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Lipid bilayer nanodisc platform for investigating polyprenol-dependent enzyme interactions and activities

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Membrane-bound polyprenol-dependent pathways are important for the assembly of essential glycoconjugates in all domains of life. However, despite their prevalence, the functional significance of the extended linear polyprenyl groups in the interactions of the glycan substrates, the biosynthetic enzymes that act upon them, and the membrane bilayer in which they are embedded remains a mystery. These interactions are investigated simultaneously and uniquely through application of the nanodisc membrane technology. The Campylobacter jejuni N-linked glycosylation pathway has been chosen as a model pathway in which all of the enzymes and substrates are biochemically accessible. We present the functional reconstitution of two enzymes responsible for the early membrane-committed steps in glycan assembly. Protein stoichiometry analysis, fluorescence-based approaches, and biochemical activity assays are used to demonstrate the colocalization of the two enzymes in nanodiscs. Isotopic labeling of the substrates reveals that undecaprenyl-phosphate is coincorporated into discs with the two enzymes, and furthermore, that both enzymes are functionally reconstituted and can sequentially convert the coembedded undecaprenyl-phosphate into undecaprenyl-diphosphate-linked di-saccharide. These studies provide a proof-of-concept demonstrating that the nanodisc model membrane system represents a promising experimental platform for analyzing the multifaceted interactions among the enzymes involved in polyprenol-dependent glycan assembly pathways, the membrane-associated substrates, and the lipid bilayer. The stage is now set for exploration of the roles of the conserved polyprenols in promoting protein–protein interactions among pathway enzymes and processing of substrates through sequential steps in membrane-associated glycan assembly.

Cellular membranes accommodate abundant biological activities, including the transport of small molecules and proteins, energy production, and multisite biosynthetic transformations. These functions are crucial for cell viability; however, studying these processes in biophysical and biochemical detail is challenging because of the complexity of working with both integral and peripheral membrane proteins in lipid bilayer systems. An important class of membrane-associated pathways involves the assembly of complex glycoconjugates, which is dependent on the extended linear polyprenols (1–4). The products of these pathways are essential for cellular viability in all domains of life and, intriguingly, the polyprenols that are used in glycan assembly vary between organisms, with considerable differences in the overall length and degrees of unsaturation (2, 5). For example, bacteria generate peptidoglycan components on the membrane-anchored undecaprenyl-diphosphate before cell wall assembly (6), whereas eukaryotes produce glycans for N-linked protein glycosylation via dolichyl-diphosphate–linked intermediates, which feature polyprenols ranging from 14–25 isoprene units (1, 2, 7). Despite the ubiquitous presence of linear polyprenols as glycan carriers in these important biosynthetic pathways, it remains unclear why these structures have been so faithfully conserved throughout evolution and what might be their functional significance, particularly because extended polyprenols have no other known role in cells (2, 4, 5).

The discovery (8) and biochemical investigation (9–11) of N-linked protein glycosylation in the Gram-negative bacterium Campylobacter jejuni has revealed a canonical polyprenol-dependent glycan assembly pathway. The C. jejuni protein glycosylation (pgl) pathway is an appealing subject for in-depth analysis because the component enzymes can be heterologously expressed and purified in good yields, and can be subjected to protein engineering approaches for the introduction of tags and labels. As illustrated in Fig. 1A, in the pgl pathway, a heptasaccharide is assembled onto undecaprenyl-diphosphate (Und-P-P) by the sequential action of five membrane proteins, designated as PglC, PglA, PglJ, PglH, and PglI. Of these proteins, PglC and PglI are predicted to be integral membrane proteins (12), whereas the other glycan assembly enzymes (PglA, PglJ, and PglH) lack discrete transmembrane domains (TMDs) and are peripheral membrane proteins. Both the integral and peripheral membrane Pgl proteins form insoluble aggregates in the absence of detergent, which further supports a model wherein these enzymes are recruited to the membrane to collaborate in the sequential glycan assembly process. After biosynthesis of the undecaprenyl-diphosphate heptasaccharide is complete, a flippase (PglK) translocates the assembled product to the periplasmic face of the inner membrane (13), where the oligosaccharyltransferase (PgbL) transfers the assembled glycan to asparagine residues in selected acceptor proteins (10, 14). After translocation through the outer membrane, glycosylated proteins...
are displayed on the cellular surface and appear to be involved in adhesion, colonization, and host-cell invasion (15).

