Novel Serine/Threonine-O-glycosylation with N-Acetylneuraminic acid and 3-Deoxy-D-manno-octulosonic acid by Maf glycosyltransferases

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Supplementary figures S1 to S13, supplementary tables S1 to S23, and additional supplementary data containing SEQUEST-annotated MS/MS spectra of O-glycosylated peptides with Modscore values of ≥ 19 for Site 1 Position_A and Site 1 Position_B are provided as supporting information for this manuscript.

Abstract

Some bacterial flagellins are O-glycosylated on surface-exposed Serine/Threonine residues with nonulosonic acids such as pseudaminic acid, legionaminic acid, and their derivatives by flagellin nonulosonic acid glycosyltransferases, also called Motility associated factors (Maf). We report here two new glycosidic linkages previously unknown in any organism, Serine/Threonine-O-linked N-Acetylneuraminic acid (Ser/Thr-O-Neu5Ac) and Serine/Threonine-O-linked 3-Deoxy-D-manno-octulosonic acid (Ser/Thr-O-KDO), both catalysed by *Geobacillus kaustophilus* Maf (putative flagellin sialyltransferase) and *Clostridium botulinum* Maf (putative flagellin legionaminic acid transferase). We identified these novel glycosidic linkages in recombinant *G. kaustophilus* and *C. botulinum* flagellins that were co-expressed with their cognate recombinant Maf protein in *Escherichia coli* strains producing the appropriate nucleotide sugar glycosyl donor. The glycosylation of *G. kaustophilus* flagellin with KDO, and that of *C. botulinum* flagellin with Neu5Ac and KDO indicates that Maf glycosyltransferases display donor substrate promiscuity. Maf glycosyltransferases have the potential to radically expand the scope of neoglycopeptide synthesis and posttranslational protein engineering.

Significance Statement

Glycosylation, the modification of proteins with sugars, is one of the most common post-translational modifications observed in proteins. While glycosylation is versatile, the most common forms of glycosylation are N-glycosylation, where the N atom of Asparagine is modified with a glycan, and O-glycosylation where the O atom of serine or threonine residues is modified with a glycan. Here, we report a novel type of O-glycosylation in the bacterial flagellin proteins of two Gram-positive bacteria, *Geobacillus kaustophilus* and *Clostridium botulinum*. We demonstrate for the first time that the enzyme flagellin Maf glycosyltransferase is capable of transferring the monosaccharides, N-acetylneuraminic acid

and 3-Deoxy-D-manno-octulosonic acid, on to serine and threonine residues of these proteins.

Introduction

Glycosylation is the most common and versatile post translational modification in proteins ¹. Initially identified in eukaryotes ², glycans are most commonly N-linked to asparagine or O-linked to serine or threonine ³ residues. N-linked and O-linked glycosylation have been well documented in prokaryotic proteins, too ^{4, 5, 6, 7}. O-glycosylation occurs in bacterial pilins, flagellins, autotransporter adhesion proteins and several other proteins ⁷.

Flagellins from both Gram-negative and Gram-positive bacteria are known to be O-glycosylated ^{7, 8} with a wide variety of monosaccharide or oligosaccharide glycan structures on varying numbers of glycosites, ranging from two to 19 sites ^{9, 10, 11, 12, 13, 14, 15, 16, 17}. The glycan structures that are commonly found on flagellar proteins are derivatives of pseudaminic acid (**Figure 1**) (in *C. jejuni*, *Campylobacter coli*, *Helicobacter pylori*, *Aeromonas caviae*) and legionaminic acid (**Figure 1**) (in *C. coli* and *Clostridium botulinum*), which are non-sialic acid nonulosonic acids ^{9, 11, 12, 18}. Nonulosonic acids are nine-carbon sugars with a carboxylate group at C-1 and an exocyclic side chain C-7 to C-9; sialic acids are nonulosonic acids with a glycerol-like exocyclic side chain, eg. N-acetylneuraminic acid (Neu5Ac) ¹⁹ (**Figure 1**). Also found on flagellar proteins are rhamnose or rhamnose-linked oligosaccharides (in *Pseudomonas aeruginosa*), and N-acetylglucosamine (GlcNAc) (in *L. monocytogenes*) ^{10, 13, 14}. Glycans on some flagellins are acylated with acyl groups or peptides, as in the case of *C. jejuni* and *Clostridium difficile* ^{15, 16}.

Several lines of evidence indicate that Motility associated factor (Maf) proteins are the flagellin nonulosonic acid glycosyltransferases. The *maf* genes are present in the flagellar locus along with genes responsible for glycan biosynthesis and transport ^{20, 21, 22}. Insertional mutagenesis or inactivation of *maf* does not affect biosynthesis of the glycan moiety but results in a non-flagellated, non-motile phenotype in *C. jejuni* ^{21, 22, 23}, *H. pylori* ¹², *Aeromonas hydrophila* ^{24, 25, 26}, *A. caviae* ²⁷, and *Magnetospirillum magneticum* ²⁸. Maf directly interacts with flagellin in vivo in *A. caviae* ²⁹. Further, the crystal structure of *M. magneticum* Maf,

putative flagellin pseudaminic acid transferase (PDB ID: 5mu5) indicates that the central Maf_flag10 domain (PF01973 or DUF115 in Pfam database) has a modified glycosyltransferase GT-A topology and is structurally related to family GT42 sialyltransferases with striking structural resemblance to *C. jejuni* sialyltransferase Cst-II (PDB ID: 1ro7)³⁰ in the donor substrate binding region²⁸.

In this article, we explicitly demonstrate the flagellin nonulosonic acid glycosyltransferase activity of Maf proteins from Gram-positive bacteria by employing suitable heterologous expression systems. We describe the mass spectrometry analysis of recombinant *Geobacillus kaustophilus* HTA426 flagellins, *GkFlaA1* and *GkFlaA2*, and *C. botulinum* F Str. Langeland flagellin *CbFla* heterologously expressed in *E. coli* strains with or without co-expression of the cognate recombinant Maf proteins, *GkMaf* and *CbMaf*, respectively. We report two new glycosidic linkages, Serine/Threonine-O-linked N-Acetylneuraminic acid (Neu5Ac) and Serine/Threonine-O-linked 3-Deoxy-D-manno-octulosonic acid (or keto-deoxyoctulosonate; KDO) catalysed by these Maf proteins in their cognate flagellins, and concomitantly demonstrate the donor substrate promiscuity of this class of enzymes.

Results:

Strategy for heterologous co-expression of Maf and flagellin proteins from *Geobacillus* sp.:

A recent comparative genomics study of 36 strains of the Gram-positive, aerobic, thermophilic genus *Geobacillus* by Maayer et al demonstrated the occurrence of five distinct types of flagellin glycosylation islands (FGI-I to FGI-V) amongst 18 of these strains³¹. These islands are present within the flagellar biosynthesis locus and contain glycan biosynthesis and *maf* or glycosyltransferase genes³¹. Based on the different glycan biosynthesis genes present in the flagellin glycosylation islands (FGI-I to FGI-V), predictions of the glycan moieties on the *Geobacillus* flagellins are possible³¹. The type-I FGI, present in the type strain, *G. kaustophilus* DSM 7263 (or ATCC 8005 or NBRC 102445, isolated from

pasteurized milk in USA ^{32, 33, 34}), and strains, *G. kaustophilus* HTA426 (isolated from deep sea sediment in the Mariana trench ³⁵) (**Figure 2A**) and *G. thermoglucosidans* C56-YS93 (isolated from a hot spring in Obsidian, USA ³⁶), is unique in that it encodes Neu5Ac biosynthetic genes as well as *maf* genes (a single *maf-1* gene in the first and second strains, and two genes, *maf-3* and *maf-4*, in the third strain) ³¹; this suggests that the Maf proteins encoded by them might be flagellin sialyltransferases. In contrast, FGI-II, -III and -IV harbour *maf* genes as well as genes for pseudaminic acid biosynthesis, suggesting that these *maf* genes might encode for flagellin pseudaminic acid transferases, and the type-V FGI has genes for rhamnose biosynthesis but lacks *maf* genes ³¹. Flagellin glycosylation has not been reported in the literature for *Geobacillus kaustophilus* or *G. thermoglucosidans*. The only known glycosylated flagellin from a *Geobacillus* sp. is that of *Geobacillus stearothermophilus* wherein the flagellin was reported to be glycosylated based on positive staining with the Periodic acid-Schiff reagent but without definitive mass spectrometry based characterization ³⁷.

Albeit de novo synthesis and/or metabolism of sialic acids (such as Neu5Ac) occur in pathogenic bacteria ^{19, 38, 39, 40} such as *Leptospira* ⁴¹, *C. jejuni* ⁴², and *E. coli* ⁴³, there is no report of any sialic acid being incorporated in flagellins. There is also no evidence, to our knowledge, of protein O-sialylation in any organism to date. Considering the novelty of protein O-linked sialic acids, we decided to study a putative flagellin sialyltransferase protein encoded by *Geobacillus* FGI type-I. We selected the putative flagellin sialyltransferase protein encoded by *maf1* (NCBI accession no. BAD77414.1; protein referred to here as *GkMaf*) of *G. kaustophilus* HTA426 (which is 100% identical in amino acid sequence to *maf1* of *G. kaustophilus* DSM 7263, NCBI accession no. WP_011232599.1), together with its putative acceptor substrates - the two flagellins, encoded by genes *flaA1* (NCBI accession no. BAD77427.1; protein referred to here as *GkFlaA1*, which does not find a homologue in *G. kaustophilus* DSM 7263), and *flaA2* (NCBI accession no. BAD77416.1, protein referred to here as *GkFlaA2*, which is 100% identical in amino acid sequence to flagellin of *G.*

kaustophilus DSM 7263, NCBI accession no. WP_011232601.1), for this study considering the presence of a single *maf* gene in this organism as opposed to two *maf* genes in *G. thermoglucosidans* C56-YS93 (*maf-3* and *maf-4*, which are similar to the *maf* genes observed in FGI-II and FGI-III clusters containing pseudaminic acid biosynthesis genes). *GkMaf* is a member of the Pfam 1973 family ⁴⁴ with the conserved Maf_flag10 domain characteristic of Maf proteins. The two flagellins, *GkFlaA1* and *GkFlaA2* are ~71% identical but vary in length. *GkFlaA1* (604 aa long) resembles *Salmonella typhimurium* flagellin in domain organization ⁴⁵ and it has D2 and D3 domains. *GkFlaA2* (297 aa long) resembles *Bacillus subtilis* flagellin ⁴⁶ and lacks D2 and D3 domains.

