

Supplementary material

Table S1. Summary results of fluorescence binding analysis obtained with twelve different lectins in *A. thiooxidans* wild type cells.

| Lectin | Specificity ^a | <i>A. thiooxidans</i> ^T |
|--------|--|------------------------------------|
| AAL | L-Fucose α (1,6) N-Acetyl-D-Glucosamine | + |
| BPA | N-Acetyl-D-Galactosamine | + |
| ConA | Internal D-Mannose and D-Glucose | + |
| DBA | Terminal α -N-Acetyl-D-Galactosamine | - |
| GS-I | α -D-Galactose | - |
| GS-II | N-Acetyl-D-Glucosamine | + |
| LPA | N-acetylneuraminic acid | - |
| MPA | α -D-Galactose | - |
| PNA | Galactose β (1,4)Glucose | - |
| SBA | Galactose | - |
| UEA-I | Linked α (1,2) L-Fucose | - |
| WGA | GlcNac β (1,4) GlcNac β (1,4) GlcNac | - |

^a, according to the manufacturer's information (EY Laboratories®, San Mateo, CA, USA).

Table S2. Primers used in this work.

| Name | Sequence 5'-3' ¹ |
|----------------|-----------------------------|
| <i>pelA1_F</i> | CCGATTGCCGCAGTTATTTATT |
| <i>pelA1_R</i> | GCTGTCTTGATGGCTTTGATG |
| <i>pelD_F</i> | CACAAGTTGGCATCCTGGTTCGTT |
| <i>pelD_R</i> | CATGCTGCCTGCGAAAGGTAACAA |
| <i>wgcA_F</i> | GAACTTGTC AATGCGCCATC |
| <i>wgcA_R</i> | GGCCAGCAATAAATCCTGAATAC |
| <i>flaA_F</i> | CTGGTCACGGCCATCAATAA |
| <i>flaA_R</i> | CAAAGTCCCGCCAGATGTAATA |
| 16S-F3 | ATGGCCTTTATGTCCAGGGCTACA |
| 16S-R3 | AATCCGAACTACGACGCGCTTTCT |
| <i>map_F</i> | GGACCGGATTTGTCACGATTA |
| <i>map_R</i> | GACGTGGTTGAGGGAAATACA |

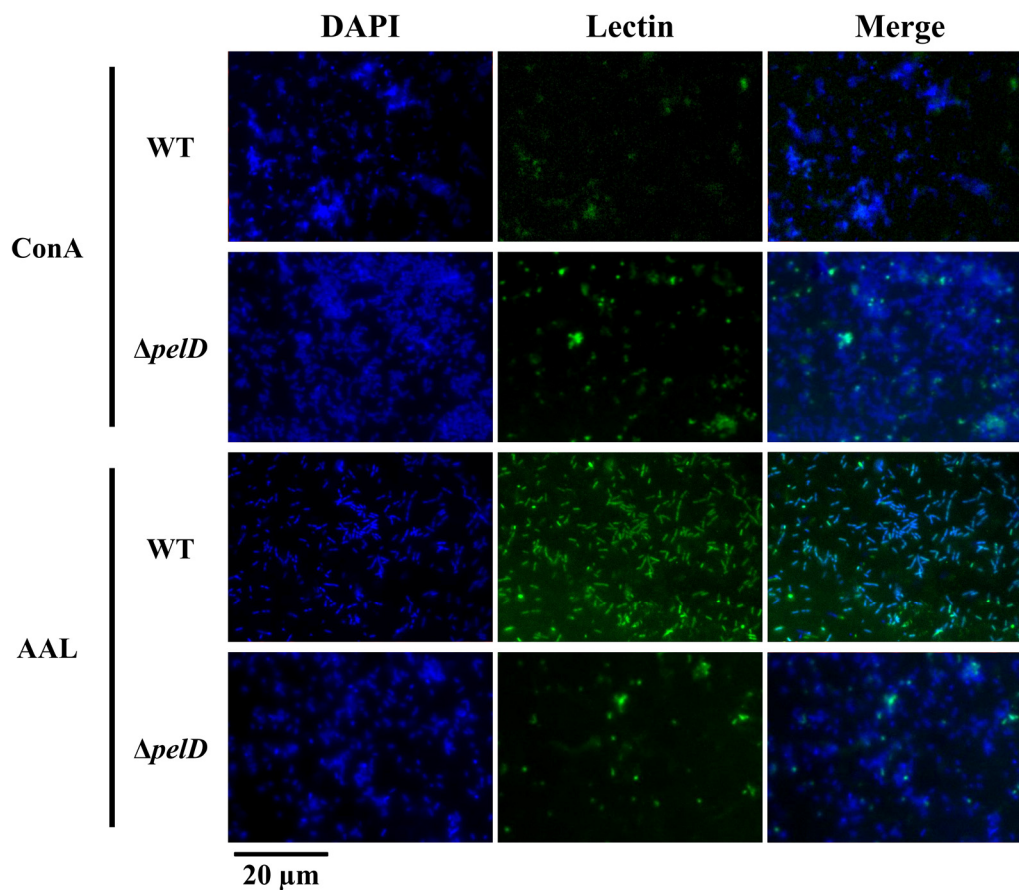


Figure S1. Analysis of PEL exopolysaccharide glycoconjugate composition by using epifluorescence microscopy coupled to FLBA. S^0 -coupons colonized by *A. thiooxidans*^T (WT) or mutant derived ($\Delta pelD$) cells were extracted from 5-days growth cultures and incubated with FITC-conjugated AAL or ConA lectins. Then, they were stained with DAPI before microscopy imaging. Size bars represent 20 μm .

