

**Curli synthesis and biofilm formation in enteric bacteria are controlled by a dynamic small RNA module made up of a pseudoknot assisted by an RNA chaperone.**

Valérie Bordeau, Brice Felden

► **To cite this version:**

Valérie Bordeau, Brice Felden. Curli synthesis and biofilm formation in enteric bacteria are controlled by a dynamic small RNA module made up of a pseudoknot assisted by an RNA chaperone.. *Nucleic Acids Research*, Oxford University Press, 2014, 42 (7), pp.4682-96. <10.1093/nar/gku098>. <inserm-00941995>

**HAL Id: inserm-00941995**

**<http://www.hal.inserm.fr/inserm-00941995>**

Submitted on 4 Feb 2014

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

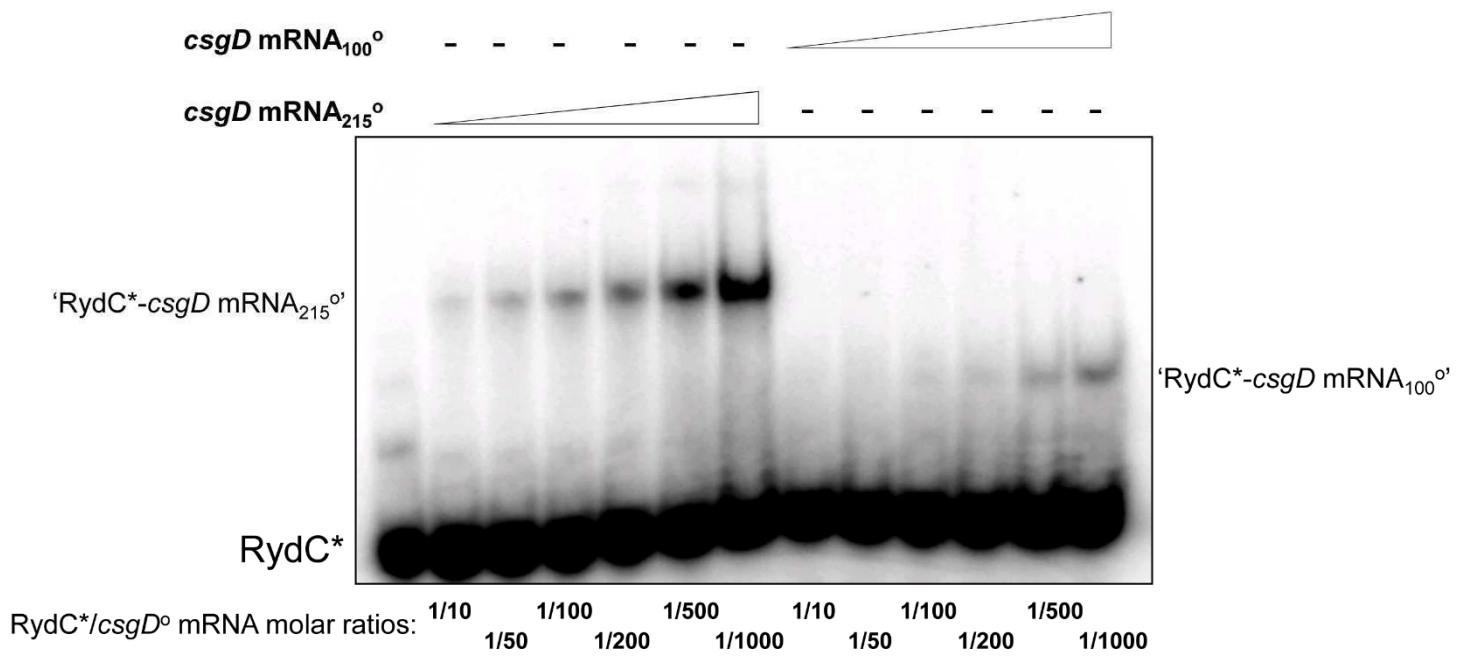
Curli synthesis and biofilm formation in enteric bacteria is controlled by a dynamic small RNA module made up of a pseudoknot assisted by an RNA chaperone.