One of the major hurdles in deciphering the discrete biochemical and biological roles of polyprenols in membrane-associated pathways is implementing methods to simultaneously investigate all the three components involved in polyprenol action: the lipid bilayer, membrane-associated proteins, and polyprenyl-linked substrates. Prior studies on polyprenol-dependent pathways have principally focused on redacted experimental systems representing two of the three key variables. For example, the effect of varying the substrate polyprenol groups has been studied in model membrane systems including variants of phosphatidylcholine (PC), phosphatidylethanolamine (PE), and phosphatidylglycerol (PG), as well as E. coli lipid extracts (25). Diverse membrane proteins have been incorporated into nanodiscs and studies on these systems have revealed fascinating nuances of protein structure, protein oligomeric state, protein–protein interactions, substrate binding, and enzyme activity (30–36). In addition, particularly noteworthy for the current study, the effects of lipid composition on enzymes have been probed in a highly reproducible manner relative to other membrane mimetic systems (37, 38).

To address the fundamental challenge of defining the physical and biochemical roles of polyprenols in membrane-associated pathways, we present the development and validation of an experimental strategy to reconstitute the first two membrane-committed steps of the N-linked glycosylation pathway of C. jejuni (9, 11) in membrane bilayer nanodiscs (28). The approach in this study renders the simultaneous and controlled manipulation of all three determining elements in polyprenol-dependent glycan assembly at the membrane bilayer a tangible objective.

**Results**

**Incorporation and Characterization of PglC and PglA in Membrane Bilayer Nanodiscs.** PglC is a phosphoglycosyltransferase containing one predicted N-terminal TMD (11). PglC catalyzes the transfer of phospho-N,N′-diacytitylcarbamoisine from UDP-N,N′-diacytitylcarbamoisine (UDP-diNACab) to undecaprenyl-diphosphate (Und-P) (Fig. 1B). For these studies the GB1 domain of Ig binding protein G–PglC fusion construct was engineered in which a His6-tag was inserted N-terminal to the GB1 domain (39). The GB1 domain vastly improved the expression and purification of PglC, which was critical for these studies. The His6-GB1-PglC construct expresses well in E. coli (2–5 mg/L cell culture) and can be solubilized from membrane lipids with detergent and purified using Ni-NTA affinity chromatography for reconstitution in the nanodisc system (*SI Text*).

PglA is a glycosyltransferase that catalyzes the transfer of GalNac from UDP-GalNac to form Und-P-P-diNACab-GalNac (9) (Fig. 1B). Although there are no predicted TMDs for PglA (12), size-exclusion chromatographic (SEC) analysis of the His6-tobacco etch virus (TEV)-PglA construct in buffer without detergent reveals that the protein aggregates. Based on this behavior and the fact that PglA interacts with a membrane-bound substrate (Und-PP-diNACab), PglA is designated as a peripheral membrane protein. Well-behaved monodisperse preparations of PglA can be achieved in the presence of β-o-dodecamyltrosate at 0.05% (wt/vol). Typical yields of PglA after purification and TEV protease treatment for His6-tag removal range from 2 to 4 mg/L cell culture (*SI Text*).

Nanodisc preparation was carried out following literature protocols (29) and is illustrated in Fig. 2. For the preparation of nanodiscs involving PglC (PglC-NDs). A polar E. coli lipid extract with a ratio PE/PG/cardiolipin of 67:23:10 (wt %) was used because the phospholipid composition of E. coli is expected to be similar to that of C. jejuni, as both are Gram-negative bacteria. The MSP1E3 variant used in these studies forms nanodiscs with a Stokes hydrodynamic diameter of 12.1 nm, as measured previously by SEC, or a diameter of 12.9 nm, as measured by small-angle X-ray scattering (25). The His6-TEV-MSP1E3 construct was expressed, purified, and subjected to TEV proteolysis to afford high yields of purified protein (60 mg/L cell culture). For the PglC-ND preparation, a 10:1 MSP:PglC (5:1 ND:PglC) ratio afforded a discrete population of discs, which could be purified away from empty discs and the remaining nanodisc assembly components via Ni-NTA chromatography using the unique His6-tag on PglC (Fig. 2B). To estimate the number of PglCs per disc, gel densitometry by quantitative Coomassie staining was carried out and revealed the presence of one PglC species per nanodisc assembly (Fig. 3 and Fig. S1). In addition, SEC analysis of the

