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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Vibrio fischeri* SR5, a Strain Isolated from the Light Organ of the Mediterranean Squid *Sepiola robusta*

Mattias C. Gyllborg,[a] Jason W. Sahl,[b] David C. Cronin III,[a] David A. Rasko,[b] and Mark J. Mandel[a]

Department of Microbiology-Immunology, Northwestern University Feinberg School of Medicine, Chicago, Illinois, USA,[a] and University of Maryland School of Medicine, Institute for Genome Sciences, Department of Microbiology and Immunology, Baltimore, Maryland, USA[b]

Here, we describe the draft genome sequence of *Vibrio fischeri* SR5, a squid symbiotic isolate from *Sepiola robusta* in the Mediterranean Sea. This 4.3-Mbp genome sequence represents the first *V. fischeri* genome from an *S. robusta* symbiont and the first from outside the Pacific Ocean.

Vibrio-squid mutualisms represent valuable models for the study of mechanisms that underlie the development and maintenance of specific microbe-host symbioses. The most-detailed studies have come from the specific association between the Hawaiian bobtail squid, *Euprymna scolopes*, and *Vibrio fischeri* (5, 8, 10). Here, we report the draft genome sequence of *V. fischeri* strain SR5 (3), which was isolated from the Mediterranean sepiolid squid, *Sepiola robusta*. *S. robusta* exhibits unique anatomical and behavioral features compared to *E. scolopes* (4), but some symbionts of *S. robusta*, including SR5, can also colonize *E. scolopes* efficiently, making them valuable isolates for mechanistic studies.

Paired-end 454 (2.5-kb inserts) and Illumina (300-bp inserts) libraries were constructed and sequenced to depths of approximately 30-fold (454 GS FLX Titanium) and 60-fold (Illumina GA II), respectively. Contigs were assembled with MIRA version 3.2.1.17 (1) and Seqman NGen 3.0 (DNASTAR, Madison, WI). The resulting 73 contigs represent a high-confidence draft sequence for the 4.3-Mbp *V. fischeri* SR5 genome, with an N_{50} of 490 kb. Contigs spanning the presumed chromosomal replication origins were split into two, and the resulting 75 contigs were oriented similarly to other sequenced *V. fischeri* genomes with Mauve Contig Mover (2, 7).

Mapping of the contigs against the genome of the monocentrid fish symbiont, *V. fischeri* MJ11 (6), suggested that the completed *V. fischeri* SR5 genome will be colinear with MJ11. From this analysis, SR5 contigs were assigned to chromosome I ($n = 8$ contigs, 2.8 Mbp), to chromosome II ($n = 4$ contigs, 1.3 Mbp), or as unmapped ($n = 61$ contigs, 0.1 Mbp). The large number of unmapped SR5 contigs are largely flanked by repetitive sequences, including *rrn* operon genes (rRNA/tRNA) and genes that are found in multicopy within the *V. fischeri* chromosome (e.g., RTX genes) and are thought to be difficult genomic regions rather than extrachromosomal DNA.

Analysis of orthologs (2, 6) among SR5, MJ11, and ES114 identified protein-coding genes unique to each sequenced *V. fischeri* strain. The SR5-specific genes are in small islets distributed across both chromosomes, typically consisting of 1 to 20 genes. The islets often encode members of phosphotransferase systems (PTS) and other metabolic genes, suggesting that this strain may encode novel and/or enhanced metabolic capacities that enable the expanded host range relative to MJ11. Absent from SR5 are the ES114-specific biofilm regulator *rscS* (9, 11) and the putative siderophore biosynthesis and receptor genes conserved between MJ11 and ES114 (VF_A0156 to VF_A0165). These observations suggest a number of intriguing issues for future studies as to what biological activities are required for squid colonization and how SR5 is able to efficiently colonize its natural host and the heterologous *E. scolopes* when MJ11 cannot.

Nucleotide sequence accession number. The *V. fischeri* SR5 whole-genome shotgun project has been deposited in GenBank under the accession number AHIH00000000.

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Address correspondence to Mark J. Mandel, m-mandel@northwestern.edu.

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