Valérie Bordeau and Brice Felden\*

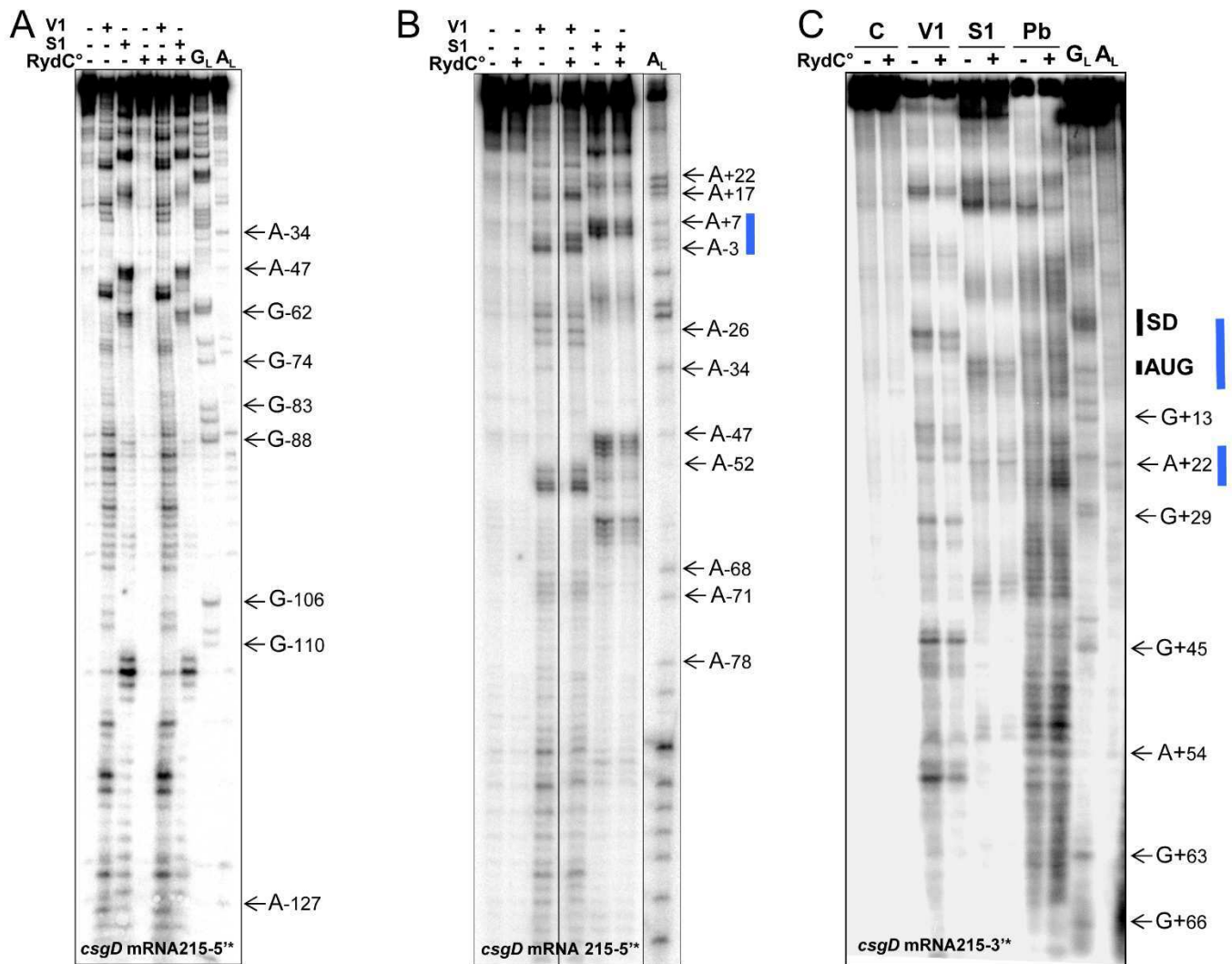
Université de Rennes I, Inserm U835-UPRES EA2311, Biochimie Pharmaceutique, 2 avenue du Prof. Léon Bernard 35043 Rennes, France.

