DprA recruits ComM to facilitate recombination during natural transformation in Gram-negative bacteria

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ABTRACT

Natural transformation (NT) represents one of the major modes of horizontal gene transfer in bacterial species. During NT, cells can take up free DNA from the environment and integrate it into their genome by homologous recombination. While NT has been studied for >90 years, the molecular details underlying this recombination remain poorly understood. Recent work has demonstrated that ComM is an NT-specific hexameric helicase that promotes recombinational branch migration in Gram-negative bacteria. How ComM is loaded onto the post-synaptic recombination intermediate during NT, however, remains unclear. Another NT-specific recombination mediator protein that is ubiquitously conserved in both Gram-positive and Gram-negative bacteria is DprA. Here, we uncover that DprA homologs in Gram-negative species contain a C-terminal winged helix domain that is predicted to interact with ComM by AlphaFold. Using *Helicobacter pylori* and *Vibrio cholerae* as model systems, we demonstrate that ComM directly interacts with the DprA winged-helix domain, and that this interaction is critical for DprA to recruit ComM to the recombination site to promote branch migration during NT. These results advance our molecular understanding of recombination during this conserved mode of horizontal gene transfer. Furthermore, they demonstrate how structural modeling can help uncover unexpected interactions between well-studied proteins to provide deep mechanistic insight into the molecular coordination required for their activity.

SIGNIFICANCE STATEMENT

Bacteria can acquire novel traits like antibiotic resistance and virulence through horizontal gene transfer by natural transformation. During this process, cells take up free DNA from the environment and integrate it into their genome by homologous recombination. Many of the molecular details underlying this process, however, remain incompletely understood. In this study, we identify a new protein-protein interaction between ComM and DprA, two factors that promote homologous recombination during natural transformation in Gram-negative species. Through a combination of bioinformatics, structural modeling, cell biological assays, and complementary genetic approaches, we demonstrate that this interaction is required for DprA to recruit ComM to the site of homologous recombination.

INTRODUCTION

Natural transformation (NT) is a broadly conserved mechanism of horizontal gene transfer present in diverse Gram-positive and Gram-negative eubacteria, as well as some archaeal species[1,2]. During this process, cells translocate single-stranded transforming DNA (tDNA) across the cytoplasmic membrane[3-5], which can then be integrated into the genome by homologous recombination. This can promote the acquisition of novel traits including antibiotic resistance and virulence factors in bacterial pathogens.

During NT, the primary bacterial recombinase, RecA, binds to tDNA and both (1) facilitates a homology search and (2) initiates the recombination reaction by promoting strand invasion of the bacterial chromosome to generate a 3-stranded D-loop structure. This 3-stranded intermediate is distinct from the more canonical recombination intermediates that form between two dsDNA substrates during DNA repair. For example, the 3-stranded intermediate during NT can never form a classical Holliday junction. As a result, the recombination reaction that occurs during NT must be distinct from more canonical forms of dsDNA recombination. Consistent with this, there are a number of proteins that have been characterized that are uniquely required for recombination during NT.

One of those proteins is DprA, which is present in all naturally transformable species[2]. DprA is a ssDNA-binding recombination mediator protein. During NT, DprA has been implicated in both (1) protecting ssDNA that has been internalized into the cytoplasm and (2) facilitating recombination by aiding in the recruitment of RecA[6-10]. Thus, to date, DprA has primarily been associated with the early pre-synaptic steps of recombination that lead to formation of the D-loop.

Another NT-specific recombination protein is ComM, which is only conserved in Gram-negative naturally transformable species[11]. ComM is a NT-specific helicase that binds to the crossover junctions (*i.e.*, branches) of the D-loop to expand them via recombinational branch migration[11,12]. This activity facilitates the integration of heterologous sequences during NT.

While most of the proteins involved in recombination during NT have been identified and characterized to some degree, the molecular coordination between these factors remains poorly understood. Here, we uncover that an extended C-terminal winged-helix domain of Gram-negative DprA homologs helps to recruit ComM to the site of tDNA recombination.

RESULTS

ComM-DprA interactions promote NT in Helicobacter pylori

DprA is broadly conserved in bacterial species and is always found in species capable of NT[2]. Prior work characterized the structure of the C-terminal winged helix domain of *Helicobacter pylori* DprA, which is present in a subset of DprA proteins[13]. The $DprA_{Hp}$ C-terminal domain is not involved in DNA-binding despite displaying a winged helix fold[13,14]. Because this domain is required for efficient NT, it was proposed that its function could be to establish interactions with other NT-specific proteins[13]. We therefore analyzed DprA in a diverse set of bacterial species and uncovered that the DprA homologs among Gram-negative species commonly encode this extended C-terminal winged helix domain, but it is absent in the DprA homologs of Gram-positive species (**Fig. S1, Dataset S1**). This distribution largely mirrors the distribution of ComM, where species that contain a ComM homolog also encode a DprA homolog with a C-terminal winged-helix domain (**Fig. S1, Dataset S1**).

Thus, we hypothesized that the DprA winged-helix domain may directly interact with ComM to facilitate NT. To test this, we first used *H. pylori* as a model system. Consistent with our hypothesis, AlphaFold 3 (AF3)[15] predicts a high-confidence interaction between the $DprA_{Hp}$ winged-helix domain and $ComM_{Hp}$ (ipTM = 0.76; pTM = 0.86)(**Fig. 1A**). To test whether these proteins interact empirically, we performed bacterial adenylate cyclase two-hybrid (BACTH) assays between the $DprA_{Hp}^{C\text{-}ter}$ (winged-helix domain) and full length ComM. In these assays, LacZ activity is directly linked to the interaction of these proteins[16]. This BACTH analysis revealed that $DprA_{Hp}$ and $ComM_{Hp}$ interact with one another (**Fig. 1B**, **Fig. S2**).

To test whether the interaction between $ComM_{Hp}$ and $DprA_{Hp}$ is functionally relevant, we sought to assess the impact of disrupting these interactions on NT frequency in *H. pylori*. For these assays, $dprA_{Hp}$ and $comM_{Hp}$ alleles were expressed ectopically at the *ureA* locus. Importantly, ectopic expression of the wildtype alleles ($comM_{Hp}$ and $dprA_{Hp}$) restored NT in the strains where the native gene was deleted (**Fig. 1C**). When cells were complemented with an allele of *dprA* lacking the C-terminal winged-helix domain ($dprA_{Hp}^{\Delta C\text{-}ter}$) the NT frequency was indistinguishable from $\Delta comM_{Hp}$ (**Fig. 1C**). Importantly, $dprA_{Hp}^{\Delta C\text{-}ter}$ transformed at rates significantly higher than $\Delta dprA$, suggesting that deleting the $DprA_{Hp}$ winged-helix did not abolish all DprA activity. Thus, we hypothesized that the reduced NT frequency observed in $dprA_{Hp}^{\Delta C\text{-}ter}$ was due to ablation of $DprA_{Hp}$-$ComM_{Hp}$ interactions. To test this more rigorously, we assessed the phenotype of a $dprA_{Hp}^{\Delta C\text{-}ter}$ $\Delta comM_{Hp}$ double mutant. If the reduced NT observed in $dprA_{Hp}^{\Delta C\text{-}ter}$ is due to ablation of $DprA_{Hp}$-$ComM_{Hp}$ interactions, we hypothesized that these mutations should be epistatic. Indeed, we found that the phenotype of $dprA_{Hp}^{\Delta C\text{-}ter}$ $\Delta comM_{Hp}$ double mutant was not significantly different from either the $dprA_{Hp}^{\Delta C\text{-}ter}$ or $\Delta comM_{Hp}$ single mutants (**Fig. 1C**). This result is consistent with $DprA_{Hp}$-$ComM_{Hp}$ interactions facilitating NT.

To test this further, we analyzed the AF3 model of $DprA_{Hp}$-$ComM_{Hp}$ interactions and found that $DprA_{Hp}^{L252}$ is buried within the interface of these two proteins (**Fig. 1A**). Thus, we hypothesized that introducing a charged amino acid at this site should disrupt $DprA_{Hp}$-$ComM_{Hp}$ interactions. Consistent with this, we found that $DprA_{Hp}^{L252E}$ no longer interacts with $ComM_{Hp}$ in BACTH assays (**Fig. 1B**). Moreover, $dprA_{Hp}^{L252E}$ phenocopies $dprA_{Hp}^{\Delta C\text{-}ter}$ in NT frequency assays (**Fig. 1C**). All together, these data strongly suggest that $DprA_{Hp}$-$ComM_{Hp}$ interactions are critical for $ComM_{Hp}$ activity in *H. pylori*.

ComM-DprA interactions promote recombination of tDNA during NT in V. cholerae

The DprA C-terminal winged-helix domain is widely distributed among Gram-negative bacteria (**Fig. S1**). This includes *Vibrio cholerae*, the organism in which ComM was first characterized as a branch migration factor, and a species in which many tools have already been established for studying ComM activity[11,17]. So next, we sought to use *V. cholerae* as a model system to elucidate (1) whether ComM-DprA interactions are broadly conserved and if so, (2) how DprA-ComM interactions mechanistically promote NT.

First, we found that AF3 predicted a high confidence interaction between the $DprA_{Vc}$ winged-helix domain and $ComM_{Vc}$ (ipTM = 0.92; pTM = 0.85) (**Fig. 2A**). Consistent with this, we found that the $DprA_{Vc}$ winged-helix domain and $ComM_{Vc}$ interact with one another in BACTH assays (**Fig. 2B**).

