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THE GENOME-WIDE PREVALENT ANTI-SENSE RNA EXPRESSION
FOR TRANSLATIONAL REGULATION IN *SYNECHOCYSTIS* SP.

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Synechocystis sp. PCC6803 has a compact genome where 87% of the base
are protein coding. Furthermore, the *Synechocystis* genome is known to
contain a vast amount of antisense RNA. Although the regulatory roles of
some antisense RNAs have been identified, there is a lack of genome-wide
study that comprehensively reports the anti-sense regulation of translation.
Here, we used strand-specific RNA-seq and ribosome profiling to
understand the genome wide effects of antisense RNA on translation
regulation. Under different light intensity and temperature conditions, we
observed a numerous untranscribed transcripts overlapped with the antisense
direction of the adjacent genes, which lead to a huge decrease in the
translation efficiency. This data suggests that untranscribed transcripts
prevent translation and possibly degrade the transcripts in the antisense. In
addition to the regulatory mechanism of the untranscribed transcripts, this
study is the first report of ribosome profiling on *Synechocystis*, which can
be used as a resource for understanding its underlying mechanism of
translational regulation. This study was supported by the Basic Core
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