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GENOME ANNOUNCEMENT

Complete Genome Sequence of the Fruiting Myxobacterium *Corallococcus coralloides* DSM 2259

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***Corallococcus coralloides*, like most other myxobacteria, undergoes a developmental program culminating in the formation of fruiting bodies. *C. coralloides* fruiting bodies are morphologically distinct from those of other fruiting myxobacteria for which full-length genome sequences are available. The genome sequence of the 10.0-Mb *C. coralloides* genome is presented herein.**

In response to starvation, most myxobacteria initiate a developmental program that culminates in the formation of multicellular, spore-filled fruiting bodies (8). Fruiting body morphology is species specific, i.e., genetically determined, and highly variable (2, 12). While the fruiting bodies of the model organism *Myxococcus xanthus* are relatively simple morphologically, resembling haystacks, numerous myxobacterial species construct fruiting bodies that exhibit a high degree of morphological complexity, including stalks, sporangioles, and appendages. To date, we understand little about the genetic mechanisms underlying this morphological complexity and diversity.

Among bacteria, fruiting body formation is restricted to myxobacteria (12), suggesting that the last common ancestor of the myxobacteria already harbored the genetic program for fruiting body formation. Surprisingly, recent comparative genomic analyses indicate that the genetic programs for fruiting body formation are likely not highly conserved in different myxobacteria (5). To provide a framework for understanding the evolution of the genetic program(s) for fruiting body formation and morphology, we sequenced and annotated the genome of *Corallococcus coralloides* DSM 2259, a member of the suborder *Cystobacterineae*. *C. coralloides* forms fruiting bodies with coral-shaped appendages that extend up and away from the central fruiting body structure (2).

C. coralloides DSM 2259 was obtained from the DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH), and fruiting body formation was verified. Sequence data were generated using the 454 XLR Titanium platform (42-fold coverage). A total of 981,135 filtered reads were assembled into a single scaffold using combined Newbler (10) and Celera (11) assembly results. Sanger-based sequencing was performed to verify the assembly and to close gaps. Genome annotation was generated by manually curating the combined results of MAGPIE (3), RAST (1), PRODIGAL (6), and BASys (14) annotation predictions.

The complete genome sequence of the *C. coralloides* DSM 2259 chromosome contains 10,080,619 bp, with a GC content of 69.9%. A total of 8,033 protein-coding genes (CDSs) were identified, with an average length of 1,148 bp. Fifty-nine tRNA genes and three rRNA operons were identified. In total, the predicted genes account for approximately 91.7% of the genome sequence length. Functional assignments, obtained using database comparisons, were determined for 58% of the CDSs. These findings are similar to those determined for other genome sequences of fruiting myxobacteria, i.e., *Sorangium cellulosum* (13), *Haliangium ochraceum* (7), *M. xanthus* (4), *Myxococcus fulvus* (9), and *Stigmatella aurantiaca* (5), with genome sizes of 13.0 Mb, 9.4 Mb, 9.1 Mb, 9.0 Mb, and 10.3 Mb, respectively. Further, global synteny is apparent between the four *Cystobacterineae* genomes of *C. coralloides*, *M. xanthus*, *S. aurantiaca*, and *M. fulvus*, and *C. coralloides* shares the inversion described for *M. fulvus* (9).

The *C. coralloides* genome sequence will allow us to analyze with greater resolution the evolution of the genetic programs leading to fruiting body formation and may provide new insights regarding genetic determinants of fruiting body morphology.

Nucleotide sequence accession number. The genome sequence was deposited in GenBank under accession number CP003389.

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REFERENCES

1. **Aziz RK, et al.** 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics **9**:75.
2. **Dawid W.** 2000. Biology and global distribution of myxobacteria in soils. FEMS Microbiol. Rev. **24**:403–427.
3. **Gaasterland T, Sensen CW.** 1996. Fully automated genome analysis that reflects user needs and preferences. A detailed introduction to the MAGPIE system architecture. Biochimie **78**:302–310.
4. **Goldman BS, et al.** 2006. Evolution of sensory complexity recorded in a myxobacterial genome. Proc. Natl. Acad. Sci. U. S. A. **103**:15200–15205.
5. **Huntley S, et al.** 2011. Comparative genomic analysis of fruiting body formation in Myxococcales. Mol. Biol. Evol. **28**:1083–1097.
6. **Hyatt D, et al.** 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics **11**:119.
7. **Ivanova N, et al.** 2010. Complete genome sequence of *Haliangium ochraceum* type strain (SMP-2T). Stand. Genomic Sci. **2**:96–106.
8. **Konovalova A, Petters T, Søgaard-Andersen L.** 2010. Extracellular biology of *Myxococcus xanthus*. FEMS Microbiol. Rev. **34**:89–106.

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9. **Li Z-F, et al.** 2011. Genome sequence of the halotolerant marine bacterium *Myxococcus fulvus* HW-1. J. Bacteriol. **193**:5015–5016.
10. **Margulies M, et al.** 2005. Genome sequencing in microfabricated high-density picolitre reactors. Nature **437**:376–380.
11. **Miller JR, et al.** 2008. Aggressive assembly of pyrosequencing reads with mates. Bioinformatics **24**:2818–2824.
12. **Reichenbach H.** 1999. The ecology of the myxobacteria. Env. Microbiol. **1**:15–21.
13. **Schneiker S, et al.** 2007. Complete genome sequence of the myxobacterium *Sorangium cellulosum.* Nat. Biotechnol. **25**:1281–1289.
14. **Van Domselaar GH, et al.** 2005. BASys: a Web server for automated bacterial genome annotation. Nucleic Acids Res. **33**:W455–W459.