To test whether the interaction between these proteins is functionally relevant, we mutated 4 residues that lie at the predicted $DprA_{Vc}$-$ComM_{Vc}$ interface (**Fig. 2A**). Two of these residues represented a potential electrostatic interaction ($comM_{Vc}^{R497}$, $dprA_{Vc}^{E353}$), so we mutated these residues by “flipping” their charge: $comM_{Vc}^{R497E}$ and $dprA_{Vc}^{E353R}$. We also mutated two leucine

153 residues buried within the interface (*comM*$_{Vc}^{L455}$, *dprA*$_{Vc}^{L350}$) to a charged amino acid:
154 *comM*$_{Vc}^{L455E}$, *dprA*$_{Vc}^{L350E}$. Three of these alleles – D*prA*$_{Vc}^{E353R}$, *ComM*$_{Vc}^{L455E}$, *DprA*$_{Vc}^{L350E}$ –
155 disrupted DprA$_{Vc}$-ComM$_{Vc}$ interactions, while ComM$_{Vc}^{R497E}$ did not (**Fig. 2B**). Consistent with
156 DprA$_{Vc}$-ComM$_{Vc}$ interactions playing a functional role in *V. cholerae*, the 3 alleles that disrupted
157 interactions (d*prA*$_{Vc}^{E353R}$, *comM*$_{Vc}^{L455E}$, *dprA*$_{Vc}^{L350E}$) all phenocopied Δ*comM* in NT frequency
158 assays, while the allele that did not disrupt interactions (*comM*$_{Vc}^{R497E}$) had no effect on NT (**Fig.
159 2C**). Importantly, the point mutations in *dprA* (d*prA*$_{Vc}^{E353R}$ and *dprA*$_{Vc}^{L350E}$), did not completely
160 inhibit NT (as in Δ*dprA*), indicating that some functions of DprA remain intact (**Fig. 2C**).
161 Furthermore, d*prA*$_{Vc}^{E353R}$ and *dprA*$_{Vc}^{L350E}$ were both epistatic with Δ*comM* (**Fig. 2C**). Together,
162 this suggests that disrupting DprA$_{Vc}$-ComM$_{Vc}$ interactions disrupts ComM$_{Vc}$ activity during NT,
163 which is consistent with what was observed above in *H. pylori* (**Fig. 1**).
164
165 To more rigorously test this model, we took advantage of the potential electrostatic interaction
166 between ComM$_{Vc}^{R497}$-DprA$_{Vc}^{E353}$. Our results demonstrate that flipping the charge on DprA
167 (*dprA*$_{Vc}^{E353R}$) disrupts DprA$_{Vc}$-ComM$_{Vc}$ interactions and ComM activity, which may be due to
168 electrostatic repulsion between DprA$_{Vc}^{E353R}$ and ComM$_{Vc}^{R497}$ based on the AF3 model. If so, we
169 hypothesized that flipping the charge of the interacting residue on ComM (ComM$_{Vc}^{R497E}$) should
170 restore ComM activity by restoring DprA$_{Vc}$-ComM$_{Vc}$ interactions. Indeed, we found that NT in
171 *dprA*$_{Vc}^{E353R}$ *comM*$_{Vc}^{R497E}$ was partially restored when compared to the *dprA*$_{Vc}^{E353R}$ single mutant
172 (**Fig. 2C**). Importantly, NT of *dprA*$_{Vc}^{L350E}$ *comM*$_{Vc}^{R497E}$ was not restored when compared to
173 *dprA*$_{Vc}^{L350E}$ (**Fig. S3A**). This indicates that there is specificity to the recovery observed in
174 *dprA*$_{Vc}^{E353R}$ *comM*$_{Vc}^{R497E}$, and demonstrates that *comM*$_{Vc}^{R497E}$ is not simply a gain-of-function
175 allele of ComM. This data strongly suggests that DprA$_{Vc}^{E353}$ and ComM$_{Vc}^{R497}$ interact, which
176 further validates the AF3 model.
177
178 While we see partial recovery for NT in *dprA*$_{Vc}^{L350E}$ *comM*$_{Vc}^{R497E}$, we did not see recovery of
179 interaction with these proteins in BACTH assays (**Fig. 2B**). One possibility is that the recovered
180 protein-protein interaction is below the detection limit for this assay. This is supported, in part, by
181 the fact that NT is only partially restored in *dprA*$_{Vc}^{E353R}$ *comM*$_{Vc}^{R497E}$.
182
183 Prior work shows that ComM is not required for the uptake of tDNA into the cytoplasm, instead,
184 it is only required for the recombination of tDNA into the genome[11,18]. Consistent with this, NT of
185 Δ*comM* is indistinguishable from the parent when a replicating plasmid is used as the tDNA[11],
186 which does not require recombination (**Fig. 2D**). DprA, however, has a presynaptic role in
187 protecting tDNA from being degraded in the cytoplasm prior to tDNA integration[6]. Consistent
188 with that, NT of Δ*dprA* is significantly reduced when a replicating plasmid is used as tDNA (**Fig.
189 2D**). The point mutations in DprA$_{Vc}$ that disrupt DprA$_{Vc}$-ComM$_{Vc}$ interactions (*dprA*$_{Vc}^{L350E}$ and
190 *dprA*$_{Vc}^{E353R}$), however, do not affect NT with a replicating plasmid. This suggests that these DprA
191 alleles retain their presynaptic function; namely, the ability to protect tDNA in the cytoplasm.
192
193 ***DprA$_{Vc}$-ComM$_{Vc}$ interactions are required for branch migration during NT***
194 Our data thus far suggest that DprA-ComM interactions are critical for ComM activity because
195 mutations that disrupt this interaction phenocopy a Δ*comM* mutant. Also, these mutations are
196 epistatic with a Δ*comM* mutation. ComM is required for recombinational branch migration during
197 NT. Thus, we next sought to test whether DprA$_{Vc}$-ComM$_{Vc}$ interactions are critical for ComM-
198 dependent branch migration. To do this, we used a previously established assay to evaluate
199 branch migration activity *in vivo*[11]. This assay indirectly measures branch migration by
200 assessing the comigration of two linked genetic markers: a Trimethoprim antibiotic resistance
201 marker (Tm^R) and a premature stop codon in *lacZ* (*lacZ**) (**Fig. 3A**). We employed two different
202 tDNA products, one where Tm^R and *lacZ** are separated by 243 bp and another where they are
203 separated by 820 bp. Consistent with ComM playing an important role in branch migration

during NT, Δ*comM* exhibits significantly reduced comigration for these markers with both tDNA products (**Fig. 3B**). In this assay, we found that the mutations that disrupt $DprA_{Vc}$-$ComM_{Vc}$ interactions (*dprA*$_{Vc}^{L350E}$, *dprA*$_{Vc}^{E353R}$, and *comM*$_{Vc}^{L455E}$) had a significant reduction in comigration that was similar to Δ*comM* (**Fig. 3B**).

Furthermore, we found that comigration in *dprA*$_{Vc}^{E353R}$ *comM*$_{Vc}^{R497E}$ was restored when compared to the *dprA*$_{Vc}^{E353R}$ single mutant (**Fig. 3B**). In fact, comigration of *dprA*$_{Vc}^{E353R}$ *comM*$_{Vc}^{R497E}$ was restored to parental levels, despite the fact that NT is only partially restored in this background (**Fig. 3B**, **Fig. 2C**). This is consistent with $DprA_{Vc}$-$ComM_{Vc}$ interactions being restored when the charge on both sides of this electrostatic interaction are flipped, which further supports the validity of the AF3 model. Importantly, comigration was not restored in *dprA*$_{Vc}^{L350E}$ *comM*$_{Vc}^{R497E}$ when compared to *dprA*$_{Vc}^{L350E}$ indicating that the recovery observed was specific and not due to *comM*$_{Vc}^{R497E}$ being a gain-of-function ComM allele (**Fig. S3B**).

$DprA_{Vc}$ recruits $ComM_{Vc}$ to the recombination site during NT

DprA has predominantly been characterized for the presynaptic role it plays during NT. In particular, it plays an important role in recruiting RecA to the tDNA via a direct protein-protein interaction[6-10]. Our data suggest that DprA-ComM interactions are critical for ComM-dependent branch migration. And while it is clear that ComM activity is required for NT and not for other forms of recombination, the mechanism by which this specificity is determined is unclear. Thus, we hypothesized that DprA recruits ComM to the recombination site during NT.

We have previously shown that in single cells undergoing NT, a fluorescent fusion of ComM (GFP-$ComM_{Vc}$) forms foci that are (1) dependent on RecA, (2) only formed in the presence of exogenous tDNA, (3) specifically formed at the chromosomal locus homologous to the tDNA, and (4) transient and highly dynamic, which all together indicates that these foci represent active ComM complexes acting at the recombination site during NT[17]. So, to test whether $DprA_{Vc}$-$ComM_{Vc}$ interactions help recruit $ComM_{Vc}$ to the recombination site, we assessed GFP-$ComM_{Vc}$ focus formation in cells incubated with tDNA (**Fig. 4A**). Consistent with prior work, we found that the parent strain forms many GFP-$ComM_{Vc}$ foci (**Fig. 4B-C**), with ~60% of cells exhibiting at least 1 GFP-$ComM_{Vc}$ focus within the timelapse imaging window. By contrast, point mutants that disrupt $DprA_{Vc}$-$ComM_{Vc}$ interactions (*dprA*$_{Vc}^{L350E}$ and *comM*$_{Vc}^{L455E}$) reduce GFP-$ComM_{Vc}$ focus formation to the limit of detection (**Fig. 4B-C**). These data are consistent with a model in which DprA helps recruit ComM to the recombination site during NT.

DprA promotes ComM-dependent branch migration for NT in species-specific manner

Despite DprA-ComM interactions being preserved in both *H. pylori* and *V. cholerae*, the interaction interfaces between these proteins are distinct. For example, the electrostatic interaction that we demonstrate is critical for $DprA_{Vc}$-$ComM_{Vc}$ interactions, is absent in the $DprA_{Hp}$-$ComM_{Hp}$ model (**Fig. 1A, 2A**). Consistently, ectopically expressed $ComM_{Hp}$ in *V. cholerae* could not complement the defect in NT and branch migration of a *V. cholerae* Δ*comM* mutant (**Fig. 5A-B**). Thus, we hypothesized that DprA-ComM interactions may be species specific (*i.e.*, $DprA_{Vc}$ cannot recruit $ComM_{Hp}$ and *vice versa*). If this is the case, ectopic expression of both $DprA_{Hp}$ and $ComM_{Hp}$ in *V. cholerae* should be sufficient to rescue ComM activity. First, we find that ectopic expression of $DprA_{Hp}$ in *V. cholerae* results in a slight decrease in NT frequency (**Fig. S4**), but deletion of native *comM* in this background still diminishes NT ~100-fold as expected (**Fig. 5**). When $DprA_{Hp}$ and $ComM_{Hp}$ are both ectopically expressed in *V. cholerae*, we found that NT was unchanged when native *comM* is deleted in this background (**Fig. 5A**) and branch migration activity was restored (**Fig. 5B**). This result is

consistent with $DprA_{Hp}$ recruiting $ComM_{Hp}$ to facilitate ComM-dependent branch migration activity in *V. cholerae*. These results also suggest that DprA and ComM represent the "functional unit" that facilitates branch migration during NT in Gram-negative species.

DISCUSSION

The results presented above advance our understanding of the molecular coordination underlying tDNA integration during horizontal gene transfer by NT. Specifically, they demonstrate that in Gram-negative species, the winged-helix domain of DprA directly binds to ComM to recruit this branch migration factor to the recombination site during NT.