\*Corresponding author: [bfelden@univ-rennes1.fr](mailto:bfelden@univ-rennes1.fr)

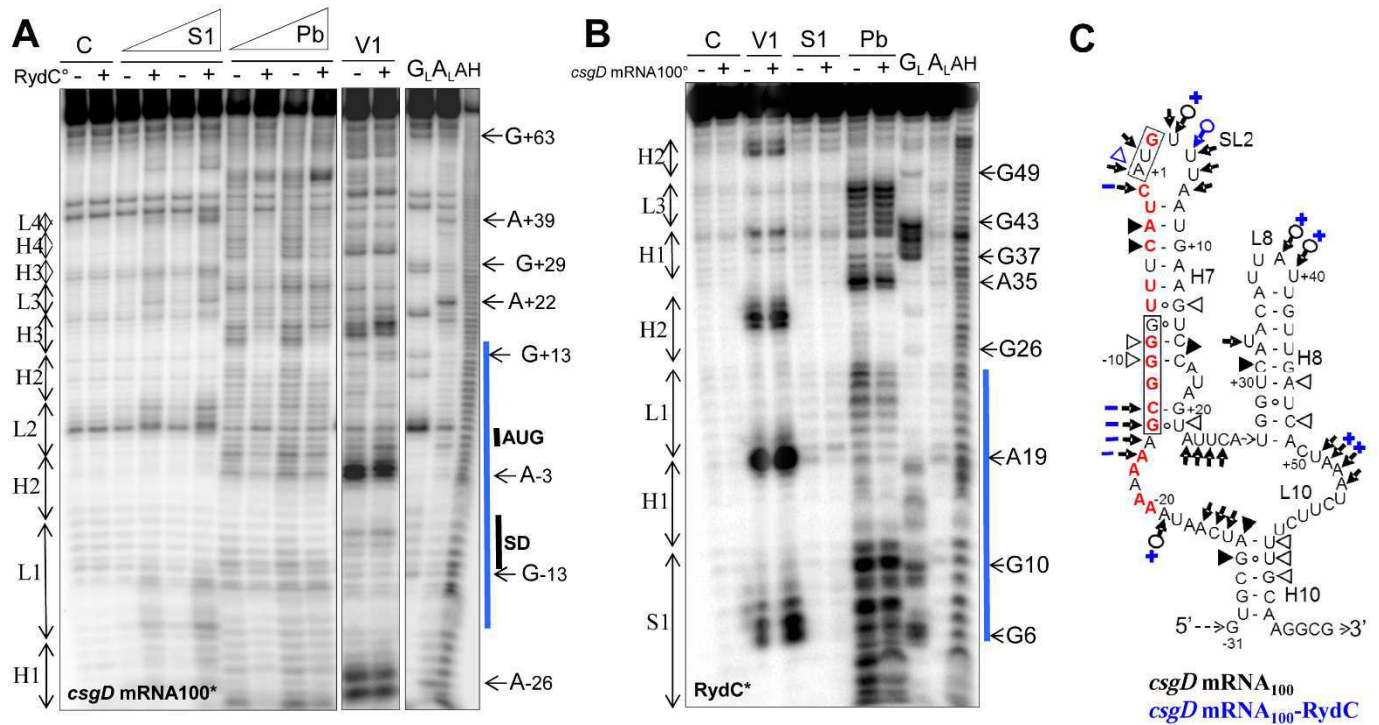
*Supplemental Material*



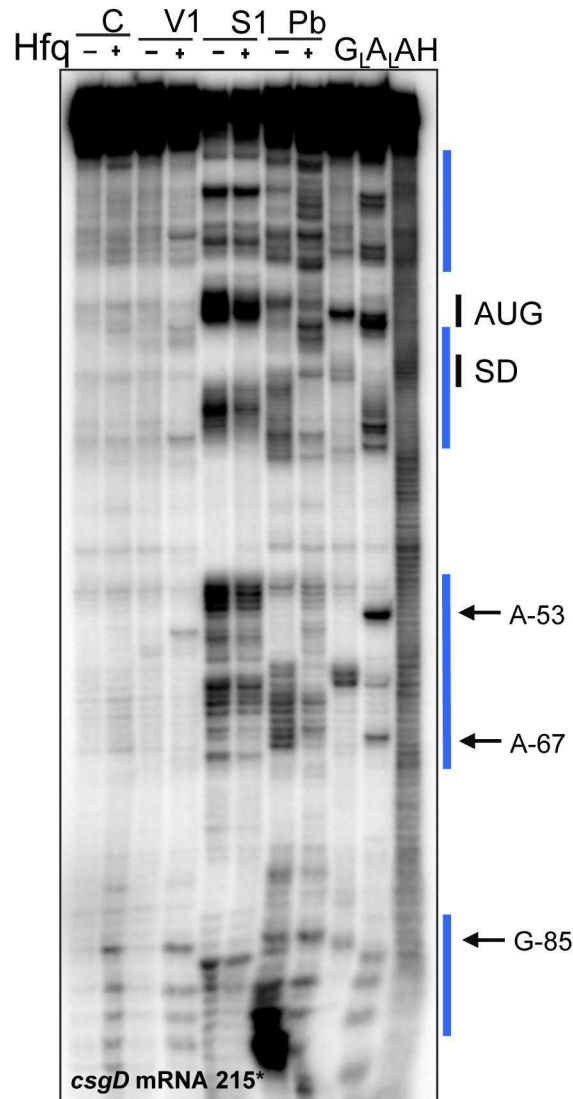
**Figure S1. Complex formation between RydC and two  $csgD$  mRNA fragments of different lengths.**  $csgD$  mRNA<sub>100</sub> and  $csgD$  mRNA<sub>215</sub> correspond to 100 and 215 nts from the  $csgD$  mRNA 5'-end, respectively. Native gel retardation assays of purified labelled RydC with increasing amounts of unlabelled  $csgD$  mRNA<sub>215</sub> and  $csgD$  mRNA<sub>100</sub> (10 to 1000-fold more than RydC) in the absence of the Hfq protein. This indicates that in the absence of the Hfq protein, the affinity between the two RNAs is weak.



**Figure S2. Structural analysis of the conformational changes in *csgD* mRNA<sub>215</sub> induced by complex formation with RydC.** Autoradiograms of the cleavage products of 5'- (A, B) or 3'-labelled (C) *csgD* mRNA<sub>215</sub> by RNases V<sub>1</sub> (5.10<sup>-5</sup> unit) and nuclease S<sub>1</sub> (2 units) in the presence or absence of unlabelled RydC at a 1:100 molar ratio. Lanes G<sub>L</sub>, RNase T<sub>1</sub> hydrolysis ladder; lanes A<sub>L</sub>, RNase U<sub>2</sub> hydrolysis ladder. The RNA sequences are indexed on the right sides of each panel. The conformational changes of the *csgD* mRNA upon complex formation with RydC are indicated with vertical blue bars. The SD sequence and AUG initiation codon of the mRNA are also shown.



