Identification of YsrT and evidence that YsrRST constitute a unique phosphorelay system in Yersinia enterocolitica

Kimberly A. Walker  
Washington University School of Medicine in St. Louis

Markus W. Obrist  
University of North Carolina School of Medicine

Shirly Mildiner-Earley  
Washington University School of Medicine in St. Louis

Virginia L. Miller  
Washington University School of Medicine in St. Louis

Follow this and additional works at: https://digitalcommons.wustl.edu/open_access_pubs

Recommended Citation
Identification of YsrT and Evidence that YsrRST Constitute a Unique Phosphorelay System in *Yersinia enterocolitica*

Kimberly A. Walker, Markus W. Obrist, Shirly Mildiner-Earley and Virginia L. Miller

Identification of YsrT and Evidence that YsrRST Constitute a Unique Phosphorelay System in \textit{Yersinia enterocolitica}\textsuperscript{7}

Kimberly A. Walker,\textsuperscript{1,3}\textsuperscript{*} Markus W. Obrist,\textsuperscript{1,3} Shirly Mildiner-Earley,\textsuperscript{3}\textsuperscript{†} and Virginia L. Miller\textsuperscript{1,2,3}

\textsuperscript{1}Department of Genetics and \textsuperscript{2}Microbiology and Immunology, \textsuperscript{2}University of North Carolina School of Medicine, Chapel Hill, \textsuperscript{3}North Carolina 27599, and \textsuperscript{3}Department of Molecular Microbiology, Washington University School of Medicine, St. Louis, Missouri 63110

Received 25 June 2010/Accepted 10 September 2010

Two-component systems (TCS) and phosphorelay systems are mechanisms used by bacteria and fungi to quickly adapt to environmental changes to produce proteins necessary for survival in new environments. Bacterial pathogens use TCS and phosphorelay systems to regulate genes necessary to establish infection within their hosts, including type III secretion systems (T3SS). The \textit{Yersinia enterocolitica} ysa T3SS is activated in response to NaCl by YsrS and YsrR, a putative hybrid sensor kinase and a response regulator, respectively. Hybrid TCS consist of a sensor kinase that typically has three well-conserved sites of phosphorylation: autophosphorylation site H1, D1 within a receiver domain, and H2 in the histidine phosphotransferase (HPt) domain. From H2, the phosphoryl group is transferred to D2 on the response regulator. A curious feature of YsrS is that it lacks the terminal HPt domain. We report here the identification of the HPt-containing protein (YsrT) that provides this activity for the Ysr system. YsrT is an 82-residue protein predicted to be cytosolic and α-helical in nature and is encoded by a gene adjacent to ysrS. To demonstrate predicted functions of YsrRST as a phosphorelay system, we introduced alanine substitutions at H1, D1, H2, and D2 and tested the mutant proteins for the ability to activate a \textit{ysaE-lacZ} reporter. As expected, substitutions at H1, H2, and D2 resulted in a loss of activation of \textit{ysaE} expression. This indicates an interruption of normal protein function, most likely from loss of phosphorylation. A similar result was expected for D1; however, an intriguing “constitutive on” phenotype was observed. In addition, the unusual feature of a separate HPt domain led us to compare the sequences surrounding the \textit{ysrS-ysrT} junction in several \textit{Yersinia} strains. In every strain examined, \textit{ysrT} is a separate gene, leading to speculation that there is a functional advantage to YsrT being an independent protein.

\textit{Yersinia enterocolitica} is a human pathogen that causes several gastrointestinal conditions, with symptoms that include fever, vomiting, and diarrhea. In an otherwise healthy host, the infection is usually self-limiting, lasting 1 to 2 weeks (44). However, individuals with high blood iron levels or with compromised immune systems can develop a systemic \textit{Y. enterocolitica} infection that is often fatal (8). Pigs are a major reservoir of some biotypes of pathogenic \textit{Y. enterocolitica} (28), and while it is often isolated from the tonsils and intestinal tract, \textit{Y. enterocolitica} does not cause obvious disease in swine (10). The bacteria are shed into the environment via feces or can contaminate pork products during processing, both of which can lead to contamination of human food and water supplies. In addition, \textit{Y. enterocolitica} is frequently found during surveys of food-borne pathogens in milk supplies (22). The prevalence of \textit{Y. enterocolitica} in contaminated meat and milk products may be enhanced by its ability to grow at cool temperatures, even as low as 0°C (3).