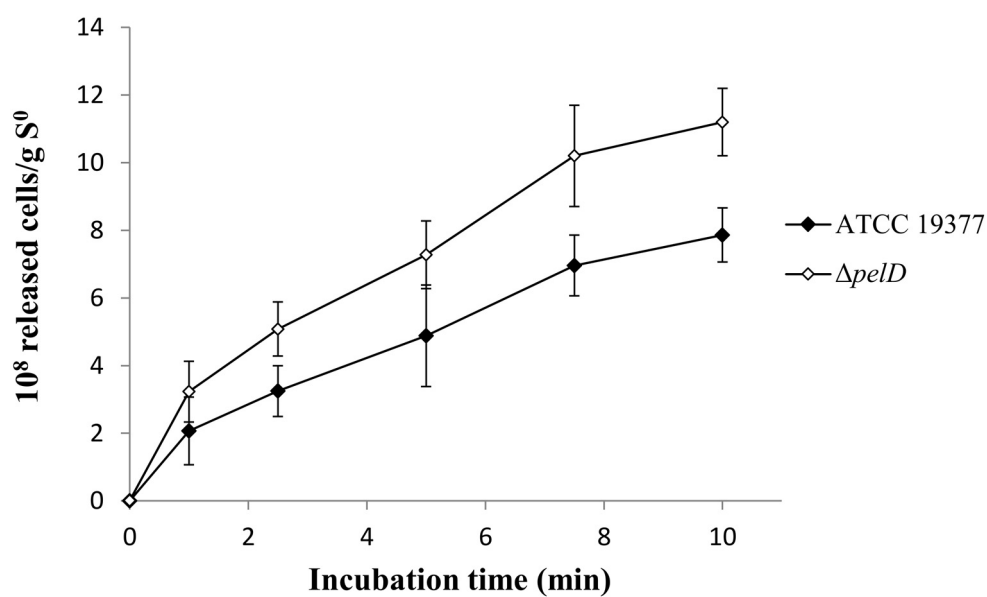


Figure S2. The loss of PEL exopolysaccharide contributes to the production of a fragile biofilm in *A.*

thiooxidans. Inoculated S⁰-coupons were extracted from 5-days growth cultures and treated with 0.05 % Triton X-100. Then they were vortexed during 10 min. Number of cells released from the wild type and $\Delta pelD$ null-mutant biofilms subjected to the mechanical stress was determined with a Petroff-Hausser counting chamber and normalized against mass of sulfur. Standard deviations were calculated from three independent cultures.

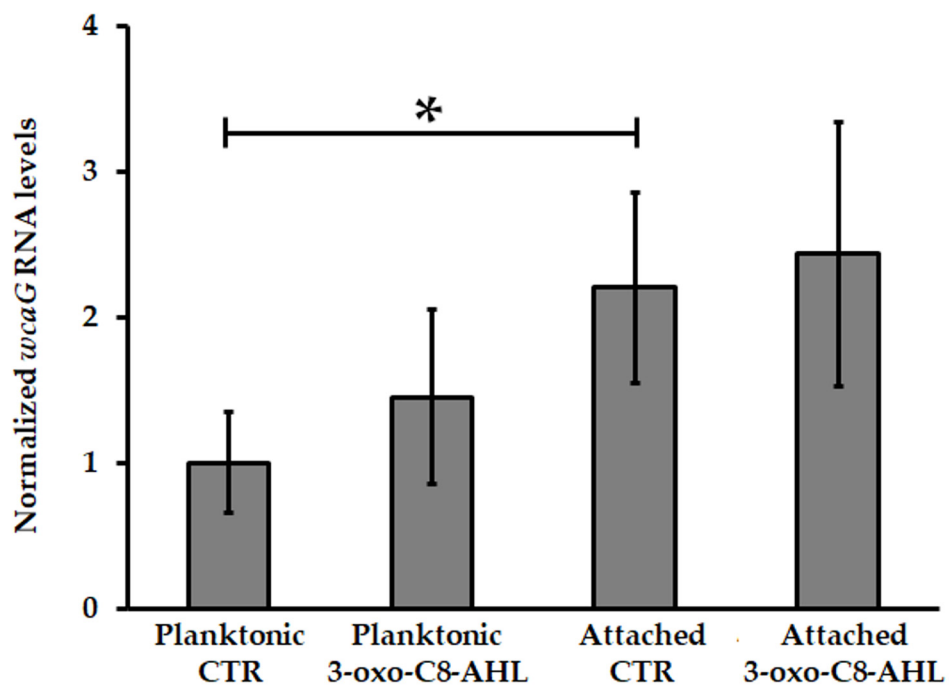


Figure S3. Addition of QS molecule 3-oxo-C8-AHL has no significant effect on transcription levels of *wcaG* from *A. thiooxidans*^T. Total RNAs were extracted from *A. thiooxidans* WT cells obtained from 5-days growth cultures. Transcript levels of *wcaG* were measured by qPCR and then normalized using DNA 16S and *map* genes. Values represent the average of 4 independent experiments \pm standard deviation. Significant differences calculated by a one-way ANOVA test ($p < 0.05$) are noted (*). CTR, DMSO 0.01 % without AHL.

