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RESEARCH ARTICLE

Natural Strain Variation Reveals Diverse Biofilm Regulation in Squid-Colonizing *Vibrio fischeri*

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ABSTRACT The mutualistic symbiont *Vibrio fischeri* builds a symbiotic biofilm during colonization of squid hosts. Regulation of the exopolysaccharide component, termed Syp, has been examined in strain ES114, where production is controlled by a phosphorelay that includes the inner membrane hybrid histidine kinase RscS. Most strains that lack RscS or encode divergent RscS proteins cannot colonize a squid host unless RscS from a squid symbiont is heterologously expressed. In this study, we examine *V. fischeri* isolates worldwide to understand the landscape of biofilm regulation during beneficial colonization. We provide a detailed study of three distinct evolutionary groups of *V. fischeri* and find that while the RscS-Syp biofilm pathway is required in one of the groups, two other groups of squid symbionts require Syp independent of RscS. Mediterranean squid symbionts, including *V. fischeri* SR5, colonize without an RscS homolog encoded by their genome. Additionally, group A *V. fischeri* strains, which form a tightly related clade of Hawaii isolates, have a frameshift in *rscS* and do not require the gene for squid colonization or competitive fitness. These same strains have a frameshift in *sypE*, and we provide evidence that this group A *sypE* allele leads to an upregulation in biofilm activity. Thus, this work describes the central importance of Syp biofilm in colonization of diverse isolates and demonstrates that significant evolutionary transitions correspond to regulatory changes in the *syp* pathway.

IMPORTANCE Biofilms are surface-associated, matrix-encased bacterial aggregates that exhibit enhanced protection to antimicrobial agents. Previous work has established the importance of biofilm formation by a strain of luminous *Vibrio fischeri* bacteria as the bacteria colonize their host, the Hawaiian bobtail squid. In this study, expansion of this work to many natural isolates revealed that biofilm genes are universally required, yet there has been a shuffling of the regulators of those genes. This work provides evidence that even when bacterial behaviors are conserved, dynamic regulation of those behaviors can underlie evolution of the host colonization phenotype. Furthermore, this work emphasizes the importance of investigating natural diversity as we seek to understand molecular mechanisms in bacteria.

KEYWORDS *Aliivibrio fischeri*, BinK, RscS, *Vibrio fischeri*, biofilm, phosphorelay

A fundamental question in studying host-associated bacterial communities is understanding how specific microbial taxa assemble reproducibly in their host. Key insights into these processes were first obtained by studying plant-associated microbes, and the discovery and characterization of Nod factors in rhizobia were valuable to understanding how partner choice between microbe and host could be mediated at the molecular level (1, 2). There are complex communities in humans and other vertebrate animals, yet metagenomic and imaging analyses of these communities have

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revealed striking reproducibility in the taxa present and in the spatial arrangement of those taxa (3–5). Invertebrate animal microbiomes provide appealing systems in which to study microbiome assembly in an animal host: the number of taxa are relatively small, and examination and manipulation of these organisms have yielded abundant information about processes underlying host colonization (6). For this work, we focused on the binary symbiosis between *Vibrio fischeri* and bobtail squids, including the Hawaiian bobtail squid, *Euprymna scolopes*. Bobtail squid have an organ for the symbiont termed the light organ, and passage of specific molecules between the newly hatched host and the symbiont leads to light organ colonization specifically by planktonic *V. fischeri* and not by other bacteria (7–9). The colonization process involves initiation, accommodation, and persistence steps, resulting in light organ crypt colonization by *V. fischeri*. Upon colonization of the squid light organ, bacteria accumulate to high density and produce light. The bacterial light is modulated by the host to camouflage the moonlight shadow produced by the nighttime foraging squid in a cloaking process termed counterillumination (10, 11). A diel rhythm leads to a daily clearing of 90 to 95% of the bacteria from the crypts and regrowth of the remaining cells (12). However, the initial colonization process, including biofilm-based aggregation on the host ciliated appendages, occurs only in newly hatched squid. This work examines regulation of biofilm formation in diverse squid-colonizing *V. fischeri* strains.

In the well-studied *V. fischeri* strain ES114, biofilm formation is required to gain entry into the squid host. RscS is a hybrid histidine kinase that regulates *V. fischeri* biofilm formation through a phosphorelay involving the hybrid histidine kinase SypF and the response regulator and σ^{54}-dependent activator SypG (13–15). This pathway regulates transcription of the symbiosis polysaccharide (Syp) locus, which encodes regulatory proteins (SypA, SypE, SypF, and SypG), glycosyltransferases, factors involved in polysaccharide export, and other biofilm-associated factors (14, 16). The products of the ES114 *syp* locus direct synthesis and export of a biofilm exopolysaccharide that is critical for colonization. Additional pathways have been identified to influence biofilm regulation in ES114, including the SypE-SypA pathway, and inhibition of biofilm formation by BinK and HahK (17–21).

V. fischeri biofilm regulation is connected to host colonization specificity. In the Pacific Ocean, the presence of *rscS* DNA is strongly correlated to the ability to colonize squid (22). As one example, while the fish symbiont MJ11 carries a complete *syp* locus, it lacks RscS and does not robustly colonize squid. Heterologous expression of ES114 RscS in MJ11 activates the biofilm pathway and is sufficient to enable squid colonization (22). Similarly, addition of ES114 RscS to *mjapo*.8.1, a fish symbiont that encodes a divergent RscS that is not functional for squid colonization, allows the strain to colonize squid (22). RscS has also been shown to be necessary for squid colonization in certain strains. In addition to ES114, interruption of *rscS* in *V. fischeri* strains KB1A97 and MJ12 renders them unable to colonize squid. Previous phylogenetic analysis revealed that genomes of ancestral *V. fischeri* strains do not carry *rscS* and that it was acquired once during the organism's evolution, likely allowing for an expansion in host range. From this analysis, it was concluded that strains with *rscS* can colonize squid, with the only exception being the fish symbionts that harbor the divergent RscS, including *mjapo*.8.1 (22).

There are similar *Vibrio*-squid associations worldwide, yet only *V. fischeri* and the closely related *Vibrio logei* have been isolated from light organs (23–26). Our 2009 study revealed that although most symbionts have *rscS* DNA, there are Mediterranean *V. fischeri* strains (e.g., SR5) that do not have *rscS* yet can colonize squid (22, 24, 27). This unexpected finding prompted the current work to examine whether strains such as SR5 colonize with the known biofilm pathway or with a novel pathway. Here, we show that all *V. fischeri* strains tested require the *syp* locus to colonize a squid host, and we identify two groups of isolates that colonize with novel regulation. Given the exquisite specificity by which *V. fischeri* bacteria colonize squid hosts, this work reinforces the importance of biofilm formation and reveals different regulatory modes across the evolutionary tree.

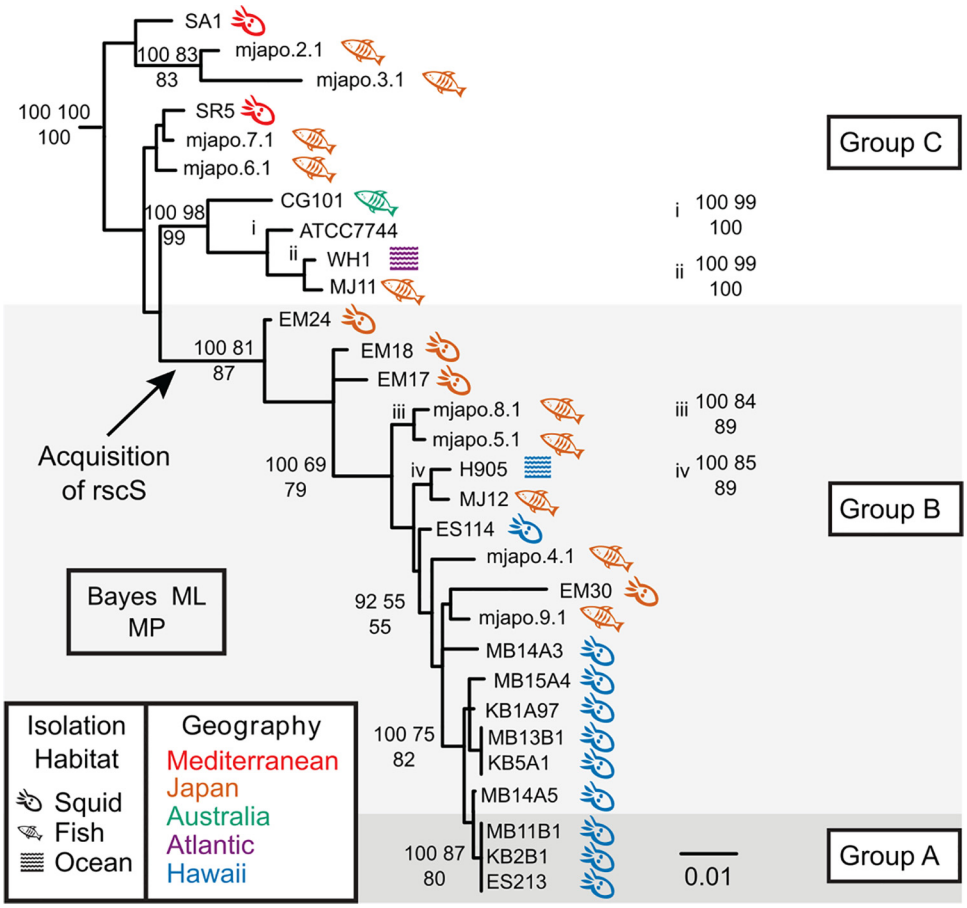

FIG 1 Bayesian phylogram (50% majority-rule consensus) inferred with a SYM+I+Γ model of evolution for the concatenated gene fragments *recA*, *mdh*, and *katA*. In this reconstruction, the root connected to a clade containing the four non-*V. fischeri* outgroup taxa. Statistical support is represented at nodes by the following three numbers: upper left, Bayesian posterior probability (of approximately 37,500 nondiscarded samples) multiplied by 100; upper right, percentage of 1,000 bootstrap maximum likelihood pseudoreplicates; bottom, percentage of 1,000 bootstrap maximum parsimony pseudoreplicates. Statistical support values are listed only at nodes where more than 2 methods generated support values of ≥50%. Strains sharing identical sequences for a given locus fragment are listed next to a vertical bar at a leaf; because of a lack of space, some support values have been listed immediately to the right of their associated nodes and are marked with lowercase roman numerals in the phylogram. The isolation habitat and geography of each strain are indicated by symbol and color, respectively. The scale bar represents 0.01 substitution/site.

RESULTS

Most *V. fischeri* strains synthesize biofilm in response to RscS overexpression. Biofilm formation is required for squid colonization, and overexpression of the biofilm regulator RscS in strain ES114 stimulates a colony biofilm on agar plates (15). Our previous work demonstrated that *V. fischeri* strain MJ11 synthesizes a colony biofilm under similar inducing conditions, which is notable because MJ11 does not encode RscS in its chromosome (22). While the ancestral strain MJ11 did not encode RscS, it had what seemed to be an intact *syp* locus, and overexpression of the heterologous RscS from ES114 was sufficient to enable robust squid colonization (22). We examined a phylogenetic tree of *V. fischeri* isolates (Fig. 1), and in this study we expand our analysis of RscS-Syp biofilm regulation in a wider group of *V. fischeri* strains.