Based on biochemical properties, \textit{Y. enterocolitica} strains are subdivided into several biovars. Interestingly, there is a considerable range in the severity of disease caused by the different biovars. Biovar 1B strains are the most highly pathogenic for humans, and 1B is the only biovar that is lethal in a mouse model of yersiniosis (37, 38, and references therein). Not surprisingly, these isolates contain virulence factors not found in other biovars (19, 41). Among these is the chromosomally encoded \textit{Ysa} type III secretion system (T3SS). In mouse infection studies, deletion of apparatus genes (\textit{ysa}) or individual effector genes (\textit{ysp}) results in a modest attenuation only at 24 h postinfection (27, 45) and a 10-fold increase in the 50% lethal dose, both following oral inoculation (17). Thus, the role of the Ysa T3SS in pathogenicity is subtle in the mouse model, leading to speculation that the secreted effectors (called Ysps) are important for gastroenteritis but not for systemic infection (45). \textit{In vitro}, secretion of Ysps through the Ysa T3SS apparatus is only detected when the bacteria are cultured at 26°C and in the presence of a high concentration of salt (e.g., NaCl) (17, 50). Subsequent studies provided evidence that the genes encoding both the apparatus and effector proteins are up-regulated by growth in a high concentration of salt, indicating that the salt dependence is at the level of transcription (45–47).

As \textit{Y. enterocolitica} exists as both a commensal and a pathogenic organism and has the capacity to grow in a wide range of temperatures, the expression of many genes must...
be tightly regulated to ensure survival under these often stressful conditions. One mechanism widely used by prokaryotes to respond to changes in their environment is signal transduction via two-component systems (TCS) (49). In the canonical TCS, a membrane-bound sensor histidine kinase (HK) autophosphorylates at a conserved histidine (His) residue in response to an environmental cue. The phosphoryl group is then transferred to a conserved aspartate (Asp) residue in the receiver domain of a response regulator (RR) protein. RR proteins also contain an effector domain, which is often a DNA-binding moiety; phosphorylation of the receiver domain activates the effector domain to bind DNA and alter gene transcription (13). A common variation of the canonical TCS is a phosphorelay (2). Phosphorelays involve two or more proteins and three phosphoryl group transfer events (His→Asp→His→Asp). In one subclass of the phosphorelay group, a hybrid sensor kinase contains not only an HK domain but also receiver (REC) and histidine phosphotransferase (HPt) domains, and the first two phosphotransfer events are within the sensor protein. The final phosphotransfer event is to the RR protein. Additionally, variations on this theme have been reported where three or four proteins are required to provide the domains necessary for the phosphorelay (5, 12, 36, 39).

Studies conducted in our laboratory and others showed that the putative TCS proteins YsrR and YsrS are required for expression of the ysa apparatus genes and specifically of the ysaE promoter (Fig. 1A) (30, 45–47). Deletion of either gene results in a lack of NaCl-induced activation of the ysa genes. Furthermore, the level of ysaE expression in a ΔysrS mutant strain is the same as that in a wild-type strain grown in the absence of NaCl, thus implying that YsrS responds to the NaCl (46). One conundrum of this model is that YsrS appears to belong to the hybrid class of sensor kinases but lacks the terminal HPt domain presumably required to transfer the phosphate to YsrR. In this study, we report the identification of a gene encoding this HPt function and demonstrate genetically that the Ysr proteins do indeed conduct a phosphorelay cascade that leads to activation of the ysaE promoter and, hence, the ysa and ysp genes.
## MATERIALS AND METHODS

### Bacterial strains and growth conditions

The bacterial strains and plasmids used in this work are listed in Table 1 and described below. All cultures of *Escherichia coli* strains were grown in LB (1% tryptone, 0.5% yeast extract, 170 mM NaCl; Difco) at 37°C. Cultures of *Y. enterocolitica* were grown at 26°C in LB, or LB broth (1% tryptone, 0.5% yeast extract, 290 mM NaCl). For preparation of secreted proteins, brain heart infusion broth (BHI; Difco) and BHI with 490 mM NaCl were used. Antibiotics were added as needed at the following concentrations: kanamycin, 100 μg/ml; nalidixic acid, 20 μg/ml; chloramphenicol, 12.5 μg/ml.

### Plasmid and strain construction

The plasmids and strains used in this study are listed in Table 1, and the primers used are listed in Table 2. All of the strains were grown at 26°C in LB, or LB broth with 290 mM NaCl (referred to as LB-290). For preparation of secreted proteins, brain heart infusion broth (BHI; Difco) and BHI with 490 mM NaCl were used. Antibiotics were added as needed at the following concentrations: kanamycin, 100 μg/ml; nalidixic acid, 20 μg/ml; chloramphenicol, 12.5 μg/ml.

