Mobile Elements within the Burkholderiaceae

Helena M.B. Seth-Smith, Matthew T.G. Holden & Julian Parkhill
Pathogen Sequencing Unit, Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, U.K.

Abstract
The genus Burkholderia, formerly categorised within Pseudomonas, contains in excess of 30 species, which occupy a wide range of ecological niches. They have been reported as soil organisms, plant root colonisers, biocontrol agents, bioremediation agents and pathogens of plants, animals and humans. Burkholderia mallei and Burkholderia pseudomallei are category B biotreat agents, causing glanders and meliodosis, respectively, and some members of the Burkholderia cepacia complex are considered to be opportunistic human pathogens. Many Burkholderia genomes, each of which comprise multiple replications, are in the process of being sequenced. Five of these have been completed and released, covering four different species. In addition, the deep shotgun sequencing of microbes from the Sargasso Sea contained high sequence coverage of a member of the Burkholderiaceae. A wealth of data now exists, from which information on mobile DNA elements can be extracted.

Burkholderia cenocepacia strain J2315 annotation
The genome of B. cenocepacia strain J2315 is currently being annotated (Figure 1). Particular attention has been paid to the annotation of IS elements. Several new elements have been described, and submitted to IS Finder (ISBcen).

General genome characteristics
Burkholderia pseudomallei K92243 (BP), 1710b (1710b): two strains with similar IS composition
Burkholderia mallei (BM): clone of pseudomallei which has undergone enormous IS expansion, now host restricted
Burkholderia sp. SAR1 (SAR1 - unfinished and unannotated): relatively few ISs: two novel Burkholderia cepacia complex
Burkholderia sp. strain 383 (383): only one multicopy IS (from criteria in methodology)
Burkholderia cenocepacia strain HI2424 (HI2424 - unfinished and unannotated): more than 9 novel ISs
Burkholderia cepacia strain J2315 and J2315: genome and chromosome number

ISs can mediate genome rearrangements
Comparing B. pseudomallei gene order along chromosome 1, to that of B. mallei chromosome 1, it is clear that the rearrangements have been mediated by recombination between IS elements (Figure 9). Comparing gene order between B. cepacia complex strains J2315 and 383, there has been little rearrangement, and that which exists is not due to insertion sequences (Figure 10).

Introns within the Burkholderiaceae
Group I introns
Each of the strains investigated appears to contain a group I intron. This seems to border a low GC region, possibly an island, in some strains.

Group II introns
There appear to be two types of Group II intron in the Burkholderia studied. In strain J2315, one of these contains ISBcen3 (Figure 11).

References
1. http://www.sanger.ac.uk/pub/contig/assembly

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