Supporting Information
http://www.genetics.org/cgi/content/full/genetics.110.122002/DC1

Glycosylation Genes Expressed in Seam Cells Determine Complex Surface Properties and Bacterial Adhesion to the Cuticle of *Caenorhabditis elegans*

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DOI: 10.1534/genetics.110.122002
FIGURE S1.—Total RNA was isolated from N2 mixed stages using TRIzol (Invitrogen); 1 μg of total DNase-treated RNAs were reverse transcribed using the Superscript VILO cDNA Synthesis Kit (Invitrogen), according to the manufacturer's instructions. Semi-quantitative PCR was carried out using a Techne TC512 thermal cycler. Each reaction contained: 0.2 μM of forward and reverse primers and 1 μl of cDNA (1:20 RNA dilution) in a total volume of 50 μl. Gene specific primers were as follows:

*bus-2* _forw: 5′ GTCGAAATGGCTTCAAAACGAC 3′
*bus-2* _rev: 5′ GATCCCAACCACCTGCATAGAAC 3′,

*bus-4* _forw: 5′ GGGAGGAAGTGGCTATGTGATG 3′,
*bus-4* _rev: 5′ TCTGCCTACCCTTCTCATCTCG 3′,

*ama-1* _forw: 5′ CCTACGATGTATCGAGCAAA 3′,
*ama-1* _rev: 5′ CCTCCCTCCGGTGTAATAATG 3′,

*rla-1* _forw: 5′ GAAGATCGCTACCCTTCTCAAG 3′
*rla-1* _rev: 5′ CAGAAGTGATGGGTTTCTCAC 3′.

Thermocycling was performed under conditions consisting of an initial denaturation step (95°C for 5 min), followed by 15/20/25 or 30 cycles of 95°C for 30 s, 58°C for 30 s, and 72°C for 1 min. 30 μl of each transcript were analyzed on a 2% agarose gel and *bus-2* and *bus-4* levels were determined by comparison to the endogenous control genes *ama-1* and *rla-1* for the 4 cycle times tested. Detected levels were consistent in the 3 biological replicates analyzed. Similar results were obtained using a different pair of primers for *bus-2*.

Quantitation of relative RNA levels for these genes, and also for *bus-12*, was independently obtained from RNAsSeq data obtained by deep-sequencing RNA from intestinal cells (Simon Haenni and André Furger, personal communication). Read numbers for these genes in this dataset were as follows:

*bus-2*: 26
*bus-4*: 96
*bus-12*: 299
*ama-1*: 2537
*rla-1*: 4100
FIGURE S2. Impaired recognition of Bus and Srf mutants by wildtype males. Each point is a measure of the fraction of time that wildtype or mutant hermaphrodites experienced sliding and mating contact with wildtype males, during a 50 minute observation period. Six separate experiments were carried out, assaying the seven genotypes in parallel in each experiment. Mean and standard deviation values are given below, together with significant differences from wildtype for each mutant (2-tailed T-test).