

## Supplemental Material for:

# Cellulose as an architectural element in spatially structured *Escherichia coli* biofilms

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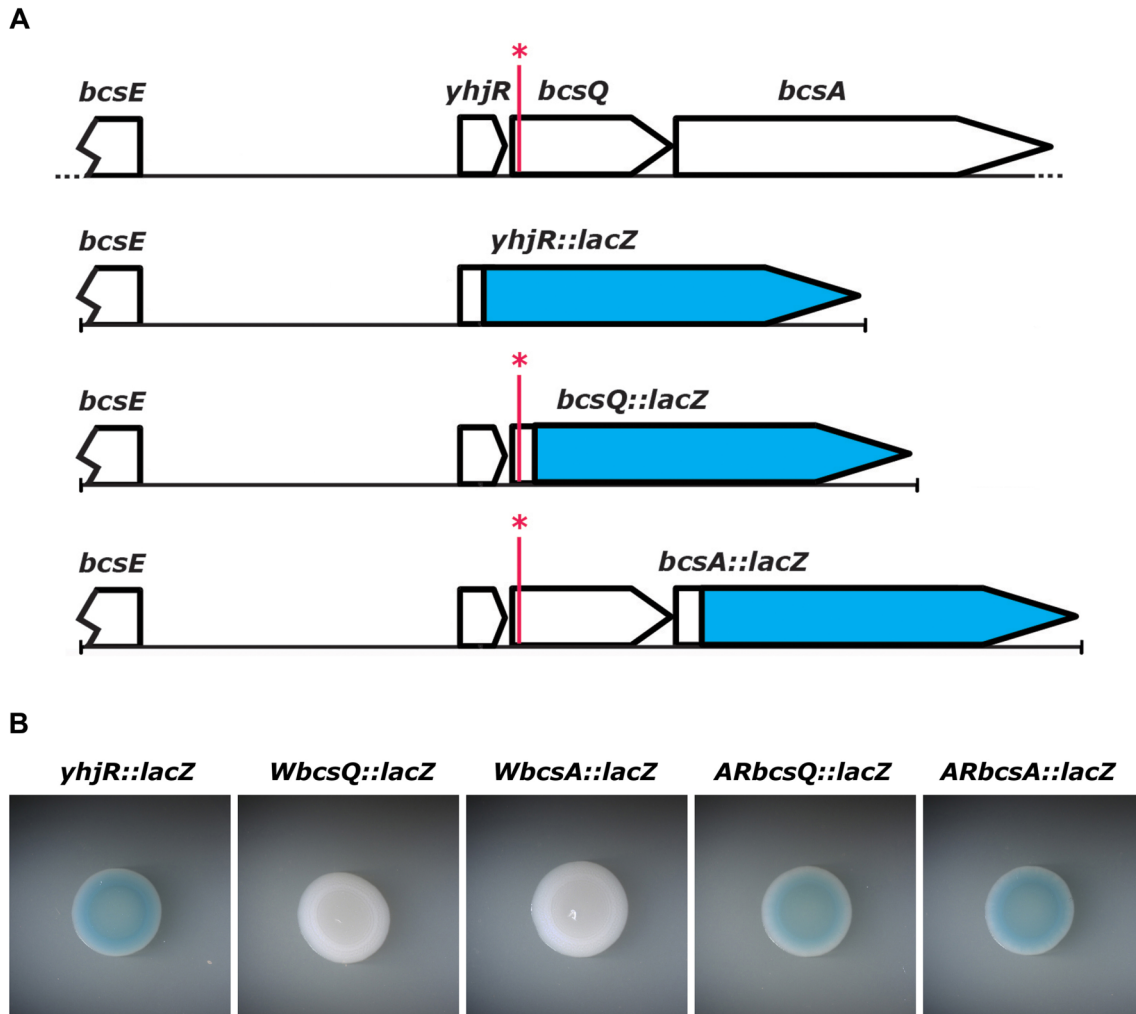
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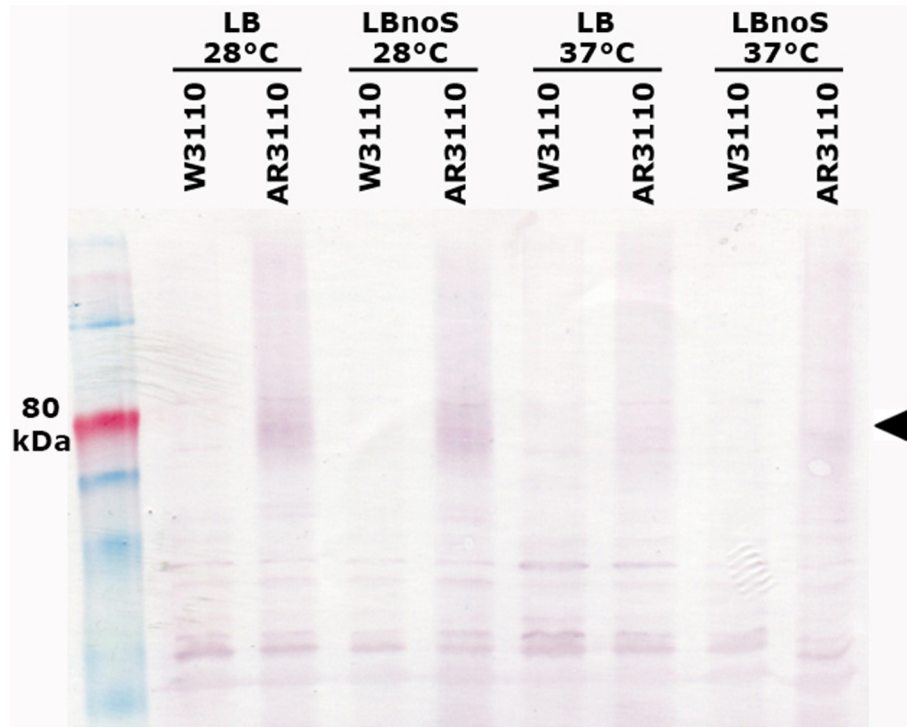
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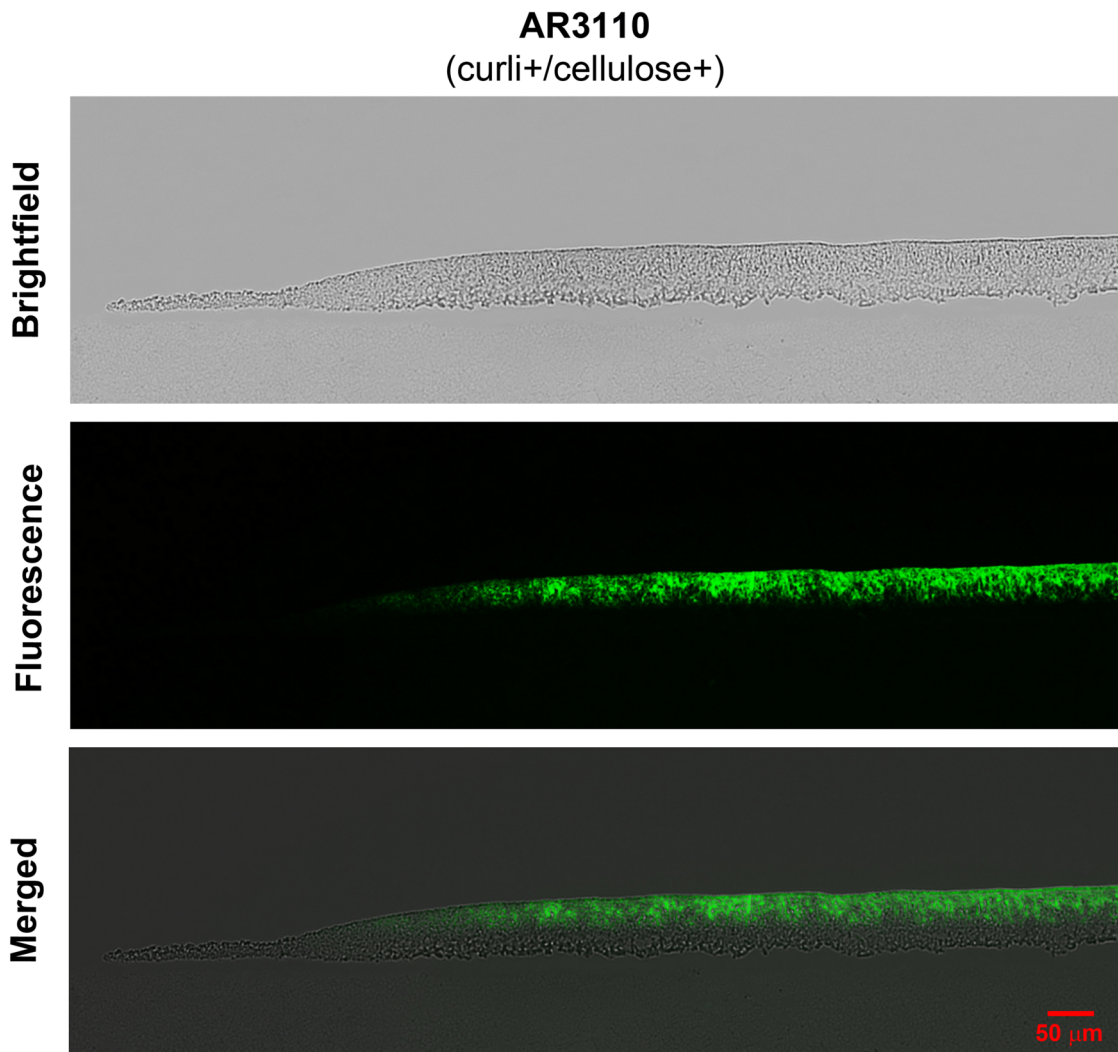
- Movie S1: Dissolution by shear forces of a cellulose- and curli-free macrocolony
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**Figure S1. Construction of single copy *lacZ* reporter fusions to *yhiR*, *bcsQ* and *bcsA* and  $\beta$ -galactosidase activities in colonies of fusion-carrying strains. **A:** The latter two fusions were constructed with TAG ('W' fusions) or TTC ('AR' fusions) in codon 6 of *bcsQ* (position indicated by a red asterisk). Lengths of genes and intergenic regions are not drawn to scale. **B:** Different  $\beta$ -galactosidase activities conferred by these *lacZ* fusions integrated into the chromosome of strain W3110 are shown qualitatively in colonies grown for 2 days on salt-free LB containing the indicator XG.**



