Multiplexed Competition in a Synthetic Squid Light Organ Microbiome Using Barcode-Tagged Gene Deletions

Hector L. Burgos, Emanuel F. Burgos, Andrew J. Steinberger, Garret Suen, Mark J. Mandel

ABSTRACT Beneficial symbioses between microbes and their eukaryotic hosts are ubiquitous and have widespread impacts on host health and development. The binary symbiosis between the bioluminescent bacterium Vibrio fischeri and its squid host Euprymna scolopes serves as a model system to study molecular mechanisms at the microbe-animal interface. To identify colonization factors in this system, our lab previously conducted a global transposon insertion sequencing (INSeq) screen and identified over 300 putative novel squid colonization factors in V. fischeri. To pursue mechanistic studies on these candidate genes, we present an approach to quickly generate barcode-tagged gene deletions and perform high-throughput squid competition experiments with detection of the proportion of each strain in the mixture by barcode sequencing (BarSeq). Our deletion approach improves on previous techniques based on splicing by overlap extension PCR (SOE-PCR) and tfoX-based natural transformation by incorporating a randomized barcode that results in unique DNA sequences within each deletion scar. Amplicon sequencing of the pool of barcoded strains before and after colonization faithfully reports on known colonization factors and provides increased sensitivity over colony counting methods. BarSeq enables rapid and sensitive characterization of the molecular factors involved in establishing the Vibrio-squid symbiosis and provides a valuable tool to interrogate the molecular dialogue at microbe-animal host interfaces.

IMPORTANCE Beneficial microbes play essential roles in the health and development of their hosts. However, the complexity of animal microbiomes and general genetic intractability of their symbionts have made it difficult to study the coevolved mechanisms for establishing and maintaining specificity at the microbe-animal host interface. Model symbioses are therefore invaluable for studying the mechanisms of beneficial microbe-host interactions. Here, we present a combined barcode-tagged deletion and BarSeq approach to interrogate the molecular dialogue that ensures specific and reproducible colonization of the Hawaiian bobtail squid by Vibrio fischeri. The ability to precisely manipulate the bacterial genome, combined with multiplex colonization assays, will accelerate the use of this valuable model system for mechanistic studies of how environmental microbes—both beneficial and pathogenic—colonize specific animal hosts.

KEYWORDS barcode sequencing, amplicon sequencing, sequence-tagged gene deletions, Vibrio fischeri, Aliivibrio fischeri, BarSeq

Beneficial symbioses are ubiquitous in the environment and have substantial impacts on the health and development of animal hosts. In animals, symbionts can affect host organ morphogenesis, immune system development, reproduction, susceptibility to disease, and even behavior (1–4). In humans, the gut, skin, lungs, and urogenital tract all have specific microbiomes for which their dysbiosis has been associated with disease


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It is clear that molecular communication between animal hosts and their microbial partners leads to selection and retention of the cognate microbiome: while many microbes are obtained from the environment, the composition of mature microbiomes is often largely stable and resilient within members of a host species (9, 10). While microbial communities have been characterized using metagenomic, transcriptomic, and metabolomic approaches (11), the complexity of animal-associated microbiomes and the inability to culture and genetically manipulate many symbionts make it difficult to study the precise molecular mechanisms that establish specific relationships.

The binary symbiosis between genetically tractable *Vibrio fischeri* and the Hawaiian bobtail squid *Euprymna scolopes* serves as a model system to study the molecular interactions underlying microbiome assembly (11–16). The squid hatch aposymbiotically (without symbiont) and are colonized by *V. fischeri* in a multistep process that leads to the specific recruitment of the symbiont from a marine environment in which the bacteria are <0.1% of the bacterioplankton (14, 17). The symbionts are housed in the dedicated light organ (LO) within the squid’s mantle cavity, where they generate light that the host uses for counterillumination to hide its shadow while hunting at night (18). The host provides the symbionts with a protected niche, nutrients, and oxygen (15). Once the symbiosis is irreversibly established in juvenile squid, a daily cycle proceeds where 90 to 95% of the bacteria are expelled from the LO at dawn. The remaining symbionts grow during the day until they fill the LO, and at night the dense population of symbionts provides light (19). Because the aposymbiotic hatchlings can be cultured in the lab and infected with genetically tractable *V. fischeri*, colonization experiments can be performed to study the molecular factors that play a role during this process (12, 16, 20). In addition, the translucent nature of the LO in squid hatchlings allows for visualization of the colonization process by microscopy (21–23).

Microbe-host signaling mechanisms and developmental transitions ensure specificity during colonization (14, 17). Upon detection of bacterium-derived peptidoglycan, the ciliated appendages on the surface of the LO secrete mucus that traps bacteria circulating within the mantle cavity (13, 24, 25). In the mucus field, *V. fischeri* bacteria bind to cilia and form aggregates by expressing symbiosis polysaccharide (syp) genes, a locus of 18 structural and regulatory genes whose products contribute to biofilm formation (26, 27). Approximately 3 to 4 h postinoculation, bacterial aggregates migrate through the host mucus toward the pores that lead into the LO ducts (25). While the initial migration is independent of flagellar motility (28), at the pores squid-produced chitin oligosaccharides serve as a chemotacttractant to direct the symbiotic bacteria into the host crypts (21). Motility and chemotaxis are required for colonization, and strains with mutations in genes required for these processes—such as *cheA, fliA*, and *rpoN*—are unable to successfully colonize the squid LO (21, 28). Once within the LO *V. fischeri* generates light through expression of the *lux* operon in a quorum sensing-dependent process (29). Symbionts that fail to produce luminescence, such as strains with mutations in the autoinducer synthase genes *ainS* and *luxI*, or deletions of the *lux* operon, are unable to persist in the symbiosis (30, 31).