Work from our group and others has characterized the molecular and structural basis of ComM-dependent branch migration of D-loops during NT in Gram-negative species[11,12,19]. D-loop structures are also generated as intermediates during DNA repair, however, ComM does not facilitate this process and is instead uniquely required for tDNA integration during NT[11]. This suggests that ComM may be specifically loaded onto the D-loops generated during NT. However, the basis for ComM loading has remained elusive. Our results demonstrate DprA is likely required to load ComM onto D-loops during NT. Thus, DprA-dependent loading of ComM may explain why this branch migration factor is exclusively associated with recombination during NT.

Our prior work has demonstrated that ComM is a bidirectional helicase that can translocate both 5' → 3' and 3' → 5' on model branched DNA substrates *in vitro*[11]. If this directionality is unregulated, then ComM would facilitate (*i.e.*, expand the D-loop) and inhibit (*i.e.*, collapse the D-loop) tDNA integration with equal probability. Indeed, this is exactly what is observed *in vitro* with purified ComM[11]. Single cell tracking of the spatiotemporal dynamics of tDNA integration, however, suggest that the recombination reaction is highly efficient[17], which suggests that there may be additional factors that regulate ComM directionality *in vivo*. Here, we show that DprA-ComM interactions are required for branch migration activity *in vivo*. Thus, it is tempting to speculate that DprA-dependent loading of ComM onto the D-loop regulates the directionality of branch migration, which is something we will test moving forward.

This discovery of DprA-dependent recruitment of ComM is notable for a number of reasons. DprA has primarily been characterized for its presynaptic roles during NT. This includes its role in protecting single-stranded tDNA in the cytoplasm, eviction of SSB, and recruitment of RecA[6-10]. Together, these activities help promote RecA-mediated strand invasion to initiate the recombination process. Our results demonstrate that DprA is also required to initiate branch migration, which indicates that it also plays a postsynaptic role during NT by recruiting ComM. DprA has also been implicated in playing a regulatory role in some systems like *Streptococcus pneumoniae*, where DprA directly interacts with the master regulator of competence, ComE, to shut-off competence[20]. Due to its varied roles during NT, most of which are facilitated by direct protein-protein interactions, it is tempting to speculate that DprA serves as the master "hub" that coordinates this complex process. On a related note, ComM has previously only been implicated in the postsynaptic step of branch migration. The recruitment of ComM by DprA may also suggest that ComM aids in a presynaptic step of recombination (*e.g.*, the homology search or initiation of strand invasion).

The highly varied roles for DprA during NT also highlight the value of the approach used in this study. Because of the critical presynaptic roles that DprA performs during NT, deletion of DprA completely inhibits NT. Thus, uncovering its postsynaptic role would not have been possible

using classical genetic approaches like transposon screens. While genetic screens can help identify the genes and proteins necessary for a particular phenotype, they may fail to reveal the underlying molecular coordination necessary for their activity – especially in cases where factors have more than one function. The structural modeling approach used here, however, helped reveal unexpected interactions that led to testable hypotheses, which ultimately uncovered how these factors coordinate to carry out their activity. Advances in structural modeling are developing at breakneck speed, and recent work demonstrates that genome-wide unbiased searches for novel protein-protein interactions are now highly feasible[21,22]. These unbiased genome-wide *in silico* screens hold great promise in accelerating the discovery of these types of unexpected interactions moving forward.

METHODS

Bacterial strains and culture conditions

All *V. cholerae* strains used throughout this study are derivatives of strain E7946[23]. Cells were routinely grown in LB Miller broth and agar supplemented with spectinomycin (200 µg/mL), kanamycin (50 µg/mL), trimethoprim (10 µg/mL), tetracycline (0.5 µg/mL), sulfamethoxazole (100 µg/mL), chloramphenicol (1 µg/mL), erythromycin (10 µg/mL), carbenicillin (20 µg/mL), and/or zeocin (100 µg/mL) as appropriate.

All *H. pylori* strains used in this study are derivatives of strain 26695[24]. Cultures were grown under microaerophilic conditions (5% O_2, 10% CO_2, using the Don Whitley system) at 37°C. Blood agar base medium (BAB) supplemented with 10% defibrillated horse blood (ThermoFisher Scientific) was used for plate cultures. An antibiotic mix containing polymyxin B (0.155 mg/ml), vancomycin (6.25 mg/ml), trimethoprim (3.125 mg/ml), and amphotericin B (1.25 mg/ml) was added to both plate and liquid cultures. Additional antibiotics were added as required: kanamycin (20 µg/ml), apramycin (12.5 µg/ml), and chloramphenicol (8 µg/ml) streptomycin (10 µg/ml).

Construction of mutant strains

For *V. cholerae*, all strains were generated by natural transformation using splicing-by-overlap-extension (SOE) PCR mutant constructs exactly as previously described[25,26]. Ectopic expression constructs were generated by SOE PCR and integrated onto the *V. cholerae* genome exactly as previously described[27].

For generating mutant variants in *H. pylori* the specific gene regions (with 200bp of flanking sequences) were amplified from genomic DNA (gDNA) of *H. pylori* 26695 using sequence specific primers and cloned into pjET1.2 plasmid using sequence- and ligation-independent cloning (SLIC)[28]. Replacement of the ORF by antibiotic resistant cassettes (either chloramphenicol, kanamycin or apramycin) was carried out by SLIC. The constructs were introduced in *H. pylori* by natural transformation and at least two independent clones were selected for each construct. For complementation by expression from the *ureA* locus the corresponding gene ORFs were amplified by PCR and cloned by SLIC into a pjET2.1 plasmid carrying an antibiotic resistance cassette flanked by 200 bp upstream and downstream of the *ureA* gene. The resulting construct was introduced in *H. pylori* by natural transformation.

All strains were confirmed by PCR and/or sequencing. For a detailed list of all strains, see **Table S1.** For a complete list of oligos used to generate mutant constructs, see **Table S2**.

357
358 ***Bioinformatic analysis of DprA homologs***
359 Using BLAST[29], we searched for DprA homologs in a set of bacterial genomes where ComM
360 homologs had previously been searched[11]. For all identified DprA homologs, we performed
361 protein structure prediction using AlphaFold v2.3[30] as implemented in the ColabFold v1.5.2
362 pipeline[31]. We ran MMseqs2[32] against the UniRef30_2202 database to generate multiple
363 sequence alignments used as input to the AlphaFold2 structure prediction module. We then
364 generated 5 structural models for each DprA homolog using 3 recycles. We structurally
365 superimposed the best models (highest pTM score for each species) with PyMOL (v3.0) and
366 aligned them to the experimental structure of the $DprA_{Hp}$ C-terminal domain[13] (PDB identifier:
367 6GW7). We visually identified the presence of a C-terminal winged helix domain in all species
368 with an identified ComM homolog, apart from *B. burgdoferi* (Fig S1 and Dataset S2). To validate
369 the presence of a C-terminal winged helix domain, we annotated Pfam[33] domains in all DprA
370 homolog sequences by HH-suite homology search[34]: we ran 5 iterations of HHblits against the
371 UniRef30_2202 database to generate multiple sequence alignments, used as input for
372 HHsearch against Pfam v35.0 (with 80% maximum pairwise sequence identity). We identified a
373 winged helix Pfam domain (PF17782, PF10771.12 or PF15977.8) with HHsearch probability
374 above 90% in all species with ComM homologs, except for *E. coli* (probability 88.2%), *F.*
375 *nucleatum* (probability 89.7%)*, H. pylori* (probability 23%)*, C. jejuni* (probability 31.7%), and *L.*
376 *interrogans* (probability 59%). Note that the $DprA_{Hp}$ C-terminal domain is not annotated in Pfam
377 despite being structurally characterized.
378
379
380 ***Natural transformation assays***
381 For *V. cholerae*, strains were engineered to bypass the native signals required for NT.
382 Specifically, strains had P_{tac}-*tfoX* and Δ*luxO* mutations, which ectopically express the master
383 competence regulator (TfoX) and genetically lock cells in a high cell density state as previously
384 described[35]. Chitin-independent transformation assays to determine NT frequency were
385 performed exactly as previously described[35]. Briefly, cells were grown at 30ºC rolling in LB
386 supplemented with 100 μM IPTG, 20 mM $MgCl_2$, 10 mM $CaCl_2$ to late-log phase. Then, ~10^8
387 CFUs were diluted into instant ocean medium (7g/L; Aquarium Systems). Then, 100 ng of
388 transforming DNA (tDNA) was added to each reaction. The tDNA used to assess transformation
389 frequency was a linear ΔVC1807::Erm^R PCR product. VC1807 is a frame-shifted transposase
390 gene. Control reactions were also performed for each strain where no tDNA was added. Cells
391 were incubated with tDNA overnight at 30ºC static. Then, reactions were outgrown by adding
392 1mL of LB and shaking at 37ºC for 3 hours. Reactions were then plated for quantitative culture
393 by dribble plating on LB agar supplemented with erythromycin to quantify transformants, and
394 plain LB to quantify total viable counts. Transformation frequency is defined as the CFU/mL of
395 transformants divided by the CFU/mL of total viable counts.
396
397 For assays where branch migration was indirectly assessed via linkage analysis in *V. cholerae*,
398 transformation reactions were performed exactly as described above except that they were
399 plated onto LB agar supplemented with trimethoprim and X-gal (40 μg/mL). On these plates, all
400 cells integrated the Tm^R marker, and if cells integrated the genetically linked *lacZ* nonsense
401 mutation they would make white colonies. If they did not integrate the linked lacZ nonsense
402 mutation, they would make blue colonies on these plates. Thus, the comigration frequency is
403 defined as the percent of Tm^R colonies that were white on these plates.
404
405 Natural transformation frequencies for *H. pylori* were determined as follows. Total chromosomal
406 DNA (600 ng) from a streptomycin resistant 26695 strain was mixed with 45 μL of a culture at
407 OD_{600} = 4.0. Then, three 15μL drops of the mix were spotted on solid medium and incubated

overnight at 37°C. Next day, cells were resuspended in 300 µL of peptone water and 10 µl drops of serial dilutions were deposited on BAB plates with and without streptomycin (10 µg/mL). Transformation frequency is defined as the CFU/mL of streptomycin resistant transformants divided by the CFU/mL of total viable counts.

