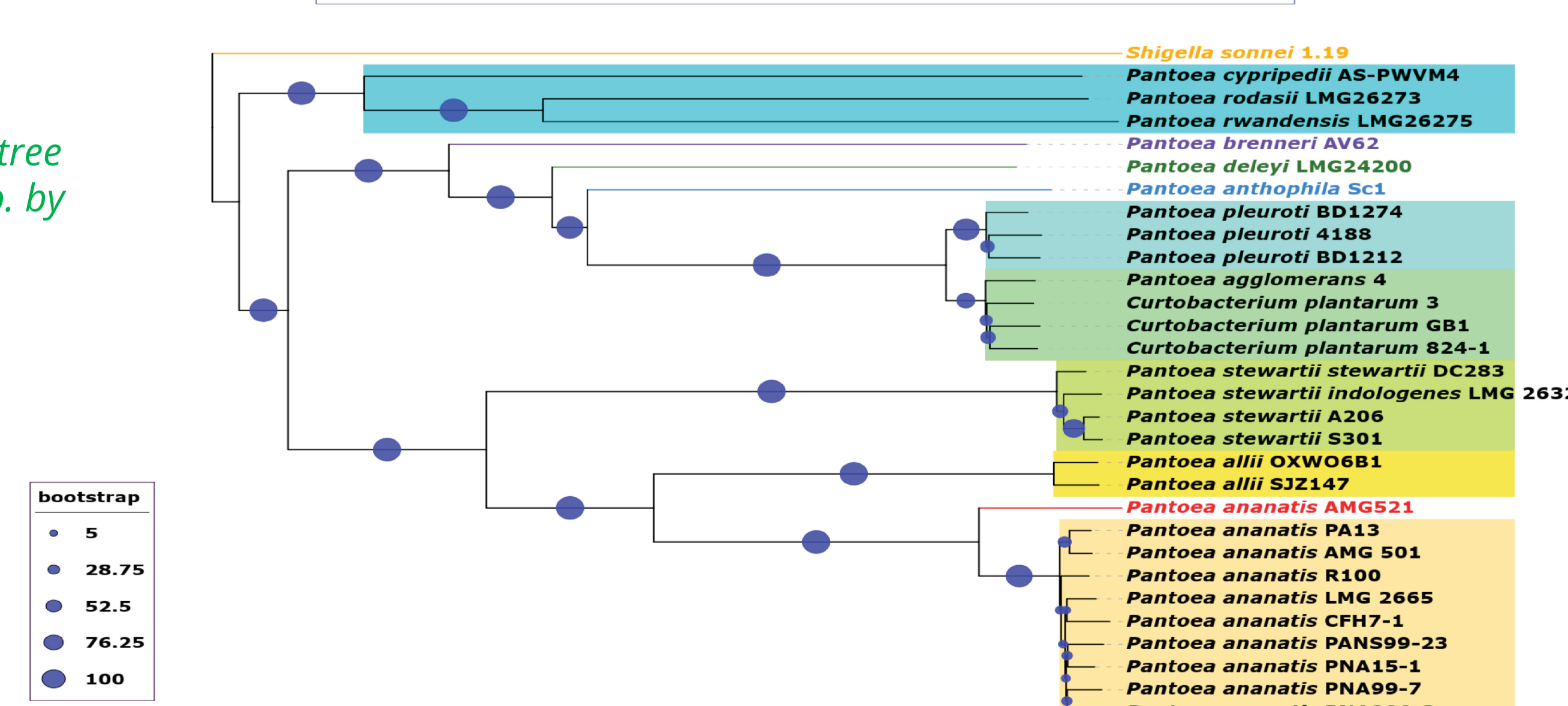
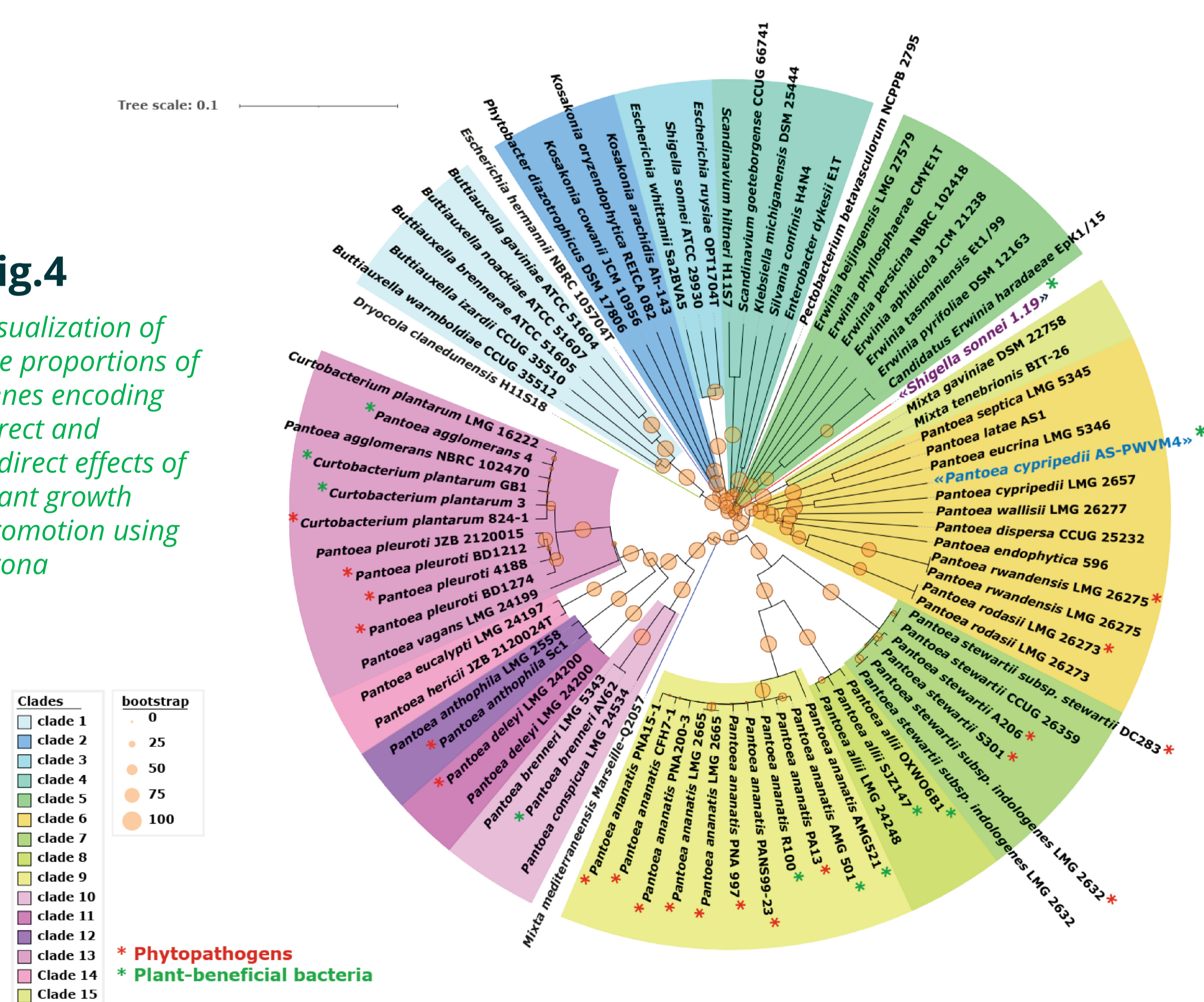


Fig.4

Visualization of the proportions of genes encoding direct and indirect effects of plant growth promotion using Krona



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