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### *Streptomyces coelicolor* genome

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*Streptomyces coelicolor* is a soil-dwelling, filamentous bacterium responsible for producing most of the natural antibiotics used in human and veterinary medicine. In the May 9 [Nature](#), Stephen Bentley and colleagues from [The Wellcome Trust Sanger Institute](#), Cambridge, UK and the [John Innes Centre](#), Norwich, UK, report the complete genome sequence of the model actinomycete *S. coelicolor* A3(2).

Bentley *et al.* used an ordered cosmid library to sequence the *S. coelicolor* genome. They observed that at 8,667,507 base pairs the linear chromosome of this organism has the largest number of genes so far discovered in a bacterium - 7,825 - many located in 20 gene clusters coding for known or predicted secondary metabolites.

"The genome contains an unprecedented proportion of regulatory genes, predominantly those likely to be involved in responses to external stimuli and stresses, and many duplicated gene sets that may represent 'tissue-specific' isoforms operating in different phases of colonial development, a unique situation for a bacterium," wrote the authors.

In addition, there is an ancient synteny between the central 'core' of the chromosome and the whole chromosome of *Mycobacterium tuberculosis* and *Corynebacterium diphtheriae* - two other pathogenic actinomycetes.

"The genome sequence will greatly increase our understanding of microbial life in the soil as well as aiding the generation of new drug candidates by genetic engineering" conclude the authors.

## References

1. Bentley SD, Chater KF, Cerdeño-Tárraga A-M, Challis GL, Thomson NR, James KD, Harris DE, Quail MA, Kieser H, Harper D, *et al.*: Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2). *Nature* 2002, 417:141-147., [<http://www.nature.com>]
2. The Wellcome Trust Sanger Institute, [<http://www.sanger.ac.uk/>]
3. John Innes Centre, [<http://www.jic.bbsrc.ac.uk/>]