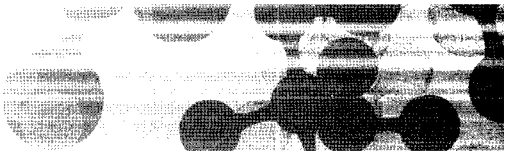

S9-1

Functional networks of noncoding RNAs in *Escherichia coli*

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The large number of noncoding RNAs (ncRNAs) are identified from bacteria to mammals in recent years. They are involved in a variety of cellular functions although many of them remain to be elucidated. In this study, we identified functional relations between 6S RNA and RygC. The *rygC* gene is located downstream of the *ssrS* gene encoding 6S RNA and in vitro transcription of *ssrS* extends to *rygC*. 6S RNA binds to RNA polymerase (RNAP)σ^{70}-holoenzyme ($E\sigma^{70}$) and reduces its activity, making it possible to alter the utilization of $E\sigma^{70}$ to ES in the stationary phase of growth. We found that 6S RNA is transcribed from two tandem promoters, designated P1 and P2, which are proximal and distal to the mature 6S RNA sequence, respectively. P1 is a canonical σ^{70}-dependent promoter, while P2 is both a σ^{70}- and a S-dependent promoter. Hence, transcription of 6S RNA can be regulated by switching factors for the formation of specific RNAP holoenzymes, in response to environmental signals. RygC RNA was previously identified as about 140-nt RNA, but its function remains unclear. RygC has a significant sequence homology with other ncRNAs, RygD, RyeC, and RyeD. The *rygC*-knockout strain did not show any mutant phenotype, while the strain overexpressing RygC entered the stationary phase earlier than the control strain. A comparative proteomic analysis showed that the RygC-overexpressing cells increased *pspA* expression as the 6S RNA-deficient cells did. Our results suggest that function of RygC is reciprocally related to that of 6S RNA.