**Figure S2. FLAG-tagging reveals the expression and temperature regulation of cellulose synthase (BcsA) in strain AR3110 but not in W3110.** W3110 and AR3110 carrying FLAG-tagged *bcsA* in the chromosome were grown in LB or salt-free LB at 28°C or 37°C as indicated and FLAG-tagged proteins were detected in colonies growing for four days at 28 °C (40  $\mu$ g total protein per lane) by immunoblot analysis using an anti-FLAG serum. Note that as an overall hydrophobic membrane protein, BcsA runs as a diffuse band and more rapidly than expected for its actually molecular mass (99.8 kDa).



**Figure S3. Cryosection through the outer growth zone of a 5-day-old macrocolony of strain AR3110 grown in the presence of thioflavine S.** A thin section (5  $\mu$ m) of a representative AR3110 macrocolony was visualized at low magnification by brightfield and fluorescence microscopy, the latter was false-colored green for TS and the two images were merged. Brightfield in the merged image appears on a dark grey background to better visualize the location of the fluorescence.

**Table supplement 1.** Oligonucleotides used in this study.

**I. Primers for 2-step mutagenesis of *bcsQ* SNP<sup>1:2</sup>**

Primer	Sequence
<i>BcsQ</i> HP1 pKD54	5'-CTGCCTGATCCCGCGATAGGCTATATCTTCCAGAATGATATT GTGGCGTTTCAGA <b>AGAACTCGTCAAGAAG</b> -3'
<i>bcsQ</i> HP2 pKD45	5'-TAGCGCAACCCAGCGTCACGCCAGTCCTGGCCATCCAGCA TCGCTCTGGCCGGA <b>TATTATCGTGAGGATG</b> -3'
<i>bcsQ</i> mut1 rev	5'-CTGGGATT <u>GC</u> AGGGGG -3'
<i>bcsQ</i> mut2 fw	5'-CCCTGCA <u>AT</u> CCCAGTACG -3'

<sup>1</sup>Cat/Kan cassette-specific sequences are shown in **boldface**.

<sup>2</sup>mutation introduced at the natural SNP position is underlined.

**II. Primers for generating knockout mutations by one-step inactivation<sup>1</sup>**

$\Delta bcsQ::cat$	5'- TGGCCGTA <b>CTGGGATTGCAGGGGGT</b> GCGGGGAGGCCGTGG GGACAACAACCGT <b>GTAGGCTGGAGCTGCTTC</b> -3' 5'- TGGTGGGTTATCTGCGAGGCATCACGCGGTAAGT <b>CGATTA</b> AAATCCACTGCATATGAATATCCTCCTTAG -3'
$\Delta bcsEFG::kan$	5'- GATAAGTTTTAATTTCAATGGTAGGTTTATTTCTTAGCTTTC GCTAGGT <b>GTAGGCTGGAGCTGCTTC</b> -3' 5'-TTACTGCGGGTAAGGCACCCAGTCGCCGCCGTT <b>CAGGCGA</b> ACGTACGGATTCCGGGGATCCGTCGACC -3'
$\Delta yhjR::cat$	5'- ATGAATAACAATGAACCAGATACTCTGCCTGATCCCGCGATAG GCTATAT <b>GTGTAGGCTGGAGCTGCTTC</b> -3' 5'- CTACTTTTGTGCGCAA <b>ACTCTGCCAGCAACGGCCAGCGTTTT</b> AATGCCGCATATGAATATCCTCCTTAG -3'

<sup>1</sup>Cat/Kan cassette-specific sequences are shown in **boldface**.

**III. Primers for generating *lacZ* reporter fusions<sup>3</sup>**

<i>yhjR</i> EcoRI	5'-GCTCAGGA <b>ATTCTGATTCGCCAGACTGATAGC</b> -3'
<i>yhjR</i> HindIII	5'-GCA <b>AGCTTGCAGAGTATCTGGTTCATT</b> -3'
<i>bcsQ</i> HindIII	5'-GCA <b>AGCTT</b> GATGGTTGTTGTCCCCACGCC -3'
<i>bcsA</i> HindIII	5'-GCA <b>AGCTT</b> GGATAAGCAACCACGGGTCAG -3'

<sup>3</sup>Restrictions sites are shown in **boldface**.

**IV. Primers used for C-terminally 3xFLAG-tagging of BcsA**

<i>bcsA</i> H1Flag	5'-CGGCACAACCATCGGATCAGGCTTTGGCTCAACAA -3'
<i>bcsA</i> H2Flag	5'-AAATCCAGAATAGTTTTCTTTTCATCGCGTTATCA -3'