Initially, we asked whether responsiveness to RscS overexpression would yield a similar colony biofilm in this diverse group of strains. We took the same approach as our previous study and introduced plasmid pKG11, which overexpressed ES114 RscS, into strains across the evolutionary tree (22, 28). We observed that almost all strains tested, including those that lack *rscS*, were responsive to overexpression of ES114 RscS (Fig. 2). The morphology of the colony biofilms differed across isolates, but in most cases colony

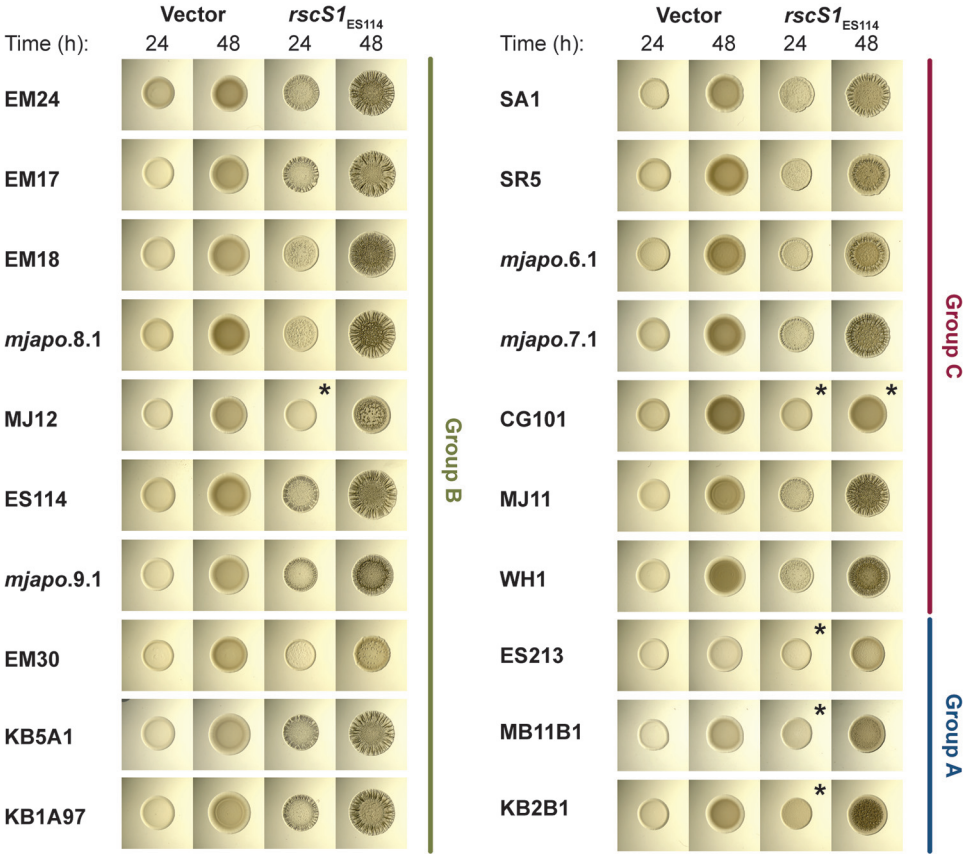

FIG 2 Most *V. fischeri* strains tested form colony biofilm in response to RscS overexpression. Shown are spot assays of the indicated *V. fischeri* strains carrying pKV69 (vector) or pKG11 (*rscS1*; overexpressing ES114 *rscS*) after 24 and 48 h. Strains are MJM1268, MJM1269, MJM1246, MJM1247, MJM1266, MJM1267, MJM1219, MJM1221, MJM1238, MJM1239, MJM1104, MJM1106, MJM1276, MJM1277, MJM1270, MJM1271, MJM1258, MJM1259, MJM1254, MJM1255, MJM1242, MJM1243, MJM1240, MJM1241, MJM1272, MJM1273, MJM1274, MJM1275, MJM1278, MJM1279, MJM1109, MJM1111, MJM1280, MJM1281, MJM1260, MJM1261, MJM1244, MJM1245, MJM1256, and MJM1257. Different phenotypes were observed in the isolates examined. In most cases we observed wrinkled colonies, but in some cases we observed only a subtle pocked pattern (EM30), and in other cases we did not observe any change in colony morphology compared to that of the vector control (noted by an asterisk).

biofilm was evident at 24 h and prominent at 48 h. All of the strains exhibited some wrinkled colony morphology at 48 h with the exception of CG101, which was isolated from the pineapplefish *Cleidopus gloriamaris* (25). These results demonstrated that most *V. fischeri* strains can produce biofilm in response to RscS overexpression, and this includes strains that presumably have not encountered *rscS* in their evolutionary history.

One unexpected observation was that there was a subset of *rscS*-encoding strains that were reproducibly delayed in their colony biofilm and had only a mild wrinkled colony phenotype at 48 h (strains MB11B1, ES213, and KB2B1) (Fig. 2). We considered whether this was due to differential growth of the strains, but resuspension of spots and dilution plating to determine CFU/spot demonstrated no significant growth difference between these strains and ES114 under these conditions. The strains are closely related (Fig. 1), and a previous study had noted that this group shared a number of phenotypic characteristics, e.g., reduced motility in soft agar (29). Those authors termed this tight clade "group A" *V. fischeri* (30). Our results shown in Fig. 2 argue that group A strains do not respond to RscS in the same manner as other *V. fischeri* strains, which prompted us to investigate the evolution of the RscS-Syp signaling pathway. We have maintained the group A nomenclature here, and furthermore we introduce the nomenclature of group B (a paraphyletic group of strains that contain *rscS*; this group includes the common ancestor of all *rscS*-containing strains) and group C (a paraphyl-

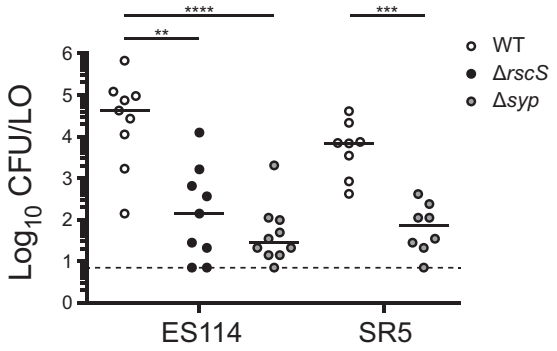

FIG 3 Squid colonization in group C strain SR5, which does not encode RscS, is dependent on the *syp* polysaccharide locus. Single-strain colonization experiments were conducted, and circles represent individual animals. The limit of detection for this assay, represented by the dashed line, is 7 CFU/light organ (LO), and the horizontal bars represent the median for each set. Hatchling squid were inoculated with 1.5×10^3 to 3.2×10^3 CFU/ml bacteria, washed at 3 h and 24 h, and assayed at 48 h. Strains are MJM1100, MJM3010, MJM3062, MJM1125, and MJM3501. Statistical comparisons were done with the Mann-Whitney test. **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$.

etic group of strains that contains the common ancestor of all *V. fischeri* strains; these strains do not contain *rscS*), as shown in Fig. 1.

Colonization of *E. scolopes* by ancestral group C squid isolates is independent of RscS and dependent on Syp. Group C strains generally cannot colonize squid, yet there are Mediterranean squid isolates that appear in this group (Fig. 1) (22). The best-studied of these strains, SR5, was isolated from *Sepiola robusta*, is highly luminous, and can colonize the Hawaiian bobtail squid *E. scolopes* (24). Nonetheless, this strain lacks *rscS* (27). We first asked whether the strain can colonize under our laboratory conditions, and we confirmed that it colonizes robustly, consistent with the result previously published by Fidopiastis et al. (24) (Fig. 3). We next asked whether it uses the Syp biofilm to colonize. To address this question, we deleted the 18-kb *syp* locus (i.e., *sypA* through *sypR*) in strains SR5 and ES114. Deletion of *rscS* or the *syp* locus in ES114 led to a substantial defect in colonization, consistent with a known role for these factors (Fig. 3). Similarly, deletion of the *syp* locus in SR5, a strain that does not contain *rscS*, led to a dramatic reduction in colonization (Fig. 3). Therefore, even though strain SR5 does not contain *rscS*, it can colonize squid, and it requires the *syp* locus to colonize normally.

RscS is dispensable for colonization in group A strains. We noted in the wrinkled colony biofilm assays shown in Fig. 2 that group A strains exhibited a more modest response to overexpression of RscS. Sequencing of the native *rscS* gene in these strains revealed a predicted −1 frameshift (ΔA1141) between the PAS domain and the histidine kinase CA domain. Whereas ES114 and other group B strains have nine adenines at this position, the group A strains have eight, leading to a frameshift and then truncation at an amber stop codon, raising the possibility that group A strains have a divergent biofilm signaling pathway (Fig. 4A). Given the importance of RscS in the group B strains, including ES114, we considered the possibility that this apparent frameshift encoded a functional protein, either through ribosomal frameshifting or through the production of two polypeptides that together provided RscS function; there is precedent for both of these concepts in the literature (31, 32). We first introduced a comparable frameshift into a plasmid-borne overexpression allele of ES114 *rscS*, and this allele did not function with the deletion of the single adenine (Fig. 4B). This result suggested to us that the frameshift in the group A strains are not functional. Therefore, we proceeded to delete *rscS* in two group A strains (MB11B1 and ES213) and two group B strains (ES114 and MB15A4). The group B strains required RscS for squid colonization (Fig. 5A). However, the group A strains exhibited no deficit in the absence of *rscS* (Fig. 5A). We next attempted a more sensitive assay in which a group A strain was competed against MB15A4. Previous studies have demonstrated that in many cases group A strains outcompete group B strains (30, 33). We competed group