### Point mutations made by overlap extension for ysrT

Point mutations were introduced into the ysrT gene using overlap extension PCR (18). Overlapping forward and reverse primers were designed with the desired mutation. These primers were used in two separate PCRs with appropriate cognate primers. The two products were gel purified and used as template DNA for PCR with the flanking forward and reverse primers to amplify the intact full-length product. The product was digested with Sall and NotI and cloned into those sites. The resulting product was digested with XbaI and Sall and cloned into those sites. The resulting product was digested with Sall and NotI and cloned into those sites. The resulting product was digested with Sall and NotI and cloned into those sites. The resulting product was digested with Sall and NotI and cloned into those sites. The resulting product was digested with Sall and NotI and cloned into those sites.
mosomal copy of \(\text{ysrR}\)-D75A, the megaprimer was synthesized using genomic DNA for the template and primers \(\text{ysrR-delA}\) and D75A-R. The full-length product was amplified using the megaprimer and \(\text{ysrR-delID}\). This product was digested with Sall and NotI and cloned into those same sites of pSR47S to generate pKW75.

**Introduction of chromosomal point mutations for \(\text{ysrR}\) and \(\text{ysrT}\).** Chromosomal copies of genes encoding point mutations were constructed using the same methods employed to delete genes. Plasmids pKW78 (\(\text{ysrT}\)) and pKW75 (\(\text{ysrR}\)) were conjugated into the \(\text{Y. enterococci}\) strain bearing a deletion of the targeted gene. Following counterselection, individual colonies were screened by PCR for the presence of the full-length gene. The regions surrounding the engineered point mutations were amplified and sequenced to verify that the desired strain had been constructed without errors. The resulting strains are referred to as \(\text{ysrR-D75A-R}\) and \(\text{ysrR-D75A-F}\). The resulting strains are referred to as \(\text{ysrR-D75A-R}\) and \(\text{ysrR-D75A-F}\).

**β-Galactosidase assays.** Saturated cultures grown overnight in L broth were diluted into fresh L broth or LB-290 to an initial optical density at 600 nm (OD600) of 0.2 and grown for 2 h at 26°C with agitation. Antibiotics were added as necessary to retain plasmids and chromosomal integrations. Assays were performed as described previously (29). Individual assays were conducted using at least three independent cultures for each strain tested, and the assays were repeated at least three times to ensure reproducibility. Representative assays are shown.

**Preparation of secreted proteins.** Proteins secreted into culture supernatants were collected essentially as described previously (46), except that the base growth medium was BHI or BHI with 490 mM NaCl. Briefly, overnight cultures were collected essentially as described previously (46), except that the base growth medium was BHI or BHI with 490 mM NaCl. The cells were pelleted and discarded. Supernatants were filtered and precipitated with 10% trichloroacetic acid at 4°C overnight. Protein pellets were resuspended in sample buffer at a concentration of 1 OD equivalent per 10 μl. Approximately 2.5 OD equivalents were subjected to 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and stained with Coomassie blue.

**DNA sequencing and analysis.** All DNA sequencing was performed by ELON Bioscience, Inc., at their North Carolina facility. For sequencing of the \(\text{ysrTs}\) region of the biovar-1A isolates (listed in Table 1), genomic DNA was prepared and used as templates for PCR using primers \(\text{ysrR-delC}\) and \(\text{ysrR-delID}\). The PCR products were gel purified and sequenced with primer \(\text{ysrR-delC}\).

<table>
<thead>
<tr>
<th>Name</th>
<th>Sequence* (5’ → 3’)</th>
</tr>
</thead>
<tbody>
<tr>
<td>ysrT-delA</td>
<td>ACGGCGTACGACGGCCCTATTATTCTGCGGGCTG</td>
</tr>
<tr>
<td>ysrT-delB</td>
<td>CCGGATCCTGAAGGTGCATCATGTAGTTCC</td>
</tr>
<tr>
<td>ysrT-delC</td>
<td>CGGGATCTGATAAGACGTCGTAAGATGAG</td>
</tr>
<tr>
<td>ysrT-delID</td>
<td>ATAGAAGATGCGGGCCATCAAACGGAATGATGAG</td>
</tr>
<tr>
<td>ysrT-delF</td>
<td>GCGTACGTGCCGCTGGTGGCGCCGAATATGGGCAGGC</td>
</tr>
<tr>
<td>ysrT-delG</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delH</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delI</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delJ</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delK</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delL</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delM</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delN</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delO</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delP</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delQ</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delR</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delS</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delT</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delU</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delV</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delW</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delX</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delY</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
<tr>
<td>ysrT-delZ</td>
<td>CGGGATCCCTAGATAACAGCTAAATAAATAGCCCCGGC</td>
</tr>
</tbody>
</table>

---

* Restriction sites are underlined (six- to eight-base sequences).
* Published elsewhere (46) and included here for completeness.