To identify novel colonization factors in *V. fischeri*, our lab previously used a global transposon insertion sequencing approach (INSeq) to identify bacterial mutants that were depleted after 48 h in the squid host (32). This approach successfully identified previously known colonization factors, such as *rscS, rpoN, ompU*, various motility factors, and the *syp* biofilm locus, and in addition revealed 344 putative novel colonization factors. Twenty candidates were tested in competitive colonization assays of wild-type (WT) versus mutant strains, and the results showed that nine factors had colonization defects. Some of the validated factors encompass roles in protein quality control (DnaJ and DegS) and copper detoxification (CopA and CusC), inner membrane proteins predicted to play a role in secretion of autotransporters (*TamB/YtfN*), and other poorly characterized factors (YdhC, YapD, and YhcB). This global approach was crucial in identifying putative colonization factors. However, further study is required...
to address which genes are true colonization factors, when they act during colonization, and how their products modulate the interaction with the host.

Approximately 32% of putative colonization factors identified by INSeq did not fall into a curated Clusters of Orthologous Groups (COGs) category, suggesting that the ability to interrogate the function of these colonization factors will reveal novel biology. Traditional genetic engineering techniques in V. fischeri are either random (transposon mutagenesis) or labor-intensive (plasmid-based allelic exchange) (32–34). We therefore considered approaches by which we could isolate mutants and examine phenotypes in a multiplexed fashion. One possible approach was to retrieve transposon insertions of interest from an arrayed library (35–37). A second approach we considered was to adapt a newly developed method for transformation-mediated mutagenesis using linear DNA (38) with an in-frame barcoding strategy to facilitate precise mutations. The latter option was attractive in that we hoped that it would limit the effects of polar mutations and provide a set of defined deletions that can be characterized by amplicon PCR. Barcode sequencing (BarSeq), in which each strain is uniquely labeled and identified using high-throughput next-generation sequencing, has been used successfully to track population dynamics in multiple systems, including in yeast genomic libraries, during Vibrio cholerae infection, and to track and phenotype laboratory-evolved Escherichia coli (39–43). Here, we describe an approach to generate barcode-tagged gene deletions in V. fischeri and perform high-throughput colonization experiments using BarSeq. We also describe the baseq python computational package used to analyze the results.

RESULTS

Generation of barcoded gene deletions. To generate barcoded deletions of specific V. fischeri genes, we designed an approach that takes advantage of splicing by overlap extension PCR (SOE-PCR) and tfoX-based natural transformation (Fig. 1) (38, 44–46). The first step uses PCR to amplify DNA fragments upstream and downstream of the gene targeted for deletion, fused to the left and right linker sequences, respectively (Fig. 1A). A separate PCR is performed with pHB1 as a template to generate the central fragment of DNA containing the linker sequences, a selectable marker (erm, conferring erythromycin resistance) surrounded by FLP recombination target (FRT) sites, and the semirandom barcode sequence. The barcode is provided by the reverse primer, which contains a region of semirandomized sequence. The three resulting DNA fragments—upstream, central, and downstream—are then fused into one fragment via their overlapping linker sequences by SOE-PCR (46) and transformed into V. fischeri upon tfoX induction (44). Finally, the erm cassette is removed via FLP recombinase (45).

The resulting 138-bp deletion scar (barcode scar, or “bar” scar, Fig. 1B) lies between the deleted gene’s first codon and last seven codons (i.e., the final six amino acid-encoding codons plus the stop codon). The scar is designed to be in-frame to prevent polar effects on gene expression when targeting genes within operons. The terminal codons were retained in case they contain a ribosomal binding site for downstream gene(s) (47). In addition to the barcode, the additional sequence in the scar includes left and right linker sequences that are shared among all of the mutants, which allows us to identify and quantify the abundance of each barcodes strain using amplicon sequencing, while minimizing amplification bias by using common primers that amplify the same size product.

To test this new approach, we investigated the copA gene. Among Gammaproteobacteria, CopA is the main exporter of cytoplasmic copper and is the most widely conserved copper detoxification factor (48, 49). Although our laboratory previously demonstrated that copA is a squid colonization factor, its role in copper resistance has not been examined (32). We therefore targeted copA for deletion using our mutagenesis approach as a proof of concept and subsequently tested its role in copper resistance in V. fischeri. To ensure that the deletion process worked as intended, we used four sets of diagnostic PCR primers that would report on correct erm insertion, subsequent removal of the erm cassette
by FLP recombinase, and absence of the targeted gene from the bacterial chromosome.