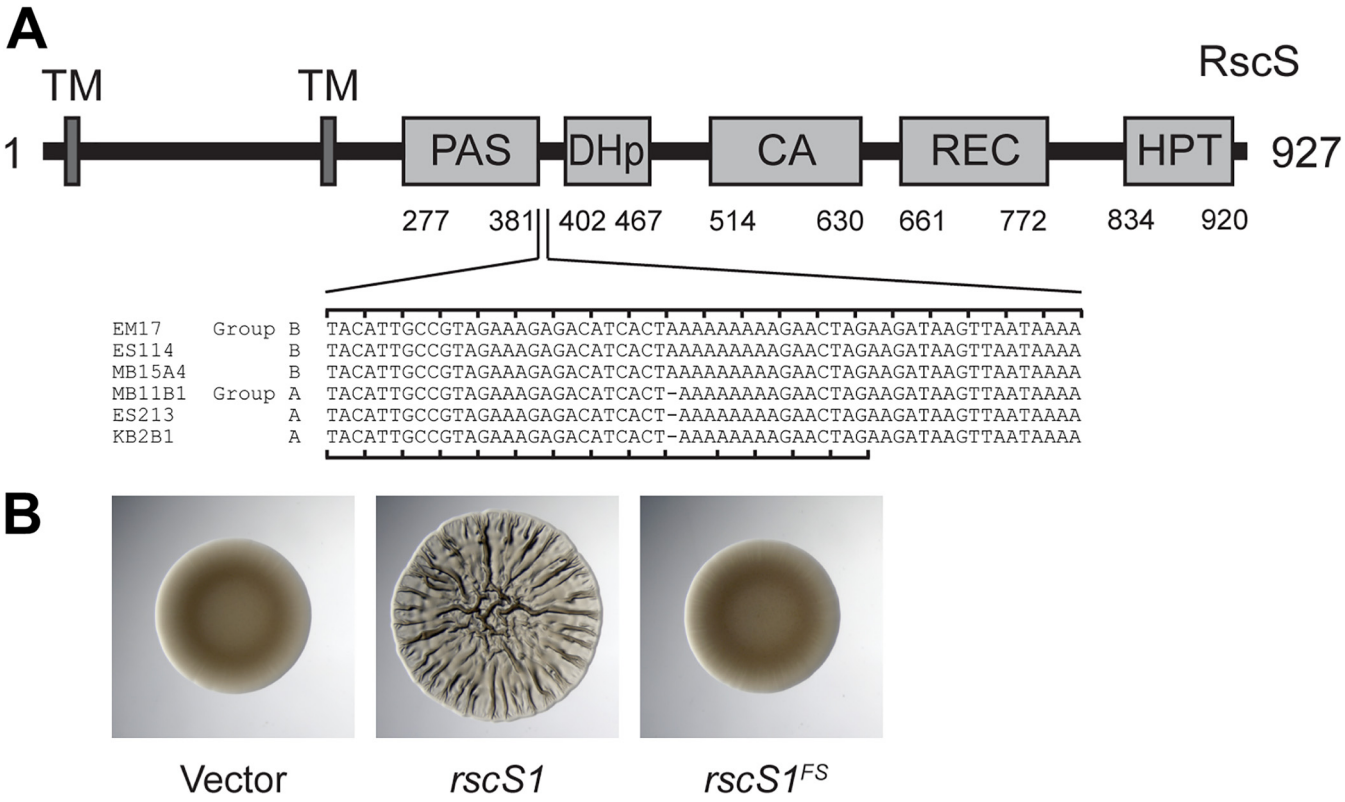

FIG 4 Group A strains have a frameshift in *rscS*. (A) ES114 RscS protein domains. Nucleotides 1114 to 1173 in ES114 RscS (GenBank accession no. AF319618) and their homologous sequences in the other group B and group A strains are listed. The −1 frameshift is present in the group A *rscS* alleles. The ES114 reading frame is noted on the top of the alignment and the group A reading frame on the bottom, which is predicted to end at the amber stop codon. (B) Deletion of nucleotide A1141 in ES114 to mimic this frameshift in pKG11 renders it unable to induce a colony biofilm in a spot assay at 48 h. Strains are MJM1104, MJM1106, and MJM2226.

A strain MB11B1 against group B strain MB15A4 and observed a significant competitive advantage for the group A strain, as was observed previously (30). Deletion of *rscS* in the group A strain did not affect competitive fitness, demonstrating that MB11B1 can outcompete a group B strain even if MB11B1 lacks RscS (Fig. 5B).

The *syp* locus is broadly required for squid colonization. Given that group A strains seemed to represent a tight phylogenetic group in which RscS was not required for colonization or competitive fitness, we next asked whether this group requires the Syp biofilm for colonization. We proceeded to delete the entire *syp* locus in two group A and two group B strains and to conduct single-strain colonization analysis. In each strain assayed, the *syp* locus was required for full colonization, and we observed a 2- to 4-log-unit reduction in CFU per animal in the absence of the *syp* genes, pointing to a critical role for Syp biofilm in these strains (Fig. 6). In group A strains in particular, no colonization was detected in the absence of the *syp* locus.

Group A strains carry an alternate allele of SypE. It seemed curious to us that group A strains do not encode a functional RscS and do not require *rscS* for colonization, yet in many cases group A strains can outcompete group B strains (e.g., MB11B1 in Fig. 5B) (30, 33). We reasoned that if the Syp biofilm had a different regulatory architecture in group A strains, e.g., constitutively activated or activated by a different regulatory protein, then this could explain the Syp regulation independent of RscS. Genome sequencing of SR5 and MB11B1 did not identify a unique histidine kinase that was likely to directly substitute for RscS (27, 33). Given that the *syp* locus encodes biofilm regulatory proteins, we examined *syp* conservation. We used TBLASTN with the ES114 Syp proteins as queries to determine amino acid conservation in the other *V. fischeri* group A strain MB11B1, group C strain SR5, and the *Vibrio vulnificus* type strain

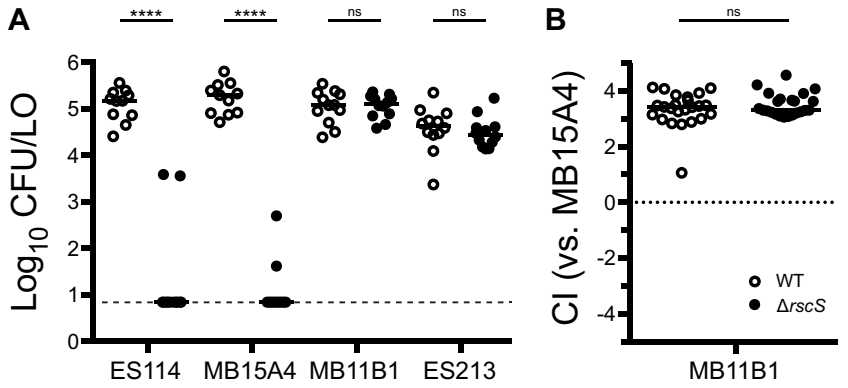

FIG 5 Group A strains MB11B1 and ES213 do not require RscS for squid colonization. Wild-type (WT) and Δ*rscS* derivatives of the indicated strains were assayed in a single-strain colonization assay (A) and competitive colonization against group B strain MB15A4 (B). Hatchling squid were inoculated at 3.5×10^3 to 14×10^3 CFU/ml bacteria, washed at 3 h and 24 h, and assayed at 48 h. Each dot represents an individual squid. (A) Strains are MJM1100, MJM3010, MJM2114, MJM3042, MJM1130, MJM3046, MJM1117, and MJM3017. The limit of detection is represented by the dashed line, and the horizontal bars represent the median for each set. In both panels, open dots are the wild type and filled dots are the Δ*rscS* strain. (B) The competitive index (CI) is defined in Materials and Methods and is shown on a $\log_{10}$ scale. Strains are MJM1130 and MJM3046, each competed against MJM2114. Values greater than 1 indicate more MB11B1. Statistical comparisons were made with the Mann-Whitney test. ns, not significant; ****, $P < 0.0001$.

ATCC 27562 (34, 35). As shown in Fig. 7, ES114 SypE, a response regulator and serine kinase/phosphatase that is a negative regulator of the Syp biofilm (17, 36), exhibited the lowest level of conservation among *syp* locus products. *V. vulnificus* does not encode a SypE ortholog (37), as the syntenic (but not homologous) RbdE gene encodes a predicted ABC transporter substrate-binding protein. The closest hit for SypE was AOT11_RS12130 (9% identity), compared to 7% identity for RbdE. Due to the reduced conservation at both the strain and species levels, we analyzed *V. fischeri* MB11B1 SypE in greater detail. Examination of the *sypE* coding sequence revealed an apparent −1 frameshift mutation in which position 33 (guanine in ES114 and adenine in other group B and C strains examined) is absent from group A strains (Fig. 7B). We therefore considered the hypothesis that SypE is nonfunctional in group A, and that these strains can colonize because they lack a functional copy of this negative regulator that is itself regulated by RscS.

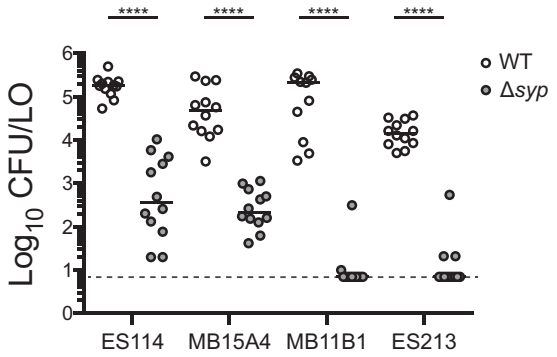

FIG 6 Group B and group A strains require the *syp* locus for robust squid colonization. The wild type (WT) and Δ*syp* derivatives of the indicated strains were assayed in a single-strain colonization assay. Hatchling squid were inoculated with 6.7×10^2 to 32×10^2 CFU/ml bacteria (ES114 and MB15A4 backgrounds) or 5.2×10^2 to 8.9×10^2 CFU/ml bacteria (MB11B1 and ES213 backgrounds), washed at 3 h and 24 h, and assayed at 48 h. Each dot represents an individual squid. The limit of detection is represented by the dashed line, and the bars represent the median for each set. Strains are MJM1100, MJM3062, MJM2114, MJM3071, MJM1130, MJM3065, MJM1117, and MJM3068. Statistical comparisons were done with the Mann-Whitney test. ****, $P < 0.0001$.

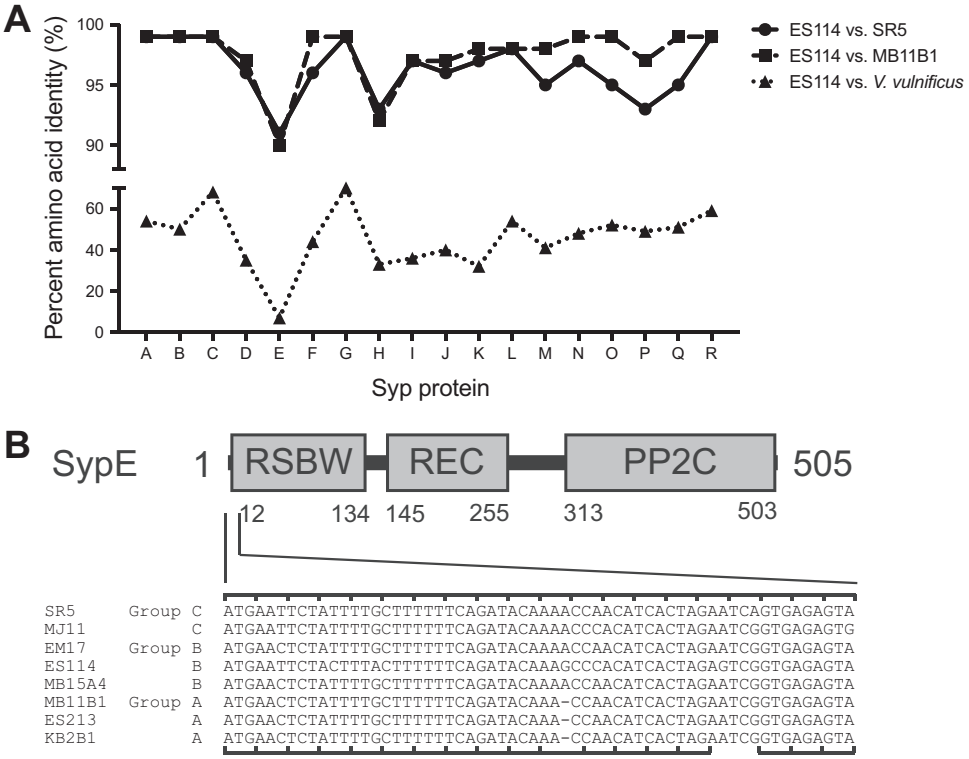

FIG 7 Group A strains have a frameshift in *sypE*. (A) Amino acid identity in the Syp locus. Results show the identity from TBLASTN query using the *V. fischeri* ES114 protein sequences as queries against genes in the homologous loci in *V. fischeri* strains or *V. vulnificus* ATCC 27562. The identity for SypE against *V. vulnificus* is plotted for the syntenous RbdE, although this is not the highest TBLASTN hit, as described in the text. (B) ES114 SypE protein domains. Nucleotides 1 to 60 in ES114 *sypE* and their homologous sequences in the other group C, B, and A strains are listed. A −1 frameshift is present in the group A *sypE* alleles. The ES114 reading frame is noted on the top of the alignment and the group A reading frame on the bottom, which is predicted to end at the amber stop codon. A possible GTG start codon for the resumption of translation in the ES114 reading frame is present at the position corresponding to the 18th codon in ES114 *sypE*.