Our strategy for studying the function of the *G. kaustophilus* Maf with putative sialyltransferase function involved co-expressing *GkMaf* along with *GkFlaA1* or *GkFlaA2* in a heterologous host producing appropriate nucleotide sugar donor and analysing the recombinant flagellins for the presence of any glycosylation by mass spectrometry (**Figure 2B**). CMP-sialic acid is the donor substrate of sialyltransferases ⁴⁷. In order to ensure sufficient donor substrate availability for the putative flagellin sialyltransferase in our study, we employed as our model heterologous expression system, *E. coli* K12-K1 hybrid strains that were engineered by Vimr and coworkers ^{48, 49} to accumulate abundant CMP-sialic acid in the cytosol. Strains EV136 (*neuS*-) and EV240, (*nanA*- *neuS*-) accumulate abundant CMP-sialic acid in the cytosol due to their lacking a functional capsule polysialyltransferase (*neuS*) whereas EV36 is the wild type K12-K1 hybrid strain with an insignificant pool of CMP-sialic acids ^{49, 50}. We confirmed by borohydride reduction ⁵¹ and periodate-resorcinol assays ⁵² that chemically competent cells of EV136 and EV240 cells accumulated significant intracellular CMP-sialic acid and total sialic acid (**data not shown**).

We confirmed co-expression of recombinant *GkMaf* and *GkFlaA2* in EV136, EV36 and EV240 cells by western analysis with anti-S-tag and anti-6XHis-tag antibodies, respectively (**Figures 2C and 2D, Supplementary figure S1**) and enriched recombinant *GkFlaA2* from these cells by immobilized metal affinity chromatography (**Supplementary figures S2A-C**).

We also singly expressed and purified recombinant *GkFlaA2* (**Figures 2C and 2D, Supplementary figures S1 and S2A-C**).

***GkMaf* is a flagellin sialyltransferase:**

We subjected *GkFlaA2* to on-blot periodate oxidation and aniline-catalyzed oxime ligation (PAL) with aminoxy-biotin⁵³ in order to detect sialylation, if any. We found that *GkFlaA2* co-expressed with *GkMaf* in EV136, EV36 and EV240 strains displayed less electrophoretic mobility than singly expressed *GkFlaA2* and was detected by HRP-conjugated streptavidin following on-blot PAL (**Figure 3A**), suggesting the presence of a vicinal 1,2-diol moiety (such as in sialic acid) that was biotinylated by PAL. The biotinylation was more intense in EV136 and EV240 cells than in EV36 cells. Singly expressed *GkFlaA2* from EV136, EV36 and EV240 strains was not biotinylated (**Figure 3A**). This suggested that *GkMaf* catalysed the sialylation of *GkFlaA2* in EV136, EV36 and EV240 cells.

We also subjected purified *GkFlaA2*, singly expressed or co-expressed in the presence of *GkMaf*, from EV36, EV136 and EV240 cells to mass spectrometry for intact mass analysis (**Figure 3B and 3C, and Supplementary Figure S3**). The ionisation spectrum of *GkFlaA2* was a multiply charged bell shaped envelope characteristic of intact proteins (**Figures 3B and 3C and Supplementary Figure S3**). Singly expressed *GkFlaA2* purified from EV136 cells had a molecular mass of 32.927 kDa (**Figure 3B, upper panel**). The theoretically predicted average molecular mass of recombinant *GkFlaA2* is 33.057 kDa, suggesting that the protein undergoes N-ter Met cleavage. In contrast, *GkFlaA2* co-expressed with *GkMaf* in EV136 cells displayed four prominent additional peaks of molecular masses of 33.219 kDa, 33.510 kDa, 33.802 kDa, and 34.093 kDa, each differing by 291 Da from the previous peak, and thus indicative of the presence of up to at least four moieties of 291 Da on *GkFlaA2* (**Figure 3B, lower panel**). Similar results were obtained with *GkFlaA2* coexpressed with *GkMaf* in EV240 cells (**Supplementary Figure S3**). The sialic acid, N-acetylneuraminic acid (Neu5Ac), has a molecular mass of 309 Da, and a sialic acid moiety transferred to protein

with loss of water (18 Da) would result in the addition of a 291 Da moiety. These results thus indicated that *GkMaf* is a flagellin sialyltransferase.

***GkMaf* displays donor substrate promiscuity:**

As mentioned above, EV36 cells do not accumulate CMP-sialic acid ⁴⁹ although they actively synthesize the same. *GkFlaA2* singly expressed from EV36 cells also had a molecular mass of 32.928 kDa. However, when co-expressed with *GkMaf* in EV36 cells, *GkFlaA2* displayed additional peaks of molecular masses, 33.147 kDa, 33.368 kDa, 33.587 kDa and 33.805 kDa, corresponding to protein modification with up to four moieties of 220 Da. No molecular species corresponding to modification with Neu5Ac (291 Da) was present. The sugar, 3-deoxy-manno-octulosonic acid (or keto-deoxyoctulosonate; KDO) (**Figure 1**) has a molecular mass of 238 Da and a KDO moiety transferred to protein with loss of water (18 Da) would result in the addition of a 220 Da moiety. KDO is known to be present in the lipopolysaccharide lipid-A component of *E. coli* ^{54, 55, 56, 57, 58}, and from the apparent Km value (0.29 mM) of CMP-KDO synthetase (from *E. coli* B cells) for KDO ⁵⁹, KDO is likely to be present at sub-millimolar concentration. We conjecture that CMP-3-deoxy-manno-octulosonic acid (CMP-KDO) is present at micromolar concentration in *E. coli* B, *E. coli* K12 and their derivative strains because the Km value of *E. coli* KDO transferase is 88 µM for CMP-KDO ⁶⁰. Considering this, we predicted the 220 Da moiety observed on *GkFlaA2* to be KDO. The putative modification of flagellin with KDO, an octulosonic acid by *GkMaf* is suggestive of the donor substrate promiscuity of *GkMaf*.

Glycosylation sites of *GkFlaA2*:

We subjected *GkFlaA2*, singly expressed or co-expressed along with *GkMaf* in EV136 and EV36 cells, to protease digestion and liquid-chromatography-tandem mass spectrometry (LC-MS/MS) (performed by Taplin Biomedical Mass Spectrometry Facility, Harvard Medical School) in order to identify sites of O-glycosylation. Parameters used for searching for O-glycosylated peptides are listed (**Supplementary Table S1**). The FASTA sequence of

GkFlaA2 was used as the database for matching spectra to peptides and the reverse sequence was used to ensure specificity of hits. We achieved high sequence coverage ($\geq 75\%$) upon tandem mass spectrometry of tryptic and GluC- digested peptides from *GkFlaA2* expressed singly or co-expressed with *GkMaf* from EV136 as well as EV36 cells (**Figures 4A and 4B, Supplementary Tables S2-S6**). We found ≤ 5 peptide hits in the searches using the reverse sequence as the database; in contrast, we found > 1500 hits to the FASTA sequence of *GkFlaA2* in all samples analyzed (**Supplementary Table S6**).

We employed the Modscore algorithm⁶¹ to search for peptides with modifications of 291 Da (Neu5Ac) or 220 Da (KDO) on Ser/Thr residues of *GkFlaA2* co-expressed with *GkMaf* in EV136 and EV36 cells (**Supplementary Tables S7a, S7b, S8a and S8b**). We applied a probabilistic-based approach to assign protein modification sites⁶¹, filtering these peptide hits to retain only those with Modscore values of ≥ 19 ($P \leq 0.01$) for Site 1 Position_A and Site 1 Position_B scores in *GkFlaA2* co-expressed with *GkMaf* from EV136 and EV36 cells (**Figures 4A and 4B, Supplementary Tables S7c, S7d, S8c, and S8d, and additional supplementary data**). We expect these glycosylation sites to be confidently assigned. No such peptide hits were obtained in *GkFlaA2* singly expressed from EV36 or EV136 cells, confirming that *GkMaf* was essential for these observed modifications.

Ions indicating confident assignment of the glycosylation sites are evident in the spectra of the modified peptide hits (**Figures 4C and 4D**). For instance, the underlined Thr residue in the peptide, NIALSTSGSGNVGVMQTQSGAEQAIIIDDAAIK from *GkFlaA2* co-expressed with *GkMaf* in EV136 cells is predicted to be O-sialylated based on the presence of fragment ions retaining a 291 Da moiety (b25 to b28, b30, b31, y8 to y19, y21 to y23, and y25 to y31). Similarly, in the spectrum of the peptide FTKNNILTQAAQAMLAQANQQPQGVLLRLLE from *GkFlaA2* co-expressed with *GkMaf* in EV36 with two 220 Da (KDO) modified Thr residues (underlined in the sequence), singly charged ions, b6 and b7, and doubly charged ions, b4 and b5 can be used to assign the KDO moiety on the first (towards N-terminal) Thr residue, b ions, b4 to b7, can be used to assign the KDO moiety on the first Thr residue, y

ions, y25, y27 and y30, can be used to assign the KDO moiety on the second Thr residue, and many b ions (b8 to b15, b18 to b21, and b23 to b31) retain the KDO moiety on both residues (**Figure 4C**). (**Figures 4D and 4E**). The spectra of modified peptides with Modscore values ≥ 19 ($P \leq 0.01$) for Site 1 Position_A and Site 1 Position_B scores are available as additional **Supplementary data**. The residues identified as O-sialylated are located in and around the loop region of the D1 domain and in the D0 helices (**Figures 4E and 4F**).