**Figure S3. Structural analysis of the conformational changes of RydC and *csgD mRNA*<sub>100</sub> induced by complex formation with *csgD mRNA*<sub>100</sub> and RydC, respectively.** **A, B.** Autoradiograms of cleavage products of 5'-labelled *csgD mRNA*<sub>100</sub> (100 nts-long) (A) or 5'-labelled RydC (B) by RNases V<sub>1</sub> (5.10<sup>-5</sup> unit), nuclease S<sub>1</sub> (0.5 and 1 unit) and lead acetate (0.5 and 1 mM) in the presence or absence of either unlabelled RydC (A) or unlabelled *csgD mRNA*<sub>100</sub> (B) at 1:100 molar ratios. The *csgD mRNA*<sub>100</sub> or RydC structural domains are indicated on the left sides of each panel. Upon complex formation, the conformational changes of *csgD mRNA*<sub>100</sub> or RydC are highlighted by vertical blue bars. **C.** Secondary structure of the *csgD mRNA*<sub>100</sub> inferred from the probing results, which support the proposed model. Triangles are V<sub>1</sub> cuts; arrows capped by a circle are S<sub>1</sub> cuts; uncapped arrows are lead cuts. The cut and cleavage intensities are proportional to the darkness of the symbols. The structural domains are indicated and the AUG and SD sequences are outlined. The red nucleotides are those proposed to interact with RydC. Structural changes detected in the *csgD mRNA*<sub>100</sub> upon RydC complex formation are in blue.