To test this hypothesis, we relied on knowledge of the biofilm regulatory pathway from ES114, in which overexpression of SypG produces a wrinkled colony phenotype, but only in strains lacking SypE activity (38, 39). Therefore, we introduced the SypG-overexpressing plasmid pEAH73 into strains as a measure of whether the SypE pathway was intact. In the ES114 strain background, we observed cohesive wrinkled colony formation at 48 h in an ES114 Δ*sypE* strain but not in the wild-type parent (Fig. 8A). If the *sypE* frameshift observed in MB11B1 led to a loss of function, then introduction of that frameshift into ES114 would lead to a strain that is equivalent to the Δ*sypE* strain. We constructed this strain, and upon SypG overexpression we observed wrinkled colony formation. Surprisingly, the biofilm phenotype was observed earlier (i.e., by 24 h) and leads to more defined colony biofilm architecture at 48 h. While the lack of SypE leads to increased and more rapid biofilm formation, in this assay we observed an even greater increase as a result of the frameshift in *sypE* (Fig. 8A).

We proceeded to conduct a similar assay in the MB11B1 strain background. The colony biofilm phenotypes were muted compared to that in the ES114 background, but the pattern observed is the same. Strains lacking the additional nucleotide at position 33 (i.e., the native MB11B1 allele) exhibited the strongest cohesion, whereas strains with the nucleotide to mimic ES114 *sypE* [i.e., added back in MB11B1 *sypE*(nt::33G)] were not cohesive (Fig. 8B). These results argue that a novel allele of *sypE* is found in group A strains, and this allele results in more substantial biofilm formation than it does in a Δ*sypE* strain.

Our finding that the MB11B1 *sypE* allele promotes biofilm formation bolstered the model that this allele contributes to the ability of MB11B1 to colonize squid indepen-

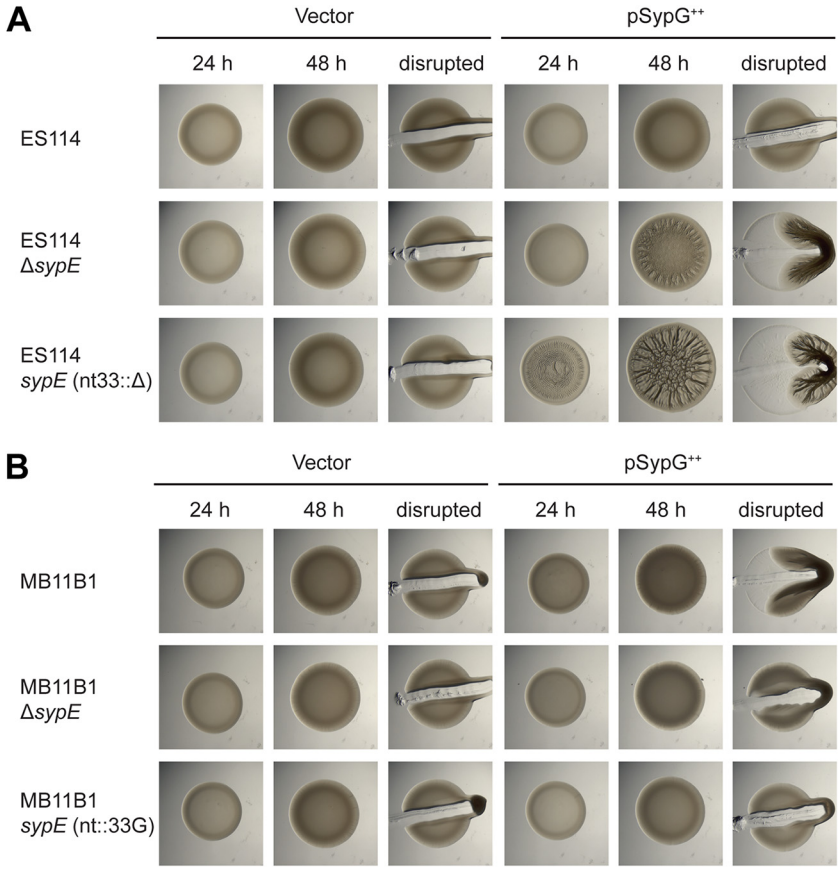

FIG 8 MB11B1 *sypE* frameshift leads to an enhanced biofilm phenotype upon SypG overexpression. Shown are spot assays of strains carrying the pKV69 vector or pEAH73 SypG overexpression plasmid. (A) ES114 strain background. Strains lacking SypE produce a wrinkled colony phenotype upon SypG overexpression. Deletion of nucleotide 33 in *sypE* to mimic the group A frameshift led to earlier wrinkling and a more pronounced colony biofilm at 48 h. Strains are MJM1104, MJM3455, MJM3418, MJM3419, MJM3364, and MJM3365. (B) Group A strain MB11B1, which naturally carries a −1 frameshift in *sypE*, exhibits a cohesive phenotype at 48 h with overexpression of SypG. Deletion of *sypE* reduces this phenotype, and repairing the frameshift by addition of a guanosine at nucleotide 33 further reduces the cohesiveness of the spot. Strains are MJM3370, MJM3371, MJM3411, MJM3412, MJM3398, and MJM3399.

dent of RscS. To test this model, we introduced the frameshift into ES114 or corrected the frameshift in MB11B1. We then conducted single-strain colonization assays, and in each case the *sypE* allele alone was not sufficient to alter the overall colonization behavior of the strain (Fig. 9). Therefore, these data suggest that the frameshift in the MB11B1 *sypE* is not sufficient to explain its ability to colonize independently of RscS, and therefore other regions of SypE and/or other loci in the MB11B1 genome contribute to its ability to colonize independently of RscS.

BinK is active in group A, B, and C strains. We recently described the histidine kinase BinK, which negatively regulates *syp* transcription and Syp biofilm formation (18). In ES114, overexpression of BinK impairs the ability of *V. fischeri* to colonize. We therefore reasoned that if BinK could function in group A strains and acted similarly to repress Syp biofilm, then overexpression of BinK would reduce colonization of these strains. We introduced the pBinK plasmid (i.e., ES114 *binK* [18]) and asked whether multicopy *binK* would affect colonization. In strain MB11B1, BinK overexpression led to a dramatic reduction in colonization (Fig. 10A). Therefore, there is a clear effect for BinK overexpression on the colonization of the group A strain MB11B1.

We attempted to ask the same question for group C strain SR5, but the pES213-origin plasmids were not retained during squid colonization. Therefore, we instead asked whether deletion of BinK, a negative regulator of ES114 colonization, has a

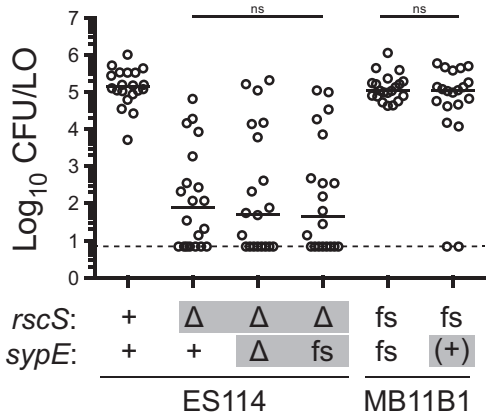

FIG 9 *sypE* −1 frameshift allele is not sufficient to affect colonization ability. The indicated strains were assayed in a single-strain colonization assay. Gray boxes denote alleles distinct from their wild-type background. Frameshift "fs" refers to alleles, relative to an ES114 reference, that lack *rscS* nucleotide A1141 or that lack *sypE* nucleotide G33. The wild-type MB11B1 strain contains natural frameshifts in these loci, and the ES114 nt33::ΔG allele was constructed. Addition back of the nucleotide in MB11B1 *sypE* is denoted (+). Hatchling squid were inoculated with 6.8×10^2 to 8.4×10^2 CFU/ml bacteria (MB11B1 background) or 4.0×10^3 to 5.4×10^3 CFU/ml bacteria (ES114 background), washed at 3 h and 24 h, and assayed at 48 h. Each dot represents an individual squid. The limit of detection is represented by the dashed line, and the bars represent the median for each set. Strains are MJM1100, MJM3010, MJM4323, MJM3394, MJM1130, and MJM3397. Statistical comparisons were done with the Mann-Whitney test. ns, not significant.

comparable effect in SR5 (18). We deleted *binK* and observed a 2.4-fold competitive advantage during squid competition (Fig. 10B), arguing that BinK in this group C strain is active and performs an inhibitory function similar to that in ES114.

We next examined the colony biofilm phenotype for strains lacking BinK. The MB11B1 Δ*binK* strain exhibited a mild colony biofilm phenotype at 48 h, as evidenced by the cohesiveness of the spot when disrupted with a toothpick (Fig. 10C). The colonies also exhibited an opaque phenotype. In a minority of experimental replicates, wrinkled colony morphology was evident at 48 h, but in all samples wrinkled colony morphology was visible at 7 days (data not shown). The SR5 Δ*binK* strain also exhibited slightly elevated biofilm morphology at 48 h, although the cells were not as cohesive as those of the MB11B1 Δ*binK* strain (Fig. 10C). Together, the results shown in Fig. 10 argue that BinK, a factor that has been characterized as a negative regulator of Syp biofilm, plays similar roles in group A and group C strains and has a widely conserved function across the *V. fischeri* evolutionary tree.