Microscopy for GFP-ComM focus formation

Assays to assess GFP-ComM focus formation in the presence of tDNA were performed exactly as previously described[17]. Briefly, cells were grown as described above for natural transformation assays. Then, ~10^7 cells were mixed with ~650 ng of a linear ~6 kb tDNA product that is homologous to the host chromosome, and placed under an 0.2% gelzan pad. Samples were then subjected to timelapse imaging. Phase contrast and fluorescence images were collected every 3 min for a total of 90 mins on a Nikon Ti-2 microscope using a Plan Apo 60X objective, a GFP filter cube, a Hamamatsu ORCA Flash 4.0 camera and Nikon NIS Elements imaging software. The number of GFP-ComM foci was determined by analyzing 60 cells per replicate.

Bacterial Adenylate Cyclase Two-Hybrid (BACTH) Assays

Gene inserts were amplified by PCR and cloned into the pUT18C, pUT18, pKT25, or pKNT25 vectors to generate N- and C- terminal fusions to the T18 and T25 fragments of adenylate cyclase. Miniprepped vectors were then cotransformed into *E. coli* BTH101. Then, single colonies were picked and grown in LB supplemented with kanamycin 50 µg/mL and carbenicillin 100 µg/mL. Next, 3 µL of each strain was spotted onto LB agar plates supplemented with kanamycin 50 µg/mL, carbenicillin 100µg/mL, 0.5 mM IPTG and 40 µg/mL X-gal. Plates were incubated at 30°C for 24 hours prior to imaging.

To quantify the strength of BACTH interactions, five colonies were collected and used to inoculate 3 mL of LB containing both antibiotics and allowed to grow overnight at 30°C. The OD_{600} of the culture was determined and cells from 1mL were pelleted and resuspended in 1mL of buffer Z (60 mM Na_2HPO_4, 40 mM NaH_2PO_4, 10 mM KCl, 1 mM $MgSO_4$, 50 mM β-mercaptoethanol, pH 7). Next, 100 µL of chloroform was added and reactions were vortexed for 20 s. Then, 20 µL of the upper phase was mixed in 96-well microplates with 180 µL of buffer Z with 0.7 mg/mL of ortho-nitrophenyl-β-galactoside (ONPG) but without β-mercaptoethanol. Absorbance measures at 540 and 414 nm were carried out every 5 minutes for 2 h. β-galactosidase activity (A) was defined as: $A = 1000 * (OD_{414}(t) - (1.75 * OD_{540}(t)) / (t * V_{sample} *$ initial $OD_{600})$ and expressed as Miller units (A414/min mL OD_{600})

Statistics

Statistical differences were assessed using GraphPad Prism software. The statical tests employed are indicated in figure legends. Descriptive statistics for all samples, and a comprehensive list of statistical comparisons can be found in **Dataset S2**.

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REFERENCES

1 Dubnau, D. & Blokesch, M. Mechanisms of DNA Uptake by Naturally Competent Bacteria. *Annu Rev Genet* **53**, 217-237 (2019).

2 Johnston, C., Martin, B., Fichant, G., Polard, P. & Claverys, J. P. Bacterial transformation: distribution, shared mechanisms and divergent control. *Nat Rev Microbiol* **12**, 181-196 (2014).

3 Fox, M. S. & Allen, M. K. On the Mechanism of Deoxyribonucleate Integration in Pneumococcal Transformation. *Proc Natl Acad Sci U S A* **52**, 412-419 (1964).

4 Dubnau, D. & Davidoff-Abelson, R. Fate of transforming DNA following uptake by competent Bacillus subtilis. I. Formation and properties of the donor-recipient complex. *J Mol Biol* **56**, 209-221 (1971).

5 Mejean, V. & Claverys, J. P. Use of a cloned DNA fragment to analyze the fate of donor DNA in transformation of Streptococcus pneumoniae. *J Bacteriol* **158**, 1175-1178 (1984).

6 Mortier-Barriere, I. *et al.* A key presynaptic role in transformation for a widespread bacterial protein: DprA conveys incoming ssDNA to RecA. *Cell* **130**, 824-836 (2007).

7 Lisboa, J. *et al.* Molecular determinants of the DprA-RecA interaction for nucleation on ssDNA. *Nucleic Acids Res* **42**, 7395-7408 (2014).

8 Quevillon-Cheruel, S. *et al.* Structure-function analysis of pneumococcal DprA protein reveals that dimerization is crucial for loading RecA recombinase onto DNA during transformation. *Proc Natl Acad Sci U S A* **109**, E2466-2475 (2012).

9 Yadav, T. *et al.* Bacillus subtilis DprA recruits RecA onto single-stranded DNA and mediates annealing of complementary strands coated by SsbB and SsbA. *J Biol Chem* **288**, 22437-22450 (2013).

10 Bakhlanova, I. *et al.* Mechanisms of RecA filament nucleation on ssDNA by the DprA protein. *bioRxiv*, 2024.2005.2007.592916 (2024).

11 Nero, T. M. *et al.* ComM is a hexameric helicase that promotes branch migration during natural transformation in diverse Gram-negative species. *Nucleic Acids Res* **46**, 6099-6111 (2018).

12 Hardy, L. *et al.* YraN is a helicase-associated nuclease fostering extended recombination events by natural transformation. *bioRxiv*, 2024.2002.2006.579203 (2024).

13 Lisboa, J. *et al.* The C-terminal domain of HpDprA is a DNA-binding winged helix domain that does not bind double-stranded DNA. *FEBS J* **286**, 1941-1958 (2019).

14 Dwivedi, G. R. *et al.* Insights into the Functional Roles of N-Terminal and C-Terminal Domains of Helicobacter pylori DprA. *PLoS One* **10**, e0131116 (2015).

15 Abramson, J. *et al.* Accurate structure prediction of biomolecular interactions with AlphaFold 3. *Nature* **630**, 493-500 (2024).

16 Karimova, G., Pidoux, J., Ullmann, A. & Ladant, D. A bacterial two-hybrid system based on a reconstituted signal transduction pathway. *Proc Natl Acad Sci U S A* **95**, 5752-5756 (1998).

17 Dalia, A. B. & Dalia, T. N. Spatiotemporal Analysis of DNA Integration during Natural Transformation Reveals a Mode of Nongenetic Inheritance in Bacteria. *Cell* **179**, 1499-1511 e1410 (2019).

18 Gwinn, M. L., Ramanathan, R., Smith, H. O. & Tomb, J. F. A new transformation-deficient mutant of Haemophilus influenzae Rd with normal DNA uptake. *J Bacteriol* **180**, 746-748 (1998).

19 Rosa, L. T., Vernhes, E., Soulet, A. L., Polard, P. & Fronzes, R. Structural insights into the mechanism of DNA branch migration during homologous recombination in bacteria. *EMBO J* (2024).

20 Mirouze, N. *et al.* Direct involvement of DprA, the transformation-dedicated RecA loader, in the shut-off of pneumococcal competence. *Proc Natl Acad Sci U S A* **110**, E1035-1044 (2013).
21 Humphreys, I. R. *et al.* Protein interactions in human pathogens revealed through deep learning. *Nat Microbiol* **9**, 2642-2652 (2024).
22 Gao, M., Nakajima An, D., Parks, J. M. & Skolnick, J. AF2Complex predicts direct physical interactions in multimeric proteins with deep learning. *Nat Commun* **13**, 1744 (2022).
23 Miller, V. L., DiRita, V. J. & Mekalanos, J. J. Identification of toxS, a regulatory gene whose product enhances toxR-mediated activation of the cholera toxin promoter. *J Bacteriol* **171**, 1288-1293 (1989).
24 Tomb, J. F. *et al.* The complete genome sequence of the gastric pathogen Helicobacter pylori. *Nature* **388**, 539-547 (1997).
25 Dalia, A. B. Natural Cotransformation and Multiplex Genome Editing by Natural Transformation (MuGENT) of Vibrio cholerae. *Methods Mol Biol* **1839**, 53-64 (2018).
26 Dalia, A. B., McDonough, E. & Camilli, A. Multiplex genome editing by natural transformation. *Proc Natl Acad Sci U S A* **111**, 8937-8942 (2014).
27 Dalia, T. N., Chlebek, J. L. & Dalia, A. B. A modular chromosomally integrated toolkit for ectopic gene expression in Vibrio cholerae. *Sci Rep* **10**, 15398 (2020).
28 Li, M. Z. & Elledge, S. J. SLIC: a method for sequence- and ligation-independent cloning. *Methods Mol Biol* **852**, 51-59 (2012).
29 Altschul, S. F., Gish, W., Miller, W., Myers, E. W. & Lipman, D. J. Basic local alignment search tool. *J Mol Biol* **215**, 403-410 (1990).
30 Jumper, J. *et al.* Highly accurate protein structure prediction with AlphaFold. *Nature* **596**, 583-589 (2021).
31 Mirdita, M. *et al.* ColabFold: making protein folding accessible to all. *Nat Methods* **19**, 679-682 (2022).
32 Steinegger, M. & Soding, J. MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. *Nat Biotechnol* **35**, 1026-1028 (2017).
33 Paysan-Lafosse, T. *et al.* InterPro in 2022. *Nucleic Acids Res* **51**, D418-D427 (2023).
34 Steinegger, M. *et al.* HH-suite3 for fast remote homology detection and deep protein annotation. *BMC Bioinformatics* **20**, 473 (2019).
35 Ellison, C. K. *et al.* Retraction of DNA-bound type IV competence pili initiates DNA uptake during natural transformation in Vibrio cholerae. *Nat Microbiol* **3**, 773-780 (2018).