Glycosylation sites of *GkFlaA1*:

As mentioned above, the genome of *G. kaustophilus* HTA426, encodes for two flagellins, *GkflaA1* and *GkFlaA2*. We also studied glycosylation in *GkFlaA1*, the longer flagellin (theoretically predicted average molecular mass of 65.107 kDa), following a similar strategy of expression in EV136 cells with or without co-expressing *GkMaf* (**Supplementary Figure S4A**). Following purification (**Supplementary Figures S4B and S4C**), protease digestion and tandem mass spectrometry analysis (**Supplementary Tables S9a, S9b, S9c, S10, and S11**), the ion fragmentation patterns could be used to assign two glycosylation sites, LSSGLR wherein the underlined Ser residue was modified with a 221 Da (KDO) moiety and LSSGLR wherein the underlined Ser residue was modified with a 291 Da (Neu5Ac) moiety (**Supplementary Figure S5, Supplementary Tables S12a-e, and additional Supplementary data**). These glycosylation sites map to the distal end of the N-terminal D0 domain at the loop adjoining the D1 domain. We did not identify any glycosylation sites in the D2 and D3 domains, or in the conserved Thr residues of the sequence identical D1 loop region corresponding to the O-sialylated T213 and T270 residues in recombinant *GkFlaA2*, perhaps because *GkMaf* could not effectively glycosylate *GkFlaA1* under these conditions or because these residues are not surface exposed in *GkFlaA1* due to the presence of the D2 and D3 domains.

***C. botulinum* Maf displays promiscuous sialyltransferase activity in *E. coli* strains overproducing CMP-Neu5Ac:**

Flagellins of different strains of the human pathogen *C. botulinum* have been reported to be modified with various glycan moieties such as a legionaminic acid derivative, 7-acetamido-5-(N-methyl-glutam-4-yl)-amino-3,5,7,9-tetradexy-D-glycero-alpha-D-galacto-nonulosonic acid, a di-acetamido-substituted hexuronic acid sugar, a tri-acetamido-substituted hexuronic acid sugar, and a glycan of mass 696 Da⁹. Flagellins from *C. botulinum* F Str. Langeland and *C. botulinum* strain FE9909ACS Alberta are glycosylated with the legionaminic acid derivative, 7-acetamido-5-(N-methyl-glutam-4-yl)-amino-3,5,7,9-tetradexy-D-glycero-alpha-D-galacto-nonulosonic acid, and share 100% amino acid sequence identity, and seven glycosylation sites have been identified in the flagellin from *C. botulinum* strain FE9909ACS Alberta⁹. The flagellar locus of *C. botulinum* F Str. Langeland comprises genes for flagellum structural components, flagellin genes, genes for flagellin glycan biosynthesis and a single *maf* gene (NCBI accession no. WP_003359189.1; encoding a protein with a Maf_flag10 domain typical of Maf proteins) neighbouring a flagellin gene, *fla* (NCBI accession no. WP_003359201.1) (**Figure 5A**). We selected this Maf-flagellin pair (referred to here as *CbMaf* and *CbFla*, respectively) for heterologous expression in the *E. coli* strains, EV36, EV136 and EV240, with the expectation that *CbMaf*, being a putative flagellin legionaminic acid transferase, might display donor substrate promiscuity and accept CMP-Neu5Ac instead of CMP-legionaminic acid as donor substrate (**Figure 5B**). We based our assumption on the close stereochemical structural similarity of Neu5Ac and legionaminic acid, and on evidence for the reverse scenario, i.e., that mammalian and engineered bacterial sialyltransferases are able to use CMP-legionaminic acid instead of CMP-Neu5Ac as donor substrate^{62, 63, 64}.

We confirmed co-expression of recombinant *CbMaf* and *CbFla* in EV136, EV36 and EV240 cells by western analysis with anti-6XHis-tag antibody (**Figures 4C and 4D, Supplementary figure S6**) and enriched recombinant *CbFla* from these cells by immobilized metal affinity

chromatography (**Supplementary figure S7**). We also singly expressed and purified recombinant *CbFla* (**Figures 4C and 4D, Supplementary figures S6 and S7**).

We performed on-blot periodate oxidation and aniline-catalyzed oxime ligation (PAL) with aminooxy-biotin⁵³ and found that *CbFla* was heavily biotinylated in the EV136 and EV240 strains when co-expressed with *CbMaf* but not when expressed singly (**Figure 6A**). *CbFla*, when coexpressed with *CbMaf*, also displayed less electrophoretic mobility compared to the singly expressed *CbFla* in these strains (**Figure 6A**). *CbFla*, coexpressed with *CbMaf* in the EV36 strain, also displayed less electrophoretic mobility than singly expressed *CbFla* but displayed relatively little biotinylation (**Figure 6A**). This result suggested that whereas *CbMaf* displayed robust flagellin sialyltransferase activity in EV136 and EV240 cells, it displayed lower flagellin sialyltransferase activity in EV36 cells, perhaps due to the lower level of CMP-Neu5Ac in this strain.

We performed intact mass analysis of *CbFla* by liquid chromatography - mass spectrometry. *CbFla* singly expressed and purified from EV136 cells had a molecular mass of 30.143 kDa (theoretically predicted average molecular mass: 30.270 kDa) (**Figure 6B upper panel**). This suggests that the recombinant protein undergoes N-ter Met cleavage. However, in addition to a peak of molecular mass 30.139 kDa, the deconvoluted intact mass spectrum of *CbFla* purified from EV136 cells co-expressing *CbMaf* displayed seven additional prominent peaks of molecular masses, 30.431 kDa, 30.722 kDa, 31.016 kDa, 31.305 kDa, 31.595 kDa, 31.886 kDa, and 32.175 kDa, each differing by 291 Da from the previous peak and indicative of the presence of up to at least seven Neu5Ac moieties on *CbFla* (**Figure 6B lower panel**).

Singly expressed *CbFla* purified from EV36 cells had a molecular mass of 30.141 kDa (**Figure 6C, upper panel**). Intact mass analysis of *CbFla* purified from EV36 cells co-expressing *CbMaf* indicated the presence of two Neu5Ac modified peaks of molecular masses, 30.429 kDa and 30.720 kDa, differing by 291 Da and 582 Da, respectively, from the unmodified peak of molecular mass 30.138 kDa (**Figure 6C lower panel**). Additionally, we

observed peaks of molecular masses, 30.358 kDa, 30.580 kDa, and 30.798 kDa, differing by 220 Da, 440 Da, and 660 Da, respectively, from the unmodified peak, and indicative of the presence of up to three KDO moieties (**Figure 6C lower panel**). We also identified peaks of molecular masses 30.650 kDa, corresponding to modification with one Neu5Ac moiety and one KDO moiety, 30.871 kDa, corresponding to modification with one Neu5Ac and two KDO moieties, and 30.939 kDa, corresponding to modification with two Neu5Ac and two KDO moieties (**Figure 6C lower panel**). Similar results were obtained upon intact mass analysis of *CbFla* purified from EV240 cells (**Supplementary Figure S8**).

Glycosylation sites of *CbFla*:

We obtained ~100 peptide hits with confidently assigned glycosylation sites by tandem mass spectrometry of protease-released peptides from *CbFla* purified from EV136 cells or EV36 cells with or without *CbMaf* co-expression followed by searches with Modscore algorithm⁶¹ (**Supplementary tables S13a-b, S14, S15, S16, S17, S18a-e and S19a-b, and additional Supplementary data**). A single peptide of *CbFla* singly expressed and purified from EV136 cells passed the threshold of Modscore value ≥ 19 ($P \leq 0.01$) for Site 1 Position_A and Site 1 Position_B, indicating a low frequency of non-specific hits (**Supplementary table S18c**). The glycosylation sites that we identified in *CbFla* include all the seven Ser residues previously identified as glycosylated with the legionaminic acid derivative in *C. botulinum*⁹. Additionally, we identified five Thr residues in and around the D1 loop region to be glycosylated (**Figure 7A, 7B**). Annotated spectra of a sample peptide from *CbFla* expressed in EV136 and EV36 cells, SM*VFQIGANKDQVMELTIAGMGTSALK, is provided, which indicates the presence of fragment ions retaining the glycan moiety, Neu5Ac (291 Da) or KDO (220 Da), respectively (**Figure 7C, 7D**). The structural model of *CbFla* depicting the glycosites identified in this study are shown in **Figures 7E and 7F**.

***CbMaf* and *GkMaf* amino acid residues involved in catalytic activity:**

Sulzenbacher et al have previously demonstrated that E324 and D415 are critical for the enzyme activity of *M. magneticum* Maf (PDB ID: 5mu5)²⁸. In order to validate the flagellin glycosyltransferase activity observed for *CbMaf* and *GkMaf*, we performed site-directed mutagenesis of the corresponding residues in sequence/structure (**Supplementary Figure S9A, S9B, and S9C**) - D272A and D357A in *CbMaf*, and D285A and N379A in *GkMaf*. We additionally mutated a Ser residue (S334 and S356 in *CbMaf* and *GkMaf*, respectively), conserved in sequence among Maf proteins (**Supplementary Figures S9A, S9B and S9C**), and present in the three-dimensional vicinity of the amino acid residues demonstrated to be important for catalysis, to assess if it was also important for enzymatic activity. We did not observe any flagellin glycosyltransferase activity upon co-expression of any of these Maf mutants with their cognate flagellins – *CbFla*/*GkFla*A2 (**Figure 8A and Supplementary Figures S10a and S10b**) as evident from lack of sensitivity to periodate oxidation and reaction with aminooxy biotin (**Figure 8B and Supplementary Figures S10c and S10d**), and absence of any modified peaks in intact mass analysis (**Figure 8C**). We conclude that these residues are important for the catalytic activity of Maf.

***C. botulinum* Maf displays promiscuous KDO transferase activity in *E. coli* BL21:**

We also assayed *CbMaf* for flagellin KDO transferase activity in the commonly used *E. coli* lab strain, BL21(DE3), which is known to have KDO₂-Lipid(IV)-A in its outer membrane, and should therefore contain CMP-KDO^{57, 65, 66, 67} (**Figure 9A**). *CbFla*, purified from *E. coli* BL21(DE3) cells co-expressing *CbMaf* (**Figure 9B, Supplementary Figure S11**), was mildly reactive to periodate oxidation and subsequent reaction with aminooxy-biotin (**Figure 9C**) and intact mass analysis confirmed that it was modified by at least six KDO moieties (**Figure 9D**). We subjected *CbFla* purified from BL21(DE3) cells to protease digestion, tandem mass spectrometry and Modscore analysis (**Supplementary tables S20a-c, S21a-c, S22, S23a-d**) and assigned glycosylation sites (**Supplementary table S23e and Supplementary Figure S12A-C, and additional Supplementary data**). The glycosylation sites included Ser and Thr residues identified as glycosylated in *CbFla* expressed from EV136 cells.