PCR with various pairs of oligonucleotides that target the copA gene and its deletion constructs produced amplicons of the expected size in each strain (Fig. 2A). These results show that the erm cassette was successfully inserted into copA generating ΔcopA:erm-bar and subsequently removed by FLP recombination to generate the in-frame deletion scar in ΔcopA::bar. Furthermore, sequencing of the deletion scar for several ΔcopA:erm-bar candidates showed that after a single round of mutagenesis, multiple uniquely barcoded deletion strains were generated (Fig. 2B). These results demonstrate that our deletion method is successful in generating uniquely barcoded mutant strains of V. fischeri.
The presence of a barcode within a gene deletion does not alter mutant phenotypes. To test that the barcoded scar does not affect the mutant phenotypes, we measured the copper sensitivity of strains deleted for copA using various methods. In addition to the mutants generated using our deletion approach (ΔcopA::erm-bar and ΔcopA::bar), we constructed a deletion of copA using plasmid-based allelic exchange.

FIG 2 Evaluating the genotype of a copA deletion strain. (A) Representative 1% agarose gel showing the products generated by PCR when using the specified primer pairs and templates. DNA ladder is the 1-kb Plus DNA ladder (New England BioLabs). Oligos, oligonucleotides. (B) Table showing several unique barcode sequences within the ΔcopA::erm-bar deletion scar of various deletion candidates that were generated from a single round of mutagenesis. The diagram is not drawn to scale.
(ΔcopA) (33) and obtained a copA transposon mutant isolated from our previous study (copA::Tnerm) (32). We then tested the growth of these copA mutants in the presence of various amounts of copper. Our results show that, regardless of the mutagenesis method, the growth of copA mutants is similarly impeded in the presence of copper, with the severity of the growth defect increasing in proportion to the concentration of copper: at 0.2 μM Cu2+, the copA mutants were able to grow slightly, whereas at 20 μM Cu2+, these strains were unable to grow (Fig. 3A). This is in contrast to the WT strain that achieved the same growth yield regardless of the concentration of copper present. The ΔcopA::erm-bar and ΔcopA::bar mutants showed the same degree of copper sensitivity (Fig. 3A).

To corroborate that the observed growth defects were due specifically to excess copper, we measured the growth of the ΔcopA::bar mutant in the presence of copper, with and without the copper chelator bathocuproinedisulfonic acid (BCS). As expected, ΔcopA::bar was unable to grow in the presence of 20 μM Cu2+, whereas the WT is unaffected (Fig. 3B). However, growth of ΔcopA::bar in the presence of copper was rescued by addition of 80 μM BCS (Fig. 3B), suggesting that free copper is indeed responsible for the observed lack of growth in the mutant. To verify that the absence of CopA was responsible for susceptibility to copper toxicity, we complemented copA at the chromosomal attTn7 site in the ΔcopA::bar strain and observed that growth was rescued in the presence of copper (Fig. 3B). On the basis of these results, we conclude that CopA
is required for resistance to copper in *V. fischeri*, consistent with its function in other Gammaproteobacteria (48).

To further test our deletion method, we generated mutants in multiple genes required for *V. fischeri* motility—rpoN, flrA, and flaA—and tested the resulting strains’ motility phenotypes on soft agar plates (28, 50, 51). We also included a WT strain tagged with the deletion scars at the *att*Tn7 site (WT-1) and copA mutants as controls. While the motility of WT *V. fischeri* resulted in a migration disc with a diameter of 26 mm from the inoculation point on soft agar plates, deleting flaA resulted in a drastic reduction in migration (9 mm), while deleting either flrA or rpoN resulted in no motility (1.5 mm) (Fig. 4). We observed that both the *erm-bar* and *bar* versions of the gene deletions displayed equivalent phenotypes, showing that the strains behave as null alleles regardless of whether the scar contains the *erm* cassette (Fig. 4). The motility of both the WT-1 and copA strains is comparable to that of the WT, showing that motility defects are due to the deleted loci and not to the insertion of the deletion scars.

Removing the erythromycin resistance cassette minimizes polar effects of the barcoded deletions. While the presence or absence of the *erm* cassette does not prevent deletion strains from manifesting the corresponding phenotypes (Fig. 3A and 4), we were concerned about polar effects on downstream gene expression upon insertion of the 1,049-bp heterologous *erm* cassette (52–54). To test the effect of the *erm* cassette on downstream gene expression, we used reverse transcriptase quantitative PCR (RT-qPCR) to measure expression of genes immediately upstream and downstream of a targeted gene deletion for three different predicted operons. In each case, we measured the ratio in expression levels of the downstream versus upstream genes in the mutant, normalized to the ratio in WT *V. fischeri* (defining this normalized value as the "polarity ratio"). For both rpoN and cheA, deletion scars of either *erm-bar* or *bar* resulted in negligible changes in the polarity ratio (Fig. 5). In contrast, the polarity ratio of ΔcusA: *erm-bar* was 26-fold higher than WT, whereas removal of the *erm* cassette to form the in-frame deletion scar restored the polarity ratio to basal levels (Fig. 5). We conclude that, in at least some cases, gene::*bar* deletion scars can alleviate collateral effects on flanking genes that are caused by inserting an antibiotic resistance cassette.