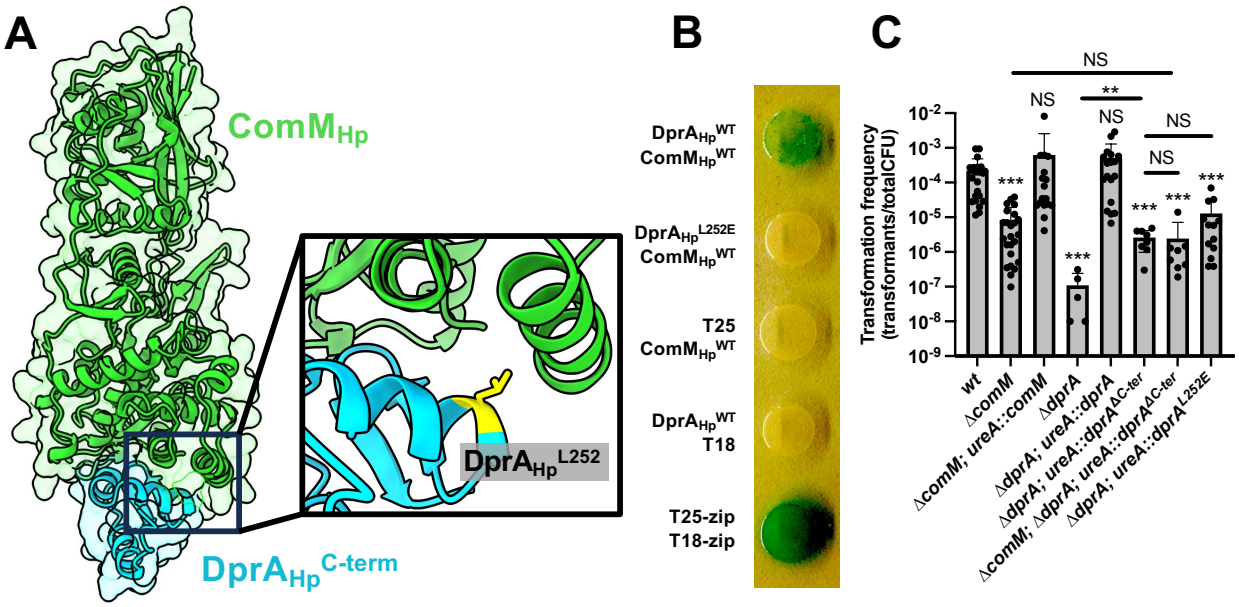

Fig. 1. **ComM-DprA interactions promote NT in *H. pylori*.** (**A**) AlphaFold 3 model of $ComM_{Hp}$-$DprA_{Hp}^{C\text{-}term}$ interactions. The inset shows the $DprA_{Hp}^{L252}$ interaction interface residue targeted for mutagenesis in yellow. (**B**) BACTH analysis to assess the interaction between the indicated alleles of DprA and ComM. All DprA constructs for BACTH consisted of C-terminal fusions of T25 to the terminal 53 amino acids of the indicated $DprA_{Hp}$ allele. The ComM construct for BACTH consisted of C-terminal fusions of T18 to full length $ComM_{Hp}$. The T25-zip and T18-zip constructs represent a known interacting pair and are a positive control in this assay. Data are representative of two independent experiments. (**C**) Natural transformation assays of the indicated *H. pylori* strains using linear tDNA that integrates onto the genome. Data are from at least 5 independent biological replicates and shown as the mean ± SD. Statistical comparisons were made by one-way ANOVA with Tukey's multiple comparison test of the log-transformed data. NS, not significant. *** = $p < 0.001$. Statistical identifiers directly above bars represent comparisons to the *wt*.

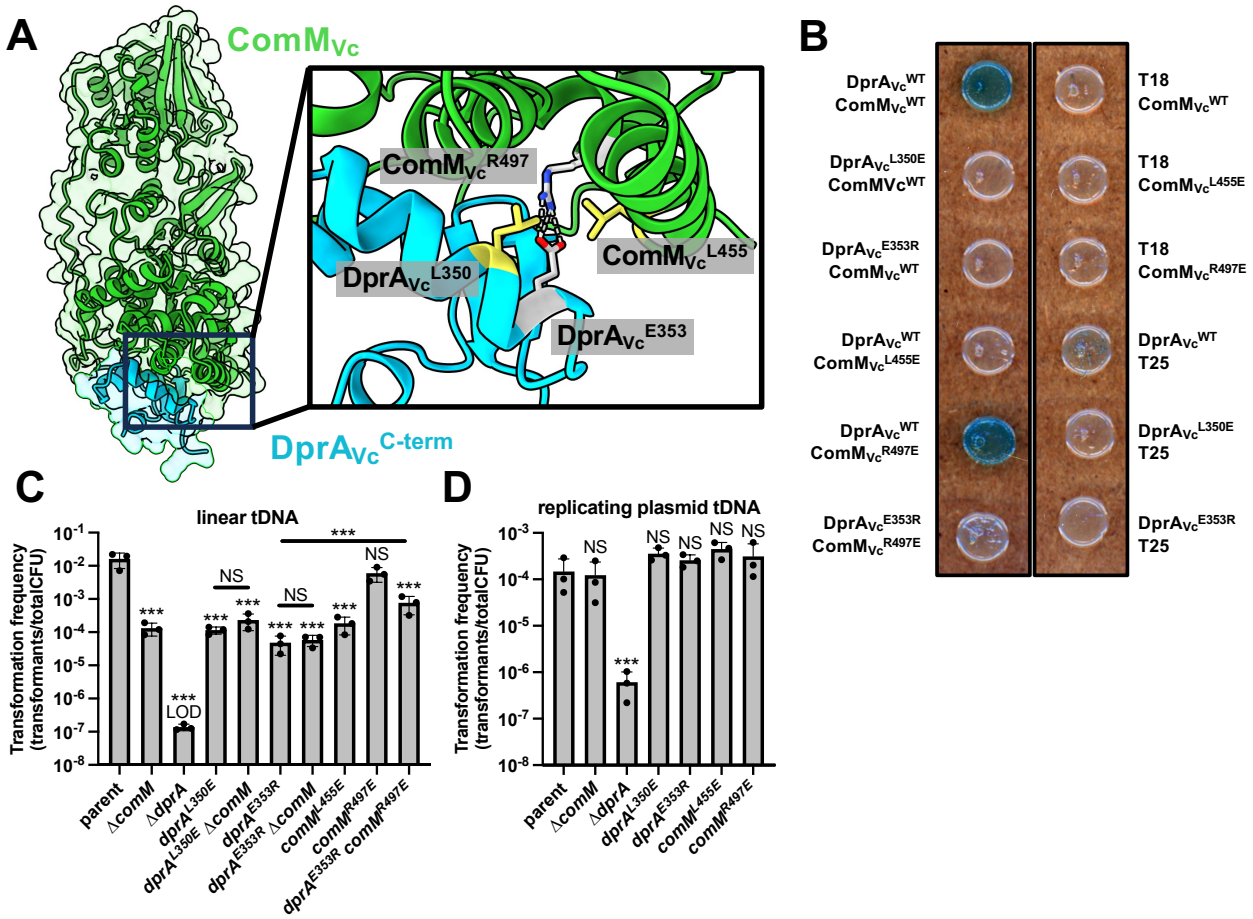

Fig. 2. **ComM-DprA interactions promote recombination of tDNA during NT in *V. cholerae*.** (**A**) AlphaFold 3 model of $ComM_{Vc}$-$DprA_{Vc}^{C\text{-term}}$ interactions. The inset shows the interaction interface residues targeted for mutagenesis. The residues that form a putative electrostatic interaction ($ComM_{Vc}^{R497}$ and $DprA_{Vc}^{E353}$) are in gray with charged atoms in blue (positive) or red (negative), while the two leucine residues within the interface ($DprA_{Vc}^{L350}$ and $ComM_{Vc}^{L455}$) are colored yellow. (**B**) BACTH analysis to assess the interaction between the indicated alleles of DprA and ComM. All DprA constructs for BACTH consisted of N-terminal fusions of T18 to the terminal 71 amino acids of the indicated DprA allele. All ComM constructs for BACTH consisted of C-terminal fusions of T25 to full length ComM allele indicated. Data in **B** are representative of two independent experiments. (**C**) Natural transformation assays of the indicated strains using linear tDNA that integrates onto the genome. (**D**) Natural transformation assays of the indicated strains using a replicating plasmid as the tDNA. Data in **C** and **D** are from at least 3 independent biological replicates and shown as the mean ± SD. Statistical comparisons were made by one-way ANOVA with Tukey's multiple comparison test of the log-transformed data. NS, not significant. *** = $p < 0.001$. LOD, limit of detection. Statistical identifiers directly above bars represent comparisons to the parent.

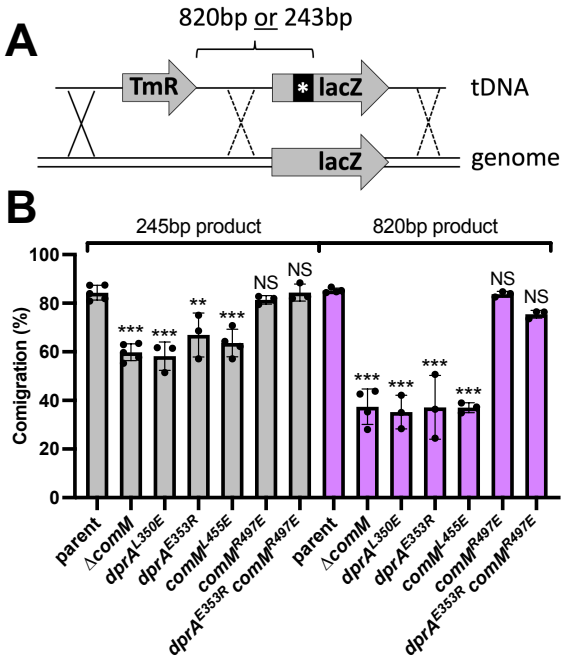

Fig. 3. **ComM$_{Vc}$-DprA$_{Vc}$ interactions are required for branch migration during NT.** (**A**) Schematic of the experimental setup to assess branch migration via linkage analysis between a trimethoprim resistance marker (Tm^R) and a nonsense mutation in *lacZ*. Two different tDNAs were used: one where the *lacZ* nonsense mutation was 243 bp away from the Tm^R cassette, and another where the spacing was 820 bp. (**B**) The two tDNA products described in **A** were transformed into the indicated strains and the comigration frequency (i.e., the linkage frequency between the Tm^R and *lacZ* nonsense mutation) is reported. All strains in these assays contained a Δ*mutS* mutation to prevent mismatch repair from confounding the results. Data are from at least 3 independent biological replicates and shown as the mean ± SD. Statistical comparisons were made by one-way ANOVA with Tukey's multiple comparison test of the log-transformed data for each tDNA product. NS, not significant. *** = $p < 0.001$, ** = $p < 0.01$. Statistical identifiers directly above bars represent comparisons to the parent.