Our results reiterate the donor substrate promiscuity of *CbMaf* and indicate that the commonly used *E. coli* BL21(DE3) strain can be employed for further molecular characterization of this class of enzymes.

Identification of glycan moiety on *CbFla* and *GkFlaA2*:

We employed mild acid hydrolysis to release acidic sugar moieties from the glycosylated flagellins, and LC-MS/MS to confirm the identities of the glycan moieties. The tandem mass spectrum of the mild acid hydrolysate of *CbFla* purified from EV136 cells matched that of standard Neu5Ac (**Figure 10A**), and the tandem mass spectrum of the mild acid hydrolysate of *CbFla* purified from BL21(DE) cells matched that of standard KDO (**Figure 10B**), thereby confirming that the glycans modifying the flagellins in these *E. coli* strains were indeed Neu5Ac and KDO.

Discussion:

In this study, we have employed heterologous recombinant co-expression of flagellin and Maf proteins and mass spectrometry to demonstrate that *GkMaf*, predicted to be a flagellin sialyltransferase based on gene neighbourhood analysis, and *CbMaf*, a putative flagellin legionaminic acid transferase, can glycosylate Ser/Thr residues of their cognate flagellins with Neu5Ac and KDO. We have also demonstrated here the catalytic involvement of a conserved Ser residue in the Maf_flag10 domain, in addition to residues equivalent to Asp324 and Glu415 residues of *M. magneticum* Maf previously demonstrated to be critical for enzyme activity²⁸.

Sialic acids are the most abundant terminal saccharides in eukaryotic glycoconjugates^{19, 68}. The Carbohydrate-Active enZymes database (CAZy⁶⁹) family, GT29, comprises eukaryotic sialyltransferases such as ST3Gal, ST6Gal, ST6GalNAc and ST8Sia sialyltransferases that transfer sialic acid (Sia) to glycan residues on glycoconjugates, catalysing the following glycosidic bonds – Sia α 2-3Gal, Sia α 2-6Gal, Sia α 2-6GalNAc and Sia α 2-8Sia¹⁹. Among prokaryotes, sialic acids are especially prevalent in pathogenic bacteria^{39, 40}. Bacterial

sialyltransferases are classified in the CAZy families, GT4, GT38, GT42, GT52, GT38, GT80, GT97 and GT100, and also catalyse transfer of sialic acids to glycan residues to form the glycosidic bonds - Sia α 2-3Gal, Sia α 2-6Gal, Sia α 2-8Sia, and Sia α 2-9Sia^{69, 70, 71, 72}. To our knowledge, there is no existing report in the literature of direct Ser/Thr O-sialylation in proteins. Therefore, our study of the putative flagellin sialyltransferase, *GkMaf*, and the putative legionaminic acid transferase, *CbMaf*, provides the first evidence for the glycosidic bond, Ser/Thr O-linked Neu5Ac, in any living system. A cursory analysis of flagellar loci in bacterial genomes in the Integrated Microbial Genomes & Microbiomes system v. 5.0 (IMG/M v.5.0) database⁷³ indicate that besides other *Geobacillus kaustophilus* strains, several other bacilli such as *Bacillaceae bacterium* mt8 (Ga0121794_112), *Sporosarcina* sp. P21c (Ga0338388_15), *Cenibacillus caldisaponilyticus* B157 (Ga0302714_1002), *Virgibacillus* sp. SK-1 (Ga0069221_126), *Brevibacillus massiliensis* phR (HGBMDRAFT_CAGW01000083_1.83), *Lysinibacillus sphaericus* LMG 22257 (Ga0175015_11), and *Sporosarcina* sp. P19 (Ga0338387) might also display O-sialylation in their flagellins. Also, *Burkholderia pseudomallei* flagellin is reportedly modified with an unidentified glycan of 291 Da that undergoes fragmentation with neutral losses of water, acetyl group, formic acid, acetamidino group and ammonia; it is possible that this glycan moiety is also Neu5Ac⁷⁴.

Albeit KDO transferases are involved in the synthesis of lipopolysaccharide and some bacterial and plant polysaccharides^{75, 76, 77, 78, 79}, KDO is not known to modify proteins and there are no reported glycosyltransferases that transfer KDO on to amino acid residues. We could find no entry of any protein modification with KDO in these protein modification databases - FindMod^{80, 81}, UniProt^{82, 83}, DeltaMass (<https://abrf.org/delta-mass>)^{84, 85}.

Our demonstration of the novel glycosidic linkages, Ser/Thr O-linked Neu5Ac in *CbFla* and Ser/Thr O-linked KDO in *CbFla* and *GkFla*, also highlights the donor substrate promiscuity of *CbMaf* and *GkMaf* proteins. Donor substrate promiscuity is quite prevalent in glycosyltransferases (including sialyltransferases⁸⁶), and is frequently exploited to label

glycoconjugates in living cells using metabolic oligosaccharide engineering⁸⁷ or chemoenzymatic glycan labelling⁸⁸. In this context, we would like to note that Liu et al have previously demonstrated transfer of azido-labeled pseudaminic acid by *C. jejuni* Maf⁸⁹.

The non-sialic acid nonulosonic acids, legionaminic acid, pseudaminic acid and their derivatives have been known to decorate Ser/Thr residues in the flagellin of several bacteria such as *C. jejuni*, *C. coli*, *H. pylori*, *A. caviae*, *A. hydrophila*, *M. magneticum*, *Shewanella oneidensis*, *Treponema denticola*, *C. botulinum*⁸. Gene deletion or mutation and complementation studies in the Gram negative bacteria, *A. caviae*, *A. hydrophila*, *H. pylori*, *C. jejuni*, and *M. magneticum*, and structural studies of the *M. magneticum* Maf protein indicate that Maf proteins are flagellin nonulosonic acid glycosyltransferases^{12, 21, 22, 23, 24, 25, 26, 27, 28}. Our study of recombinant GkMaf and CbMaf in *E. coli* strains provides the first direct evidence of the flagellin nonulosonic acid transferase activity of Maf in a heterologous expression system lacking other cognate genes of the flagellar locus. Further, whereas *E. coli* K12 (which is the genetic background of the EV136, EV36 and EV240 strains used here) is known to have a flagellar locus identical to that of *Salmonella*⁹⁰, *E. coli* B (which is the genetic background of BL21(DE3)) lacks 21 *fli* genes encoding flagellar components and is non-motile⁶⁵. Therefore, albeit we have not yet successfully demonstrated glycosyltransferase activity in in vitro assays employing recombinant purified CbMaf, CbFla and CMP-Neu5Ac, the glycosyltransferase activity of CbMaf in BL21(DE3) that we report in this study indicates that Maf might not require any flagellar context to function as a glycosyltransferase. This is in agreement with the notion that native flagellin glycosylation likely occurs in the cytoplasm prior to chaperone binding and protein secretion²⁹. Flagellin glycosylation has been observed in the absence of flagellin chaperone (FlaJ) and FlaJ has been demonstrated to preferentially bind to glycosylated flagellin, thus favoring secretion and assembly of glycosylated flagellin²⁹.

In pathogens such as *Campylobacter jejuni* and *Helicobacter pylori*, flagellin glycosylation is required for flagellum assembly, bacterial motility, and colonization ability, and therefore

associated with virulence⁸. Flagellin glycosylation therefore offers potential as an anti-virulence target, and hence small molecule inhibitors of nonulosonic acid biosynthesis⁹¹ or of flagellin glycosyltransferases might inhibit motility and thus virulence. Biosynthetic pathways of flagellin nonulosonic acids, legionaminic acid and pseudaminic acid are well-characterized, and CMP-legionaminic acid and CMP-pseudaminic acid biosynthesis have been reconstituted in vitro using enzymes from *C. jejuni*, and *H. pylori*, respectively^{18, 92, 93, 94}. Albeit these systems are available for studying putative legionaminic acid and pseudaminic acid transferases, our demonstration of donor substrate promiscuity (especially with respect to KDO transferase activity) has the implication that Maf proteins may be easily subjected to high-throughput screening for small molecule inhibitors or to other biochemical characterization using a common lab strain of *E. coli*.

On a broader note, we anticipate that the ability to directly sialylate proteins via Ser/Thr-O-linked sialic acids will dramatically expand the scope of neoglycopeptide synthesis. Further biochemical studies aimed at understanding the sequence/structural prerequisites for glycosylation by Maf will facilitate the development of facile posttranslational protein engineering strategies to install sialic acid moieties and thereby alter the physiochemical properties of recombinant proteins.

Materials and methods:

Cloning of recombinant Maf and flagellin proteins:

The *Clostridium botulinum* F Str. Langeland *maf* (*Cb-maf*, NCBI accession number WP_003359189) and flagellin gene (*Cb-fla*, NCBI accession number WP_003359201), and the *Geobacillus kaustophilus* HTA426 *maf* (*Gk-maf*, NCBI accession number BAD77414.1) and flagellin genes, *flaA1* (*Gk-flaA1*, NCBI accession number BAD77427.1) and *flaA2* (*Gk-flaA2*, NCBI accession number BAD77416.1), were codon optimized for expression in *E. coli* host strains and custom synthesized as clones in pUC57 vector (Genscript, Piscataway, NJ).

Supplementary figure S13 lists details of all expression plasmid constructs used in the study. Cloned inserts in expression plasmids were confirmed by DNA sequencing.