**Development of a computational pipeline to analyze *V. fischeri* BarSeq data.** With the ability to quickly generate precise barcoded deletions, we next sought to compete the Δgene::*bar* deletions en masse during host colonization. We therefore developed a BarSeq sample preparation protocol, and an accompanying computational package to analyze the data (Fig. 6). To accomplish this, we mixed barcoded strains to generate an input library (i.e., a synthetic microbiome). This library was then used to inoculate media and/or squid hatchlings, which were then sampled at the

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**FIG 4** Assaying the phenotype of strains deleted for motility factors. Representative TBS agar trays showing the migration of strains from the inoculation point after incubation at 28°C for 4 h. WT is MJM1100 (ES114), while WT-1 represents the *att*Tn7-marked MJM1100 strain with barcode 1 (either WT::*erm-bar* or WT::*bar*). Bar graph shows the quantified data from five independent replicates with error bars showing the standard deviations of the means (*n* = 5). Statistical analysis was performed using a two-way ANOVA test. ****, *P* < 0.0001.
desired time points. Samples were then processed to extract genomic DNA (gDNA), and PCR was performed with dual-index Illumina sequencing primers to obtain double-stranded DNA (dsDNA) fragments containing the barcoded deletion scars. The resulting library was then sequenced on an Illumina MiSeq and demultiplexed based on the unique dual indexes (55). The resulting sequence data were then analyzed using the barseq package, which identifies and counts the barcodes present in the samples, assigns strain identity, normalizes strain counts, and calculates relative frequency and the competitive index (CI) for each strain within the samples. The BarSeq protocol provides a streamlined and effective way to measure population dynamics throughout squid colonization.

BarSeq enables sensitive multiplex competition experiments. To test our BarSeq protocol in tracking individual strains within a population, we performed an in vitro competition and a competitive colonization experiment using an input library of seven different barcoded strains mixed in an equivalent ratio. In addition to several mutant strains, we included three WT::bar strains that had the bar scar inserted at the attTn7 site that could be similarly tracked using amplicon sequencing but without affecting the phenotypes of the strains (WT-1, WT-2, and WT-3 in Fig. 7). After 15 generations of growth in vitro, the proportion of most strains relative to the WT::bar strains remained stable except for flaA and rpoN deletion strains, which were fourfold higher and lower, respectively, compared to WT::bar (Fig. 7A). In contrast, following 48 h of squid colonization—which corresponds to approximately 15 bacterial generations (32)—we observed reduced levels of the flaA flagellin mutant and severely reduced levels of the flaA, rpoN, and cheA strains, all of which were near the limit of detection (Fig. 7B). This result is consistent with their previously known roles as necessary factors for squid colonization, although we did observe higher levels of flaA in the competitive colonization than are observed when a transposon insertion is competed against the wild-type strain (28, 50, 51, 56). We note that there was relatively little variability among the WT::bar strains in the analysis, whereas the 4- to 5-log-unit scale in which to identify colonization defects provided a substantially greater range over which to identify and refine colonization phenotypes in vivo (Fig. 7B). Taken together, these results show that our method for targeted barcoded deletions, multiplex squid colonization, and analysis by BarSeq allows for reproducible competition experiments in vitro and in vivo with high sensitivity.
DISCUSSION

In this study, we developed a method to quickly generate gene deletions where the resulting strains are tagged with unique DNA barcodes. We demonstrated the utility of these strains in performing BarSeq high-throughput competitive colonization experiments and introduced a software package to analyze the resulting sequencing data. BarSeq provides a sensitive method to track population dynamics of squid colonization by *V. fischeri*.

**Generation of targeted, barcoded gene deletions that minimize effects on neighboring genes.** Our approach builds upon previous SOE-PCR/tfoX mutagenesis techniques to incorporate a unique barcode in each deletion strain, which enables high-throughput experiments via barcode sequencing (BarSeq). Since BarSeq relies on amplicon sequencing, library preparation is straightforward and allows for a large number of samples to be processed in parallel. The method we have employed to design the barcode and flanking sequences was planned to minimize disruption on flanking genes. Expression of bacterial genes is frequently organized by their genetic
arrangement into operons where expression of operon members is driven by a common promoter (57). However, given that some regulatory regions overlap in neighboring genes, deletion of one gene can alter the expression level of another nearby cis-tron. These off-target effects on gene expression could obfuscate the analysis of experimental results. Similar to the approach used by Baba et al. (53), our deletion approach reduces off-target effects on gene expression by ensuring the formation of an in-frame open reading frame within the deletion scar and including several codons at the end of the deletion target where the ribosome binding site of downstream genes is frequently located (Fig. 1B and Fig. 5). We do note a potential limitation any time that foreign codons are introduced. The rarest codon within the scar (normalized to the set of codons for that amino acid) comprises 2% of the arginines encoded in the genome. It is formally possible that under growth conditions not tested here, for example, a different tRNA pool in the cell could theoretically lead to distinct effects. Our polarity assay results suggest that this is not an issue under typical laboratory growth conditions (Fig. 5). Nonetheless, there may be conditions in which the introduced DNA leads to substantive effects.

BarSeq enables detailed studies of the molecular mechanisms that result in establishment of the Vibrio-squid symbiosis. Using an INSeq screen, our lab previously identified 344 putative novel squid colonization factors in V. fischeri (32). Our deletion approach, combined with BarSeq, will enable the high-throughput characterization of these factors during squid colonization by allowing multiplexing of colonization factor mutants and tracking of individual strains. By enabling a more precise study of colonization factors, BarSeq has several potential applications.