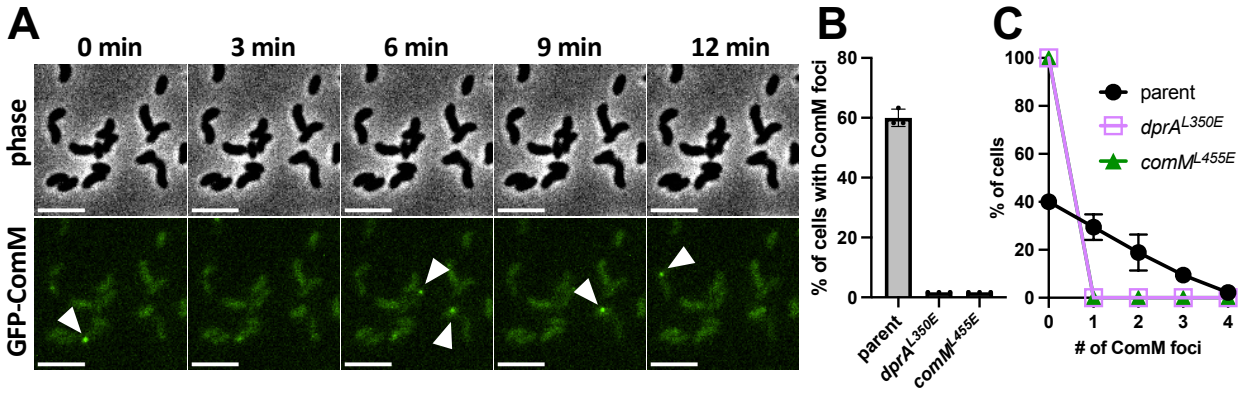

Fig. 4. **DprA$_{Vc}$ recruits ComM$_{Vc}$ to the recombination site during NT.** (**A**) Montage of timelapse imaging showing that the recruitment of ComM$_{Vc}$ to tDNA can be easily observed as fluorescent foci (white arrows) in a parent strain harboring a functional GFP-ComM$_{Vc}$ fusion at the native locus. Scale bar, 4µm. (**B**) Quantification of timelapse images for (**B**) the percent of cells that exhibited at least one GFP-ComM$_{Vc}$ focus and (**C**) the number of GFP-ComM$_{Vc}$ foci observed per cell. The indicated strains were imaged every 3 min for 1.5 hours. Data are from 3 independent replicates and shown as the mean ± SD. *n* = 60 cells analyzed per replicate.

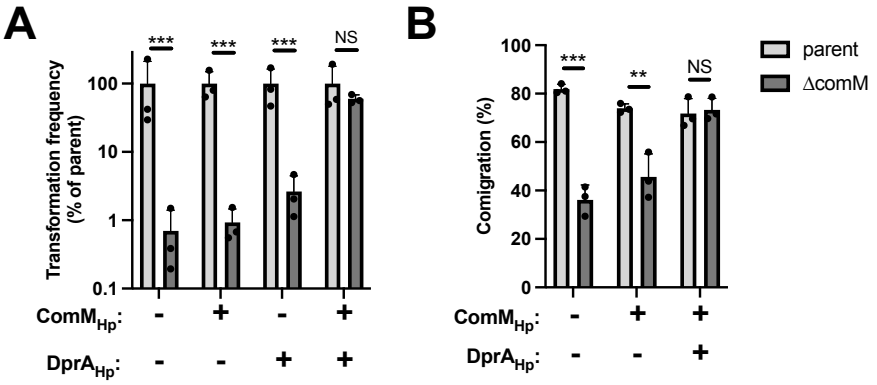

Fig. 5. **DprA-dependent recruitment of ComM is species-specific**. (**A**) Relative transformation frequency of *V. cholerae* strains where native *comM* is intact (parent; gray bars) or deleted (Δ*comM*; black bars) using linear tDNA that integrates onto the genome. Strains express *H. pylori* ComM ($ComM_{Hp}$) and/or DprA ($DprA_{Hp}$) from an ectopic locus as indicated (+ denotes that the strain expresses the indicated protein). (**B**) Comigration frequency in the indicated strain backgrounds to assess branch migration via linkage analysis between a trimethoprim resistance marker (Tm^R) and a nonsense mutation in *lacZ* as depicted in **Fig. 2A**. For the tDNA used is this experiment the *lacZ* nonsense mutation was 820 bp away from the Tm^R cassette. All data are from at least 3 independent biological replicates and shown as the mean ± SD. Statistical comparisons were made by one-way ANOVA with Tukey's multiple comparison test of the log-transformed data. NS, not significant. *** = $p < 0.001$, ** = $p < 0.01$.

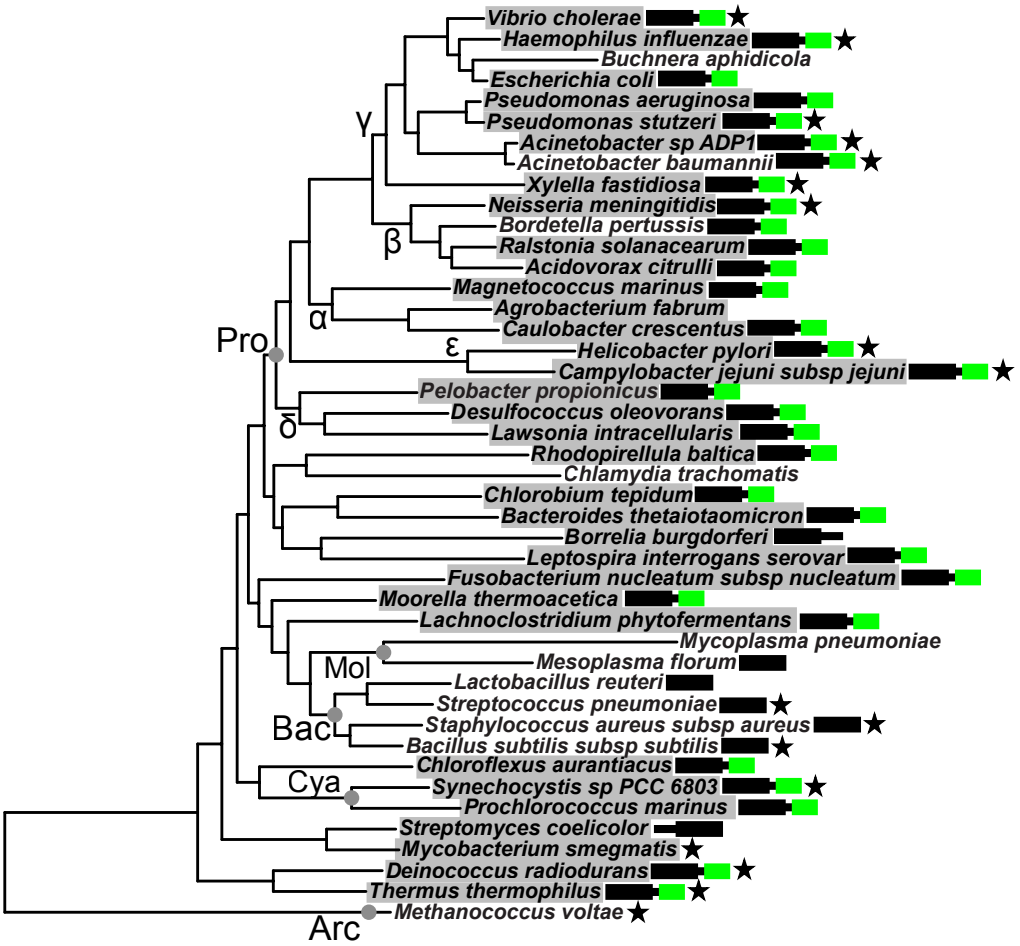

Fig. S1. **Most species with ComM encode a DprA homolog with a C-terminal winged-helix domain**. Estimated maximum likelihood phylogeny of the indicated species based on a concatenated alignment of 36 conserved proteins identified from whole genome sequences (Genome Accession numbers are available in **Dataset S1**). Species that encode a ComM homolog are highlighted in gray. The architecture of the DprA homolog (if present) is indicated to the right of each species name. The core DprA smf domain is indicated by a black box, while the presence of a C-terminal winged helix domain is demarcated by a green box (details of C-terminal domain identification are presented in Methods and **Dataset S1**). Species that have been shown to have the capacity for NT are designated by a black star. Major taxa are labeled along their nodes. Pro: Proteobacteria (Greek letters denote subdivisions); Bac: Bacilli; Mol: Mollicutes; Cya: Cyanobacteria; Arc: Archaea.

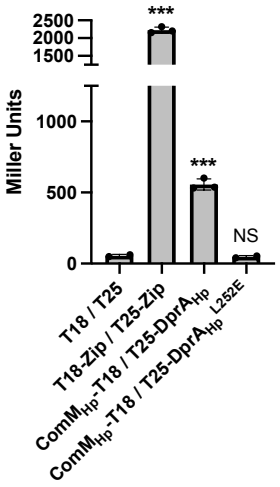

Fig. S2. Quantification of BACTH for ComM$_{Hp}$-DprA$_{Hp}$ interactions. The indicated interactions were quantitatively assessed for interactions by performing Miller Assays. Statistical identifiers directly above bars represent comparisons to the parent containing the empty vectors (T18 / T25). NS, not significant. *** = $p < 0.001$.

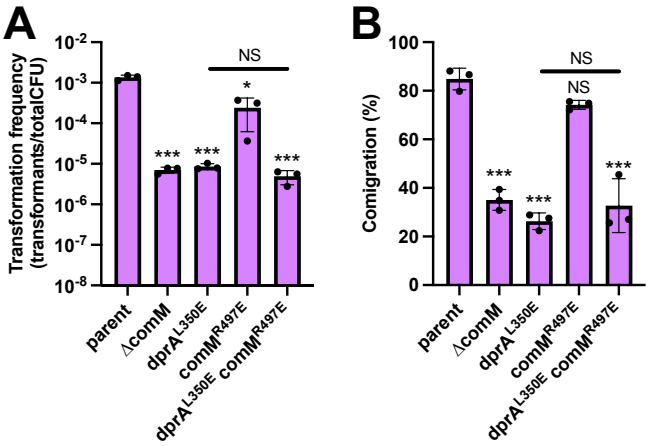

Fig. S3. **ComM^{R497E} is not a gain-of-function allele.** Branch migration was assessed via linkage analysis between a trimethoprim resistance marker (Tm^{R}) and a nonsense mutation in *lacZ* as depicted in **Fig. 2A**. For the tDNA used is this experiment the *lacZ* nonsense mutation was 820 bp away from the Tm^{R} cassette. (**A**) Transformation frequency and (**B**) comigration frequency are reported for strains with the indicated genotypes. Data are from 3 independent biological replicates. Statistical comparisons were made by one-way ANOVA with Tukey's multiple comparison test of the log-transformed data. NS, not significant. *** = $p < 0.001$, * = $p < 0.05$. Statistical identifiers directly above bars represent comparisons to the parent.