DISCUSSION

This study examines regulation of a beneficial biofilm that is critical to host colonization specificity in *V. fischeri*. The Syp biofilm was discovered fourteen years ago and has been characterized extensively for its role in facilitating squid colonization by *V. fischeri*. This work establishes that the *syp* locus is required broadly across squid symbionts, and it uncovers three groups of *V. fischeri* that use different regulatory programs upstream of the *syp* locus. A simplified phylogenetic tree showing key features of squid symbionts in these three groups is shown in Fig. 11.

There are three nested evolutionary groups of *V. fischeri* that have been described separately in the literature, and here we formalize the nomenclature of groups A, B, and C. Group A is a monophyletic group, as are groups AB and ABC (Fig. 1). This work provides evidence that squid symbionts in each group have a distinct biofilm regulatory architecture. Most *V. fischeri* isolates that have been examined from the ancestral group C cannot colonize squid; however, those that can colonize do so without the canonical biofilm regulator RscS. We show that the known targets of RscS regulation, genes in the *syp* biofilm locus, are nonetheless required for squid colonization by this group. Group B strains include the well-characterized ES114 strain, which requires RscS

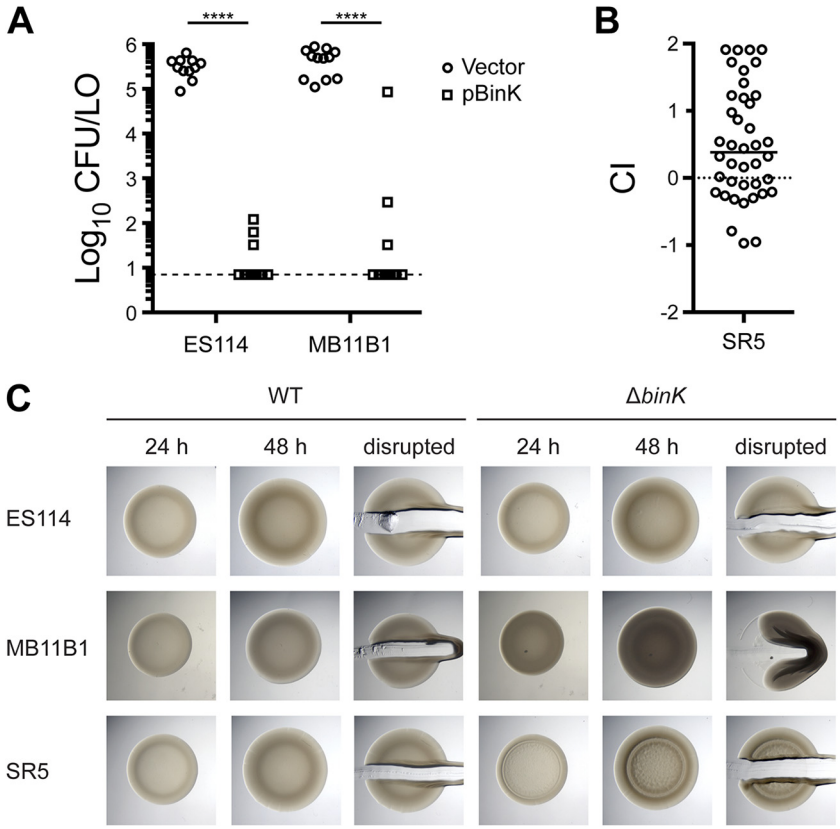

FIG 10 BinK is active in groups A, B, and C. (A) Overexpression of pBinK inhibits colonization in group A strain MB11B1. Hatchling squid were inoculated with 3.6×10^3 to 6.8×10^3 CFU/ml bacteria, washed at 3 h and 24 h, and assayed at 48 h. Each dot represents an individual squid. The limit of detection is represented by the dashed line, and the bars represent the median of each set. The vector control is pVSV104. Strains are MJM1782, MJM2386, MJM2997, and MJM2998. (B) Deletion of *binK* confers a colonization defect in group C strain SR5. Strains are MJM1125 and MJM3571. The mean inoculum was 7.2×10^3 CFU/ml, and the median competitive index (CI) was 0.38 (i.e., 2.4-fold advantage for the mutant). (C) Deletion of the native *binK* in MB11B1 yielded opaque and cohesive spots, which are stronger phenotypes than we observe in ES114. Strains are MJM1100, MJM2251, MJM1130, MJM3084, MJM2997, and MJM2998. Statistical comparisons were done with the Mann-Whitney test. ****, $P < 0.0001$.

and the *syp* locus to colonize squid. Group A strains differ phenotypically and behaviorally from the sister group B strains (30), and we demonstrate that these strains have altered biofilm regulation. Group A strains have a frameshift in *rscS* that renders it nonfunctional and a 1-bp deletion in *sypE*, and we provide evidence that the *sypE* allele promotes biofilm development in the absence of RscS. Additionally, we note that the

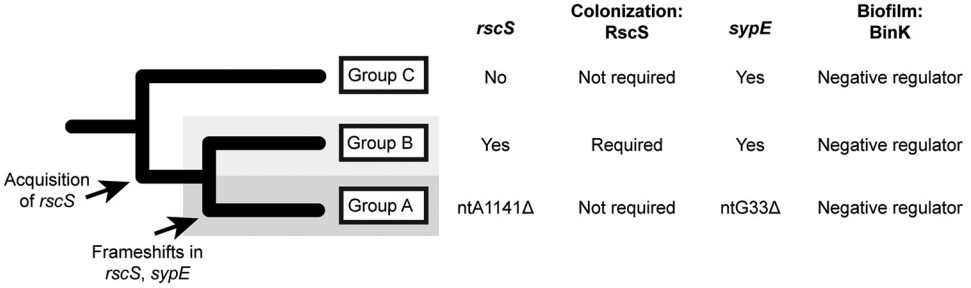

FIG 11 Summary model of distinct modes of biofilm formation in squid-colonizing *V. fischeri*. The phylogenetic tree is simplified from Fig. 1 and illustrates key features of squid symbionts in the three groups. Shown are divergent aspects (RscS and SypE) and conserved regulation (BinK). In all groups, the *syp* exopolysaccharide locus is required for squid colonization.

sypE frameshift is not present in SR5, arguing for distinct modes of biofilm regulation in groups A, B, and C.

At the same time, this study provides evidence that some aspects of biofilm regulation are conserved in diverse squid symbionts, such as the effects of the strong biofilm negative regulator BinK. Published data indicate that evolved BinK alleles can alter colonization of H905 (group B) and MJ11 (group C), and that a deletion of MJ11 *binK* leads to enhanced colonization (20). Our experiments in Fig. 10 show a clear effect for BinK in all three phylogenetic groups. We also observed responsiveness to RscS overexpression in all squid symbionts examined (Fig. 2). CG101 was the only *V. fischeri* strain examined that did not exhibit a colony biofilm in response to RscS overexpression. CG101 was isolated from the Australian fish *Cleidopus gloriamaris*; based on these findings, we suspect that the strain does not have an intact *syp* locus or otherwise has divergent biofilm regulation.

It remains a formal possibility that the entire *syp* locus is not required in group A or group C but instead that only one or a subset of genes in the locus is needed. Aggregation in squid mucus has been observed for the group A strain MB13B2, and this aggregation is dependent on *sypQ* (40). In our data we note that group A strains were completely unable to colonize in the absence of the *syp* locus, unlike the tested group B and C strains that exhibited reduced colonization in their respective mutants (Fig. 3 and 6). Therefore, the simplest explanation is that the *syp* locus is required to function in divergent strains in a manner similar to how it is used in ES114. We think that the ability to completely delete the *syp* locus is an effective way to determine whether the locus is required for specific phenotypes, and our strains are likely to be useful tools in probing Syp protein function in diverse *V. fischeri* isolates.

It is intriguing to speculate as to how the two frameshifts in the group A strains arose and why the nonfunctional RscS is tolerated in this group. One possible scenario is that the group A strains acquired a new regulatory input into the Syp pathway, and that the presence of this new regulator bypassed the requirement for RscS. We note that comparative genomic analysis of Hawaiian D (dominant)-type strains, which largely overlap group A, revealed an additional 250 kb of genomic DNA not seen in other isolates, yielding a large cache of genes that could play a role in this pathway (33). A related possibility is that *rscS*-independent colonization results from altered regulation of the *syp* locus due to changes in regulators (e.g., SypF) or sites that are conserved with group B. An additional possibility is that the *sypE* frameshift enabled group A strains to colonize independently of *rscS*. Given that correction of this frameshift in MB11B1 does not significantly affect colonization ability (Fig. 9), this sequence of events seems less likely, and we expect that another regulator in MB11B1 is required for the RscS-independent colonization phenotype. There is evidence that under some conditions LuxU can regulate the *syp* biofilm (41), and as this protein is conserved in *V. fischeri*, it may play an important role in group A or group C.

Results from two experimental conditions suggest that the group A strains have an elevated baseline level of biofilm formation. Our data indicate that in the absence of BinK or upon SypG overexpression, MB11B1 colonies exhibit strong cohesion under conditions in which ES114 does not (Fig. 8 and 10). Furthermore, we note that the group A strain MB11B1, when lacking BinK, also exhibits a darker, or more opaque, colony phenotype (Fig. 10). This phenotype has been observed in some ES114 mutants (16) but not in the corresponding ES114 Δ*binK* strain (Fig. 10). The entire colonization lifecycle likely requires a balance between biofilm formation/cohesion and biofilm dispersal, and these data argue that group A strains are more strongly tilted toward the biofilm-producing state. There is evidence that strains lacking BinK exhibit a colonization advantage in the laboratory (18, 20), suggesting that this strategy of more readily forming biofilms provides a fitness advantage in nature. At the same time, the biofilm negative regulator BinK is conserved among *V. fischeri* strains examined (including MB11B1 [Fig. 10]), arguing that there is a benefit to reducing biofilm formation under some conditions.

Our study provides hints as to the role of SypE in MB11B1 and other group A strains.

In ES114, the C terminus is a PP2C serine kinase domain, whereas the N terminus of SypE is an RsbW serine phosphatase domain. SypE acts to phosphorylate and dephosphorylate SypA Ser-56, with the unphosphorylated SypA being the active form to promote biofilm development (17). The balance between SypE kinase and phosphatase is modulated by a central two-component receiver domain (17). Our data that the MB11B1 *sypE* allele promotes biofilm formation suggest that the protein is tilted toward the phosphatase activity. In MB11B1, the frameshift early in *sypE* suggests that there is a different (later) start codon. An alternate GTG start codon in MB11B1 occurs corresponding to codon 18 in ES114 *sypE* (Fig. 7), and this is likely the earliest start for the MB11B1 polypeptide. We attempted to directly identify the SypE N terminus by mass spectrometry, yet we could not identify the protein from either strain. Additional study is required to elucidate how MB11B1 SypE acts to promote biofilm formation.

V. fischeri strains are valuable symbionts in which to probe the molecular basis to host colonization specificity in animals (22, 25, 26). A paradigm has emerged in which biofilm formation through the RscS-Syp pathway is required for squid colonization but not for fish colonization. This study affirms a role of the Syp biofilm but at the same time points out divergent (RscS-independent) regulation in group C and group A isolates. In another well-studied example of symbiotic specificity, rhizobial Nod factors are key to generating specificity with the plant host, yet strains have been identified that do not use this canonical pathway (42, 43). Future work will elaborate on these RscS-independent pathways to determine how noncanonical squid colonization occurs in diverse natural isolates.