Expression of recombinant Maf and flagellin proteins in *E. coli* K12-K1 hybrid strains:

We obtained *E. coli* K12-K1 hybrid strains EV36, EV136 and EV240 as kind gifts from Prof. Eric R. Vimr. In order to enable overexpression of recombinant proteins under the strong T7 promotor, we used Targe Tron vector pAR1219 (Sigma) that expresses T7 RNA polymerase under the IPTG inducible lac UV5 promotor. For co-expression of Maf and Fla in EV36, EV136 and EV240 cells, we co-transformed *Cb-maf*-pET-28a(+) (pMB1/colE1 *ori*) and *Cb-fla*-pCDFDuet-1 plasmids (CDF *ori*) or the *Gk-maf*-pCDFDuet-1 with *Gk-flaA1*-pET-28a(+) / *Gk-flaA2*-pET-28a(+) plasmids in the cells along with Targe Tron vector pAR1219 (pMB1/colE1 *ori*). We used kanamycin (Goldbio) and ampicillin (Goldbio) as selection markers for pET-28a(+) and pAR1219, respectively (there was no obvious plasmid incompatibility⁹⁵). We used spectinomycin (Goldbio) as selection marker for pCDFDuet-1 clones as EV36, EV136 and EV240 cells carry selection marker for streptomycin. In the case of EV36 cells, which we found to be inefficient for transformation, we transformed the cells with pAR1219 first and then prepared chemically competent cells of these for further transformation with the Fla and/or Maf expression vectors. We grew secondary cultures of successfully transformed EV36, EV136, or EV240 cells in Luria Bertani liquid medium until the cell density was equivalent to an OD_{600nm} of 0.9, upon which we induced recombinant protein expression by the addition of 1 mM IPTG. Following this, we incubated cells at 37°C with shaking at 200 rpm for 5 hours.

Expression of recombinant Maf and flagellin proteins in *E. coli* BL21(DE3):

For co-expression in *E. coli* BL21(DE3) (Stratagene), we co-transformed *Cb-maf*-pETDuet-1 (pMB1/colE1 *ori*) and *Cb-fla*-pET-28a(+) plasmids in the cells using ampicillin (Goldbio) and kanamycin (Goldbio) as selection markers, respectively. We grew secondary cultures of successfully transformed *E. coli* BL21(DE3) cells at 37 °C in Luria Bertani liquid medium until

the cell density was equivalent to an OD_{600nm} of 0.8, upon which we induced recombinant protein expression by the addition of 1 mM IPTG. Following this, we incubated cells at 37°C with shaking at 200 rpm for 4 hours.

Western analysis of Maf and flagellin proteins:

We confirmed Maf and flagellin co-expression by western blotting the soluble supernatant and insoluble pellet fractions obtained by high-speed centrifugation of cell lysates. We detected co-expressed *CbMaf* and *CbFla* in EV strains by using mouse anti-6X-His tag monoclonal antibody (Invitrogen). We detected the co-expression of *CbMaf* and *CbFla* in *E. coli* BL21(DE3) cells and that of *GkMaf* and *GkFlaA2* in EV strains by using mouse anti-S-tag monoclonal antibody (Novagen) (for the S-tagged Maf proteins) and mouse anti-6X-His tag monoclonal antibody (for the hexahistidine tagged flagellin proteins).

Purification of flagellin proteins:

We purified recombinant hexahistidine tagged flagellin proteins by Ni-NTA metal ion affinity chromatography. Briefly, we lysed cells by sonication in Tris-buffered saline (TBS), i.e., Tris 20 mM, pH 7.5 with 150 mM NaCl, containing N-laurylsarcosine sodium salt at concentration 0.5% for *CbFla* and 1% for *GkFlaA2*. We incubated the cell-free supernatant (obtained following lysis and high-speed centrifugation) with His bind Ni-NTA resin (Pierce), washed the resin with 30 mM imidazole in TBS, and eluted the protein with 300 mM imidazole in TBS. We assessed eluates for purity by SDS-PAGE. We performed acetone precipitation by mixing imidazole eluates with pre-chilled acetone at a ratio of 1:5 and freezing them overnight in a -80 °C freezer. The following day, we washed pellets five times with acetone:water::4:1 and then stored the pellets in a freezer at -20 °C until mass spectrometry analysis.

Site-directed mutagenesis of Maf:

We generated *CbMaf* mutants - D272A, S334A, and D357A, and *GkMaf* mutants - D285A, S356A, and N379A, by using appropriate oligonucleotide primers and Quikchange Lightning site directed mutagenesis kit as per manufacturer's instructions. We co-expressed mutant Maf proteins with the cognate flagellins similar to the wild type Maf proteins.

Biotinylation of glycosylated flagellin:

We performed on-blot biotinylation of sialic acids⁵³. We subjected recombinant, purified flagellins to SDS-PAGE and western blotting on to nitrocellulose membrane. We performed on-blot oxidation with 1 mM sodium metaperiodate in phosphate buffered saline (PBS) (30 mM sodium phosphate, pH 7.4 with 150 mM NaCl) at 4°C for 20 minutes. We then washed the blot with PBS and incubated it in PBS, freshly adjusted to pH 6.7 and containing 250 µM amino-oxybiotinoyl-hydrazine (Invitrogen) and 10 mM aniline, for one hour at room temperature in the dark. We followed this up with washing the blot, overnight blocking in 5% skimmed milk, and probing the blot with HRP-conjugated streptavidin (Jackson ImmunoResearch) followed by detection with Luminata Forte western HRP substrate (Merck-Millipore).

Mass spectrometry analysis for intact mass measurement:

We obtained intact mass data of purified flagellins using Agilent G6550A Quadrupole Time of Flight (Q-TOF) mass spectrometer (CSIR-IMTECH mass spectrometry facility). We dissolved acetone precipitates in 10% acetonitrile, and subjected samples to liquid chromatography in Zorbax 300SB-C8 column (Agilent) at a flow rate of 0.4 ml/minute with acetonitrile as the mobile phase solvent (in concentration gradient). Sample components separated by LC were infused in MS Q-TOF mass spectrometer at a scan rate of 1 scan/minute with the acquisition range 200-3200 m/z. Ionisation source was electrospray ionisation (dual AJS-ESI) in positive ion mode. We analysed the data generated in Agilent Mass-Hunter software in-house. *CbFla* typically eluted between 7.4-9 minutes, while *GkFlaA2* eluted between 9-9.5 minutes.

GkFlaA2, both expressed singly and co-expressed with *GkMaf*, was purified by Ni-NTA metal affinity chromatography, acetone precipitated and subjected to intact mass analysis by liquid chromatography coupled electrospray ionisation mass spectrometry. Acetone precipitated purified flagellin is dissolved in 10% acetonitrile to use for mass spectrometry and periodate oxidation and biotinylation.

Mass spectrometry analysis for identification of glycosylation sites:

We obtained results of MS/MS analysis of proteolytic digests of flagellins from Taplin Mass Spectrometry facility, Harvard Medical School, USA employing an LTQ Orbitrap Velos Pro ion-trap mass spectrometer (Thermo Fisher Scientific, Waltham, MA). For this, we subjected the proteins to be analysed to SDS-PAGE and Coomassie staining. Excised gel bands containing the protein (approximately 1 mm³ pieces) were subjected to in-gel protease digestion⁹⁶ at Taplin Mass Spectrometry facility, Harvard Medical School, USA. Gel pieces were washed and dehydrated with acetonitrile for 10 min followed by removal of acetonitrile and drying in a speed-vac, and rehydration in 50 mM bicarbonate. The samples were reduced with 1 mM DTT (in 50 mM ammonium bicarbonate) at 60 °C for 30 minutes, and then cooled to room temperature, Iodoacetamide (in 50 mM ammonium bicarbonate) was added to a final concentration of 5 mM. Following an incubation for 15 minutes at room temperature in the dark, DTT was added to a final concentration of 5 mM to quench the reaction, and sequence grade trypsin was added to a concentration of 5 ng/μl, and the reaction incubated overnight at 37 °C. Peptides were later extracted by removing the ammonium bicarbonate solution, followed by one wash with a solution containing 50% acetonitrile and 1% formic acid. The extracts were desalted by a desalting column made in-house, and then dried in a speed-vac (~1 hr) and stored at 4 °C until analysis. On the day of analysis the samples were reconstituted in 5 - 10 μl of HPLC solvent A (97.5% water, 2.5% acetonitrile, and 0.1% formic acid). A nano-scale reverse-phase HPLC capillary column was created by packing 2.6 μm C18 spherical silica beads into a fused silica capillary (100 μm inner diameter x ~30 cm length) with a flame-drawn tip (Peng, J and Gygi S.P. Proteomics:

The move to mixtures, *J. Mass Spec.* Oct:36(10):1083-91). After equilibrating the column each sample was loaded via a Famos auto sampler (LC Packings, San Francisco CA) onto the column. A gradient was formed and peptides were eluted with increasing concentrations of solvent B (97.5% acetonitrile, 2.5% water, and 0.1% formic acid). As peptides eluted they were subjected to electrospray ionization and then entered into an LTQ Orbitrap Velos Pro ion-trap mass spectrometer (Thermo Fisher Scientific, Waltham, MA). Peptides were detected, isolated, and fragmented to produce a tandem mass spectrum of specific fragment ions for each peptide. Peptide sequences (and hence protein identity) were determined by matching the protein database with the acquired fragmentation pattern by the software program, SEQUEST (Thermo Fisher Scientific, Waltham, MA) ⁹⁷. All databases included a reverse version of the sequence used and data were filtered to <2% peptide false discovery rate.

The search parameters allowed for a variable modification of 15.994915 Da on methionine. The Modscore algorithm was used to search for modifications of 291 Da (Neu5Ac) or 220 Da (KDO) on Ser/Thr residues. Two scores – Site 1 Position_A and Site 1 Position_B – were used with fragment ion tolerance settings of 0.6 Da and 0.3 Da, respectively. If the Modscore values for Site 1 Position_A and Site 1 Position_B scores were both above 19 for the same site then the location was considered confidently assigned. If the value was 1000 then it was an unequivocal assignment due to there being only one Ser/Thr in the peptide ⁶¹. Residue numbering and glycosylation site position are according to the amino acid sequence of the recombinant proteins and includes an additional Ala residue following the initial Met residue, and a C-terminal hexahistidine tag.

The mass spectrometry proteomics data reported in the manuscript have been deposited to the ProteomeXchange Consortium ⁹⁸ via the PRIDE ⁹⁹ partner repository with the dataset identifier PXD018167.