BarSeq can be applied to the study of strain variation and evolution of colonization mechanisms in the Vibrio-squid symbiosis. V. fischeri strain variation is an important consideration when studying the mechanisms of colonization of the squid LO (58, 59). Previous studies have shown that multiple strains can cocolonize the squid LO and that they do so at different rates (60–62). More recent studies have focused on deciphering the specific mechanisms that result in differing colonization behavior (63, 64). The barcode-tagged mutagenesis method presented here can be applied to generate uniquely tagged WT or mutant strains of the various phylogenetically distinct V. fischeri strains and assayed in multiplexed format during squid colonization using BarSeq. We have already successfully used our SOE-PCR/tfoX mutagenesis approach to make targeted deletions in strain SRS, showing that this method is applicable to V. fischeri strains that are evolutionarily distant to the frequently used ES114 strain (63).
BarSeq can also be used in directed evolution experiments to examine the functional evolution of colonization factors. Directed evolution experiments have recently been applied to study colonization factors in *V. fischeri* (65). The ease of tracking large numbers of individual *V. fischeri* strains using BarSeq could enable tracking of strain lineages in long-term evolution experiments, as has been conducted in other organisms (39, 42, 43).

**Phenotypes of rpoN and flrA mutants during competitive growth in media.** Both *rpoN* and *flrA* deletion strains showed a statistically significant fourfold decrease and increase, respectively, during competitive growth in media compared to WT (Fig. 7A). Due to the nature of the factors they encode, the observed growth defects are likely due to changes in energetic and nutritional requirements when *rpoN* and *flrA* are deleted. The *rpoN* gene encodes the alternative $\sigma^{54}$ factor that is responsible for expression of various systems involved in squid colonization, including Syb biofilm formation, flagellar motility, and luminescence (51, 66, 67). Therefore, it is not surprising that deleting the gene encoding $\sigma^{54}$ has pleiotropic effects on gene expression due to misregulation of the RpoN regulon and could reduce the ability of the mutant strain to effectively compete for growth *in vitro*, though further experiments are necessary to define the precise mechanism for the defect. FlrA is the $\sigma^{54}$-dependent transcription factor that activates expression of the flagellar biosynthesis cascade and is required for motility and squid colonization (50). The high energetic cost of expressing all genes related to flagellar biosynthesis (68), which in *V. cholerae* requires FlrA-dependent regulation of 52 genes (69) and in *V. fischeri* between 39 and 131 genes (28), is consistent with the observed increase in growth of the *flrA* deletion strain compared to WT during competitive growth in media (Fig. 7A). Nonetheless, even though the changes observed in competitive growth of the *rpoN* and *flrA* mutants *in vitro* are in opposing directions (less versus more growth, respectively), both are severely defective in squid colonization (Fig. 7B). Future experiments using BarSeq to probe bacterial growth *in vitro* and during colonization have the potential to elucidate heretofore hidden phenotypes.

**Discrepancy in flaA colonization efficiency measured by BarSeq versus traditional competitive squid colonization experiments.** In our BarSeq experiment, the known colonization factor *flaA* shows only a small (ca. twofold) colonization defect after 48 h post-squid inoculation (Fig. 7B). In contrast, Millikan and Ruby showed that a *flaA* deletion made by insertion of a Kan cassette is severely defective during competitive colonization against WT *V. fischeri* (56). Using confocal microscopy, their work showed that LO colonization by *flaA* is delayed compared to WT by $\sim$8 h. However, because our competitive colonization experiment using BarSeq was done at 48 h postinoculation, this delayed colonization is not enough to explain the observed discrepancy. Previous work has shown that the concentration of *V. fischeri* in the inoculum can affect the number of different strains that can cocolonize the squid LO (70). This raises the possibility that the inoculum amount or the ratio of strains within the synthetic microbiome might affect the observed colonization defect. To address this, future experiments should examine how inoculum amount and the ratio of mutant strains to WT within a synthetic barcode-tagged population affects colonization efficiency for the different strains in the population.

In summary, we provide a new method for constructing barcoded deletions of *V. fischeri* genes, we demonstrate the utility of this method for generating in-frame deletions and discovering new functions of squid colonization factors, and we combine this approach with a computational tool to conduct multiplex animal colonization assays using barcode sequencing.

**MATERIALS AND METHODS**

**Bacterial strains, growth conditions, plasmids, and primers.** Bacterial strains used in this study are listed in Table 1, with Table S1 in the supplemental material containing an extended Table 1 showing the oligonucleotides used to generate the specified barcode-tagged gene deletions. Plasmids are listed in Table 2, and DNA oligonucleotides are listed in Table S2. DNA oligonucleotides were synthesized by Integrated DNA Technologies (Coralville, IA), and Sanger DNA sequencing was performed through the
When necessary, growth media was solidified in Luria-Bertani broth (LB) medium (per liter, 25 g Difco LB broth, 10 g NaCl, and 50 ml 1 M Tris buffer [pH 7.0] in distilled water) at 25°C with aeration.