MATERIALS AND METHODS

Bacterial strains and growth conditions. *V. fischeri* and *Escherichia coli* strains used in this study can be found in Table 1. Plasmids are listed in Table 2. *E. coli* strains, used for cloning and conjugation, were grown in Luria-Bertani (LB) medium (25 g Difco LB broth [BD] per liter). *V. fischeri* strains were grown in Luria-Bertani salt (LBS) medium (25 g Difco LB broth [BD], 10 g NaCl, and 50 ml 1 M Tris buffer, pH 7.0, per liter). Growth media were solidified by adding 15 g Bacto agar (BD) per liter. When necessary, antibiotics (Gold Biotechnology) were added at the following concentrations: tetracycline, 5 μg/ml for *V. fischeri*; erythromycin, 5 μg/ml for *V. fischeri*; kanamycin, 50 μg/ml for *E. coli* and 100 μg/ml for *V. fischeri*; and chloramphenicol, 25 μg/ml for *E. coli*, 2.5 to 5 μg/ml for group B *V. fischeri*, and 1 to 2.5 μg/ml for group A *V. fischeri*. The two MB11B1/pKV69 strains listed reflect two separate constructions of this strain, although we have not identified any differences between them.

Phylogenetic analysis. Phylogenetic reconstructions assuming a tree-like topology were created with three methods—maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (Bayes)—as previously described (22, 30). Briefly, MP reconstructions were performed by treating gaps as missing, searching heuristically using random addition, tree-bisection reconnection with a maximum of 8 for swaps, and swapping on best only with 1,000 repetitions. For ML and Bayesian analyses, likelihood scores of 1,500+ potential evolutionary models were evaluated using both the corrected and uncorrected Akaike information criterion, the Bayesian information criterion, and decision theory (performance-based selection) as implemented by jModelTest2.1 (44). For all information criteria, the most optimal evolutionary model was a symmetric model with a proportion of invariable sites and a gamma distribution of rate heterogeneity (SYM+I+Γ).

ML reconstruction was implemented via PAUP*4.0a163 (45) by treating gaps as missing, searching heuristically using random addition, tree-bisection reconnection for swaps, and swapping on best only with 1,000 repetitions. Bayesian inference was done by invoking the nst=6, rates=invgamma, and statefreqpr=fixed(equal) settings in the software package MrBayes3.2.6 (46). The Metropolis-coupled Markov chain Monte Carlo (MCMCMC) algorithm, used to estimate the posterior probability distribution for the sequences, was set up with temp=0.2 and one incrementally "heated" chain with three "cold" chains; these four chains were replicated two times per analysis to establish convergence of the Markov chains (i.e., "stationarity," as defined in reference 47 and interpreted previously in reference 30). For this work, stationarity was achieved after approximately 50,000 samples (5,000,000 generations) were collected, with 25% discarded. The ~37,500 samples included were used to construct a 50% majority-rule consensus tree from the sample distribution generated by MCMCMC and assess clades' posterior probabilities. For ML and MP analyses, the statistical confidence in the topology of each reconstruction was assessed using 1,000 bootstrap replicates. Phylogenetic trees were visualized with FigTree 1.4.3 (http://tree.bio.ed.ac.uk/software/figtree); the final tree was edited for publication with Inkscape 0.91 (http://inkscape.org/) and GIMP 2.8.22 (http://www.gimp.org/).

DNA synthesis and sequencing. Each of the primers listed in Table 3 was synthesized by Integrated DNA Technologies (Coralville, IA). Full inserts from all cloned constructs were verified by Sanger DNA sequencing through ACGT, Inc., via the Northwestern University Feinberg School of Medicine NUSeq Core Facility or the University of Wisconsin—Madison Biotechnology Center. Sequence data were analyzed with SeqMan Pro (DNAStar software), SnapGene (GSL Biotech), and Benchling.

TABLE 1 Bacterial strains

Strain	Genotype	Source or reference(s)
V. fischeri		
MJM1059	MJ11	25, 53
MJM1100	ES114	54
MJM1104	ES114 (MJM1100)/pKV69	This study
MJM1106	ES114 (MJM1100)/pKG11	This study
MJM1109	MJ11 (MJM1059)/pKV69	This study
MJM1111	MJ11 (MJM1059)/pKG11	This study
MJM1114	MJ12	53
MJM1115	CG101	25
MJM1117	ES213	55
MJM1119	EM18	25, 53
MJM1120	EM24	53, 56
MJM1121	EM30	53
MJM1122	WH1	57
MJM1125	SR5	24
MJM1126	SA1	24
MJM1127	KB1A97	29
MJM1128	KB2B1	29
MJM1129	KB5A1	29
MJM1130	MB11B1	29
MJM1136	EM17	56
MJM1147	*mjapo*.6.1	22
MJM1149	*mjapo*.7.1	22
MJM1151	*mjapo*.8.1	22
MJM1153	*mjapo*.9.1	22
MJM1219	*mjapo*.8.1/pKV69	This study
MJM1221	*mjapo*.8.1/pKG11	This study
MJM1238	MJ12 (MJM1114)/pKV69	This study
MJM1239	MJ12 (MJM1114)/pKG11	This study
MJM1240	SR5 (MJM1125)/pKV69	This study
MJM1241	SR5 (MJM1125)/pKG11	This study
MJM1242	SA1 (MJM1126)/pKV69	This study
MJM1243	SA1 (MJM1126)/pKG11	This study
MJM1244	MB11B1 (MJM1130)/pKV69	This study
MJM1245	MB11B1 (MJM1130)/pKG11	This study
MJM1246	EM17 (MJM1136)/pKV69	This study
MJM1247	EM17 (MJM1136)/pKG11	This study
MJM1254	KB1A97 (MJM1127)/pKV69	This study
MJM1255	KB1A97 (MJM1127)/pKG11	This study
MJM1256	KB2B1 (MJM1128)/pKV69	This study
MJM1257	KB2B1 (MJM1128)/pKG11	This study
MJM1258	KB5A1 (MJM1129)/pKV69	This study
MJM1259	KB5A1 (MJM1129)/pKG11	This study
MJM1260	ES213 (MJM1117)/pKV69	This study
MJM1261	ES213 (MJM1117)/pKG11	This study
MJM1266	EM18 (MJM1119)/pKV69	This study
MJM1267	EM18 (MJM1119)/pKG11	This study
MJM1268	EM24 (MJM1120)/pKV69	This study
MJM1269	EM24 (MJM1120)/pKG11	This study
MJM1270	EM30 (MJM1121)/pKV69	This study
MJM1271	EM30 (MJM1121)/pKG11	This study
MJM1272	*mjapo*.6.1 (MJM1147)/pKV69	This study
MJM1273	*mjapo*.6.1 (MJM1147)/pKG11	This study
MJM1274	*mjapo*.7.1 (MJM1149)/pKV69	This study
MJM1275	*mjapo*.7.1 (MJM1149)/pKG11	This study
MJM1276	*mjapo*.9.1 (MJM1151)/pKV69	This study
MJM1277	*mjapo*.9.1 (MJM1151)/pKG11	This study
MJM1278	CG101 (MJM1115)/pKV69	This study
MJM1279	CG101 (MJM1115)/pKG11	This study
MJM1280	WH1 (MJM1122)/pKV69	This study
MJM1281	WH1 (MJM1122)/pKG11	This study
MJM1782	ES114 (MJM1100) pVSV104	18
MJM2114	MB15A4	29
MJM2226	ES114 (MJM1100)/pMJM33	This study

(Continued on next page)

TABLE 1 (Continued)

Strain	Genotype	Source or reference(s)
MJM2251	ES114 (MJM1100) Δ*binK*	18
MJM2386	ES114 (MJM1100)/pBinK	This study
MJM2997	MB11B1 (MJM1130)/pVSV104	This study
MJM2998	MB11B1 (MJM1130)/pBinK	This study
MJM2999	ES213 (MJM1117)/pVSV104	This study
MJM3000	ES213 (MJM1117)/pBinK	This study
MJM3010	ES114 (MJM1100) Δ*rscS*	This study
MJM3017	ES213 (MJM1117) Δ*rscS*	This study
MJM3042	MB15A4 (MJM2114) Δ*rscS*	This study
MJM3046	MB11B1 (MJM1130) Δ*rscS*	This study
MJM3062	ES114 (MJM1100) Δ*syp*	This study
MJM3065	MB11B1 (MJM1130) Δ*syp*	This study
MJM3068	ES213 (MJM1117) Δ*syp*	This study
MJM3071	MB15A4 (MJM2114) Δ*syp*	This study
MJM3084	MB11B1 (MJM1130) Δ*binK*	This study
MJM3354	ES114 (MJM1100) *sypE*(ntG33Δ)	This study
MJM3364	ES114 (MJM1100) *sypE*(ntG33Δ)/pKV69	This study
MJM3365	ES114 (MJM1100) *sypE*(ntG33Δ)/pEAH73	This study
MJM3370	MB11B1 (MJM1130)/pKV69	This study
MJM3371	MB11B1 (MJM1130)/pEAH73	This study
MJM3394	ES114 (MJM1100) Δ*rscS sypE*(ntG33Δ)	This study
MJM3397	MB11B1 (MJM1130) *sypE*(nt33::G)	This study
MJM3398	MB11B1 (MJM1130) *sypE*(nt33::G)/pKV69	This study
MJM3399	MB11B1 (MJM1130) *sypE*(nt33::G)/pEAH73	This study
MJM3410	MB11B1 (MJM1130) Δ*sypE*	This study
MJM3411	MB11B1 (MJM1130) Δ*sypE*/pKV69	This study
MJM3412	MB11B1 (MJM1130) Δ*sypE*/pEAH73	This study
MJM3417	ES114 (MJM1100) Δ*sypE*	This study
MJM3418	ES114 (MJM1100) Δ*sypE*/pKV69	This study
MJM3419	ES114 (MJM1100) Δ*sypE*/pEAH73	This study
MJM3423	ES114 (MJM1100) Δ*rscS* Δ*sypE*	This study
MJM3455	ES114 (MJM1100)/pEAH73	This study
MJM3501	SR5 (MJM1125) Δ*syp*	This study
MJM3751	SR5 (MJM1125) Δ*binK*::*erm*	This study
E. coli		
MJM534	CC118 λpir/pEVS104	58
MJM537	DH5α λpir	Laboratory stock
MJM570	DH5α/pEVS79	58
MJM580	DH5α λpir/pVSV104	59
MJM581	DH5α/pKV69	60
MJM583	DH5α/pKG11	15
MJM639	XL1-Blue/pMJM33	This study
MJM658	BW23474/pEVS107	61
MJM2384	DH5α λpir/pBinK	18
MJM2540	KV5264/pEAH73	39
MJM3008	DH5α/pEVS79-Δ*rscS*[MJM1100]	This study
MJM3014	DH5α λpir/pEVS79-Δ*rscS*[MJM1117]	This study
MJM3039	DH5α λpir/pEVS79-Δ*rscS*[MJM2114]	This study
MJM3043	DH5α λpir/pEVS79-Δ*rscS*[MJM1130]	This study
MJM3060	NEB5α/pEVS79-Δ*syp*[MJM1100]	This study
MJM3063	NEB5α/pEVS79-Δ*syp*[MJM1130]	This study
MJM3066	DH5α λpir/pEVS79-Δ*syp*[MJM1117]	This study
MJM3069	DH5α λpir/pEVS79-Δ*syp*[MJM2114]	This study
MJM3082	NEB5α/pEVS79-Δ*binK*[MJM1130]	This study
MJM3287	NEB5α/pHB1	This study
MJM3338	DH5α λpir/pEVS107-*sypE*[MJM1130](nt33::G)	This study
MJM3340	DH5α λpir/pEVS107-*sypE*[MJM1100](ntG33Δ)	This study
MJM3351	NEB5α/pEVS79-*sypE*[MJM1130](nt33::G)	This study
MJM3352	NEB5α/pEVS79-*sypE*[MJM1100](ntG33Δ)	This study
MJM3409	NEB5α/pEVS79-Δ*sypE*[MJM1130]	This study
MJM3416	NEB5α/pEVS79-Δ*sypE*[MJM1100]	This study