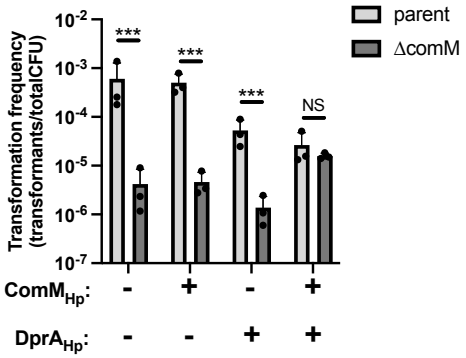

Fig. S4. DprA-dependent recruitment of ComM is species-specific. Transformation frequency assays of the indicated *V. cholerae* strains where native *comM* is intact (parent; gray bars) or deleted (Δ*comM*; black bars). Strains also express $ComM_{Hp}$ and/or $DprA_{Hp}$ from an ectopic locus as indicated (+ denotes that the strain expresses the indicated allele). These are the raw transformation frequencies for the data presented in **Fig. 5A**.

Table S1 - *Strains used in this study*

Strain #*	Genotype	Figures	Use in manuscript
***Helicobacter pylori* strains**			
LR1	*wild-type*	Fig. 1C	wt for NT frequency assays
LR1187	*ΔcomM::Kan^R*	Fig. 1C	Δ*comM* for NT frequency assays
LR1241	Δ*comM::Kan^R, P$_{ureA}$::comM::Cm^R*	Fig. 1C	Δ*comM; ureA::comM* for NT frequency assays
LR827	Δ*dprA::Cm^R*	Fig. 1C	Δ*dprA* for NT frequency assays
LR853	Δ*dprA::Kan^R, P$_{ureA}$::dprA::Apra^R*	Fig. 1C	Δ*dprA; ureA::dprA* for NT frequency assays
LR918	Δ*dprA::Kan^R, P$_{ureA}$::dprA$^{C\text{-}ter}$::Apra^R*	Fig. 1C	Δ*dprA; ureA::dprA$^{C\text{-}ter}$* for NT frequency assays
LR1373	Δ*dprA::kan^R*, Δ*comM::Cm^R, P$_{ureA}$::dprA$^{C\text{-}ter}$::Apra^R*	Fig. 1C	Δ*comM;* Δ*dprA; ureA::dprA$^{C\text{-}ter}$* for NT frequency assays
LR1255	Δ*dprA::Kan^R, P$_{ureA}$::dprA^{L252E}::Cm^R*	Fig. 1C	Δ*dprA; ureA::dprA^{L252E}* for NT frequency assays
***Vibrio cholerae* strains**			
TND0905 / SAD2468	*P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Zeo^R*	Fig. 2C, 2D	parent for NT frequency assays
TND2245 / SAD3567	Δ*comM::Carb^R, P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Zeo^R*	Fig. 2C, 2D	Δ*comM* for NT frequency assays
TND1072 / SAD3569	Δ*dprA::Cm^R, P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Zeo^R*	Fig. 2C, 2D	Δ*dprA* for NT frequency assays
TND4143 / SAD3589	*dprA^{L350E}, P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Cm^R*	Fig. 2C, 2D	*dprA^{L350E}* for NT frequency assays
TND4148 / SAD3590	Δ*comM::Carb^R, dprA^{L350E}, P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Cm^R*	Fig. 2C	*dprA^{L350E}* Δ*comM* for NT frequency assays
TND4145 / SAD3591	*dprA^{E353R}, P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Cm^R*	Fig. 2C, 2D	*dprA^{E353R}* for NT frequency assays
TND4150 / SAD3592	Δ*comM::Carb^R, dprA^{E353R}, P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Cm^R*	Fig. 2C	*dprA^{E353R}* Δ*comM* for NT frequency assays
TND4146 / SAD3593	*comM^{L455E}, P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Cm^R*	Fig. 2C, 2D	*comM^{L455E}* for NT frequency assays
TND4147 / SAD3594	*comM^{R497E}, P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Cm^R*	Fig. 2C, 2D	*comM^{R497E}* for NT frequency assays
TND4152 / SAD3595	*dprA^{E353R}, comM^{R497E}, P$_{tac}$-tfoX*, Δ*luxO, lacZ::lacI^q, pilA^{S67C},* Δ*VC1807::Kan^R*	Fig. 2C	*dprA^{E353R}, comM^{R497E}* for NT frequency assays
SAD1063	Δ*mutS, Kan^R-P$_{tac}$-tfoX*	Fig. 3B, 5B, S3	parent for branch migration assays
SAD1071	Δ*comM::Spec^R,* Δ*mutS, Kan^R-P$_{tac}$-tfoX*	Fig. 3B, 5B, S3	Δ*comM* for branch migration assays
TND4153 / SAD3596	*dprA^{L350E},* Δ*VC1807::Cm^R,* Δ*mutS, Kan^R-P$_{tac}$-tfoX*	Fig. 3B, S3	*dprA^{L350E}* for branch migration assays
TND4151 / SAD3597	*dprA^{E353R},* Δ*VC1807::Cm^R,* Δ*mutS, Kan^R-P$_{tac}$-tfoX*	Fig. 3B	*dprA^{E353R}* for branch migration assays
TND4155 / SAD3598	*comM^{L455E},* Δ*VC1807::Cm^R,* Δ*mutS, Kan^R-P$_{tac}$-tfoX*	Fig. 3B	*comM^{L455E}* for branch migration assays
TND4156 / SAD3599	*comM^{R497E},* Δ*VC1807::Cm^R,* Δ*mutS, Kan^R-P$_{tac}$-tfoX*	Fig. 3B, S3	*comM^{R497E}* for branch migration assays
TND4169 / SAD3600	*dprA^{E353R}, comM^{R497E},* Δ*VC1807::Cm^R,* Δ*mutS, Kan^R-P$_{tac}$-tfoX*	Fig. 3B	*dprA^{E353R} comM^{R497E}* for branch migration assays
SAD1924	P$_{tac}$-*tfoX*, Δ*luxO::Spec^R, comEA-mCherry*, Δ*VC1807::Cm^R, pilA^{S67C}*, 0.11 Mbp::*parS$_{MT1}$, gfp-comM*, Δ*lacZ::P$_{lac}$-cyPet-parB$_{MT1}$ Zeo^R*	Fig. 4A-C	parent for GFP-ComM focus formation assay
TND4178 / SAD3601	*dprA^{L350E}*, P$_{tac}$-*tfoX*, Δ*luxO::Spec^R, comEA-mCherry*, Δ*VC1807::Kan^R,*	Fig. 4A-C	*dprA^{L350E}* for GFP-ComM focus formation assay

	pilA^{S67C}, 0.11 Mbp::*parS*$_{MT1}$, *gfp-comM*, Δ*lacZ*::*P*$_{lac}$*-cyPet-parB*$_{MT1}$ *Zeo*^{R}		
TND4177 / SAD3602	*comM*^{L455E}, P$_{tac}$*-tfoX*, Δ*luxO*::*Spec*^{R}, *comEA-mCherry*, Δ*VC1807*::*Kan*^{R}, *pilA*^{S67C}, 0.11 Mbp::*parS*$_{MT1}$, *gfp-comM*, Δ*lacZ*::*P*$_{lac}$*-cyPet-parB*$_{MT1}$ *Zeo*^{R}	Fig. 4A-C	*comM*^{L455E} for GFP-ComM focus formation assay
TND4441 / SAD3603	*igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-gfp,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*-gfp, P*$_{tac}$*-tfoX*, Δ*luxO, lacZ::lacI*^{q}, *pilA*^{S67C}, Δ*VC1807::Zeo*^{R}	Fig. 5A, S4	parent for NT frequency assays
TND4450 / SAD3604	Δ*comM::Spec*^{R}*, igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-gfp,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*-gfp, P*$_{tac}$*-tfoX*, Δ*luxO, lacZ::lacI*^{q}, *pilA*^{S67C}, Δ*VC1807::Zeo*^{R}	Fig. 5A, S4	Δ*comM* for NT frequency assays
TND4406 / SAD3605	*igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-gfp,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*-comM*$_{Hp}$*, P*$_{tac}$*-tfoX*, Δ*luxO, lacZ::lacI*^{q}, *pilA*^{S67C}, Δ*VC1807::Zeo*^{R}	Fig. 5A, S4	Ectopic *comM*$_{Hp}$ for NT frequency assays
TND4426 / SAD3606	Δ*comM::Spec*^{R}*, igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-gfp,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*-comM*$_{Hp}$*, P*$_{tac}$*-tfoX*, Δ*luxO, lacZ::lacI*^{q}, *pilA*^{S67C}, Δ*VC1807::Zeo*^{R}	Fig. 5A, S4	Δ*comM* native + ectopic *comM*$_{Hp}$ for NT frequency assays
TND4410 / SAD3607	*igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-dprA*$_{Hp}$*,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*-gfp, P*$_{tac}$*-tfoX*, Δ*luxO, lacZ::lacI*^{q}, *pilA*^{S67C}, Δ*VC1807::Zeo*^{R}	Fig. 5A, S4	Ectopic *dprA*$_{Hp}$ for NT frequency assays
TND4427 / SAD3608	Δ*comM::Spec*^{R}*, igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-dprA*$_{Hp}$*,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*-gfp, P*$_{tac}$*-tfoX*, Δ*luxO, lacZ::lacI*^{q}, *pilA*^{S67C}, Δ*VC1807::Zeo*^{R}	Fig. 5A, S4	Δ*comM* native + ectopic *dprA*$_{Hp}$ for NT frequency assays
TND4353 / SAD3609	*igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-dprA*$_{Hp}$*,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*-comM*$_{Hp}$*, P*$_{tac}$*-tfoX*, Δ*luxO, lacZ::lacI*^{q}, *pilA*^{S67C}, Δ*VC1807::Zeo*^{R}	Fig. 5A, S4	Ectopic *comM*$_{Hp}$ and *dprA*$_{Hp}$ for NT frequency assays
TND4357 / SAD3610	Δ*comM::Spec*^{R}*, igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-dprA*$_{Hp}$*,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*- comM*$_{Hp}$*, P*$_{tac}$*-tfoX*, Δ*luxO, lacZ::lacI*^{q}, *pilA*^{S67C}, Δ*VC1807::Zeo*^{R}	Fig. 5A, S4	Δ*comM* native + ectopic *comM*$_{Hp}$ and *dprA*$_{Hp}$ for NT frequency assays
TND4370 / SAD3611	Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*-comM*$_{Hp}$*,* Δ*mutS, Kan*^{R}*-P*$_{tac}$*-tfoX*	Fig. 5B	Ectopic *comM*$_{Hp}$ for branch migration assays
TND4385 / SAD3612	Δ*comM::Spec*^{R}*,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*-comM*$_{Hp}$*,* Δ*mutS, Kan*^{R}*-P*$_{tac}$*-tfoX*	Fig. 5B	Δ*comM* native + ectopic *comM*$_{Hp}$ for branch migration assays
TND4388 / SAD3613	*igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-dprA*$_{Hp}$*,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*- comM*$_{Hp}$*,* Δ*mutS, Kan*^{R}*-P*$_{tac}$*-tfoX*	Fig. 5B	Ectopic *comM*$_{Hp}$ and *dprA*$_{Hp}$ for branch migration assays
TND4396 / SAD3614	Δ*comM::Spec*^{R}*, igVCA0265-VCA0266::Cm*^{R}*-P*$_{tac}$*-dprA*$_{Hp}$*,* Δ*VCA0692-Carb*^{R}*-P*$_{tac}$*- comM*$_{Hp}$*,* Δ*mutS, Kan*^{R}*-P*$_{tac}$*-tfoX*	Fig. 5B	Δ*comM* native + ectopic *comM*$_{Hp}$ and *dprA*$_{Hp}$ for branch migration assays
TND4318 / SAD3615	*dprA*^{L350E}*, comM*^{R497E}*,* Δ*VC1807::Cm*^{R}*,* Δ*mutS, Kan*^{R}*-P*$_{tac}$*-tfoX*	Fig. S3	*dprA*^{L350E} *comM*^{R497E} for branch migration assays
***Escherichia coli* strains**			
PR1577	pKNT25-*dprA*$_{Hp}$	Fig. 1B	Harbors the DprA$_{Hp}$-T25 (only the C-terminal 53 residues) for BACTH analysis
PR1650	pKNT25-*dprA*$_{Hp}$^{L350E}	Fig. 1B	Harbors the DprA$_{Hp}$^{L350E}-T25 (only the C-terminal 53 residues) for BACTH analysis
PR1550	pUTN18-*comM*$_{Hp}$	Fig. 1B	Harbors the ComM$_{Hp}$-T18 vector for BACTH analysis

