

## Genomic Surveillance of Bacillus Anthracis in South Africa Revealed a Unique Genetic Cluster of B- Clade Strains

**Authors :** Kgaugelo Lekota, Ayesha Hassim, Henriette Van Heerden

**Abstract :** Bacillus anthracis is the causative agent of anthrax that is composed of three genetic groups, namely A, B, and C. Clade-A is distributed world-wide, while sub-clades B has been identified in Kruger National Park (KNP), South Africa. KNP is one of the endemic anthrax regions in South Africa with distinctive genetic diversity. Genomic surveillance of KNP B. anthracis strains was employed on the historical culture collection isolates (n=67) dated from the 1990's to 2015 using a whole genome sequencing approach. Whole genome single nucleotide polymorphism (SNPs) and pan-genomics analysis were used to define the B. anthracis genetic population structure. This study showed that KNP has heterologous B. anthracis strains grouping in the A-clade with more prominent ABr.005/006 (Ancient A) SNP lineage. The 2012 and 2015 anthrax isolates are dispersed amongst minor sub-clades that prevail in non-stabilized genetic evolution strains. This was augmented with non-parsimony informative SNPs of the B. anthracis strains across minor sub-clades of the Ancient A clade. Pan-genomics of B. anthracis showed a clear distinction between A and B-clade genomes with 11 374 predicted clusters of protein coding genes. Unique accessory genes of B-clade genomes that included biosynthetic cell wall genes and multidrug resistant of Fosfomycin. South Africa consists of diverse B. anthracis strains with unique defined SNPs. The sequenced B. anthracis strains in this study will serve as a means to further trace the dissemination of B. anthracis outbreaks globally and especially in South Africa.

**Keywords :** bacillus anthracis, whole genome single nucleotide polymorphisms, pangenomics, kruger national park

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