

Evolutionary origin of bacterial chromosomes revealed

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Researchers have unveiled the evolutionary origin of the different chromosomal architectures found in three species of *Agrobacterium*. A comprehensive comparison of the *Agrobacterium* sequence information with the genome sequences of other bacteria suggests a general model for how second chromosomes are formed in bacteria.

Agrobacteria are members of the Rhizobiaceae family, which also includes the benign, nitrogen-fixing organisms *Rhizobium* and *Sinorhizobium*. [Agrobacterium](#) *tumefaciens* C58 is the workhorse of the plant biotechnology science and industry, thanks to its ability to insert its own DNA into host plants.

Members of the Rhizobiaceae have genetic architectures that span single [chromosomes](#), multiple chromosomes and circular DNA molecules (plasmids) of various sizes. The scientists used the sequence information of the genomes of three types of *Agrobacterium* (biovars), two of which were recently completed, and compared the sequences with those of different [bacteria](#) to shed light on the origin of the different chromosomal arrangements.

Most bacteria have only one chromosome. The Rhizobiaceae is an unusual bacterial family in that all of its members have either two chromosomes or one chromosome and very large plasmids. Until this study, it was not clear how such multichromosomal architectures had evolved.

João Setubal, associate professor at the Virginia Bioinformatics Institute and the Department of Computer Science at Virginia Tech, commented: "Thanks to the efforts of the Agrobacterium [Genome Sequence Consortium](#) and the wider research community, we have sufficient sequence data available from different bacterial species to allow the inference of a general model for bacterial genome evolution. It appears that the transfer of genes from chromosomes to large plasmids mediates second chromosome formation."

"Examination of different genome sequences within the Rhizobiales family has revealed that gene migration is rife among the different replication units," said Steve Slater, professor at the University of Wisconsin. "Genes are not only migrating between organisms but they are also moving within the cell between chromosomes and plasmids. The genetic organization of even essential genes in bacteria is much more complex and fluid than has been imagined."

"The three Agrobacterium biovars for which we now have sequences - *A. tumefaciens* C58, *A. radiobacter* K84, and *A. vitis* S4 - provide an exciting snapshot of chromosome evolution in progress," said Brad Goodner, associate professor at Hiram College. "In Biovars I and III, Agrobacteria gene movements have produced second chromosomes derived from plasmids, while in the biovar II strain K84 the plasmid-based replicon has yet to reach second chromosome status."

Derek Wood, associate professor at Seattle Pacific University, remarked: "The findings in this work provide substantial new evidence that second chromosomes in all bacteria studied to date have plasmid origins. While other mechanisms leading to second chromosome formation seem possible, it is intriguing that this approach has been most productive."

"Because of the biotechnological importance of Agrobacterium, the

sequence information provided by these strains should be an invaluable resource for Agrobacterium researchers and the wider life sciences research community," said Barry Goldman, Biotechnology Prospecting Lead at Monsanto.

More information: Slater SC, Goldman BS, Goodner B, Setubal JC, Farrand SK, Nester EW, Burr TJ, Banta L, Dickerman AW, Paulsen I, Otten L, Suen G, Welch R, Almeida NF, Arnold F, Burton OT, Du Z, Ewing A, Godsy E, Heisel S, Houmiel KL, Jhaveri J, Lu J, Miller NM, Norton S, Chen Q, Phoolcharoen W, Ohlin V, Ondrusek D, Pride N, Stricklin SL, Sun J, Wheeler C, Wilson L, Zhu H, Wood DW (2009) Genome sequences of three Agrobacterium biovars help elucidate the evolution of multi-chromosome genomes in bacteria" *Journal of Bacteriology*. In press. doi:10.1128/JB.01779-08

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