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**Fig. 1.** Canonical reaction pathway of bacterial N-linked glycosylation in C. jejuni. (A) Scheme of the membrane-bound enzymatic conversions that produce the polyprenyl-diphosphate-linked glycan, which is used in protein glycosylation. (B) The reactions of the first two enzymes in the C. jejuni pathway, PglC and PglA, are shown.
Ni-NTA–purified nanodiscs showed an elution profile consistent with a PglC-ND assembly (Fig. 3B and S2). Nanodiscs were also prepared in the presence of PglC and PglA at an MSP:PglC:PglA ratio of 10:1:1 (5:1:1 ND/PglC/PglA) and subjected to affinity chromatography on Ni-NTA. In this case, the only nanodisc species binding to the stationary phase are those containing His$_6$-GB1-PglC, because the affinity tags of all other components were removed previously. At this stage, two possible outcomes were anticipated: Either there would be a statistical distribution of PglA among all of the discs, and therefore only 20% of the discs isolated after Ni-NTA purification would contain both PglC and PglA, or alternatively, a positive interaction between PglC and PglA in the discs would bias the distribution. When the purified nanodiscs were analyzed by gel densitometry, the PglC:PglA ratio was 1.0±0.7 (Fig. 3A). This result implies that PglA is colocalized with PglC in ~70% of the population.

Dynamic light scattering (DLS) was applied to estimate the hydrodynamic radii of the various nanodisc assemblies (Fig. 3C). The measurements show particles with average hydrodynamic particle radii of 6.6 nm for empty nanodiscs, 12.9 nm for PglC-NDs, and 15.4 nm PglC/PglA-NDs, which is consistent with the effect of systematically adding proteins to the nanodisc assemblies. As a control, PglC and MSP in the absence of phospholipids did not afford detectable particles, and it is likely that the protein components precipitated under detergent withdrawal conditions. We note that the measured polydispersities are somewhat high, which may indicate the presence of a population of aggregates, which has been documented previously with DLS measurements on nanodisc assemblies (33).

Fluorescence Labeling of PglC and PglA and FRET Analysis. PglC and PglA were engineered to incorporate site-specific fluorescent labels (Fig. 4A) to probe the cofacial organization of the two reconstituted proteins in the nanodisc assembly using FRET. Based on estimated distances in the PglC/PglA-ND (Fig. 4B), the known tetramethylrhodamine (TAMRA) and Cyanine5 (Cy5) FRET-pair (R$_0$ ~ 6.5 nm) was selected. For fluorophore labeling, PglC lacks native Cys residues and therefore single Cys mutations were introduced to generate two mutants for site-specific thiol-directed modification using a Cy5-maleimide derivative (SI Text and Fig. S3). The labeling sites were selected such that the Cy5 would modify either the globular domain of PglC [PglC(Cy5-globular)] or the N terminus [PglC(Cy5-terminal)], which would be localized on the distal side of the membrane bilayer (Fig. 4B and Fig. S3). The chemical labeling proceeded to ~50% conversion and the precise labeling efficiency was quantified following reconstitution of the PglC mutants into nanodiscs. With respect to PglA, the native sequence includes six Cys residues, and therefore an alternate labeling strategy was adopted. Labeling of PglA (Fig. 4A) with the TAMRA fluorophore was achieved by sortase-mediated ligation (40); this method guaranteed quantitative labeling of the donor species, which is beneficial in a static ensemble FRET experiment. For this process, a PglA variant with a C-terminal sortase A recognition sequence (LPETG) and a TAMRA-labeled, sortase-active peptide [GGGYK(TAMRA)KG] were reacted to yield the modified PglA(TAMRA). The C terminus was chosen for labeling because addition of an N-terminal peptide tag had been found to disrupt the association of PglA with PglC-NDs (Fig. S4). Fluorescence labeling was carried out as summarized in Fig. 4A and presented in the SI Text.

