Origins of replication in *Cyanothece* 51142

Welsh *et al.* (1) recently reported the complete genome of *Cyanothece* 51142 in PNAS. The authors concluded that “The origin of replication could not be determined for either the circular or linear chromosome by using standard GC skew and DnaA box analysis” (1). However, by utilizing a web-based system Ori-Finder (2), we have identified the locations of *oriC* for both the circular and linear chromosomes in *Cyanothece* 51142. For the circular chromosome, the *oriC* is predicted within the intergenic region between the ORF *cce_1862* and the *dnaN* gene (*cce_1864*), from 1,886,587 nt to 1,887,114 nt of the chromosome. The feature that *oriC* is adjacent to the *dnaN* gene is universal among the bacteria within the class *Cyanobacteria* (for more detail, please visit DoriC, a database of *oriC* regions in bacterial genomes at <http://tubic.tju.edu.cn/doric/>). This *oriC* region also contains 3 putative DnaA boxes (Fig. 1A), each with perfect match to TTTTCCACA, the “species-specific” DnaA box motif for the class *Cyanobacteria*. For the linear chromosome, the *oriC* is predicted within the intergenic region between 2 ORFs, *cce_5168* and *cce_5169*, from 373,518 nt to 373,849 nt of the chromosome. This identified *oriC* region is around the minimum of the GC disparity curve (348,971 nt) and contains 3 putative DnaA boxes (Fig. 1B), each with no more than 1 mismatch from TTATCCACA, the DnaA box motif of *Escherichia coli*. It is also observed that the *oriC* for the linear

Fig. 1. Schematic diagram of the replication origins in *Cyanothece* 51142 for the circular chromosome (A) and linear chromosome (B). DnaA box, palindromic repeat, and reverse repeat are marked in green, blue, and red, respectively.

chromosome contains a reverse repeat, TGAAGATATA-GAAGT (Fig. 1B).

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2. Gao F, Zhang CT (2008) Ori-Finder: A web-based system for finding *oriC*s in unannotated bacterial genomes. *BMC Bioinformatics* 9:79.

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The authors declare no conflict of interest.

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