**SECONDARY STRUCTURAL ANALYSIS AND MODELING.** Analysis of the secondary structure prediction for \(\text{YsrT}\) was performed using the Phyre server (http://www.sbg.bio.ic.ac.uk/phyre) (25). The sequences for the designated HPT-containing proteins in \(\text{Y. enterococci}\) were obtained from the following accession numbers: ArcB (YE3733), YP_001007887.1; BarA (YE0742), YP_001005086.1; ResD (YE1398), YP_001005711.1; CheA (YE2577), YP_001000780.1; BsgS (YE2663), YP_001000833.1. The residues that make up the HPT domain were obtained from the MIST database (43), and the alignment was generated using CLUSTAL W as described above. The YsrR receiver domain was modeled using SWISS-MODEL (16) and generated using PyMOL (The PyMOL Molecular Graphics System, version 1.2; Schrödinger, LLC). Domain sequences from \(\text{YsrR}, \text{YsrT}\), and \(\text{YsrT}\) were identified with the simple modular architecture research tool (SMART) and used to perform a BLASTp search (1). A subset of homologous proteins whose domains had been defined either genetically or biochemically were aligned using the CLUSTAL W algorithm (40) in the Geneious Pro version 5 software package (BioMatters, Ltd., New Zealand).
between YsrS and YsrR, as Ysp secretion was unaffected by these mutations (data not shown). Upon release of the annotated Y._enterocolitica genome, we noticed that a small open reading frame (ORF), designated YE3561a, was located adjacent to ysrS (Fig. 1A). BLASTp results revealed that this hypothetical protein had homology to HPt domains, and this is supported by aligning YE3561a with all of the known HPt domains found in _Y. enterocolitica_ (Fig. 1B). YE3561a encodes an 82-amino-acid protein that contains a single histidine residue (H38) located within a short stretch of somewhat conserved residues found in HPt domains (13). Protein structure prediction using the Phyre server (23) predicted a high helical content for YE3561a, with the conserved H located on an exposed region of an alpha helix. These findings are consistent with the notion that YE3561a serves as an HPt protein.

To investigate if YE3561a encodes a protein important for the function of the Ysa T3SS, we constructed an in-frame deletion of this gene and tested the resulting strain for the presence of Ysps in culture supernatants. We found that no secreted proteins could be detected from cultures grown under inducing conditions when YE3561a was deleted (Fig. 1C). This result is the same as that observed in strains lacking ysrR and ysrS (45–47). We further tested this mutant in a strain carrying a chromosomal _ysaE-lacZ_ reporter and found that _ysaE_ expression was not activated when the bacteria were grown under inducing conditions. These data are described in detail in the following sections and shown in Fig. 2. Because of the critical role in _ysa_ expression and its putative function as part of a phosphorelay, we have renamed YE3561a _ysrT_ and refer to it as such here.
YsrS, YsrT, and YsrR are phosphorelay proteins. With all of the components of a hybrid two-component system identified and shown to be requisite factors in transcriptional activation of the ysaE promoter, we wanted to determine if YsrSTR were indeed functioning as phosphorelay proteins. To this end, alanine substitutions were made at the histidine and aspartate residues predicted to participate in the phosphorelay. These residues were chosen based on alignments with other phosphorelay proteins in which the key residues had been defined (Fig. 1B; see also Fig. 3 and 4) (9). Strains carrying either plasmid or chromosomal copies of the mutated genes were used to evaluate their ability to activate ysaE expression.

**Analysis of YsrS.** In the wild-type strain (YVM925), ysaE-lacZ expression levels are very low in the absence of NaCl (L broth), resulting in about 25 Miller units (MU). In the presence of 290 mM NaCl (LB-290), ysaE-lacZ expression levels reach about 1,085 MU, a 43-fold activation (Fig. 2A). Consistent with previous observations with different ysrS mutant strains, no activation of ysaE-lacZ is observed in LB-290 in the /H9004 ysrS mutant strain (YVM1320), indicating that YsrS is required for the salt-dependent activation of ysaE expression (45–47). This phenotype can be complemented by expressing ysrS on a low-copy-number plasmid (pYsrS WT), resulting in 420 MU in L broth and 2,614 MU in LB-290 (Fig. 2A). The elevated levels are likely the consequence of the multicopy plasmid. Plasmid pYsrSH320A carries ysrS with an alanine substitution at H320, the predicted site of autophosphorylation (H1). When pYsrSH320A is transformed into YVM1320 (/H9004 ysrS), ysaE expression is the same as in a strain with no plasmid or the vector only, with about 20 MU in L broth or LB-290 (Fig. 2A). This indicates that H320 is a critical residue for the function of YsrS in its role in activating ysaE expression in response to NaCl. A similar result was expected with pYsrSD714A; D714 is the predicted site of phosphorylation in the receiver domain of YsrS (D1) (Fig. 3A). However, a very different result was observed. This mutation caused levels of ysaE to be very high both in LB-290 and in L broth, with 4,253 and 5,472 MU, respectively (Fig. 2A). These results indicate that both H320 and D714 are required for the normal function of YsrS, but only H320 interferes with the ability of YsrS to activate ysaE expression.