Fluorescently labeled proteins were reconstituted into nanodiscs using the approaches developed for the unlabeled species. Fluorescent PglC/PglA-NDs were adjusted to the same concentration.
Fig. 4. Analysis of cofacial localization of PgC and PglA in nanodiscs using FRET. (A) Preparation of fluorescent protein constructs. PgC Cys mutants were labeled with Cy5 maleimide and PglA was labeled with TAMRA using a sortase-mediated transpeptidation with a TAMRA-containing peptide. (B) Graphic of the PgC/PglA-ND. Nanodisc dimensions and the R0 of the fluorophore pair are indicated. The locations of the fluorophores are based on structure prediction models (SI Text and Fig. S3). (C) Corrected fluorescence emission spectra of PgC(Cy5-terminal)/PglA(TAMRA) nanodiscs (FRET state) and PglA(unlabeled)/PglA(TAMRA) nanodiscs (donor only). (D) Corrected fluorescence emission spectra of PgC(Cy5-globular)/PglA(TAMRA) nanodiscs (FRET state) and donor-only nanodiscs. Data from nanodiscs comprising the PgC species labeled in the globular segment reveal a higher FRET efficiency than nanodiscs containing terminally labeled PglC.

To perform the FRET experiment, TAMRA was excited at a low wavelength (515 nm) to minimize cross-excitation of the Cy5 acceptor. The fluorescence emission showed defined signals for the donor emission and excitation of the acceptor attributable to FRET (Fig. S5). The resulting spectra of the nanodisc ensembles with different PglC mutants were corrected for UV spectroscopy to determine the number of possible FRET states (see Methods and SI Text for details).

The donor signal was quenched for donor/acceptor nanodisc ensembles with both PglC mutants, revealing a higher FRET efficiency in the presence of the PglC(Cy5) acceptor labeled within the globular protein segment (E = 0.57) compared with the terminally labeled PglC(Cy5) (E = 0.43). This trend was also observed in the intensity of the acceptor signals, revealing a stronger signal for the PglC(Cy5-globular) species (Fig. 4 C and D). FRET efficiencies were estimated based on donor signal decay upon quenching, thereby avoiding the use of acceptor standards and circumventing errors arising from endogenous acceptor quenching processes, such as those caused by different probe environments. Assuming the free rotation of the appended fluorophores, the stronger energy transfer for PglC(Cy5-globular) relative to PglC(Cy5-terminal) is good evidence for a model in which the soluble globular domains of PglC and PglA obtain a cofacial arrangement in the nanodiscs, as illustrated in Fig. 4B.

Functional Reconstitution of PglC and PglA. Radioactivity tracer studies were used to assess the activities of the enzymes in the nanodisc assemblies. Specifically, undecaprenyl-[33P]phosphate (Und-[33P]P) allowed for quantification of Und-P incorporation and also provided an orthogonal radiolabel that was used in concert with [14C] or [3H]-labeled UDP-sugars (UDP-[14C]diNAcBac and UDP-[3H]GalNAc) for precise tracking of the Und-P-linked species. To establish that Und-P incorporated into the nanodiscs, PglC/PglA-NDs were prepared from PE/PG lipids (3:1) and 0.5 mol percent Und-[33P]P. The assemblies were purified by Ni-NTA chromatography, and the radioactivity present in the flow-through, wash, and elution fractions was quantified by liquid scintillation counting, which showed that ~8% of the total radioactivity was associated with nanodiscs (Fig. 5A). Because only 20% of the nanodisc ensembles included PglC, this level of Und-P incorporation was consistent with a statistical distribution of Und-P.

To validate that PglC was functionally reconstituted into the nanodiscs, PglC-NDs with Und-[33P]P were treated with soluble UDP-[14C]diNAcBac. After incubation of the reaction for 1 h, an organic-aqueous extraction of the reaction mixture was performed to assess incorporation of [14C], representing diNAcBac, into Und-[33P]P-P-[14C]diNAcBac, which would extract into the organic phase. The organic extract was analyzed by normal-phase HPLC and elution fractions were collected and analyzed by liquid scintillation counting. The [33P]-signal corresponding to Und-[33P]P eluted first, followed by [3H] and [14C] signals that coeluted in a single fraction and corresponded to Und-[33P]P-P-[14C]diNAcBac (Fig. 5B).