TABLE 2 Plasmids

Plasmid	Relevant genotype[a]	Source or reference
pEVS79	Vector backbone (Cam^r) for deletion construction	58
pKV69	Vector backbone (Cam^r/Tet^r)	60
pKG11	pKV69 carrying *rscS1*	15
pMJM33	pKG11 *rscS1*(ntA1141::Δ)	This study
pEVS104	Conjugation helper plasmid (Kan^r)	58
pEVS107	Mini-Tn*7* mobilizable vector (Erm^r Kan^r)	61
pEAH73	pKV69 carrying *sypG* from ES114	39
pVSV104	Complementation vector (Kan^r)	59
pBinK	pVSV104 carrying *binK* from MJM1100	18
pHB1	pUC19 FRT-*erm*-FRT	This study
pEVS79-Δ*rscS*[MJM1100]	pEVS79 carrying 1.6-kb US/1.6-kb DS of *rscS* from MJM1100	This study
pEVS79-Δ*rscS*[MJM1117]	pEVS79 carrying 1.6-kb US/1.6-kb DS of *rscS* from MJM1117	This study
pEVS79-Δ*rscS*[MJM2114]	pEVS79 carrying 1.6-kb US/1.6-kb DS of *rscS* from MJM2114	This study
DH5α λpir/pEVS79-Δ*rscS*[MJM1130]	pEVS79 carrying 1.6-kb US/1.6-kb DS of *rscS* from MJM1130	This study
pEVS79-Δ*syp*[MJM1100]	pEVS79 carrying 1.6-kb US of *sypA*/1.6-kb DS of *sypR* from MJM1100	This study
pEVS79-Δ*syp*[MJM1130]	pEVS79 carrying 1.6-kb US of *sypA*/1.6-kb DS of *sypR* from MJM1130	This study
pEVS79-Δ*syp[*MJM1117]	pEVS79 carrying 1.6-kb US of *sypA*/1.6-kb DS of *sypR* from MJM1117	This study
pEVS79-Δ*syp*[MJM2114]	pEVS79 carrying 1.6-kb US of *sypA*/1.6-kb DS of *sypR* from MJM2114	This study
pEVS79-Δ*binK*[MJM1130]	pEVS79 carrying 1.6-kb US/1.6-kb DS of *binK* from MJM1130	This study
pEVS107-*sypE*[MJM1130](nt33::G)	pEVS107 carrying the *sypE*(nt33::G) allele from MJM1130	This study
pEVS107-*sypE*[MJM1100](ntG33Δ)	pEVS107 carrying the *sypE*(ntG33Δ) allele from MJM1100	This study
pEVS79-*sypE*[MJM1130](nt33::G)	pEVS79 carrying the *sypE*(nt33::G) allele from MJM1130	This study
pEVS79-*sypE*[MJM1100](ntG33Δ)	pEVS79 carrying the *sypE*(ntG33Δ) allele from MJM1100	This study
pEVS79-Δ*sypE*[MJM1130]	pEVS79 carrying 1.6-kb US/1.6-kb DS of *sypE* from MJM1130	This study
pEVS79-Δ*sypE*[MJM1100]	pEVS79 carrying 1.6-kb US/1.6-kb DS of *sypE* from MJM1100	This study

[a]US, upstream; DS, downstream.

Construction of gene deletions. Deletions in *V. fischeri* strains ES114 and MB11B1 were made according to the laboratory's gene deletion protocol (https://doi.org/10.5281/zenodo.1470836). In brief, 1.6-kb upstream sequence and 1.6-kb downstream sequence of the targeted gene or locus were cloned into linearized plasmid pEVS79 (amplified with primers pEVS79_rev_690/pEVS79_for_691) using Gibson Assembly (NEBuilder HiFi DNA assembly cloning kit) with the primer combinations listed in Table S1 in the supplemental material. The Gibson mix, linking the upstream and downstream flanking regions, was transformed into *E. coli* on plates containing 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside (X-Gal) with several white colonies selected for further screening by PCR using primers flanking the upstream/downstream junction (Table 3 and Table S1). The resulting plasmid candidate was confirmed by sequencing and conjugated into the *V. fischeri* recipient by triparental mating with helper plasmid pEVS104, selecting for the chloramphenicol resistance of the plasmid backbone. *V. fischeri* colonies were first screened for single recombination into the chromosome by maintaining antibiotic resistance in the absence of selection and then screened for double recombination by the loss of both the antibiotic resistance cassette and the gene/locus of interest. Constructs were verified by PCR (Table 3) and sequencing.

Deletion of SR5 *binK* was conducted using splicing by overlap extension PCR (SOE-PCR) and natural transformation (method modified from reference 48). Oligonucleotides binK-F1 and binK-R1-LUH and oligonucleotides binK-F2-RUH and binK-R2 were used in a PCR with MJM1125 (SR5) genomic DNA as the template to amplify DNA fragments containing ~1 kb of sequence upstream and downstream, respectively, relative to *binK*. Using SOE-PCR, these fragments were fused on either side to a third DNA fragment containing an Erm^r cassette, which was amplified using pHB1 as the template and oligonucleotides HB41 and HB42. We then used natural transformation with pLostfoX (49) to insert this mutagenic DNA into MJM1125, where the flanking sequences guide the Erm^r cassette to replace *binK*, generating the desired gene deletion. Candidate SR5 Δ*binK* mutants were selected after growth on LBS-Erm5 plates. Oligonucleotides binK-F1 and binK-R2 as well as HB8 and binK-FO were used to screen candidates for the correct deletion scar by PCR, and oligonucleotides KMB_036 and KMB_037 were used to confirm the absence of *binK* in the genome. The deletion was verified by Sanger sequencing with primers HB8, HB9, HB42, and HB146. The base plasmid pHB1 contains an erythromycin resistance cassette flanked by FLP recombination target sites and was constructed using oligonucleotides HB23 and HB39 with gBlock gHB1 (sequence in File S1) (Integrated DNA Technologies, Inc.) as the template to amplify the Erm^r cassette flanked by HindIII and BamHI sites, which was then cloned into the corresponding site in pUC19.

For most constructs, the deleted genetic material was between the start codon and last six amino acids (50), with two exceptions: Δ*sypE* in MJM1130 included the ATG that is two amino acids upstream of the predicted start codon but not the canonical start codon, and the Δ*binK* alleles in MJM1117, MJM1130, and MJM2114, which were constructed to be equivalent to MJM2251 (Δ*binK* in ES114) (18). The Δ*binK* alleles in these strains include the start codon, the next six codons, two codons resulting from ATCGAT (ClaI site), and the last three codons for a predicted 12-amino-acid peptide.

Construction of *sypE* alleles. To create *sypE*(ntG33Δ) in MJM1100 and *sypE*(nt33::G) in MJM1130, the single point mutation was created by amplifying the gene in two halves, with the N-terminal portion