The “constitutive on” phenotype from pYsrS D714A is seemingly contradictory to the assumption that YsrS is a hybrid sensor kinase, as one would have predicted a loss of function. We had noticed that there are two neighboring aspartate residues: D718 and D721 (Fig. 3). Curiously, the residue located four amino acids from the phosphorylated D is typically a proline; in the case of YsrS, this is D718. One hypothesis to explain the unusual phenotype associated with D714A is that one of these other sites could be the actual site of phosphorylation or could be phosphorylated if D714 were unavailable. To test this notion, a plasmid was generated that contained alanine substitutions at all three aspartate residues. When transformed into the /H9004 ysrS mutant strain, this plasmid had the same impact on ysaE expression as pYsrS D714A: very high expression, independent of the NaCl concentration (data not shown). In addition, the YsrS receiver domain was modeled (Fig. 3B). Model of the YsrS REC domain generated using SWISS-MODEL and edited using PyMOL. Highly conserved residues important for phosphorylation, as well as unusual residue D718, are shown as sticks.
mon for D1 phosphorylation sites, whereas D714 and D721 are located in the loop between β-strand 3 and α-helix 3. Other highly conserved residues are in the proper positions, such as magnesium ion coordinating residues E670 and D671, as well as S746 and K768, which are important for signal transduction (4). Taking all of these data together, we conclude that YsrS is indeed a hybrid sensor kinase, that D714 is the D1 phosphorylation site, and that neither of the neighboring aspartate residues can substitute for D714 as a site for phosphorylation.

**Analysis of YsrT.** A similar analysis was conducted with YsrT. As mentioned above, deletion of ysrT prevented activation of ysaE expression, yielding 24 MU in L broth and 29 MU in LB-290 (Fig. 2B). When wild-type ysrT was provided in trans on pYsrTWT, ysaE levels were slightly activated in LB-290, with 73 MU. However, with pYsrTH38A, which expresses ysrT with an alanine substitution at H38, no activation of ysaE expression was observed (21 MU in L broth and LB-290). While the activation with the wild-type plasmid is subtle, the absence of this activation with H38A supports the hypothesis that YsrT possesses both kinase and phosphatase activities and that H38 is critical for both activities.

Because of the concerns of plasmid copy number, we constructed a strain with the ysrT-H38A mutation on the chromosome, designated ysrT-H38A (YVM1378). β-Galactosidase activity from the ysaE reporter in this strain is similarly low as with the ΔysrT mutant strain, further supporting the idea that H38 is required for YsrT to function properly (Fig. 2B). As was also observed with the ΔysrR mutant strain, addition of pYsrTWT to ysrT-H38A results in about a 2-fold increase in ysaE expression (not shown).

**Analysis of YsrR.** YsrR has two key domains, a C-terminal DNA-binding domain of the LuxR family of helix-turn-helix proteins and an N-terminal receiver domain. Compared to other RRs, YsrR appears to be somewhat unusual in that it has two stretches of sequence not found in other RR proteins (Fig. 4). Secondary structural analysis predicts that these regions of two stretches of sequence not found in other RR proteins (Fig. 4). Taking all of these data together, we conclude that YsrR functions as an HPt.

The lack of full complementation by pYsrTWT could be the result of the HPt domain playing a role in dephosphorylation of YsrR, which is a known function of these domains (14, 35). To test this notion, pYsrTWT was transformed into YVM925 (wild type). Expression of ysaE was markedly decreased, yielding only 70 MU in LB-290 (Fig. 2B). Transformation of pYsrTH38A into YVM925 had no negative impact on ysaE expression levels, which measured 29 and 988 MU in L broth and LB-290, respectively. Taken together, these data imply that YsrT possesses both kinase and phosphatase activities and that H38 is critical for both activities.

A similar analysis was conducted with YsrT. As mentioned above, deletion of ysrT prevented activation of ysaE expression, yielding 24 MU in L broth and 29 MU in LB-290 (Fig. 2B). When wild-type ysrT was provided in trans on pYsrTWT, ysaE levels were slightly activated in LB-290, with 73 MU. However, with pYsrTH38A, which expresses ysrT with an alanine substitution at H38, no activation of ysaE expression was observed (21 MU in L broth and LB-290). While the activation with the wild-type plasmid is subtle, the absence of this activation with H38A supports the hypothesis that YsrT possesses both kinase and phosphatase activities and that H38 is critical for both activities.

Because of the concerns of plasmid copy number, we constructed a strain with the ysrT-H38A mutation on the chromosome, designated ysrT-H38A (YVM1378). β-Galactosidase activity from the ysaE reporter in this strain is similarly low as with the ΔysrT mutant strain, further supporting the idea that H38 is required for YsrT to function properly (Fig. 2B). As was also observed with the ΔysrR mutant strain, addition of pYsrTWT to ysrT-H38A results in about a 2-fold increase in ysaE expression (not shown).