Mass spectrometry analysis for identification of glycan moiety on flagellin:

We performed mild acid hydrolysis of flagellin by incubating the protein in 0.1 M HCl at 80 °C for 60 minutes. We subjected these mild acid extracts of purified flagellin to MS/MS analysis at the High Resolution Mass Spectrometry facility at IIT Ropar using a XEVO-G2-XS-QTOF mass spectrometer. Samples were resolved on a C-18 column using a acetonitrile-water gradient on a Waters Acquity UPLC, and subjected to MS/MS in positive ionization mode. For comparison, we subjected standard solutions of Neu5Ac (Sigma) and KDO (Sigma) to MS/MS under the same conditions.

Data Availability

The mass spectrometry proteomics data reported in the manuscript have been deposited to the ProteomeXchange Consortium⁹⁸ via the PRIDE⁹⁹ partner repository with the dataset identifier PXD018167.

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Author contributions

RTNC conceived the study. AK and RTNC participated in experimental design. AK performed most of the biochemical experiments and SS performed a few biochemical experiments. RTNC, AK and SS performed data analysis. BP analyzed and interpreted the first intact mass spectrum data of glycosylated flagellin and provided the first critical insight of KDO modification of flagellin in BL21(DE3) cells. AK and RTNC wrote the first draft of the manuscript. All authors participated in editing the manuscript and approved the final version of the manuscript.

Conflict of interest

The authors declare that there are no conflicts of interest relevant to the subject of this manuscript.

References

1. Apweiler R, Hermjakob H, Sharon N. On the frequency of protein glycosylation, as deduced from analysis of the SWISS-PROT database. *Biochim Biophys Acta* **1473**, 4-8 (1999).
2. Neuberger A. Carbohydrates in protein: The carbohydrate component of crystalline egg albumin. *Biochem J* **32**, 1435-1451 (1938).
3. Spiro RG. Protein glycosylation: nature, distribution, enzymatic formation, and disease implications of glycopeptide bonds. *Glycobiology* **12**, 43R-56R (2002).

4. Mescher MF, Strominger JL. Purification and characterization of a prokaryotic glucoprotein from the cell envelope of *Halobacterium salinarium*. *J Biol Chem* **251**, 2005-2014 (1976).
5. Sleytr UB. Heterologous reattachment of regular arrays of glycoproteins on bacterial surfaces. *Nature* **257**, 400-402 (1975).
6. Sleytr UB, Thorne KJ. Chemical characterization of the regularly arranged surface layers of *Clostridium thermosaccharolyticum* and *Clostridium thermohydrosulfuricum*. *J Bacteriol* **126**, 377-383 (1976).
7. Schaffer C, Messner P. Emerging facets of prokaryotic glycosylation. *FEMS Microbiol Rev* **41**, 49-91 (2017).
8. Logan SM. Flagellar glycosylation - a new component of the motility repertoire? *Microbiology* **152**, 1249-1262 (2006).
9. Twine SM, *et al.* Flagellar glycosylation in *Clostridium botulinum*. *FEBS J* **275**, 4428-4444 (2008).
10. Schirm M, Schoenhofen IC, Logan SM, Waldron KC, Thibault P. Identification of unusual bacterial glycosylation by tandem mass spectrometry analyses of intact proteins. *Anal Chem* **77**, 7774-7782 (2005).

11. Thibault P, *et al.* Identification of the carbohydrate moieties and glycosylation motifs in *Campylobacter jejuni* flagellin. *J Biol Chem* **276**, 34862-34870 (2001).

12. Schirm M, Soo EC, Aubry AJ, Austin J, Thibault P, Logan SM. Structural, genetic and functional characterization of the flagellin glycosylation process in *Helicobacter pylori*. *Mol Microbiol* **48**, 1579-1592 (2003).

13. Schirm M, Kalmokoff M, Aubry A, Thibault P, Sandoz M, Logan SM. Flagellin from *Listeria monocytogenes* is glycosylated with beta-O-linked N-acetylglucosamine. *J Bacteriol* **186**, 6721-6727 (2004).

14. Schirm M, *et al.* Structural and genetic characterization of glycosylation of type a flagellin in *Pseudomonas aeruginosa*. *J Bacteriol* **186**, 2523-2531 (2004).

15. Logan SM, *et al.* Identification of novel carbohydrate modifications on *Campylobacter jejuni* 11168 flagellin using metabolomics-based approaches. *FEBS J* **276**, 1014-1023 (2009).

16. Bouche L, *et al.* The Type B Flagellin of Hypervirulent *Clostridium difficile* Is Modified with Novel Sulfonated Peptidylamido-glycans. *J Biol Chem* **291**, 25439-25449 (2016).

17. Zampronio CG, Blackwell G, Penn CW, Cooper HJ. Novel glycosylation sites localized in *Campylobacter jejuni* flagellin FlaA by liquid chromatography electron capture dissociation tandem mass spectrometry. *J Proteome Res* **10**, 1238-1245 (2011).

18. McNally DJ, *et al.* Targeted metabolomics analysis of *Campylobacter coli* VC167 reveals legionaminic acid derivatives as novel flagellar glycans. *J Biol Chem* **282**, 14463-14475 (2007).

19. Varki A, Schnaar RL, Schauer R. Sialic Acids and Other Nonulosonic Acids. In: *Essentials of Glycobiology* (eds rd, *et al.*) (2015).

20. Szymanski CM, Logan SM, Linton D, Wren BW. *Campylobacter*--a tale of two protein glycosylation systems. *Trends Microbiol* **11**, 233-238 (2003).

21. McNally DJ, *et al.* Functional characterization of the flagellar glycosylation locus in *Campylobacter jejuni* 81-176 using a focused metabolomics approach. *J Biol Chem* **281**, 18489-18498 (2006).

22. Karlyshev AV, Linton D, Gregson NA, Wren BW. A novel paralogous gene family involved in phase-variable flagella-mediated motility in *Campylobacter jejuni*. *Microbiology* **148**, 473-480 (2002).

23. van Alphen LB, Wuhler M, Bleumink-Pluym NM, Hensbergen PJ, Deelder AM, van Putten JP. A functional *Campylobacter jejuni* maf4 gene results in novel glycoforms on flagellin and altered autoagglutination behaviour. *Microbiology* **154**, 3385-3397 (2008).

24. Canals R, Vilches S, Wilhelms M, Shaw JG, Merino S, Tomas JM. Non-structural flagella genes affecting both polar and lateral flagella-mediated motility in *Aeromonas hydrophila*. *Microbiology* **153**, 1165-1175 (2007).

25. Canals R, *et al.* Analysis of the lateral flagellar gene system of *Aeromonas hydrophila* AH-3. *J Bacteriol* **188**, 852-862 (2006).

26. Canals R, *et al.* Polar flagellum biogenesis in *Aeromonas hydrophila*. *J Bacteriol* **188**, 542-555 (2006).

27. Parker JL, Day-Williams MJ, Tomas JM, Stafford GP, Shaw JG. Identification of a putative glycosyltransferase responsible for the transfer of pseudaminic acid onto the polar flagellin of *Aeromonas caviae* Sch3N. *Microbiologyopen* **1**, 149-160 (2012).

28. Sulzenbacher G, *et al.* Glycosylate and move! The glycosyltransferase Maf is involved in bacterial flagella formation. *Environ Microbiol* **20**, 228-240 (2018).

29. Parker JL, Lowry RC, Couto NA, Wright PC, Stafford GP, Shaw JG. Maf-dependent bacterial flagellin glycosylation occurs before chaperone binding and flagellar T3SS export. *Mol Microbiol* **92**, 258-272 (2014).

30. Chiu CP, *et al.* Structural analysis of the sialyltransferase CstII from *Campylobacter jejuni* in complex with a substrate analog. *Nat Struct Mol Biol* **11**, 163-170 (2004).

31. De Maayer P, Cowan DA. Comparative genomic analysis of the flagellin glycosylation island of the Gram-positive thermophile *Geobacillus*. *BMC Genomics* **17**, 913 (2016).

32. Priest FG, Goodfellow M, Todd C. A numerical classification of the genus *Bacillus*. *J Gen Microbiol* **134**, 1847-1882 (1988).
33. Nazina TN, *et al.* Taxonomic study of aerobic thermophilic bacilli: descriptions of *Geobacillus subterraneus* gen. nov., sp. nov. and *Geobacillus uzenensis* sp. nov. from petroleum reservoirs and transfer of *Bacillus stearothermophilus*, *Bacillus thermocatenulatus*, *Bacillus thermoleovorans*, *Bacillus kaustophilus*, *Bacillus thermodenitrificans* to *Geobacillus* as the new combinations *G. stearothermophilus*, *G. th.* *Int J Syst Evol Microbiol* **51**, 433-446 (2001).
34. Doi K, *et al.* Draft Genome Sequence of *Geobacillus kaustophilus* GBlys, a Lysogenic Strain with Bacteriophage OH2. *Genome Announc* **1**, (2013).
35. Takami H, *et al.* Thermoadaptation trait revealed by the genome sequence of thermophilic *Geobacillus kaustophilus*. *Nucleic Acids Res* **32**, 6292-6303 (2004).
36. Brumm PJ, Land ML, Mead DA. Complete genome sequence of *Geobacillus thermoglucosidasius* C56-YS93, a novel biomass degrader isolated from obsidian hot spring in Yellowstone National Park. *Stand Genomic Sci* **10**, 73 (2015).
37. Hayakawa J, Kondoh Y, Ishizuka M. Cloning and characterization of flagellin genes and identification of flagellin glycosylation from thermophilic *Bacillus* species. *Biosci Biotechnol Biochem* **73**, 1450-1452 (2009).

38. Vimr E, Lichtensteiger C. To sialylate, or not to sialylate: that is the question. *Trends Microbiol* **10**, 254-257 (2002).

39. Vimr ER, Kalivoda KA, Deszo EL, Steenbergen SM. Diversity of microbial sialic acid metabolism. *Microbiol Mol Biol Rev* **68**, 132-153 (2004).

40. Vimr ER. Unified theory of bacterial sialometabolism: how and why bacteria metabolize host sialic acids. *ISRN Microbiol* **2013**, 816713 (2013).

41. Ricaldi JN, Matthias MA, Vinetz JM, Lewis AL. Expression of sialic acids and other nonulosonic acids in *Leptospira*. *BMC Microbiol* **12**, 161 (2012).