TABLE 3 DNA oligonucleotides for PCR amplification and sequencing

Primer name	Sequence[a] (5′ to 3′)
DAT_015F	ACCAAGAAGCAGTACGACGATTAT
ES114_DS_ver	GGATGTTTTAGATGTTGCGG
ES114_indel_for	TTACTTTTTTCAGATACAAAGCCC
ES114_indel_rev	GTTGTTCTGATAGTGCGTGA
ES114_US_ver	ATCAACTCAAGAAACTCCCC
for_ver_sypE	CCGGCTCAAACTATTGCAG
Gib_ES114_binK_DS_for	attaatcgatGCGTATACATAAATAATGATTCATATATAC
Gib_ES114_binK_DS_rev	gcaggaattcgatatcaagcTTTCAATACTGTGTTTTTATGC
Gib_ES114_binK_US_for	gaggtcgacggtatcgataaGAGCCTTTTAAATCCCCTAAC
Gib_ES114_binK_US_rev	atgtatacgcATCGATTAATGACATATTATTATTCATAAAAAAC
Gib_ES114_rscS_DS_for	taatgcaatgGAGAAGTATGAAACACAATAAAC
Gib_ES114_rscS_DS_rev	gcaggaattcgatatcaagcAAAAATACATTGTTGCACTTG
Gib_ES114_rscS_US_for	gaggtcgacggtatcgataaGACGTCTAAAACTGAATCG
Gib_ES114_rscS_US_rev	catacttctcCATTGCATTAGCTCCTATAAAATAG
Gib_ES114_syp_DS_for	gcttattatgATATTTGCTCGAGGCCAATAAAAAC
Gib_ES114_syp_DS_rev	gcaggaattcgatatcaagcTGGTGAATGTAGGATCCAC
Gib_ES114_syp_US_for	gaggtcgacggtatcgataaCAACCGTAGCGCCAAATG
Gib_ES114_syp_US_rev	gagcaaatatCATAATAAGCTCCTAGGGAATAATC
Gib_ES114_sypE_C_for	cagatacaaaCCCACATCACTAGAGTCG
Gib_ES114_sypE_C_rev	ctagtggccaggtacctcgaAATTAAGCTTCCATCTTCAC
Gib_ES114_sypE_DS_for	tgtaatcatgCTGTTAATTGAGAATCAATAAAAAG
Gib_ES114_sypE_DS_rev	caactctttttccgaaggtaTTGAGTAACCGGCATAATTTAG
Gib_ES114_sypE_N_for	tagagggccctaggcgcgccTGTTTCACAACTCAATACC
Gib_ES114_sypE_N_rev	gtgatgtgggTTTGTATCTGAAAAAAGTAAAGTAG
Gib_ES114_sypE_US_for	gaggtcgacggtatcgataaTGGTCAGATGAAATGTCATTTTTAG
Gib_ES114_sypE_US_rev	caattaacagCATGATTACACCACTGTTG
Gib_ES213_rscS_US_rev	catacttctcCATTGTATTAGCTCCTATAAAATAG
Gib_MB11B1_syp_DS_for	gcttattatgATATTTGCTCGAGGTCAATAAAAG
Gib_MB11B1_syp_US_for	gaggtcgacggtatcgataaGCACACTGATAACTAAATTATTAC
Gib_MB11B1_syp_US_rev	gagcaaatatCATAATAAGCTCCTAGGG
Gib_MB11B1_sypE_C_for	cagatacaaaGCCAACATCACTAGAATC
Gib_MB11B1_sypE_C_rev	ctagtggccaggtacctcgaTCAACAATTAAGCTTCCATC
Gib_MB11B1_sypE_DS_for	cagtggtatgCTGTTAATTGAAAACCAATAGC
Gib_MB11B1_sypE_DS_rev	gcaggaattcgatatcaagcATTTAGGATGTTTTTAATAACAATTTG
Gib_MB11B1_sypE_N_for	tagagggccctaggcgcgccAGTTTCACAACTCAATACTAATAATATTC
Gib_MB11B1_sypE_N_rev	tgatgttggcTTTGTATCTGAAAAAAGCAAAATAG
Gib_MB11B1_sypE_US_for	gaggtcgacggtatcgataaGAATGGTCAGATGAAATGTC
Gib_MB11B1_sypE_US_rev	caattaacagCATACCACTGTTGATAAAAATC
Gib_pEVS79_ES_sypE_for	gaggtcgacggtatcgataaTGTTTCACAACTCAATACC
Gib_pEVS79_ES_sypE_rev	gcaggaattcgatatcaagcAATTAAGCTTCCATCTTCAC
Gib_pEVS79_MB_sypE_for	gaggtcgacggtatcgataaAGTTTCACAACTCAATACTAATAATATTC
Gib_pEVS79_MB_sypE_rev	gcaggaattcgatatcaagcTCAACAATTAAGCTTCCATC
Gib_SR5_syp_DS_for	gcttattatgATATTTGCTCGAGGACAATAAAAAG
Gib_SR5_syp_DS_rev	gcaggaattcgatatcaagcTGGTGAGTGTAGAATCCATTC
Gib_SR5_syp_US_for	gaggtcgacggtatcgataaAACCGTAGCGCCAAATGG
Gib_SR5_syp_US_rev	gagcaaatatCATAATAAGCTCCTAGGGAATAATCC
HB8	ACAAAATTTTAAGATACTGCACTATCAACACACTCTTAAG
HB9	GGGAGGAAATAATCTAGAATGCGAGAGTAGG
HB23	TTGGAGAGCCAGCTGCGTTCGCTAA
HB39	TAGGAAGCTTACGAGACGAGCTTCTTATATATGCTTCGCCAGGAAGTTCCTATTCTCTAGAAAGTA TAGGAACTTCCTTAGAAGCAAACTTAAGAGTGTG
HB41	CGATCTTGTGGGTAGAGACATCCAGGTCAAGTCCAGCCCCGCTCTAGTTTGGGAATCAAGTGCATGAGCGCTGAAG
HB42	ACGAGACGAGCTTCTTATATATGCTTCGCCAG
HB146	CGATCTTGTGGGTAGAGACATC
binK-F1	GAAATTACCATGGAGCCAACAGCAAGAC
binK-R1-LUH	ctggcgaagcatatataagaagctcgtctcgtCATAAAAAACCTAGCGCTTTATTTGTAGATATAATTATTAACTATAATCGC
binK-F2-RUH	gacttgacctggatgtctctacccacaagatcgCGCTCATTGTATCTATAGAGTATGTACTGAGTTACG
binK-R2	GGCATCATTATGGCAACCATTAAAGACG
binK-FO	CCGTTAATACTGGATTATTCGCTTGAATTTGAACG
KMB_036	CCACAATAGCAGAATACAAATTCGCTG
KMB_037	CTCAAAATGACAGTCAGAGTATCGTAGGC
JFB_287	ATGGAGTTTCTACGTCAACCAGAA
JFB_287_MB11B1	ATGGAGTTTTTACGTCAACCAGAG
JFB_288	TGTTATAACGATTACATGGCAGCG
JFB_365	GGAAAGAGAATGATTAAG
M13for	GTAAAACGACGGCCAG

(Continued on next page)

TABLE 3 (Continued)

Primer name	Sequence[a] (5′ to 3′)
M13rev	CAGGAAACAGCTATGAC
MB11B1_indel_for	GCTTTTTTCAGATACAAAGCCA
MB11B1_indel_rev	ATACCTGATGGAAACGACCT
MJM-154F	TAAAAAGGGAATTAATCCGC
MJM-306R	AACTCTAACCAAGAAGCA
pEVS107_3837	GGCGCGCCTAGGGCCCTC
pEVS107_3838	TCGAGGTACCTGGCCACTAG
pEVS79_for_691	GCTTGATATCGAATTCCTG
pEVS79_rev_690	TTATCGATACCGTCGACC
rev_ver_sypE	TTCACCATGAGTGCCAAATC
rscS_del1F	CTTATCTTCTAGTTCTTTTTTTTAGTGATGTCTCTTTCTACGGC
rscS_del1R	GCCGTAGAAAGAGACATCACTAAAAAAAAGAACTAGAAGATAAG
rscS_ver_1	GTAATTCAGTAATGCTACC
rscS_ver_2	GTCGCACCGTCAGGTATA
rscS_ver_3	AAGAAATTATTCGCTACC
rscS_ver_4	AGTTAGTAGGCCATTACG
SR5_syp_ver_for	TAGGCGTATCAAAAACCACCT
SR5_syp_ver_rev	TCAGGAATGTCGATGGCAG
Syp_ver_DS_rev	ATCGAGCATATTTTGCCAATC
Syp_ver_US_for	ACCTATCAACTCTTAAGTCGATTC
syp4F	TGAGGATCCCATCGTGCCATA
syp4R	AGCTCCTTTGCAATGTTTGCTT
syp5F	TATTAGGCCGTTTCCACCAGG
syp5F-B	TATTAGGTCGTTTCCATCAGG
sypA_out	AACAGGAATTGCGTTTTCAA
US_syp_flank_for	ACCACTGTGATAACTTGCAC
US_syp_flank_rev	ATGAGGCATAACCTGTTCCA

[a]For Gibson Assembly primers, capital letters indicate homology to the template. All primers were designed for this study, except MJM-154F and MJM-306R (22), JFB_287, JFB_288, and JFB_365 (18), and M13 for and M13 rev.

consisting of approximately 300 bp upstream of *sypE* up through nucleotide 33 and the C-terminal portion consisting of nucleotide 33 and the remaining *sypE* gene. The overlap between the two halves contained the single-nucleotide polymorphism in the primers that connected them. The altered *sypE* alleles were initially cloned into plasmid pEVS107 (linearized with primers pEVS107_3837/pEVS107_3838) using Gibson Assembly, and then the entire altered *sypE* allele was subcloned into pEVS79 with Gibson Assembly (Table S1). After double recombination of the vector into *V. fischeri*, candidate colonies for the altered *sypE* in MJM1100 were screened with primers ES114_indel_for/ES114_indel_rev. The primer set anneals more strongly to the wild-type *sypE* sequence than to *sypE*(ntG33::Δ). Candidates in the MJM1100 background with a fainter PCR band were sequenced and confirmed to have the *sypE*(ntG33::Δ) allele. For MJM1130, the primer set MB11B1_indel_for/MB11B1_indel_rev anneals more strongly to the *sypE*(nt33::G) allele than to the naturally occurring *sypE* allele, and candidates in MJM1130 that contained a more robust PCR band were selected for sequencing to be confirmed as being *sypE*(nt33::G).

Construction of pKG11 *rscS1*(ntA1141::Δ). Plasmid pKG11 encodes an overexpression allele of RscS, termed *rscS1* (15, 28). *rscS* nucleotide A1141 was deleted on the plasmid using the Stratagene QuikChange II site-directed mutagenesis kit with primers rscS_del1F and rscS_del1R. The resulting plasmid, pMJM33, was sequenced with primers MJM-154F and MJM-306R to confirm the single base pair deletion.

Squid colonization. Hatchling *E. scolopes* organisms were colonized by exposure to approximately 3×10^3 CFU/ml (ranging from 5.2×10^2 to 1.4×10^4 CFU/ml, as specified in the figure legends) for each strain in a total volume of 40 ml of FSIO (filter-sterilized Instant Ocean) for 3 h. Squid were then transferred to 100 ml of FSIO to stop the inoculation and then transferred to 40 ml FSIO for an additional 45 h, with a water change at 24 h postinoculation. For Fig. 10A, kanamycin was added to the FSIO to keep selective pressure on the plasmid. After 48 h of colonization, the squid were euthanized and surface sterilized by storage at −80°C according to standard practices (51). For determination of CFU per light organ, hatchlings were thawed and homogenized, and 50 μl of homogenate dilutions was plated onto LBS plates. Bacterial colonies from each plate were counted and recorded. Mock-treated, uncolonized hatchlings ("apo-symbiotic") were used to determine the limit of detection in the assay. The competitive index (CI) was calculated from the relative CFU of each sample in the output (light organ) versus the input (inoculum) as $\log_{10}$\{[test strain (light organ)/control strain (light organ)]/[test strain (inoculum)/control strain (inoculum)]\}. For competitions of natural isolates, the group A strain (or its Δ*rscS* derivative) was the test strain and the group B strain was the control strain. Colony color was used to enumerate colonies from each, white for group A strains MB11B1 and ES213 and yellow for group B strains ES114 and MB15A4, along with PCR verification of selected colonies. For competition between SR5 and SR5 Δ*binK*, 100 colonies per squid were patched onto LBS-Erm5 and LBS.

Colony biofilm assays. Bacterial strains were grown in LBS medium (Fig. 10C) or LBS-Cam2.5 medium (Fig. 2 and 8) for approximately 17 h, and then 10 μl (Fig. 2) or 8 μl (Fig. 8, 10C) was spotted

onto LBS plates (Fig. 10C) or LBS-Tet5 plates (Fig. 2 and 8). Spots were allowed to dry and the plates incubated at 25°C for 48 h. Images of the spots were taken at 24 and 48 h postspotting using a Leica M60 microscope and Leica DFC295 camera. After 48 h of growth, the spots were disrupted using a flat toothpick and imaged similarly.

Analysis of DNA and protein sequences *in silico*. Amino acid sequences for *V. fischeri* ES114 *syp* genes were obtained from RefSeq accession no. NC_006841.2. Local TBLASTN queries were performed for each protein against nucleotide databases for the following strains, each of which were derived from the RefSeq cds_from_genomic.fna file: *V. fischeri* SR5 (GCA_000241785.1), *V. fischeri* MB11B1 (GCA_001640385.1), and *V. vulnificus* ATCC 27562 (GCA_002224265.1). Percent amino acid identity was calculated as the identity in the BLAST query divided by the length of the amino acid sequence in ES114. Domain information is from the PFAM database (52).

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at https://doi.org/10.1128/JB.00033-19.

SUPPLEMENTAL FILE 1, PDF file, 0.1 MB.

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