**Analysis of YsrR.** YsrR has two key domains, a C-terminal DNA-binding domain of the LuxR family of helix-turn-helix proteins and an N-terminal receiver domain. Compared to other RRs, YsrR appears to be somewhat unusual in that it has two stretches of sequence not found in other RR proteins (Fig. 4). Secondary structural analysis predicts that these regions of two stretches of sequence not found in other RR proteins (Fig. 4). Taking all of these data together, we conclude that YsrR functions as an HPt.

The lack of full complementation by pYsrTWT could be the result of the HPt domain playing a role in dephosphorylation of YsrR, which is a known function of these domains (14, 35). To test this notion, pYsrTWT was transformed into YVM925 (wild type). Expression of ysaE was markedly decreased, yielding only 70 MU in LB-290 (Fig. 2B). Transformation of pYsrTH38A into YVM925 had no negative impact on ysaE expression levels, which measured 29 and 988 MU in L broth and LB-290, respectively. Taken together, these data imply that YsrT possesses both kinase and phosphatase activities and that H38 is critical for both activities.

Because of the concerns of plasmid copy number, we constructed a strain with the ysrT-H38A mutation on the chromosome, designated ysrT-H38A (YVM1378). β-Galactosidase activity from the ysaE reporter in this strain is similarly low as with the ΔysrT mutant strain, further supporting the idea that H38 is required for YsrT to function properly (Fig. 2B). As was also observed with the ΔysrR mutant strain, addition of pYsrTWT to ysrT-H38A results in about a 2-fold increase in ysaE expression (not shown).

**Analysis of YsrR.** YsrR has two key domains, a C-terminal DNA-binding domain of the LuxR family of helix-turn-helix proteins and an N-terminal receiver domain. Compared to other RRs, YsrR appears to be somewhat unusual in that it has two stretches of sequence not found in other RR proteins (Fig. 4). Secondary structural analysis predicts that these regions of two stretches of sequence not found in other RR proteins (Fig. 4). Taking all of these data together, we conclude that YsrR functions as an HPt.

The lack of full complementation by pYsrTWT could be the result of the HPt domain playing a role in dephosphorylation of YsrR, which is a known function of these domains (14, 35). To test this notion, pYsrTWT was transformed into YVM925 (wild type). Expression of ysaE was markedly decreased, yielding only 70 MU in LB-290 (Fig. 2B). Transformation of pYsrTH38A into YVM925 had no negative impact on ysaE expression levels, which measured 29 and 988 MU in L broth and LB-290, respectively. Taken together, these data imply that YsrT possesses both kinase and phosphatase activities and that H38 is critical for both activities.

Because of the concerns of plasmid copy number, we constructed a strain with the ysrT-H38A mutation on the chromosome, designated ysrT-H38A (YVM1378). β-Galactosidase activity from the ysaE reporter in this strain is similarly low as with the ΔysrT mutant strain, further supporting the idea that H38 is required for YsrT to function properly (Fig. 2B). As was also observed with the ΔysrR mutant strain, addition of pYsrTWT to ysrT-H38A results in about a 2-fold increase in ysaE expression (not shown).

**Analysis of YsrR.** YsrR has two key domains, a C-terminal DNA-binding domain of the LuxR family of helix-turn-helix proteins and an N-terminal receiver domain. Compared to other RRs, YsrR appears to be somewhat unusual in that it has two stretches of sequence not found in other RR proteins (Fig. 4). Secondary structural analysis predicts that these regions of two stretches of sequence not found in other RR proteins (Fig. 4). Taking all of these data together, we conclude that YsrR functions as an HPt.

The lack of full complementation by pYsrTWT could be the result of the HPt domain playing a role in dephosphorylation of YsrR, which is a known function of these domains (14, 35). To test this notion, pYsrTWT was transformed into YVM925 (wild type). Expression of ysaE was markedly decreased, yielding only 70 MU in LB-290 (Fig. 2B). Transformation of pYsrTH38A into YVM925 had no negative impact on ysaE expression levels, which measured 29 and 988 MU in L broth and LB-290, respectively. Taken together, these data imply that YsrT possesses both kinase and phosphatase activities and that H38 is critical for both activities.