**Figure S4. Structural analysis of the conformational changes of *csgD* mRNA<sub>215</sub> induced by complex formation with Hfq.** Autoradiograms of the cleavage products of 5' *csgD* mRNA<sub>215</sub> by RNases V<sub>1</sub> ( $15 \cdot 10^{-5}$  unit), nuclease S<sub>1</sub> (0.5 units), and lead acetate (1 mM) in the presence or absence of Hfq at a 1:20 molar ratio. Lanes G<sub>L</sub>, RNase T<sub>1</sub> hydrolysis ladder; lanes A<sub>L</sub>, RNase U<sub>2</sub> hydrolysis ladder. The RNA sequences are indexed on the right sides of the panels. Upon complex formation with Hfq, the conformational changes in *csgD* mRNA are emphasized by the vertical blue bars. The SD sequence and AUG initiation codon of the mRNA are indicated

Table S1. Strains used and constructed in this study.

| Strain   | Description  | Source,Reference |
|--|--|------------------|
| <i>E. coli</i> MG1655Z1                              | Z1(lacR tetR SpR)  | (4)              |
| <i>E. coli</i> MG1655Z1 $\Delta$ rydC                | Z1(lacR tetR SpR) $\Delta$ RNA1114::Cm                           | (4)              |
| <i>E. coli</i> MG1655Z1 pUC18                        | MG1655Z1 + pUC18   | (4)              |
| <i>E. coli</i> MG1655Z1 pUC18-rydC                   | MG1655Z1 + pUC18-RNA1114   | (4)              |
| <i>S. enterica</i> subsp. <i>bongori</i> +pUC18      | <i>Salmonella enterica</i> subsp. <i>bongori</i> + pUC18         | This study       |
| <i>S. enterica</i> subsp. <i>bongori</i> +pUC18-rydC | <i>Salmonella enterica</i> subsp. <i>bongori</i> + pUC18-RNA1114 | This study       |
| <i>S. sonnei</i> +pUC18                              | <i>Shigella sonnei</i> + pUC18                                   | This study       |
| <i>S. sonnei</i> +pUC18-rydC                         | <i>Shigella sonnei</i> + pUC18-RNA1114                           | This study       |

Table S2. DNA oligodeoxyribonucleotides used in this study.