The PglC/PglA-NDs were prepared with Und-[33P]P and activity was assessed in a similar fashion, but using first unlabeled UDP-diNAcBac and UDP-[3H]GalNAc (Fig. 5C), and then both

![Diagram](Image)

**Fig. 4.** Analysis of cofacial localization of PgC and PglA in nanodiscs using FRET.
UDP\(^{[14]C}\)diNAcBac and UDP\(^{[3]H}\)GalNAc (Fig. 5D). The \(^{[33]P}\) signal corresponding to Und-\(^{[33]P}\)P elutes first in both cases and the disaccharide product is observed with coeluting \(^{[32]P}\) and \(^{[14]C}\) or coeluting \(^{[32]P}\), \(^{[38]C}\), and \(^{[14]C}\), consistent with the coupled reactions of PglC and PglA. When UDP-diNAcBac is omitted from the coupled reaction, no final product is observed (Fig. 5E), indicating that the sequential reactions of both enzymes are required for production of the Und-P-P-disaccharide.

Because all of the substrates in the assays were discretely and quantifiable labeled with radioisotopes, the percent conversion of the nanodisc-associated Und-\(^{[33]P}\)P could be determined. After 1 h we observed that \(\sim 50\%\) of the Und-\(^{[33]P}\)P had been converted to corresponding Und-\(^{[33]P}\)P-P-linked product (Fig. 5 B–D). This finding is consistent with a model in which the Und-P is statistically distributed in the nanodisc with the phosphate oriented equally toward both faces of the membrane bilayer. Because it is well established that polyisoprenyl-phosphates do not undergo passive membrane flipping (41, 42), this finding would correlate with all of the available Und-P being processed through the active sites of the enzymes on the same face of the disc.

To monitor the time course of the coupled PglC/PglA reaction and production of the product, a similar method to that described above using unlabeled Und-P, UDP-diNAcBac, and UDP-\(^{[3]}H\) GalNAc, was applied and aliquots of the reaction mixture were quenched at multiple time points. The data show a rapid and efficient production of the labeled Und-P-P-diNAcBac-\(^{[3]}H\)GalNAc product (Fig. 6A). To assess for activity because of endogenous Und-P in the native \(E.\ coli\) lipid extract, the nanodiscs were prepared without added Und-P, and indeed a low level of background activity was observed (Fig. 6A). When this experiment was repeated with nanodiscs prepared with a lipid mixture composed of synthetic PE (67.0%) and PG (23.2%), as well as cardiolipin (9.8%)—which is comparable to the predominant \(E.\ coli\) membrane lipid components—background activity was not observed. Therefore, this observation is consistent with the commercial \(E.\ coli\) lipid extract containing a low level of endogenous Und-P.

To demonstrate the importance of colocalization in nanodiscs for enzyme activity, the enzymatic reaction rates were determined in nanodiscs and in detergent-disrupted nanodiscs. Two identical nanodisc samples were diluted with either buffer or detergent and then assayed for activity. The reaction rate of detergent-disrupted nanodiscs was \(-12.5\text{-times slower than the reaction rate of the undisrupted sample (Fig. 6B).}\)

Finally, evidence for a static colocalization of the PglC and PglA enzymatic reactions at the nanodisc surface was obtained by evaluating the reaction rates at different PglC/PglA-ND dilutions. Assuming that nanodiscs are stable macromolecular complexes containing cofacially oriented PglC, PglA, and Und-P, then the observed activity rate should not depend on the concentration of PglC, PglA, or Und-P, but rather the absolute amount of these components. To test this theory, an equimolar amount of nanodiscs was assayed at three different dilutions and the concentrations of the soluble UDP-sugars were kept constant. The initial reaction rates reflected in the slopes of the reaction turnover are the same for all dilutions (Fig. 6C). This finding is consistent with the formation of nanodiscs containing stable cofacially oriented PglC and PglA in tandem with available Und-P substrate.

**Discussion**

We present an experimental platform that exploits membrane bilayer nanodiscs for investigating the functional roles of linear long-chain polyisoprenols in glycan assembly pathways. To establish the potential of the approach, we have focused on the current studies on the first two membrane-committed steps in the \(C.\ jejuni\) Pgl pathway carried out by the phosphoglycosyltransferase PglC and the glycosyltransferase PglA, and have investigated coincorporation of the enzymes into nanodiscs using multiple biochemical and biophysical methods.

