

Genome Adaptation to Various Niches: from Land to the Sea

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Bacteria that belong to the genus *Burkholderia* are ubiquitous in the nature, living freely in the environments or associated with plants or animals. They are known as soil saprophytes, plant growth promoters, antagonists and pathogens to diverse life forms. Even in the sea, a significant level of *Burkholderia* was revealed by the recent meta-genomic expedition to the Sargaso Sea lead by Craig Venter. The enormous adaptability and diversity exhibited by the bacteria of this group are believed to have resulted from the rich repertoire of gene contents (genome size ~4 to 9 mb) carried by flexible chromosomes, which greatly facilitated genome modifications. These bacteria truly provide a valuable opportunity to study genome evolution associated with adaptation to various environments. A number of completed genomes of *Burkholderia*, although biased to pathogens, are currently available. Analysis of these genomes will help understand the evolution and mechanisms of their diversified virulence, and will ultimately lead to the development of effective countermeasures against the important human health hazards and potential bio-warfare agents, represented by *Burkholderia cepacia* complex, *Burkholderia mallei* and *Burkholderia pseudomallei*.