

Table S2. Protein sequences used for phylogenetic analyses in Fig. 2A

| Abbreviation | Species and protein name | Accession numbers |
|--------------|--|--|
| Hsa HS | <i>Homo sapiens</i> hyaluronan synthase | AAC50706 |
| Mmu HS | <i>Mus musculus</i> hyaluronan synthase | BAA11654.1 |
| Afu CS | <i>Aspergillus fumigatus</i> chitin synthase | CAA63928.1 |
| Ani | <i>Aspergillus niger</i> hypothetical protein An02g05730 | XP_001399709.1 |
| Cac | <i>Clostridium acetobutylicum</i> ATCC 824 cell wall biosynthesis glycosyltransferase | NP_348113.1 |
| Cdi | <i>Clostridium difficile</i> QCD-37x79 cellulose synthase | ZP_02726444.1 |
| Pcv | <i>Paramecium bursaria Chlorella virus 1</i> similar to <i>Acetobacter</i> cellulose synthase | AAC96840.1 |
| Sgr | <i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350 putative glycosyl transferase | YP_001826277.1 |
| Cin | <i>Ciona intestinalis</i> cellulose synthase | BAD10864 |
| Csa | <i>Ciona savignyi</i> cellulose synthase | AAR89623.1 |
| Agr | <i>Agrobacterium</i> sp. ATCC 31749 putative beta 1, 3 glucan synthase | AAD20440.2 |
| Mae | <i>Microcystis aeruginosa</i> PCC 7806 unnamed protein | CAO87270.1 |
| Sme | <i>Sinorhizobium meliloti</i> 1021 putative cellulose synthase | NP_436917.1 |
| Mpo | <i>Methylobacterium populi</i> BJ001 cellulose synthase | YP_001923985.1 |
| Msp | <i>Methylobacterium</i> sp. 4-46 cellulose synthase | YP_001770326.1 |
| Ret | <i>Rhizobium etli</i> CIAT 652 putative cellulose synthase | YP_001985895.1 |
| Rle | <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM2304 cellulose synthase | ZP_02858951.1 |
| Atu | <i>Agrobacterium tumefaciens</i> cellulose synthase | AAC41436.1 |
| Axy1 | <i>Gluconacetobacter xylinus</i> cellulose synthase | AAA85264.1 |
| Axy2 | <i>Gluconacetobacter xylinus</i> cellulose synthase | O82859.1 |
| Axy3 | <i>Gluconacetobacter xylinus</i> cellulose synthase 1 | Q9WX61.1 |
| Ppu1 | <i>Pseudomonas putida</i> F1 cellulose synthase | YP_001267459.1 |
| Ppu2 | <i>Pseudomonas putida</i> F1 cellulose synthase | NP_744779.1 |
| Sen1 | <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi str. CT18 cellulose synthase | NP_458301.1 |
| Sen2 | <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Weltevreden str. HI_N05-537 cellulose synthase | ZP_02830558.1 |
| Eco1 | <i>Escherichia coli</i> E110019 cellulose synthase | ZP_03049480.1 |
| Eco2 | <i>Escherichia coli</i> SMS-3-5 cellulose synthase | YP_001745808.1 |
| Eco3 | <i>Escherichia coli</i> O157:H7 str. Sakai putative cellulose synthase | BAB37836.1 |
| Ddi | <i>Dictyostelium discoideum</i> cellulose synthase | AAF00200.1 |
| Npu | <i>Nostoc punctiforme</i> PCC 73102 cellulose synthase | YP_001865112.1 |
| Sco | <i>Streptomyces coelicolor</i> A3(2) glycosyl transferase | NP_627065.1 |
| Ssv | <i>Streptomyces sviceus</i> ATCC 29083 glycosyl transferase | YP_002208804.1 |
| Ath CesA1-10 | <i>Arabidopsis thaliana</i> cellulose synthase 1-10 | NP_194967.1 NP_195645.1 NP_196136.1 NP_199216.2 NP_196549.1 NP_201279.1 Q95WW6.1 NP_567564.1 NP_179768.1 NP_180124.1 O49323.1 Q9LFL0.1 Q9M9M4.1 Q9SZL9.1 Q9SRW9.1 |
| Ath CslD1-5 | <i>Arabidopsis thaliana</i> cellulose synthase-like protein D1-5 | Q6AT26.1 Q84M43.1 Q69V23.1 Q5JN63.1 Q851L8.1 Q6YVM4.1 Q9AV71.1 Q84ZN6.1 Q69P51.1 |
| Osa CesA1-9 | <i>Oryza sativa</i> Japonica Group cellulose synthase 1-9 | Q8W3F9.1 Q9LHZ7.1 Q7EZW6.2 Q2QNS6.1 Q5Z6E5.1 |
| Osa CslD1-5 | <i>Oryza sativa</i> Japonica Group cellulose synthase-like protein D1-5 | Q8W3F9.1 Q9LHZ7.1 Q7EZW6.2 Q2QNS6.1 Q5Z6E5.1 |
| Zma CesA1-12 | <i>Zea mays</i> cellulose synthase 1-12 | AAF89961.1 AAF89962.1 AAF89963.1 AAF89964.1 AAF89965.1 AAF89966.1 AAF89967.1 AAF89968.1 AAF89969.1 AAR23310.1 AAR23311.1 AAR23312.1 |
| Nal CesA | <i>Nicotiana alata</i> cellulose synthase | AAK49454.1 |
| Nal CslD | <i>Nicotiana alata</i> cellulose synthase D-like protein | AAK49455.1 |