**Protein Interactions at the Membrane Interface.** We demonstrate that PglC incorporates into nanodiscs as a functional monomer (Figs. 2 and 5, and Fig. S1), which is unique in showing the oligomeric state of a phosphoglycosyltransferase being probed in a lipid bilayer. Furthermore, we show that PglC and PglA
physically and functionally interact in the presence of a lipid bilayer. Nonrandom, colocalization of PglC and PglA provides clear evidence that these enzymes undergo a specific protein–protein interaction that is dependent on the lipid bilayer interface and does not occur in the presence of detergent (Fig. 6B and Fig. S6). In addition, the sequential activities of the two enzymes in the nanodisc platform are clearly demonstrated through the application of triple isotopic-labeling approaches using the uniquely labeled substrates Und-[3H]P, UDP-[3H]diNacBac, and UDP-[14C]GalNAc (Fig. 5D). Importantly, the ability to carry out quantitative analysis of activities, for example in the disc disruption and disc dilution assays (Fig. 6 B and C), reveals the impact of enzyme colocalization in a 2D membrane. The results from such studies are crucial for deepening our understanding about how membrane-bound enzymes in multistep pathways function in vivo.

Although the current studies have focused on PglC and PglA, the native Pgl pathway comprises five glycan assembly enzymes (PglC, PglA, PglJ, PglH, and PglI, Fig. 1 A), and intriguingly only PglC and PglI are predicted to be integral membrane proteins by sequence analysis (12). Based on this established foundation of methods, the nanodisc platform should be readily applicable for investigating the specific roles of PglC and PglI in recruting the entire cluster of enzymes to the membrane bilayer interface where they function. Additionally, the opportunities for orthogonal isotopic labeling of substrates and intermediates will enable studies to examine whether substrates are transferred directly between sequential enzymes in the pathway. Because substrate processivity in glycan assembly pathways is poorly understood, this approach promises to provide the experimental system for addressing this key issue.

**Structure/Function Relationships at the Lipid Bilayer.** It is well documented that nanodiscs can be assembled from a variety of phospholipids, which may reflect native or nonnative compositions. In these studies we demonstrated that disc preparations made with native *E. coli* lipids result in a measureable background activity in the absence of added Und-P, presumably because the native *E. coli* lipid extract included a small amount of endogenous Und-P (Fig. 6A). This background activity is completely abolished with discs assembled with synthetic phospholipid components. Importantly, addition of dosed quantities of Und-P restores robust activity that can be readily quantified by using isotopically labeled substrates. These studies further show that the nanodisc platform will allow tremendous versatility in quantifying the specific effects of lipid bilayer composition on the functional efficiency of the sequential membrane enzyme activities.

The current studies take the versatility of nanodiscs one step further by showing the opportunity to investigate glycan assembly enzymes that require a membrane-bound substrate, in this case a polypropenyl-phosphate derivative. To our knowledge, this demonstration of enzymes acting on coincorporated membrane-bound substrates in nanodiscs is unique. Previously, the activity of a series of diverse polypropenyl-phosphate derivatives were investigated using PglC as a detergent micelle preparation (16). The studies revealed that although unsaturation of the α-isoprene and a particular combination of E and Z isoprene units were key features determining enzyme activity, the length of the propenyl chain had significantly less impact on protein activity. However, in a detergent-based assay, the effects of propenyl length on membrane partitioning and dynamics would have been taken out of consideration. With the nanodisc approach, we are now in a unique position to quantitatively assess structure/function relationships of native and nonnative polypropenyl-linked substrates and phospholipids directly in a membrane bilayer, which will enable us to make measurements that are simply inaccessible through any other in vitro or in vivo system. Furthermore, we will be able to assess the impact of capturing the substrates and enzymes in a 2D bilayer, which is likely to have profound implications for substrate availability and propensity of the turnover (42–44).