42. Linton D, *et al.* Multiple N-acetyl neuraminic acid synthetase (neuB) genes in *Campylobacter jejuni*: identification and characterization of the gene involved in sialylation of lipo-oligosaccharide. *Mol Microbiol* **35**, 1120-1134 (2000).

43. Vimr E, Steenbergen S, Cieslewicz M. Biosynthesis of the polysialic acid capsule in *Escherichia coli* K1. *J Ind Microbiol* **15**, 352-360 (1995).

44. El-Gebali S, *et al.* The Pfam protein families database in 2019. *Nucleic Acids Res* **47**, D427-D432 (2019).

45. Yonekura K, Maki-Yonekura S, Namba K. Complete atomic model of the bacterial flagellar filament by electron cryomicroscopy. *Nature* **424**, 643-650 (2003).

46. Wang F, *et al.* A structural model of flagellar filament switching across multiple bacterial species. *Nat Commun* **8**, 960 (2017).
47. Freeze HH, Hart GW, Schnaar RL. Glycosylation Precursors. In: *Essentials of Glycobiology* (eds rd, *et al.*) (2015).
48. Steenbergen SM, Wrona TJ, Vimr ER. Functional analysis of the sialyltransferase complexes in *Escherichia coli* K1 and K92. *J Bacteriol* **174**, 1099-1108 (1992).
49. Ringenberg M, Lichtensteiger C, Vimr E. Redirection of sialic acid metabolism in genetically engineered *Escherichia coli*. *Glycobiology* **11**, 533-539 (2001).
50. Steenbergen SM, Vimr ER. Mechanism of polysialic acid chain elongation in *Escherichia coli* K1. *Mol Microbiol* **4**, 603-611 (1990).
51. Blacklow RS, Warren L. Biosynthesis of sialic acids by *Neisseria meningitidis*. *J Biol Chem* **237**, 3520-3526 (1962).
52. Bhavanandan VP, Ringler NJ, Gowda DC. Identification of the glycosidically bound sialic acid in mucin glycoproteins that reacts as "free sialic acid" in the Warren assay. *Glycobiology* **8**, 1077-1086 (1998).
53. Zeng Y, Ramya TN, Dirksen A, Dawson PE, Paulson JC. High-efficiency labeling of sialylated glycoproteins on living cells. *Nat Methods* **6**, 207-209 (2009).

54. Emiola A, George J, Andrews SS. A Complete Pathway Model for Lipid A Biosynthesis in *Escherichia coli*. *PLoS One* **10**, e0121216 (2014).

55. Finke A, Jann B, Jann K. CMP-KDO-synthetase activity in *Escherichia coli* expressing capsular polysaccharides. *FEMS Microbiol Lett* **57**, 129-133 (1990).

56. Raetz CR, Whitfield C. Lipopolysaccharide endotoxins. *Annu Rev Biochem* **71**, 635-700 (2002).

57. Klein G, Lindner B, Brade H, Raina S. Molecular basis of lipopolysaccharide heterogeneity in *Escherichia coli*: envelope stress-responsive regulators control the incorporation of glycoforms with a third 3-deoxy- α -D-manno-oct-2-ulosonic acid and rhamnose. *J Biol Chem* **286**, 42787-42807 (2011).

58. Ellwood DC. The distribution of 2-keto-3-deoxy-octonic acid in bacterial walls. *J Gen Microbiol* **60**, 373-380 (1970).

59. Ray PH, Benedict CD, Grasmuk H. Purification and characterization of cytidine 5'-triphosphate:cytidine 5'-monophosphate-3-deoxy-D-manno-octulosonate cytidyltransferase. *J Bacteriol* **145**, 1273-1280 (1981).

60. Belunis CJ, Raetz CR. Biosynthesis of endotoxins. Purification and catalytic properties of 3-deoxy-D-manno-octulosonic acid transferase from *Escherichia coli*. *J Biol Chem* **267**, 9988-9997 (1992).

61. Beausoleil SA, Villen J, Gerber SA, Rush J, Gygi SP. A probability-based approach for high-throughput protein phosphorylation analysis and site localization. *Nat Biotechnol* **24**, 1285-1292 (2006).
62. Watson DC, Leclerc S, Wakarchuk WW, Young NM. Enzymatic synthesis and properties of glycoconjugates with legionaminic acid as a replacement for neuraminic acid. *Glycobiology* **21**, 99-108 (2011).
63. Watson DC, *et al.* Preparation of legionaminic acid analogs of sialo-glycoconjugates by means of mammalian sialyltransferases. *Glycoconj J* **32**, 729-734 (2015).
64. Watson DC, *et al.* Sialyltransferases with enhanced legionaminic acid transferase activity for the preparation of analogs of sialoglycoconjugates. *Glycobiology* **25**, 767-773 (2015).
65. Jeong H, *et al.* Genome sequences of Escherichia coli B strains REL606 and BL21(DE3). *J Mol Biol* **394**, 644-652 (2009).
66. Mamat U, *et al.* Detoxifying Escherichia coli for endotoxin-free production of recombinant proteins. *Microb Cell Fact* **14**, 57 (2015).
67. Prehm P, Stirn S, Jann B, Jann K. Cell-wall lipopolysaccharide from Escherichia coli B. *Eur J Biochem* **56**, 41-55 (1975).

68. Schauer R. Achievements and challenges of sialic acid research. *Glycoconj J* **17**, 485-499 (2000).
69. Lombard V, Golaconda Ramulu H, Drula E, Coutinho PM, Henrissat B. The carbohydrate-active enzymes database (CAZy) in 2013. *Nucleic Acids Res* **42**, D490-495 (2014).
70. Li Y, Chen X. Sialic acid metabolism and sialyltransferases: natural functions and applications. *Appl Microbiol Biotechnol* **94**, 887-905 (2012).
71. Shen GJ, Datta AK, Izumi M, Koeller KM, Wong CH. Expression of alpha2,8/2,9-polysialyltransferase from Escherichia coli K92. Characterization of the enzyme and its reaction products. *J Biol Chem* **274**, 35139-35146 (1999).
72. Yamamoto T. Marine bacterial sialyltransferases. *Mar Drugs* **8**, 2781-2794 (2010).
73. Chen IA, *et al.* IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. *Nucleic Acids Res* **47**, D666-D677 (2019).
74. Scott AE, *et al.* Flagellar glycosylation in Burkholderia pseudomallei and Burkholderia thailandensis. *J Bacteriol* **193**, 3577-3587 (2011).
75. Ovchinnikova OG, Doyle L, Huang BS, Kimber MS, Lowary TL, Whitfield C. Biochemical Characterization of Bifunctional 3-Deoxy-beta-d-manno-oct-2-ulosonic Acid

(beta-Kdo) Transferase KpsC from *Escherichia coli* Involved in Capsule Biosynthesis. *J Biol Chem* **291**, 21519-21530 (2016).

76. Ovchinnikova OG, Mallette E, Koizumi A, Lowary TL, Kimber MS, Whitfield C. Bacterial beta-Kdo glycosyltransferases represent a new glycosyltransferase family (GT99). *Proc Natl Acad Sci U S A* **113**, E3120-3129 (2016).

77. Willis LM, Whitfield C. KpsC and KpsS are retaining 3-deoxy-D-manno-oct-2-ulosonic acid (Kdo) transferases involved in synthesis of bacterial capsules. *Proc Natl Acad Sci U S A* **110**, 20753-20758 (2013).

78. Belunis CJ, Clementz T, Carty SM, Raetz CR. Inhibition of lipopolysaccharide biosynthesis and cell growth following inactivation of the *kdtA* gene in *Escherichia coli*. *J Biol Chem* **270**, 27646-27652 (1995).

79. Smyth KM, Marchant A. Conservation of the 2-keto-3-deoxymanno-octulosonic acid (Kdo) biosynthesis pathway between plants and bacteria. *Carbohydr Res* **380**, 70-75 (2013).

80. Wilkins MR, *et al.* Protein identification and analysis tools in the ExPASy server. *Methods Mol Biol* **112**, 531-552 (1999).

81. Wilkins MR, *et al.* High-throughput mass spectrometric discovery of protein post-translational modifications. *J Mol Biol* **289**, 645-657 (1999).

82. Bairoch A, *et al.* The Universal Protein Resource (UniProt). *Nucleic Acids Res* **33**, D154-159 (2005).
83. UniProt C. UniProt: a worldwide hub of protein knowledge. *Nucleic Acids Res* **47**, D506-D515 (2019).
84. Creasy DM, Cottrell JS. Unimod: Protein modifications for mass spectrometry. *Proteomics* **4**, 1534-1536 (2004).
85. Avtonomov DM, Kong A, Nesvizhskii AI. DeltaMass: Automated Detection and Visualization of Mass Shifts in Proteomic Open-Search Results. *J Proteome Res* **18**, 715-720 (2019).
86. Oetke C, *et al.* Versatile biosynthetic engineering of sialic acid in living cells using synthetic sialic acid analogues. *J Biol Chem* **277**, 6688-6695 (2002).
87. Campbell CT, Sampathkumar SG, Yarema KJ. Metabolic oligosaccharide engineering: perspectives, applications, and future directions. *Mol Biosyst* **3**, 187-194 (2007).
88. Aime Lopez Aguilar JGB, Linette Yang, Ben Ovryn, Matthew Scott Macauley, Peng Wu. Tools for Studying Glycans: Recent Advances in Chemoenzymatic Glycan Labeling. *ACS Chem Biol* **12**, 611-621 (2017).

