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Burkholderia: Friend and Foe, or, How to Use Your Enemy's Weapons to Your Advantage

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ABSTRACT

The genus *Burkholderia* belongs to the class *Betaproteobacteria* within the phylum of the *Pseudomonadota.* Although recent taxonomic revisions have reduced the number of recognized *Burkholderia* species from several hundred to a few dozen, this genus remains exceptionally diverse and functionally versatile. This versatility is supported by large genomes up to 10 Mb in size typically organized into three replicons. *Burkholderia* sensu stricto species have been isolated from a wide range of sources, but accumulating evidence indicates that soil—where they associate with various plants, fungi, and protists—is their natural habitat. The genus includes two class 3 pathogens, *Burkholderia mallei* and *Burkholderia pseudomallei*, which cause glanders in horses and melioidosis in humans, respectively. In addition, an increasing number of *Burkholderia* species have been identified as opportunistic human pathogens. These bacteria show a particular affinity for the respiratory tract, with life-threatening lung infections caused by *Burkholderia cepacia* complex bacteria occurring primarily in individuals with cystic fibrosis or those requiring mechanical ventilation. *Burkholderia* species have been described as both friends and foes of humans. While they are perhaps best known for their roles as pathogens of humans, animals, and plants, numerous studies have also highlighted their biotechnological potential, in particular, their abilities to promote plant growth, control agricultural pests, and contribute to bioremediation efforts. Today, an exceptionally large number of *Burkholderia* whole-genome sequences are available. However, these data have generally failed to clearly distinguish between beneficial and harmful strains, or between those considered safe or unsafe for biotechnological applications. Nonetheless, genomic analyses combined with *in planta* experiments—now underpin a growing number of studies aimed at harnessing this genetic potential as a source of novel antibiotics and other bioactive secondary metabolites.

Keywords: *Burkholderia*, taxonomic, genomics, pathogenicity, biotechnological potential

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