

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Water bug genome

ArticleInfo		
ArticleID	:	4028
ArticleDOI	:	10.1186/gb-spotlight-20010327-03
ArticleCitationID	:	spotlight-20010327-03
ArticleSequenceNumber	:	99
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2001-03-27 OnlineDate : 2001-03-27
ArticleCopyright	:	BioMed Central Ltd2001
ArticleGrants	:	
ArticleContext	:	130592211

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Caulobacter crescentus is a Gram-negative bacterium that exhibits cell differentiation, asymmetric division and coordinated cell-cycle progression. In the March 27 [Proceedings of the National Academy of Sciences USA](#), Nierman *et al.* report the complete genome sequence of *C. crescentus* (*Proc Natl Acad Sci USA* 2001, **98**:4136-4141). The sequence was assembled by whole-genome random sequencing. The single *C. crescentus* chromosome contains about 4 megabases of DNA and encodes 3,767 genes. [Cell-cycle progression](#) is dependent on two-component signal-transduction proteins, and these are abundant in the genome (105 genes). Many of these signalling proteins function, together with outer membrane channel transporters and metabolic enzymes, to allow adaptability to environmental fluctuations and low-nutrient conditions: for example, they sense and respond to intracellular oxygen and redox states. Nierman *et al.* also suggest that DNA methylation in intergenic regions plays a role in cell-cycle regulation. Analysis of the *C. crescentus* genome should provide insights into the biology of related bacteria, such as the human pathogens [Rickettsia prowazekii](#) and [Brucella abortus](#).

References

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