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## Plant pathogen genome

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Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

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In the January 31 *Nature*, Salanoubat *et al.* report the complete genome sequence of the soil-borne plant pathogen *Ralstonia solanacearum* (*Nature* 2002, **415**:497-502). The French research team sequenced the genome of the *R. solanacearum* GMI1000 strain, which is a pathogen of *Arabidopsis thaliana*, to gain insights into pathogenicity and [host-pathogen interactions](#). The [R. solanacearum genome](#) is composed of two circular molecules of 3.7 and 2.1 Mb, encoding over five thousand predicted proteins. The larger replicon ('the chromosome') encodes all the basic mechanisms required for bacterial survival, while the smaller replicon ('the megaplasmid') is genetically dispensable. The megaplasmid may be involved in fitness and adaptation, and it harbours all the *hrp* genes required to cause disease. Salanoubat *et al.* found new genes linked to pathogenicity, or encoding hydrolytic enzymes, toxins, attachment factors and proteins required for hormone induction or resistance to oxidative stress. They identified a large number of genes encoding the type III secretion system, and the effector proteins that it delivers, which are essential for pathogenicity; they also found evidence suggesting that some of these pathogenicity genes may have been acquired by horizontal gene transfer.

## References

1. *Nature*, [<http://www.nature.com>]
2. Common and contrasting themes of plant and animal diseases.
3. *R. solanacearum* genome , [<http://sequence.toulouse.inra.fr/R.solanacearum.html>]