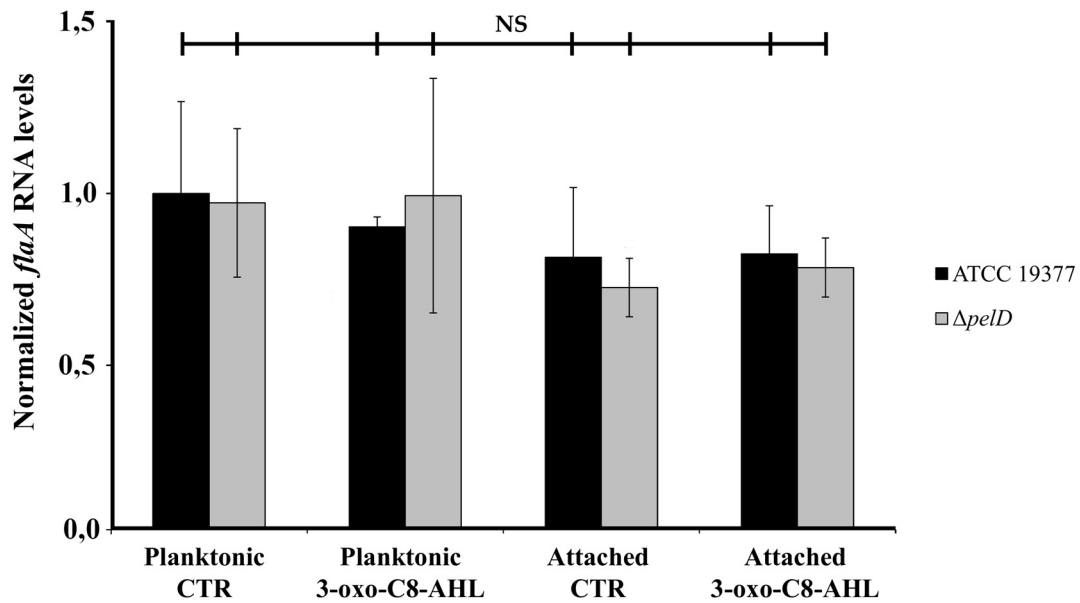


Figure S4. Transcriptional analysis of *flaA* gene from *A. thiooxidans*^T. Total RNAs were extracted from *A. thiooxidans* cells obtained from 5-days growth cultures. Transcript levels were measured by qPCR and then normalized using DNA 16S and *map* genes. Values represent the average of 4 independent experiments \pm standard deviation. NS, None significant differences were observed by a one-way ANOVA test ($p < 0.05$). CTR, DMSO 0.01 % without AHL.

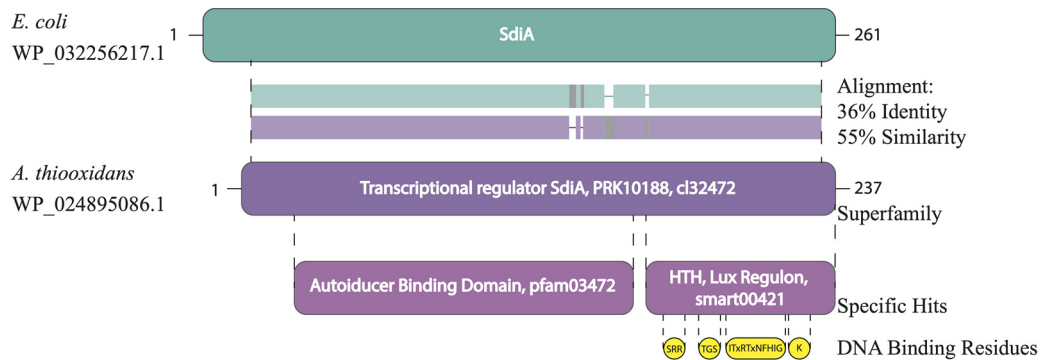


Figure S5. Bioinformatic characterization of WP_024895086.1, a SdiA-like protein present in the new available genome sequences of *A. thiooxidans*. (Top) Schematic representation of SdiA (green) and WP_024895086.1 (purple) amino acid sequence alignment. As noted, both proteins share high similarity and strong identity along over 88% of coverage. Few identified gaps are shown as lines without background color. (Bottom) Domain structure of WP_024895086.1 protein shows the distinctive two domains of canonical QS regulators: Autoinducer Binding Domain (pfam03472) and Helix-Turn-Helix Lux Domain (smart00421), whose combination is classified as PRK10188 Superfamily. Amino acids responsible for DNA binding are depicted in yellow.