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## Comparing *Xanthomonas*

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In the May 23 *Nature*, da Silva *et al.* report the comparative analysis of genomes of two bacterial **phytopathogens** that differ in their host specificity and pathogenicity (*Nature* 2002, **417**:459-463). *Xanthomonas axonopodis* pv *citri* (*Xac*) affects citrus cultivars and causes canker lesions. In contrast, *Xanthomonas campestris* pv. *campestris* (*Xcc*) affects crucifers and causes black rot. Each genome contains a circular chromosome of around 5 megabases. In addition, *Xac* carries two plasmids, of 34 and 65 kilobases. The chromosomes display a high degree of colinearity, suggesting as few as three major rearrangement events have occurred in the time that separates them, and they have as many as 80% of genes in common. Regions around the putative termini of replication contain most strain-specific genes that may be related to pathogenesis. *Xac*-specific genes include those for fungicide synthesis, secreted toxins, and nodulation pathways. *Xcc*-specific genes include those implicated in colonization, antibiotic synthesis and nitrate assimilation. The Brazilian researchers estimate the divergence time between the two is 6.5-8.9 million years. Analysis of the differences between the **Xanthomonas genomes** may provide clues to their different features of the pathogens. For example, differences in the numbers of proteases and endogluconases may explain the strain-specific effects on host tissue destruction; *Xcc*-specific genes may be related to invasion and colonization phenotypes, and *Xac* genes may explain the strongly localized *Xac* response.

## References

1. *Nature*, [<http://www.nature.com>]
2. From rags to riches: insights from the first genomic sequence of a plant pathogenic bacterium., [<http://genomebiology.com/2000/1/3/reviews/1019/>]
3. *Xanthomonas* genome projects , [<http://genoma4.iq.usp.br/xanthomonas>]