Strain Alias Genotype or description Reference(s) or source

V. fischeri strains

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E. coli strains

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<td>MJM534</td>
<td>CC118 Δpir/pEVS104</td>
<td>Δ(ara-leu) araD ΔlacX74 galE gaiK phoA20 thi-1 rpsE rpoB argE(Am) recA1, lysogenized with Δpir/pEVS104</td>
<td>33</td>
</tr>
<tr>
<td>MJM537</td>
<td>ΔH5α Δpir</td>
<td>Δ80lacZAM15 ΔlacZYA-argF U169 supE44 hsdR17 (rK mK) endA1 recA1 gyrA96 thi-1 relA1 uidA-pir&lt;p&gt; Laboratory stock&lt;/p&gt;</td>
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</tr>
<tr>
<td>MJM570</td>
<td>ΔH5α/pEVS79</td>
<td>Δ80lacZAM15 ΔlacZYA-argF U169 supE44 hsdR17 (rK mK) endA1 recA1 gyrA96 thi-1 relA1/pEVS79</td>
<td>72, 73</td>
</tr>
<tr>
<td>MJM637</td>
<td>S17-1 Δpir/pUX-BF13</td>
<td>pro res hsdR17 (rK mK) recA with an integrated RP4-2-Tc::Mu-Km:Tn7 λpir/pUX-BF13</td>
<td>72, 73</td>
</tr>
<tr>
<td>MJM658</td>
<td>BW23474/pEVS107</td>
<td>Δlac-169 robA1 creC510 hsdR514 uiddA(ΔMmul::pir16 endA(B733) recA1/pEVS107</td>
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</tr>
<tr>
<td>MJM3287</td>
<td>ΔNEB5α/ΔPB1</td>
<td>Δ80lacZAM15 ΔlacZYA-argF U169 glnV44 hsdR17 (rK mK) endA1 recA1 gyrA96 thi-1 relA1 fhuA2 phoA1/pHB1</td>
<td>63</td>
</tr>
<tr>
<td>MJM3288</td>
<td>NEB5α/Δpir/ΔPB2</td>
<td>MJM537/pΔPB2</td>
<td>This work</td>
</tr>
<tr>
<td>MJM3383</td>
<td>NEB5α/ΔPB3</td>
<td>MJM537/pΔPB2</td>
<td>This work</td>
</tr>
<tr>
<td>MJM3478</td>
<td>KV8052: p3813(pK)</td>
<td>lacI thi-1 supE44 endA1 recA1 hsdR17 gyrA462 zei-298 Tn10 ΔthylA::(erm-pir-116)/pK/V496</td>
<td>38, 71</td>
</tr>
</tbody>
</table>

Thymidine auxotroph, growth conditions in Materials and Methods.
confirmed by sequencing, generating pH83, which was conjugated into V. fischeri MJM1100 (ES114) via triparental mating with MJM534, which contains the helper plasmid pEVS104 (33). Single recombinants of pH83 into the chromosome were screened and selected by growth on chloramphenicol (MJM3400), and double recombinants were screened and selected by loss of the antibiotic resistance cassette and copA (MJM3401). The resulting constructs were verified by PCR and sequencing (Table S2).

The copA gene was inserted into the attTn7 site in the chromosome using pEVS107 (70). The copA gene including 191-bp US and 321-bp DS sequences was amplified by PCR using oligonucleotides HB27 and HB34, and the product was digested with AsclI and cloned into the AsclI site of pEVS107. The resulting constructs were verified by PCR and sequencing (Table S2).

**Construction of barcode-tagged gene deletions.** The deletion protocol demonstrated in Fig. 1A is based on splicing by overlap extension PCR (SOE-PCR) and tfoX transformation (38, 44–46) to directly delete and tag targeted genes with a randomized sequence (barcode). Our protocol was in development prior to publication of the previous method (38), so while it is conceptually similar, the sequences of the linkers and primers are distinct. First, several oligonucleotides were designed specific to the targeted genes to amplify 1 kb of US (F1 and R1-LL) and DS (F2-RL and R2) DNA tagged with the left linker (LL) and right linker (RL) sequences, respectively, to screen the deletion scar via PCR (FO and RO), and to assay for the absence of the targeted gene (FW and RW) (Fig. 1A, Table S1, and Table S2). FW and RW were designed to amplify a fragment of 500 to 1,000 bp, depending on the size of the gene. The F1 and R2 oligonucleotides were designed to anneal 1-kb US and DS, respectively, of the targeted gene. The R1 oligonucleotide was designed to anneal starting at the start codon of the targeted open reading frame (ORF) going upstream, then the reverse complement of the LL sequence (LL reverse complement, 5′-CTGGCGAAGCATATATAAGAAGCTCGTCTCGT-3′) was attached to the 5′ end of the R1 oligonucleotide, resulting in R1-LL. The F2 oligonucleotide was designed to anneal at the last seven codons (6 amino acids [aa] and stop codon) on the 3′ end of the targeted ORF going downstream, then the RL sequence

<table>
<thead>
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<th>Table 2: Plasmids used in this study</th>
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<tr>
<td><strong>Plasmid</strong></td>
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<tr>
<td>pEV579</td>
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<tr>
<td>pEV5104</td>
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<td>pEV5107</td>
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<tr>
<td>pKV496</td>
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<tr>
<td>pLostfoX</td>
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<td>pUC19</td>
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<tr>
<td>pH81</td>
</tr>
<tr>
<td>pH82</td>
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<tr>
<td>pH83</td>
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**Plasmids used in this study**

