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## Anthrax genomics

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The threat of bioterrorism has renewed interest in techniques for pathogen detection, monitoring and analysis. In the May 8 [ScienceXpress](#), Timothy Read and researchers at [The Institute for Genome Research \(TIGR\)](#) Maryland, USA, describe a genome-based analysis of *Bacillus anthracis*, the causative agent of anthrax (DOI:10.1126/science.1071837). They assembled sequences from a recent isolate of *B. anthracis* used in a series of fatal letter-based attacks in Florida that followed in the wake of the World Trade Center tragedy on September 11, and compared them with a reference strain (referred to as the Porton isolate). They discovered four sequence differences in the *B. anthracis* chromosome: two single nucleotide polymorphisms (SNPs) and two short insertions/deletions. Comparison of the pXO virulence plasmids with those from the Sterne and Pasteur strains revealed a further 38 SNPs, eight VNTRs and three large insertion/deletions. Some of these polymorphisms may have potential phenotypic effects and influence pathogenicity. In addition, these polymorphisms will be useful as genetic markers in future monitoring of bioterrorism attacks or infectious outbreaks.

## References

1. *ScienceXpress*, [<http://www.sciencemag.org/scienceexpress/recent.shtml>]
2. The Institute for Genome Research (TIGR) , [<http://www.tigr.org>]