Because of the concerns of plasmid copy number, we constructed a strain with the ysrT-H38A mutation on the chromosome, designated ysrT-H38A (YVM1378). β-Galactosidase activity from the ysaE reporter in this strain is similarly low as with the ΔysrT mutant strain, further supporting the idea that H38 is required for YsrT to function properly (Fig. 2B). As was also observed with the ΔysrR mutant strain, addition of pYsrTWT to ysrT-H38A results in about a 2-fold increase in ysaE expression (not shown).
passing the D1 and H2 residues (15, 42). Although this was subsequently found to occur only when the respective proteins were overexpressed (25), we wanted to address if YsrS<sub>D714A</sub> acts independently of YsrT. The ΔysrT mutant strain was transformed with pYsrS<sub>D714A</sub>, and ysaE-lacZ levels in this strain were the same as with the vector, indicating that YsrT is required for the constitutive on phenotype of pYsrS<sub>D714A</sub> (Fig. 5). To determine if YsrR is also required and if phosphorylation of the conserved residues is an important part of this phenotype, we transformed pYsrS<sub>D714A</sub> into the ysrT-H38A, ΔysrR, and ysrT-D75A mutant strains (Fig. 5). We observed that YsrT and YsrR must be present and phosphorylatable. If either gene is deleted or if the phosphorylation sites are mutated, ysaE levels are the same as the background (~25 to 60 MU). These results indicate that the peculiar phenotype observed with pYsrS<sub>D714A</sub> requires wild-type copies of YsrT and YsrR, indicating that no step in the phosphorelay is bypassed.

The genetic structure of YsrRST is conserved in Yersinia. In JB580v, the ysrT coding region begins within the ysrS coding region such that there is a 7-bp overlap. One theory for YsrT being a separate protein from YsrS is that a frameshift mutation was acquired at some point in our laboratory strain. To determine if this is a likely explanation, we examined the genetic arrangement of this region in several Yersinia strains. With the knowledge that several Y. enterocolitica biotype 1B isolates contain genes encoding the Ysa T3SS apparatus and effector genes (19, 41), we sequenced the region surrounding ysrT to determine if it is a separate gene in these strains. In every strain examined, ysrT was a separate gene (Fig. 6). A recent bioinformatic study of some of the nonpathogenic Yersinia strains has provided whole genome sequences for Yersinia mollaretii, Yersinia aldovae, and Yersinia ruckerii, among others (6). In these three species, genes with homology to TCS are located adjacent to remnants of what is likely the ysa locus. Closer examination revealed that Y. aldovae and Y. mollaretii have genes with reasonable similarity to ysrR, ysrX, and ysrT, and in these Yersinia strains, ysrT is encoded as a separate gene (Fig. 6). These results indicate that ysrT has been separate from ysrS since before the evolutionary divergence of these strains from the progenitor, indicating that there may be a functional purpose to YsrT being an isolated Hpt protein.

**DISCUSSION**

In this report, we present genetic evidence that the predicted two-component proteins YsrR and YsrS do indeed conduct a phosphorelay and that YsrT encodes a small protein providing the previously unidentified Hpt domain that is necessary to shuttle the phosphoryl group from the sensor to the RR. This phosphorelay leads to the activation of genes encoding the Ysa type III secretion apparatus and its effectors. These, however, are not the only genes playing a regulatory role in ysa expression, but we believe they are at or near the top of the regulatory cascade. In addition to YsrRST, RcsB is also required for activation of the ysaE promoter (45, 47). RcsB is the RR of the RcsCDB phosphorelay system (discussed below), and the mechanism by which it acts at the ysaE promoter is the current focus of research in our laboratory. YsaE itself is a transcriptional regulator that acts in conjunction with the chaperone/regulator SycB to stimulate the expression of six of the nine ysp genes (46, 47). Thus, YsrRST and RcsB are requisite factors in the transcription of the ysa and ysp genes.

While YsrR and YsrS have been predicted to conduct a phosphorelay, we sought to demonstrate this phenomenon and to understand how the phosphate was transferred from YsrR to YsrT. The identification of YsrT solved this mystery, estab-
lishing that YsrRST contain all of the predicted domains known to be required for phosphorylation. To determine if YsrRST are indeed phosphorylation proteins, we mutated all four predicted phosphorylation sites. Each mutation ablated the normal function of the proteins, and all but YsrS$_{D714A}$ (D2) produced the expected phenotype, with an inability to activate ysaE expression. While the phenotype produced by the YsrR D56A mutation was exactly as predicted, there are two structural deviations that indicate that the mechanism of how YsrR responds to phosphorylation may be atypical. First, there are two insertions of 12 and 15 amino acids, respectively, and second, a highly conserved proline residue located four residues from the phosphorylation site is absent. Both features may contribute to an altered conformation that could confer a unique function(s).

