

**Genome-based taxonomic analyses of plant pathogenic genera *Pectobacterium* and *Dickeya* suggests a larger inter- and intraspecific diversity**

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The bacterial soft rot, caused by members of the *Pectobacteriaceae* family, is one of the most notorious plant diseases worldwide. The aim of the study was to evaluate current taxonomic diversity within the genera *Pectobacterium* and *Dickeya* by using phylogenomics, average nucleotide index (ANI) and digital DNA-DNA hybridization (dDDH), core-genome alignments, and pan-genome investigation. The study conducts state-of-the-art computational methods implemented within TYGS [1] and EDGAR [2] servers.

We found a large group of strains, which were assigned as *P. brasiliense* [3], that can be characterized as paraphyletic. We performed pairwise ANI/dDDH calculations between two main clades of the species (95–96/64–69 %, respectively). It is suggesting that the identified divergent clade should be transferred to a distinct species for which the name *P. vavilovii* sp. nov. is proposed. The delineation was supported by our core-genome maximum-likelihood tree, which also identify two distinct clades. The pan-genome analysis reveals that novel species acquires the genes for agricinopine catabolism after the divergence.

It was shown that the *evf* gene distributed not only within *P. versatile* [3, 4] species, but also between some *P. odoriferum* strains. This observation suggests that the *evf* gene can be acquired by other *Pectobacterium* spp. with corresponding selective advantages. We examine potential genomic traces of recent horizontal gene transfer (HGT) event between *Photorhabdus* sp., *P. versatile*, and *P. odoriferum* using the following hallmarks [5]: (i) atypical guanine-cytosine content; (ii) the location downstream of transfer RNA gene; and (iii) the presence of integrase gene or other mobile elements near the potential acquired gene. All these hallmarks were identified for the *evf* gene suggesting that this genome region of *Pectobacterium* sp. could be horizontally acquired and ameliorated at the third codon position. We hope that our findings will be useful for investigation of the associative symbiosis between *Pectobacterium* spp. and fruit flies as their potential hosts.

Thus, our results suggesting that the genera *Pectobacterium* and *Dickeya* have a larger inter- and intraspecific diversity. Finally, we would like to conclude that our comparative genomics approach allows to identify two bacterial species of pectolytic bacteria, as following:

1) Description of *Pectobacterium vavilovii* sp. nov. (va.vi.lo'vi.i N. L. gen. n. *vavilovii*, of Nikolai Ivanovich Vavilov (1887–1943), a Russian plant geneticist postulated that the region of greatest diversity of a plant species represents its center of origin). Type strain is PCC21<sup>T</sup>.

2) Description of *Dickeya philodendri* sp. nov. (phi.lo.den'dri. N. L. gen. n. *philodendri*, of *Philodendron*, the plant genus from which the type strain was isolated). The type strain is ECH586<sup>T</sup>.

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## References

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