89. Liu F, Aubry AJ, Schoenhofen IC, Logan SM, Tanner ME. The engineering of bacteria bearing azido-pseudaminic acid-modified flagella. *Chembiochem* **10**, 1317-1320 (2009).
90. Blattner FR, *et al.* The complete genome sequence of Escherichia coli K-12. *Science* **277**, 1453-1462 (1997).
91. Menard R, *et al.* Small-molecule inhibitors of the pseudaminic acid biosynthetic pathway: targeting motility as a key bacterial virulence factor. *Antimicrob Agents Chemother* **58**, 7430-7440 (2014).
92. Schoenhofen IC, McNally DJ, Brisson JR, Logan SM. Elucidation of the CMP-pseudaminic acid pathway in Helicobacter pylori: synthesis from UDP-N-acetylglucosamine by a single enzymatic reaction. *Glycobiology* **16**, 8C-14C (2006).
93. Schoenhofen IC, Vinogradov E, Whitfield DM, Brisson JR, Logan SM. The CMP-legionaminic acid pathway in Campylobacter: biosynthesis involving novel GDP-linked precursors. *Glycobiology* **19**, 715-725 (2009).
94. Glaze PA, Watson DC, Young NM, Tanner ME. Biosynthesis of CMP-N,N'-diacetyllegionaminic acid from UDP-N,N'-diacetylbaucillosamine in Legionella pneumophila. *Biochemistry* **47**, 3272-3282 (2008).

95. Velappan N, Sblattero D, Chasteen L, Pavlik P, Bradbury AR. Plasmid incompatibility: more compatible than previously thought? *Protein Eng Des Sel* **20**, 309-313 (2007).
96. Shevchenko A, Wilm M, Vorm O, Mann M. Mass spectrometric sequencing of proteins silver-stained polyacrylamide gels. *Anal Chem* **68**, 850-858 (1996).
97. Eng JK, McCormack AL, Yates JR. An approach to correlate tandem mass spectral data of peptides with amino acid sequences in a protein database. *J Am Soc Mass Spectrom* **5**, 976-989 (1994).
98. Deutsch EW, *et al.* The ProteomeXchange consortium in 2020: enabling 'big data' approaches in proteomics. *Nucleic Acids Res* **48**, D1145-D1152 (2020).
99. Perez-Riverol Y, *et al.* The PRIDE database and related tools and resources in 2019: improving support for quantification data. *Nucleic Acids Res* **47**, D442-D450 (2019).
100. Varki A, *et al.* Symbol Nomenclature for Graphical Representations of Glycans. *Glycobiology* **25**, 1323-1324 (2015).
101. Roy A, Kucukural A, Zhang Y. I-TASSER: a unified platform for automated protein structure and function prediction. *Nat Protoc* **5**, 725-738 (2010).

Figure Legends

Figure 1: Structures of N-acetylneuraminic acid, 3-Deoxy-D-manno-octulosonic acid, pseudaminic acid and legionaminic acid.

Figure 1

Figure 2: Co-expression of *GkFlaA2* with *GkMaf*. **(A)** Flagellin glycosylation island of *Geobacillus kaustophilus* HTA426. The putative ORFs of Maf and flagellin proteins have been shown in purple and pink colour, respectively. **(B)** Strategy for T7 based co-expression of *GkFlaA2* and *GkMaf* in recombinant *E. coli* K12:K1 hybrid system overproducing the donor substrate CMP-Neu5Ac and harboring pAR1219 plasmid expressing T7 RNA Polymerase. **(C, D)** Western analysis of cell-free supernatant and cell debris fractions of cell lysates of EV136 **(C)** and EV36 **(D)** cells transformed with *GkflaA2*-pET28a(+) vector and *Gkmaf*-pCDF-Duet-1. Recombinant *GkFlaA2* and *GkMaf* were detected by western analysis with mouse anti-6XHis antibody and mouse anti-S tag antibody, respectively.

Figure 2

Figure 3: *GkMaf* glycosylates *GkFlaA2*. (A) On-blot periodate oxidation and biotinylation of *GkFlaA2* singly expressed or co-expressed with *GkMaf* in EV136, EV36 and EV240 cells. Biotinylation was detected with HRP-streptavidin. Total *GkFlaA2* protein was detected with mouse anti-6XHis antibody (B, C) Intact mass measurement of *GkFlaA2* singly expressed (upper panel) or co-expressed with *GkMaf* and purified from EV136 cells (B) or EV36 cells (C). The proteins were acetone precipitated and subjected to LC-MS in positive mode ionization. Inset shows the ionization spectrum. The satellite peaks correspond to sodiated adducts.

Figure 4: Identification of glycosites in *GkFlaA2*. (A,B) Sequence coverage of tandem mass spectrometry data obtained for *GkFlaA2* purified from EV136 **(A)** and EV36 cells **(B)**. The sequence coverage is shown as pink font. The modified sequence coverage is underlined blue (tryptic peptides) or green (Glu-C digested peptides). The sites modified have been highlighted in blue. Neu5Ac is represented by @ symbol and KDO by #. **(C, D)** MS/MS spectra indicating fragment ions of tryptic and Glu-C digested peptides of *GkFlaA2* in EV136 **(C)** and EV36 **(D)** cells as per SEQUEST⁹⁷. y- and b- ions have been shown in green and red colour, respectively. Relative percent abundances (relative to most abundant fragment ion) are plotted on the y-axis. Neu5Ac and KDO are represented by a pink diamond and a yellow hexagon, respectively, as per symbol nomenclature for graphical representations of glycans¹⁰⁰. Spectra are of peptides identified and listed in Supplementary tables S7c and S8d. **(F)** and **(G)** show structure model of *GkFlaA2*, generated by iTASSER¹⁰¹ using 5wjt as template, with Ser/Thr sites modifications (in stick form) as per MS/MS data from EV136 **(F)** and EV36 **(G)** cells.

Figure 4

Figure 5: Co-expression of *CbFla* with *CbMaf*. **(A)** Flagellin glycosylation island of *Clostridium botulinum* F strain Langeland. The putative ORFs of Maf and flagellin proteins have been shown in purple and pink colour, respectively. **(B)** Strategy for T7 based co-expression of *CbFla* and *CbMaf* in recombinant *E. coli* K12:K1 hybrid system overproducing the donor substrate CMP-Neu5Ac and harboring pAR1219 plasmid expressing T7 RNA Polymerase. **(C, D)** Western analysis of cell-free supernatant and cell debris fractions of cell lysates of EV36 **(C)** and EV136 **(D)** cells transformed with *Cbfla*-pCDF-Duet-1 vector and *Cbmaf*-pET-28a(+). Recombinant *CbFla* and *CbMaf* proteins were detected by western analysis with mouse anti-6XHis antibody.

Figure 5

Figure 6: *CbMaf* glycosylates *CbFla*. (A) On-blot periodate oxidation and biotinylation of *CbFla* singly expressed or co-expressed with *CbMaf* in EV36, EV136 and EV240 cells. Biotinylation was detected with HRP-streptavidin. Total protein was detected with mouse anti-6XHis antibody (B, C) Intact mass measurement of *CbFla* singly expressed (upper panel) or co-expressed with *CbMaf* and purified from EV136 cells (B) or EV36 cells (C). The proteins were acetone precipitated and subjected to LC-MS in positive mode ionization. Inset shows the ionization spectrum. The satellite peaks correspond to sodiated adducts.

Figure 6

Figure 7: Identification of glycosites in *CbFla*. (A, B) Sequence coverage of tandem mass spectrometry data obtained for *CbFla* purified from EV136 (A) and EV36 cells (B). The sequence coverage is shown as pink font. The modified sequence coverage is underlined blue. The sites modified have been highlighted in blue. Neu5Ac is represented by @ symbol and KDO by #. (C, D) MS/MS spectra indicating fragment ions of tryptic peptides of *CbFla* in EV136 (C) and EV36 (D) cells as per SEQUEST⁹⁷. y- and b- ions have been shown in green and red colour, respectively. Relative percent abundances (relative to most abundant fragment ion) are plotted on the y-axis. Neu5Ac and KDO are represented by a pink diamond and a yellow hexagon, respectively, as per symbol nomenclature for graphical representations of glycans¹⁰⁰ (E) and (F) show structure model of *CbFla* generated by iTASSER¹⁰¹ using 5wjt as template, with Ser/Thr sites modifications (in stick form) as per MS/MS data.

Figure 7

Figure 8: D272, D257 and S334 of *CbMaf* are required for glycosyltransferase activity.

(A) Western analysis of *CbFla* singly expressed or coexpressed with D272A, D257A and S334A mutants of *CbMaf*. *CbMaf* and *CbFla* proteins were detected with anti-S tag antibody and mouse anti-6XHis antibody, respectively. **(B)** On-blot periodate oxidation and biotinylation of *CbFla* singly expressed or co-expressed with wildtype and mutant *CbMaf* in EV136 and EV36 cells. Biotinylation was detected with HRP-streptavidin. Total *CbFla* protein was detected with mouse anti-6XHis antibody. **(C)** Intact mass measurement of *CbFla* singly expressed (upper panel) or co-expressed with *CbMaf* mutants and purified from EV136 cells. The proteins were acetone precipitated and subjected to LC-MS in positive mode ionization. Inset shows the ionization spectrum. The satellite peaks correspond to sodiated adducts.

Figure 8

Figure 9: Co-expression of *CbFla* and *CbMaf* in BL21(DE3) cells. (A) Strategy for T7 based co-expression of *CbFla* and *CbMaf* in recombinant *E. coli* BL21(DE3) producing CMP-KDO and expressing T7 RNA Polymerase. **(B)** Western analysis of cell-free supernatant and cell debris fractions of cell lysates of BL21(DE3) cells transformed with *Cbfla*-pET-28a(+) vector and *Cbmfa*-pET-Duet-1. Recombinant *CbFla* and *CbMaf* proteins were detected by western analysis with mouse anti-6XHis antibody and mouse anti-S-tag antibody, respectively. **(C)** On-blot periodate oxidation and biotinylation of *CbFla* singly expressed or co-expressed with *CbMaf* in BL21(DE3) cells. Biotinylation was detected with HRP-streptavidin. Total protein was detected with mouse anti-6XHis antibody. **(C)** Intact mass measurement of *CbFla* singly expressed (upper panel) or co-expressed with *CbMaf* and purified from BL21(DE3) cells. The proteins were acetone precipitated and subjected to LC-MS in positive mode ionization. Inset shows the ionization spectrum. The satellite peaks correspond to sodiated adducts.

Figure 9

Figure 10: Identification of glycan moiety by tandem mass spectrometry. Tandem mass spectrometry of mild acid extracts of *CbFla* co-expressed with *CbMaf* in EV136 **(A)** and BL21(DE3)cells **(B)**. Insets show standard Neu5Ac and KDO fragmentation patterns, respectively.

Figure 10