| Names                  | Sequences (5' → 3')  | Purposes  |
|------------------------|--|---|
| csgD215rev             | CGCCTGCAAAGAAGATTTAGT  | <i>csgD</i> mRNA <sub>215</sub> transcription toeprint<br><i>csgD</i> mRNA <sub>100</sub> transcription,<br><i>csgD</i> mRNA <sub>115</sub> transcription |
| csgD215for             | <u>TAATACGACTCACTATAGGATGTAATCCATTAGTTTTATATTT</u><br>ACCC           | <i>csgD</i> mRNA <sub>215</sub> transcription   |
| csgD100for             | <u>TAATACGACTCACTATAGGGTGCATCAATAAAAAAAGCGGGG</u><br>TTTCAT          | <i>csgD</i> mRNA <sub>100</sub> transcription   |
| csgD503                | TTGCAACCCTTAATTGACAACACGTTCTTGAT                                     | <i>csgD</i> mRNA <sub>503</sub> transcription   |
| csgD $\Delta$ 5'UTRfor | <u>TAATACGACTCACTATAGGTTTAATGAAGTCCATAGTA</u>                        | <i>csgD</i> mRNA $\Delta$ 5'UTR   |
| csgD115rev             | ACCTGACAGCTGCCTCTAAAA  | <i>csgD</i> mRNA <sub>115</sub> transcription   |
| csgDnorth              | CAATGTCGCGGTACGGGTAATCTTCAGGCGTATTTAGCAA                             | <i>csgD</i> mRNA northern   |
| RydCfor                | <u>CGGGATCCTAATACGACTCACTATAGGGCTTCCGATGTAGACCC</u><br>GTT           | RydC transcription  |
| RydCrev                | AAGAAAACGCCTGTACTAAAAC   | RydC transcription  |
| RydCnorth              | ACCGACCCGTGGTACAGGCG   | RydC northern   |
| RydC $\Delta$ 5'for    | <u>TAATACGACTCACTATAGGCCTGTACCACGGGTCGGTTTTAGTA</u><br>CAGGCGTTTTCTT | RydC transcription  |
| RydC $\Delta$ 5'rev    | AAGAAAACGCCTGTACTAAAACCGACCCGTGGTACAGGCCTAT<br>AGTGAGTCGTATTA        | RydC $\Delta$ 5' transcription  |
| tmRNAnorth             | GTTTTAACGCTTCAACCCCA   | tmRNA northern  |
| 5Snorth                | CTTCTGAGTTCGGCATGGGC   | 5S rRNA northern  |
| csgBAnorth             | AACTGCAGCACCGTTGCCACCACCGAACTGTTTAACCGTCATTT<br>AAT                  | <i>csgBA</i> mRNA northern  |

|                       |   |                                    |
|-----------------------|---|------------------------------------|
| Ryd <sub>H1</sub> for | <u>GAAATTAATACGACTCACTATAGGCTTCCGATGTAGACCCGTATTCTT</u><br>CGCCTGTACCTGCCAGGGTTTTAGTACAGGCGTTTTCTT  | Ryd <sub>H1</sub><br>transcription |
| Ryd <sub>H1</sub> rev | AAGAAAACGCCTGTACTAAAACCCTGGGCAGGTACAGGCGAAGAAT<br>ACGGGTCTACATCGGAAGCCTATAGTGAGTCGTATTAATTTC        | Ryd <sub>H1</sub><br>transcription |
| Ryd <sub>H2</sub> for | <u>GAAATTAATACGACTCACTATAGGCTTCCGATGTACTGGGCAATTCTT</u><br>CGCCTGTACCACGGGTCGGTTTTAGTACAGGCGTTTTCTT | Ryd <sub>H2</sub><br>transcription |
| Ryd <sub>H2</sub> rev | AAGAAAACGCCTGTACTAAAACCGACCCGTGGTACAGGCGAAGAATT<br>GCCAGTACATCGGAAGCCTATAGTGAGTCGTATTAATTTC         | Ryd <sub>H2</sub><br>transcription |
| Ryd <sub>H3</sub> for | <u>GAAATTAATACGACTCACTATAGGCTTCCGATGTACTGGGCAATTCTT</u><br>CGCCTGTACCTGCCAGGGTTTTAGTACAGGCGTTTTCTT  | Ryd <sub>H3</sub><br>transcription |
| Ryd <sub>H3</sub> rev | AAGAAAACGCCTGTACCAAACCCTGGGCAGGTACAGGCGAAGAATT<br>GCCAGTACATCGGAAGCCTATAGTGAGTCGTATTAATTTC          | Ryd <sub>H3</sub><br>transcription |
| RydCPCRQ1             | AAGAAAACGCCTGTACTAA   | Real-Time PCR                      |
| RydCPCRQ2             | CTTCCGATGTAGACCCGTA   | Real-Time PCR                      |
| tmRNAPCRQ1            | GGCAAGCGAATGTAAAGACTGA  | Real-Time PCR                      |
| tmRNAPCRQ2            | CCGCGTCCGAAATTCCTA  | Real-Time PCR                      |
| csgDPCRQ1             | CACGGAATCAGCCCTCCTTA  | Real-Time PCR                      |
| csgDPCRQ2             | GCCGATACGCAGCTTATTCAG   | Real-Time PCR                      |