**FRET Analysis of Protein Interactions in Nanodiscs.** In contrast to vesicular membrane model systems such as liposomes, both faces of the nanodisc are accessible for interactions with substrates and enzymes. Therefore, we developed orthogonal labeling strategies to prepare fluorescently modified variants of PglC and PglA to enable a FRET analysis to assess the topological relationship between the globular domains of the enzymes in the nanodiscs. The studies clearly reveal a preference for a cofacial relationship
of the globular domains; FRET efficiency is higher when PglC is labeled on the globular domain compared with N-terminal labeling, which places the label on the distal side of the membrane (Fig. 4 C and D). At the current time, further quantitative analysis of the FRET efficiency extracted from the log-log plot, because structural and functional information is not yet available on either PglC or PglA. The finding that the globular domains are cofacially oriented is corroborated by activity analyses and the functional reconstitution of the PglC/PglA-ND. In particular, in experiments using precisely quantified Und-[33]PP, all of the available of Und-P is converted to final product (Fig. 5 B–D). If the major population of discs did not include PglC and PglA oriented with cofacial active sites, the extent of conversion would be lower because assemblies with the two enzymes oriented on opposite faces would not be able to process two sequential reactions to afford Und-PP-diNAcBac-GalNAc.

Although the FRET analyses in the present studies were carried out with an ensemble of discs including only two protein species, the opportunities for fluorescent labeling of other enzymes in the glycan assembly phase of the pathway (PglJ, PglH, and PglI) using similar orthogonal labeling approaches suggests that the nanodisc platform can be extended to the entire pathway. In this context, it should be noted that although the analysis of nanodisc species as an ensemble was relatively complicated because of incomplete labeling of one of the two enzymes, single-molecule approaches would avoid this complication and render analysis of more than two differentially labeled species feasible. Single-molecule approaches have already been applied to nanodisc systems and, therefore, all of the components are in place for taking the current inquiries on the pgI pathway and the roles of polypropenols in general to the next level of complexity (45).

Conclusion
The application of nanodiscs to the well-characterized C. jejuni pgI pathway provides an exciting experimental platform for addressing the evolutionary purpose of linear polypropenols in glycan biosynthetic pathways. The present study presents key steps in establishing the platform and demonstrates that the system delivers robust quantitative measurements of activity that will be valuable for investigating the specific roles of polypropenyl-linked substrates in the integrated function of glycan assembly enzymes typified by components of the bacterial pgI pathway. The study highlights the interaction of PglC and PglA, which are responsible for the first two membrane-committed steps in the pgI pathway. Concorporation of these enzymes into nanodiscs is characterized by multiple biophysical methods that support the cospatial and cofacial localization of the proteins. In tandem with PglC and PglA, the undecaprenyl-phosphate substrate is also incorporated into nanodiscs and the functional reconstitution of a PglC-PglA complex is verified through biochemical assays. This work represents a proof-of-concept demonstrating that nanodiscs can be used for the precise manipulation and study of polypropenol-dependent pathways. The study is also unique in providing a set of evidence supporting the hypothesis that enzymes dependent on polypropenyl-phosphates associate into biosynthetic macromolecular complexes.

Methods
Protein Expression, Purification, and Site-Specific Modification of PglC and PglA Variants. Standard techniques of molecular biology and biochemistry were used to clone, express, and purify HisG81-TEV-PglC, the accompanying single Cys mutants (C7 and S145C), HisG81-TEV-PglA, and PglA-LPETGG-His6. PglC single Cys mutants were modified using Cys maleimide and PglA was modified using a sortase-mediated ligation (40) with GGGYK(TAMRA)KGC. Detailed protocols are included in SI Text. See Tables S1 and S2 for primers used in preparation of PglC and PglA DNA constructs.

Materials. All phospholipids, radioactive compounds, amino acid derivatives and fluorescent labeling agents were purchased from commercial vendors. UDP-[3H]GalNAc was prepared using the unique His6-tag handle on PglC by using Ni-NTA affinity chromatography. Nanodisc assemblies were characterized using SDS-PAGE, SEC, and DLS. Specific quantification of proteins was carried out using Coomassie blue staining followed by gel densitometry. Detailed protocols are described in SI Text.