The constitutive phenotype of the YsrS$_{D714A}$ mutant is not easily understood but is very intriguing. It has been proposed that the evolutionary advantage of hybrid sensors is the increased number of regulatory checkpoints to minimize phosphorylation of the REC under noninducing conditions (13, 20, 34). In addition to kinase activity, some HKs also appear to possess phosphatase activities (7, 14). One plausible explanation is that this mutation may have impaired the phosphatase function of YsrS without impairing the kinase activity. However, one would have to assume that a neighboring residue could substitute for D714 for the kinase activity but not for the phosphatase activity. YsrS has D resides at positions 718 and 721, but these are unlikely to become phosphorylated due to their locations just outside the active site. A curious feature of this region of YsrS is the absence of a highly conserved proline four residues from D714. It is tempting to speculate that the architecture of this loop may be altered and confer an atypical function. We are continuing experimentation with this mutant in an effort to understand this unusual phenotype. However, biochemical analyses often used to complement the genetic experiments and more definitively show transfer of phosphoryl cross communication and versatility in these important quorum-sensing regulators. While these two examples are cases of independent HPt domains, this is a relatively rare situation. Examination of the MiST2 database (43) shows that very few organisms have proteins that contain only an HPt domain. Pseudomonas aeruginosa PA01 is a rare example of an organism that has several such free HPt proteins, with four. Y. enterocolitica has an average number of HPt-containing proteins (six) compared to other bacteria, and all are part of hybrid HKs. This database does not identify YsrT as an HPt protein (search last performed on 24/6/2010), perhaps because it is such a small ORF. This suggests that there may indeed be more such proteins, but since the similarity between the known HPt domains is weak, they may be difficult to identify in silico.

The location of ysrT led us to question if a frameshift mutation may have occurred in our strain, resulting in YsrT as a protein independent of YsrS. Sequence analysis indicates that this genetic organization is conserved not only in Y. enterocolitica 1B isolates but in more distantly related nonpathogenic Yersinia strains. Whole-genome sequencing has recently been performed for several nonpathogenic Yersinia strains, and Y. ruckeri and Y. mollaretii have reasonably well-conserved ysrR and ysrS sequences and Y. mollaretii has a gene that is likely ysrT (6). The region downstream of ysrS is more divergent in Y. ruckeri, and the protein sequence for the ORF downstream of ysrS is quite different from YsrT but still has homology to HPt domains (not shown). Y. aldovae appears to contain this locus, but the sequence suggests that a number of frameshift mutations have been acquired; the DNA sequence is well conserved, however, and indicates that ysrT would have encoded a separate protein. Thus, the conservation of the genetic structure of the ysrRST genes among not only the pathogenic 1B isolates but also environmental isolates implies that there is some functional importance to YsrT being produced as a separate protein. However, one should be careful about assuming that the presence of a ysrRST locus, as well as the ysa and ysp genes, will result in secretion of Ysps. Although we have shown here that biotype 1B isolates of Y. enterocolitica have ysrT and Howard et al. previously demonstrated by microarray analysis that these biotype 1B isolates have the ysa and ysp genes (19), we have found significant differences in the abilities of these same strains to secrete Ysps under laboratory conditions (K. A. Walker, S. E. Witowski, and V. L. Miller, unpublished results).

This body of research serves to define genetically that the YsrRST system comprises a phosphorylation system and that phosphorylation is a requisite element in the normal function of these proteins in their role as activators of the ysa type III secretion genes. Several elements of this system are unusual in that (i) the hybrid sensor lacks an HPt domain, (ii) the HPt domain is provided on the small cytosolic protein YsrT, (iii) ysrT is encoded immediately downstream of ysrS, and (iv) YsrR is unique to Y. enterocolitica and nonpathogenic Yersinia species. In addition, YsrR contains stretches of amino acids that appear to be insertions not found in similar RR, indicating that it may have some unique properties/functions as well. Like many Gram-negative bacteria, Y. enterocolitica has about 30 TCS, with 24 HKs, 6 of which are hybrid HKs, and 31 RRs. Of the six hybrid HKs, two are unique to yersiniae: YsrRST and YE3578-YE3579. Curiously, YE3578 and YE3579 are nearly identical to YsrR and YsrS, respectively, on both the amino
acid and DNA levels. Adding to the intrigue of this second system is that there is no HPT-containing protein associated with YE3578-YE3579. In analogy to the LuxNUO and LusQUO systems, it is tempting to speculate that YsrT could function as the HPI for both YsrS and YE3579, thus explaining the significance of ysrT encoding a protein detached from its cognate sensor. Efforts to elucidate whether YE3578-YE3579 utilizes YsrT for regulating ysaE or other promoters are ongoing in our laboratory.

ACKNOWLEDGMENTS

We thank Ruth E. Silversmith for critical reading of the manuscript and Ruth E. Silversmith, Bob Bourett, Joshua Hall, and Matthew Lawrenz for stimulating discussions. We are indebted to Brittany Fogarty and R. Patrick Summers for technical assistance.

This research was supported by National Institutes of Health grant AI063299 awarded to V. L. Miller.

REFERENCES