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Relevant properties</th>
<th>Reference or source</th>
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<tbody>
<tr>
<td>pEVS79</td>
<td>Vector backbone for deletion construct via allelic exchange; Cam’</td>
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<tr>
<td>pEVS104</td>
<td>Conjugation helper plasmid; Kan’</td>
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<tr>
<td>pEVS107</td>
<td>Min-Tn7 mobilizable vector; Erm’ (transposon); Kan’</td>
<td>70</td>
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<tr>
<td>pKV496</td>
<td>pEVS79 containing the FLP recombinase; Kan’</td>
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<tr>
<td>pLostfoX</td>
<td>tfoX overexpression vector; Cam’</td>
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<tr>
<td>pUC19</td>
<td>Cloning vector; Carb’</td>
<td>Laboratory stock</td>
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<tr>
<td>pUX-BF13</td>
<td>Tn7 transposase helper plasmid (tns genes); Carb’</td>
<td>72</td>
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<tr>
<td>pH81</td>
<td>pUC19 containing the Ll-FRT-erm-FRT-spacer sequence in the HindIII BamHI site</td>
<td>63</td>
</tr>
<tr>
<td>pH82</td>
<td>pEV5107 containing copA (including 191 bp upstream and 321 bp downstream of the copA ORF) at the Ascl site</td>
<td>This work</td>
</tr>
<tr>
<td>pH83</td>
<td>pEVS79 containing 1.6 kb upstream/1.6 kb downstream of copA</td>
<td>This work</td>
</tr>
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</table>
The final bar scars were made by triparental mating of donor MJM3478 (α3813/pKV496) (38) and helper strain MM345 (C118α/pJRE5104) into recipient V. fischeri strains containing the erm-bar scar and selection on LBS containing 100 μg/ml kanamycin (LBS-Kan100). Plasmid pKV496 contains the FLP recombinase that removes the erm cassette and fuses the two surrounding FRT sites into one, resulting in the final bar scar as shown in Fig. 1B. The plasmid was eliminated by growing the candidates on LBS without selection twice and selecting colonies that were Erm⁻ and Kan⁺. The gene:bar candidates were screened by PCR using oligonucleotide pairs F1/R2, FO/HB146 (RL), and FW/RW, and the deletion scar was verified by Sanger sequencing using oligonucleotides HB42 and HB146. The barcode sequences were verified to match the barcode within the parental strains containing the gene:erm-bar scar.

The barcoded WT V. fischeri strains (WT::bar) were constructed using the same procedure as outlined above for the gene deletions but targeting a site next to the attTn7 site in the intergenic region of yeIR and glmS. The 1-kb US and DS arms were amplified using PCR with ES114 gDNA and oligonucleotide pairs HB239/HB240 and HB241/HB242. After SOE-PCR to form the mutagenic DNA and tfoX transformation, the WT::erm-bar candidates were screened by PCR with oligonucleotide pairs HB243/HB244 and HB243/H88. Sanger sequencing was used to confirm insertion of the erm-bar scar and record the unique barcode sequences. Triparental mating as described above was performed to remove the erm cassette using pKV496. The bar scar was confirmed by PCR with HB243/HB146 and Sanger sequencing.

**Growth assays in the presence of copper.** Colonies from freshly streaked LBS plates of the indicated V. fischeri strains were inoculated into 3 ml LBS with the appropriate antibiotics and grown for 8 h at 25°C with shaking. Three microliters of the LBS cultures was subcultured into 3 ml Tris minimal medium [per liter, 50 ml of defined seawater (DSW; 2X), 50 ml of 1 M Tris base (pH 7.5), 1 ml of 5.8% K_HPO₄, 1 ml of 10 mM FeSO₄, and 20 ml of 10% N-acetylglucosamine (GlcNAc), in distilled water; DSW (2×) = 100 mM MgSO₄, 20 mM CaCl₂, 600 ml of 1 M Tris, 100 ml of 20 mM KCl] and incubated at 25°C overnight for ≤16 h. Overnight cultures were diluted to an optical density at 600 nm (OD₆₀₀) of 0.2 in 200 ml of the same media and then 2 μl of solution with an OD₆₀₀ of 0.5 was transferred into 198 μl of fresh Tris minimal medium containing the appropriate amounts of copper and/or bathocuproinedisulfonic acid (BCS) in a 96-well plate. The plate was then incubated in a Synergy Neo2 Multi-Mode microplate reader (BioTek) at 25°C with a final melt curve analysis to ensure specificity in the reaction. The mRNA levels of rpoN, cheA, and cusF was calculated as expression of the downstream gene/expression of the upstream gene using the respective flanking genes in each putative operon (lpbB-tpnN-lpf-hpf, cheZ-cheE, cheZ-cheE, cusB, and cusF) were measured using the oligonucleotide pairs listed in Table S2. Expression levels for each gene were normalized to that of rpoD, and the mutants were normalized to WT using the 2−ΔΔCt method (76). The polarity ratio of tpoN, cheA, and cusF was calculated as "expression of the downstream gene/expression of the upstream gene." In the case of the operons ptpB-lpbB-tpnN-lpf-hpf, cheZ-cheE, and cusB-cusA-cusF, the operons were predicted using the BioCyc database for "Aliivibrio fischeri strain ES114, version 24.1," which is based on the sequenced genome in Mandel et al. (77, 78).