FRET Analysis. Nanodiscs for FRET analysis were prepared by creating nanodiscs containing the following reconstituted variants of PglC and PglA: (i) PglA(TAMRA) and unlabeled PglC; (ii) PglA(TAMRA) and PglC(Cys-terminal); (iii) PglA(TAMRA) and PglC(Cys-globular); (iv) unlabeled PglA and PglC(Cys-terminal); (v) unlabeled PglA and PglC(Cys-globular). The concentrations of the PglA(TAMRA) containing nanodisc assemblies iii–vii were adjusted to identical concentration on basis of the donor TAMRA UV-absorption signal. Acceptor-only samples iv and v were adjusted in concentration to match samples ii and iii, respectively, applying the Cys-absorption signals. FRET data were acquired by excitation at 515 nm to minimize direct acceptor excitation. Because of the different labeling strategies, the PglA construct was quantitatively labeled, whereas labeling of PglC was incomplete. To minimize errors resulting from different degrees of labeling between the two species, the fractions of labeled and nonlabeled PglC were independently quantified after nanodisc assembly to account for overestimation of the donor fluorescence because of the population of non-FRET PglC/PglA-NDs with unlabeled PglC. These non-FRET states were represented by a fraction of 45% in the case of the PglC-globular species and 56% in case of PglC-terminal. To account for this, the “donor-only” emission spectrum (i) was scaled according to the amount of the non-FRET states in each sample. The two resulting donor-only curves were used to correct the spectra of the donor/acceptor FRET samples (ii and iii). Subsequently, acceptor signal contributions stemming from direct excitation of the acceptor were subtracted using data from acceptor only samples (iv and v; full analysis is presented in Fig. S5 and SI Text).

Activity Analysis. Enzyme function in the nanodisc assemblies was assessed using isotopically labeled substrates (Und-[33]PP, UDP-[3H]diNAcBac, and UDP-[3H]GalNAc). For all concentrations and specific activities, see SI Text. For product analysis by HPLC, four nanodisc preparations containing PglC alone or PglC and PglA were prepared with 0.5 mol percentUnd-[33]PP. PglC-NDs were incubated with UDP-[3H]diNAcBac. PglA-NDs were incubated with unlabeled UDP-diNAcBac and UDP-[3H]GalNAc, or UDP-[3H]diNAcBac and UDP-[3H]GalNAc. As a control reaction, PglC/PglA-NDs were incubated with UDP-[3H]GalNAc in the absence of UDP-diNAcBac.

After 1 h, the reactions were quenched in chloroform:methanol (2:1, 1 mL) and the organic layer was washed with chloroform:methanol:0.1 M aqueous potassium chloride (3:48:4, 3 x 400 μL). The organic layer was dried and resuspended in chloroform:methanol (4:1, 100 μL) for analysis using NP-HPLC. Fractions of 1 mL were collected and each fraction was dried under an N2 stream. Radioactivity was determined by liquid scintillation counting. Activity analysis for assessing the effects of lipid composition and detergent-based nanodisc disruption was carried out using PglC/PglA-NDs prepared with unlabeled Und-P. Reactions were initiated by the addition of UDP-diNAcBac and UDP-[3H]GalNAc, and aliquots were quenched at various time points and then extracted to isolate organic soluble radiolabeled products (Und-P-P-diNAcBac-[3H]GalNAc). For nanodisc disruption, we used Triton X-100 as a nonpenetrating detergent at a concentration of 0.175% (vol/vol), which is sufficient to completely disrupt the nanodiscs as verified by Ni-NTA chromatographic analysis (Fig. S6 and SI Text). Additionally, measurements of the coupled PglC/PglA reaction show that activity is maximal at 0.175% (vol/vol) Triton X-100 (Fig. S6).

For the dilution assays, Und-[33]PP was used to enable accurate quantification of the disc-loaded substrate and the rates of enzyme-catalyzed conversions were measured by quantifying [3H]GalNAc incorporation into the Und-[33]PP-P-glycan products. Nanodiscs were assayed at 0.05 μM Und-[33]PP, 0.025 μM Und-[33]PP, or 0.017 μM Und-P, in volumes of 50 μL, 100 μL, and 150 μL such that all three reactions contained equimolar amounts of the disc preparation at different dilutions. The concentrations of UDP-diNAcBac and UDP-[3H]GalNAc remained constant. Aliquots corresponding to 15% of the total starting volume were quenched and extracted, as described above.

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