Promoter islands as instruments of bacterial evolution

O. Ozoline, K. Shavkunov, O. Glazunova, E. Fesenko, M. Tutukina, S. Kiselev

Institute of Cell Biophysiscs, RAS, Pushchino state Institute of Natural Sciences, Pushchino, Russia ozoline@rambler.ru

S. Antipov, V. Pokusaeva

Voronezh State University, Voronezh, ss.antipov@gmail.com

V.Panyukov

Institute of Mathematical Problems of Biology RAS Pushchino, Russia, panyukov@itaec.ru

Promoter islands (PIs) initially were found in the genome of *E.coli* due to the extremely high density of the transcription start points, predicted *in silico* (exemplified in Fig. 1A and B). Interacting with RNA polymerase (RNAP) better than normal promoters, PIs show surprisingly low transcriptional activity (1). To deduce biological role of these unusual elements, we evaluated their structural properties in comparison with normal promoters and non-promoter DMAs, checked the ability of PIs to produce short oligos, estimated their capacity to form complexes with nucleoid proteins and specified their genomic distribution.

Transcriptional activity of PIs was assessed using the 5'-end specific RNA-seq data, (2) which were analyzed by the software RNAMatcher. Structural parameters were measured for 3D models using the software aSHAPE (3). An ability to form complexes with nucleoid proteins and several transcription factors was assessed using available chip-on-chip data. Interaction with the nucleoid protein Dps was measured experimentally.

We found that the synthesis of normal mRNAs from PIs is deliberately quenched at the stage of promoter clearance. At least in part it is conditioned by the specific 3D structure of PIs, providing a platform for interaction with both RNAP and structuring proteins of bacterial chromosome, including H-NS and Dps. Deletion of *hns* increased the transcription output from PIs, thus confirming participation of this protein in the transcriptional silencing. We found that most PIs are located near genes presumably acquired by the horizontal transfer, while orthologs within the genomes of potential donors have normal promoters (Fig. 1).

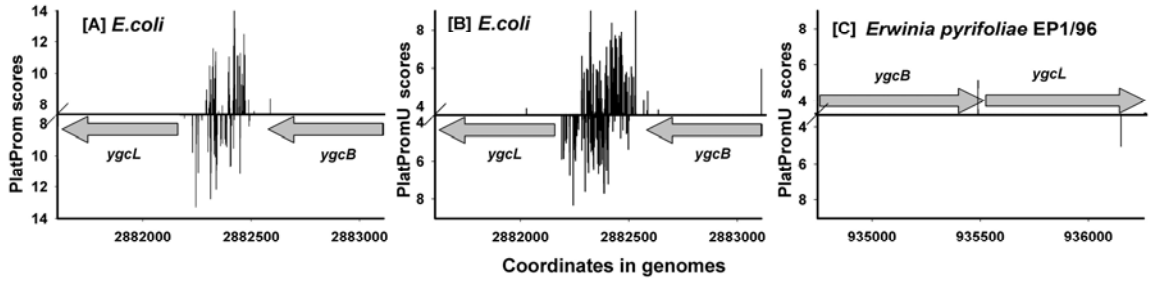

Figure 1. Distribution of potential transcription start points predicted in the *ygcL* regulatory region of *Escherichia coli* K12 MG1655 [**A** and **B**] or *Erwinia pyrifoliae* EP1/96 [**C**] by the promoter finder PlatProm [1] or PlatPromU [4]. According to predictions given in (5, 6), *E.coli* acquired genes *ygcL* and *ygcB* by horizontal transfer. Putative orthologs of these genes were found only in the genomes of two *Erwinia*. This bacterium can therefore be considered as a donor. The *promoter island* in front of *ygcL* was originally found by PlatProm [A], i.e. by the software adapted to recognize σ^{70} promoters of *E.coli*. In order to compare the density of promoter-like signals in two genomes we used the unified version of this software PlatPromU [**B** and **C**], which ignores σ^{70}-specific weight matrices. X-axes in all panels correspond to 4 StD above the background level ($p<0.00004$).

We assume that PIs evolve nearby the "alien" genes so as to suppress expression of toxic or useless genes and to offer suitable promoters for beneficial genes, thus playing a complex role in the assimilation of foreign DNA. Putative mechanism underlying accelerated evolution of promoter-rich regions will be discussed.

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