TND4189 / SAD3616	pUT18C-*dprA*$_{Vc}$	Fig. 2B	Harbors the T18-DprA$_{Vc}$ (only the C-terminal 71 residues) for BACTH analysis
TND4230 / SAD3617	pUT18C-*dprA*$_{Vc}^{L350E}$	Fig. 2B	Harbors the T18-DprA$_{Vc}^{L350E}$ (only the C-terminal 71 residues) for BACTH analysis
TND4235 / SAD3618	pUT18C-*dprA*$_{Vc}^{E353R}$	Fig. 2B	Harbors the T18-DprA$_{Vc}^{E353R}$ (only the C-terminal 71 residues) for BACTH analysis
TMN0427 / SAD3619	pKTN25-*comM*$_{Vc}$	Fig. 2B	Harbors the ComM$_{Vc}$-T25 vector for BACTH analysis
TND4231 / SAD3620	pKTN25-*comM*$_{Vc}^{L455E}$	Fig. 2B	Harbors the ComM$_{Vc}^{L455E}$-T25 vector for BACTH analysis
TND4232 / SAD3621	pKTN25-*comM*$_{Vc}^{R497E}$	Fig. 2B	Harbors the ComM$_{Vc}^{R497E}$-T25 vector for BACTH analysis
SAD2236	pKT25	Fig. 2B	Harbors the T25 empty vector for BACTH analysis
SAD2240	pUT18C	Fig. 2B	Harbors the T18 empty vector for BACTH analysis
SAD2241	pUT18C-zip	Fig. 2B	Harbors the T18-zip vector for BACTH analysis
SAD2238	pKT25-zip	Fig. 2B	Harbors the T25-zip vector for BACTH analysis

*Multiple Strain# designations indicate that the strain was stocked in two independent strain collections.

654 **Table S2** – *Primers used in this study*
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Primer	Sequence (5' → 3')	Description
***Helicobacter pylori* mutant constructs**		
Op329	gagaatattgtaggagatcttctagaaagataaggttaagatagagtatcaaaaccg	Amplify *comM* locus F
Op330	ccggatggctcgagtttttcagcaagatggttcattctgcttgatgaaagc	Amplify *comM* locus R
Op345	gtaacaaccatgattaacacgatgttttgatggctaaaatgagaatatcaccg	Insertion *Kan*^{R} in *comM* locus F
Op346	cttataaaaatccttttaagaaatctttctaaaacctaaaacaattcatccagtaaaat	Insertion *Kan*^{R} in *comM* locus R
Op478	gaaaaacactttaagaataggagaataaggaattcatgattaacacgatgttttgcg	Insertion *ComM* in *ureA* locus for ectopic expression F
Op479	gccatttattcctcctagttagtcacccgggtaccttaagaaatctttctaaaac	Insertion *ComM* in *ureA* locus for ectopic expression R
Op839	ggggataagcttttagaatacgaggagttgggtaagatcaagcgcatcaatc	*DprA* ^{L252E} site-directed mutagenesis F
Op840	gattgatgcgcttgatcttacccaactcctcgtattctaaaagcttatcccc	*DprA* ^{L252E} site-directed mutagenesis R
Op607	ggataacaatttcacacaggaaacagctatgtaccatttaaaagaaatgcctgaaatgg	Amplify C-terminal 53 residues of $dprA_{Hp}$ to clone into BACTH vector F
Op608	ccatttcaggcatttcttttaaatggtacatagctgtttcctgtgtgaaattgttatcc	Amplify C-terminal 53 residues of $dprA_{Hp}$ to clone into BACTH vector R
Op493	ggataacaatttcacacaggaaacagctatgatgattaacacgatgttttgcgcg	Amplify $comM_{Hp}$ to clone into BACTH vector F
Op495	cgcgcaaaacatcgtgttaatcatcatagctgtttcctgtgtgaaattgttatcc	Amplify $comM_{Hp}$ to clone into BACTH vector R
Vibrio cholerae* mutant constructs		
ABD820	CGCTCTTATCTGCTTGGATAATGG	Δ$dprA_{Vc}$ (*i.e.*, ΔVC0048) or *dprA* point mutants F1
ABD998	gtcgacggatccccggaatCATTAACTGGCATCATCAACC	Δ$dprA_{Vc}$ (*i.e.*, ΔVC0048) R1
ABD999	gaagcagctccagcctacaTAGCTATGATGATGGATATTTTGATG	Δ$dprA_{Vc}$ (*i.e.*, ΔVC0048) F2
ABD996	GGTTTGGTTATCCGGATCACAC	Δ$dprA_{Vc}$ (*i.e.*, ΔVC0048) or $dprA_{Vc}$ point mutants R2
ABD855	CATGAATCACTTTGGCATGAGG	Δ$comM_{Vc}$ (*i.e.*, ΔVC0032) or $comM_{Vc}$ point mutants F1
ABD856	gtcgacggatccccggaatCATTGCTTCCCTTAGTATTTGATC	Δ$comM_{Vc}$ (*i.e.*, ΔVC0032) R2
ABD857	gaagcagctccagcctacaTAGTACTCTGACCTGCAGAGTTC	Δ$comM_{Vc}$ (*i.e.*, ΔVC0032) F2
ABD858	AAATTCCAGAAAAACCACGTC	Δ$comM_{Vc}$ (*i.e.*, ΔVC0032) or $comM_{Vc}$ point mutants R2
DOG0886	GCTCAAGCTCttcGAGCTGCATCATGATATCTTGCACCGGTATCTG	$dprA_{Vc}^{L350E}$ R1
DOG0887	GATGCAGCTCgaaGAGCTTGAGCTCCTTGGGCATGTGGTTGCAGTA	$dprA_{Vc}^{L350E}$ F2
DOG0888	GCCCAAGGAGacgAAGCTCCAAGAGCTGCATCATGATATCTTGCAC	$dprA_{Vc}^{E353R}$ R1
DOG0889	CTTGGAGCTTcgtCTCCTTGGGCATGTGGTTGCAGTACCTGGTGGC	$dprA_{Vc}^{E353R}$ F2

DOG0891	TTGATAAACCttcGCGATGCAGCGCGCTTTCTAGAAATTCCGCATC	*comM*$_{Vc}^{L455E}$ R1
DOG0892	GCTGCATCGCgaaGGTTTATCAATTCGGGCTTACCATCGCATCATT	*comM*$_{Vc}^{L455E}$ F2
DOG0893	GCTGTTTGAGTAAttcATCCATGGCTCGATAGCCCAACGCCTCGGCCAA	*comM*$_{Vc}^{R497E}$ R1
DOG0894	TCGAGCCATGGATgaaTTACTCAAACAGCTCAGTGCGCAGAACGTCTAG	*comM*$_{Vc}^{R497E}$ F2
BBC4911	gcaggtggagcaggtggaTATCAAGCAACACTTTTTTCTGCTG	Amplify C-terminal 71 residues of *dprA*$_{Vc}$ to clone into BACTH vector F
TMN0211	tgtaggctggagctgcttcCTAGCCTCTCCCCTTTCTAATATAGC	Amplify C-terminal 71 residues of *dprA*$_{Vc}$ to clone into BACTH vector R
TMN0202	gcaggtggagcaggtggaGGACTTGCGATCATTCATAGC	Amplify *comM*$_{Vc}$ to clone into BACTH vector F
TMN0204	tccaccacttccacctgcGACGTTCTGCGCACTGAG	Amplify *comM*$_{Vc}$ to clone into BACTH vector R
BBC5044	caatttcacacaggatcccgggAGGAGGTCAACGAATGAAAAGCCACTTCC	Amplify *dprA*$_{Hp}$ to clone into ectopic expression construct F
BBC5045	tgtaggctggagctgcttcTCACGCTAACACCACAATGTG	Amplify *dprA*$_{Hp}$ to clone into ectopic expression construct R
BBC5047	caatttcacacaggatcccgggAGGAGGTACAACCATGATTAACACGATGTT	Amplify *comM*$_{Hp}$ to clone into ectopic expression construct F
BBC5048	tgtaggctggagctgcttcTTAAGAAATCTTTCTAAAACTCAGCGC	Amplify *comM*$_{Hp}$ to clone into ectopic expression construct R

*Lower case nucleotides on the 5' end demarcate overlap sequences for SOE PCR and/or isothermal assembly with BACTH vectors. While internal lower case nucleotides demarcate point mutations.