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1 **Figure 2-1.** Sites at which *V. fischeri* encounters acidic pH, and genes induced in response to
2 acidic pH. *A*) The light organ of *V. fischeri* (Left: indicated in black under the squid's mantle),
3 is an organ with bilateral symmetry. In newly hatched squid, the bilateral ciliated fields
4 structures present on the light organ. The structure, and metachronal beat, of these fields
5 promote the harvesting of *V. fischeri* from the bacterioplankton. Upon exposure to
6 peptidoglycan, the surfaces of the ciliated fields secrete mucus, which is acidic (~pH 6.5). *B*)
7 A comparison of *V. fischeri* transcripts expressed in pH 8.0 or 6.5 seawater containing mucins
8 (a mimic of the environment encountered upon first contact with the host), reveals a linear
9 correlation between populations of RNA ($r^2=0.97$), as well as a subset of genes differentially
10 expressed greater than 2-fold (open circles). The expression of 41 genes is greater at pH 8.0
11 than pH 6.5, while the expression of 36 genes is greater at pH 6.5 than pH 8.0. Data represent
12 an analysis of 3 independent pools of RNA. *C*) qRT-PCR was used to validate the pH-
13 dependent transcription of a subset of genes identified in the microarray, using the same
14 growth conditions (grey bars, pH 6.5; open bars, pH 8.0; error represents SD; n=6 biological
15 replicates; numbers above bars indicate the fold change in expression between pH 6.5 and pH
16 8.0 +/- standard deviation).
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1 **Table 2-2. Genes differentially regulated by exposure to acidic pH in seawater**

VF_ID	Gene	Predicted Function	Fold Δ 6.5/8.0
VF_0041	<i>mdtL</i>	Multidrug efflux system protein	-2.14
VF_0150	-	Hypothetical protein	2.14
VF_0406	<i>pyrB</i>	Aspartate carbamoyltransferase	-2.28
VF_0461	-	Sodium-dependent phosphate transporter	2.06
VF_0472	<i>carA</i>	Carbamoyl phosphate synthase small subunit	-2.17
VF_0475	<i>ompU</i>	OmpU, outer membrane protein	4.36
VF_0804	<i>asnB</i>	Asparagine synthetase B	-2.03
VF_0828	<i>znuB</i>	Zinc ABC transporter membrane protein	2.13
VF_0829	<i>znuC</i>	Zinc ABC transporter ATP-binding protein	2.39
VF_0830	<i>znuA</i>	Zinc ABC transporter periplasmic substrate-binding protein	2.48
VF_0831	<i>yebA</i>	Peptidase	2.02
VF_0833	<i>feoA</i>	Ferrous iron transport protein A	3.89
VF_0834	<i>feoB</i>	bifunctional ferrous iron transporter, protein B/ GTP-binding protein/membrane protein	2.58
VF_1010	-	Putative porin	-11.51
VF_1011	-	Putative porin	-2.29
VF_1067	<i>yqjF</i>	Quinol oxidase subunit	-10.51
VF_1068	-	Pirin	-9.80
VF_1069	-	Hypothetical protein	-8.87
VF_1076	-	Sulfite-dehydrogenase	-2.38
VF_1077	<i>nirV</i>	Formylglycine-generating sulfatase NirV	-3.52
VF_1147	<i>cstA</i>	Peptide transporter induced by carbon starvation	-6.00
VF_1160	<i>sscR</i>	6-pyruvoyl tetrahydrobiopterin synthase	2.84
VF_1373	-	Putative Fe ²⁺ /Mn ²⁺ transporter	2.24
VF_1374	<i>ybgK</i>	Allophanate hydrolase subunit 2	2.61
VF_1375	<i>ybgJ</i>	Allophanate hydrolase subunit 1	4.56
VF_1376	<i>ybgL</i>	LamB/YcsF family protein	4.64
VF_1377	-	Hypothetical protein	5.88
VF_1410	<i>abgT</i>	Aminobenzoyl-glutamate transporter	-2.19
VF_1513	<i>ydjN</i>	Sodium:dicarboxylate symporter family protein YdjN	-2.15
VF_1522	<i>zntA</i>	Zinc/cadmium/mercury/lead-transporting ATPase	-3.09
VF_1597	<i>oppA</i>	Oligopeptide-binding protein OppA	-2.17
VF_1795	<i>ompC</i>	Outer membrane protein OmpC	16.58
VF_2042	-	Methyl-accepting chemotaxis protein	-2.14
VF_2150	<i>sfuB</i>	Iron(III)-transport system permease SfuB	2.11
VF_2151	-	Iron(III) ABC transporter periplasmic binding protein	2.46
VF_2157	-	Glycerate kinase	-2.03
VF_2220	-	Ubiquinol-cytochrome c reductase iron-sulfur subunit	-2.45

VF_ID	Gene	Predicted Function	Fold Δ 6.5/8.0
VF_2265	<i>leuO</i>	Leucine transcriptional activator	3.03
VF_2394	<i>purH</i>	Bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	-2.05
VF_2446	<i>fliL2</i>	Flagellar basal body protein FliL	2.20
VF_2458	-	Hypothetical protein	2.04
VF_2492	<i>scsC</i>	Copper sensitivity protein ScsC	2.19
VF_2520	-	Cytochrome c5	-2.40
VF_2527	<i>ihvC</i>	Ketol-acid reductoisomerase	2.50
VF_2528	<i>ihvC</i>	Ketol-acid reductoisomerase	2.01
VF_A0070	-	Lipoprotein	2.06
VF_A0124	<i>tpdB</i>	Di-/tripeptide transporter permease	28.40
VF_A0210	<i>eptA</i>	Metal-dependent hydrolase	67.03
VF_A0371	-	Hypothetical protein	2.12
VF_A0447	-	Methyl-accepting chemotaxis protein	2.21
VF_A0610	-	Hypothetical protein	7.51
VF_A0738	-	Hypothetical protein	2.60
VF_A0748	<i>bioA</i>	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	-2.93
VF_A0852	<i>ycdR</i>	Fused DNA-binding transcriptional regulator/ amino transcriptional regulatory protein	-3.76
VF_A0863	<i>hcp</i>	Hydroxylamine reductase	3.47
VF_A0995	-	High-affinity iron permease	2.75
VF_A1112	<i>lysE</i>	Amino acid transporter LysE	-3.14
VF_B23	-	Hypothetical protein	-2.15
VF_B24	-	Putative conjugative region transfer protein	-2.13
VF_B27	-	Hypothetical protein	-2.11
VF_B28	-	Hypothetical protein	-2.06
VF_B30	-	Putative type II secretion component PulF	-2.01
VF_B37	-	Hypothetical protein	-2.40
VF_B38	-	Attachment mediating protein VirB2-like protein	-2.30
VF_B46	-	DNA topoisomerase III	-2.10
VF_B47	-	OmpA-like outer membrane protein	-2.13
VF_B48	-	Hypothetical protein	-2.21