**barseq bioinformatic tool.** To quantify barcodes within each sequenced sample, we developed barseq (https://github.com/mjmlab/barseq), a python package that identifies putative barcodes in the sequenced reads and matches them to a user-provided barcode library. The program iterates through each sample and uses regular expressions to search within the reads for flanking sequences on the left (GCTCATGACTTGAATCC spacer sequence) and the right (GACCTGAACCTTGTAGTGT; right linker sequence) of the barcode (Fig. 1B), while also allowing for 18 random nucleotides that represent a candidate barcode. The putative barcode sequence is then mapped against the reference barcode library and increases the count for the matched strain. barseq outputs a tab-delimited table with the barcode/strain counts for each of the samples analyzed.
intake 3 ml fresh LBS and grown to mid-log phase (OD_{600} of 0.2). Equivalent ODs of cells from each strain [volume to mix calculated as volume (in microliters) = (1.25/OD_{600}) x 50] were mixed, resulting in a multiplexed population with each strain present at a 1-to-1 ratio. A sample from this input library was harvested by collecting cells from 700 μl by centrifugation and storing the cell pellet at -80°C. The input library was then used to inoculate hatching _Euprymna scolopes_ squids at 5 x 10^7 to 9 x 10^7 CFU/ml for 3 h in FSIO (filter-sterilized Instant Ocean) as previously described (20). Squid samples (n = 24, per replicate) were harvested at 48 h postinoculation and surface sterilized by storing at 20°C prior to DNA extraction. Genomic DNA from the cell pellets was extracted and purified using the Qiagen DNeasy blood and tissue kit (Qiagen; catalog no. 69506) following the Gram-negative bacteria protocol and quantified using a NanoDrop spectrophotometer (Thermo Fisher Scientific). The barcoded scars were amplified together with dual-index Illumina sequencing primers (55). The reaction mixtures contained 50 ng of each homogenate was mixed in a 50-ml conical tube, diluted 1:20 in 70% IO (Instant Ocean), and 50 μl plated onto LBS plates in triplicate. After a 17-h overnight incubation at 25°C, the bacterial colonies from each plate were scraped with a sterile cell scraper into 1 ml of 70% IO and collected by centrifugation. Cell pellets were stored at -20°C prior to DNA extraction.

Genomic DNA from the cell pellets was extracted and purified using the Qiagen DNeasy blood and tissue kit (Qiagen; catalog no. 69506) following the Gram-negative bacteria protocol and quantified using a NanoDrop spectrophotometer (Thermo Fisher Scientific). The barcoded scars were amplified together with dual-index Illumina sequencing primers (55). The reaction mixtures contained 50 ng of gDNA, 200 nM each oligonucleotide (Table S2), 1 x Phusion Hot Start Flex Master Mix (NEB; catalog no. M0536L), and H2O up to a total volume of 50 μl. PCR conditions were 98°C for 30 s, 20 cycles with each cycle consisting of 98°C for 10 s, 60°C for 10 s, and 72°C for 10 s, with a final extension step at 72°C for 5 min. PCR products were visualized using a 2% agarose gel to confirm the dual-indexed amplicon of 231 bp and purified using a Qiagen PCR purification kit (Qiagen; catalog no. 28106). Purified PCR products were quantified using a Qubit 3 fluorometer (Life Technologies), pooled in equimolar amounts, and diluted to 4 nM. The pool was sequenced on an Illumina MiSeq using the 2 x 250 bp v2 kit with a 10% PhiX control following the manufacturer’s protocol (Illumina, Inc., San Diego, CA) and using custom primers developed from reference 55. The sequencing data were processed using the barseq python package to obtain strain counts per sample, and mutants that were in the input library but still being validated were removed from the data set. The relative frequency (RF) for each strain in a sample was calculated, normalized to the RF in the input library and the average RF in the sample, and the competitive index (CI) was then calculated using the formula: CI = log_{10} (RF_{mutant}/RF_{WT,Input} / RF_{mutant} / RF_{WT,Sample}).

**SUPPLEMENTAL MATERIAL**

Supplemental material is available online only.

**TABLE S1**, **XLSX file**, 0.01 MB.

**TABLE S2**, **XLSX file**, 0.02 MB.

**TABLE S3**, **XLSX file**, 0.01 MB.

**ACKNOWLEDGMENTS**

We thank Karen L. Visick for plasmid pKV496 and members of the Mandel lab for comments on the mutagenesis protocol and manuscript. This work was funded by NIGMS grant R33 GM119627 to M.J.M., an American Society for Microbiology Undergraduate Research Fellowship to E.F.B., and the McNair Scholars Program (E.F.B.). G.S. acknowledges support from the USDA National Institute of Food and Agriculture (NIFA), Agricultural and Food Research Initiative (AFRI) Foundation grant 2020-67015-31576, and USDA NIFA HATCH grant WIS02007.

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