Trends in Microbiology | Microbe of the Month

Shewanella algae

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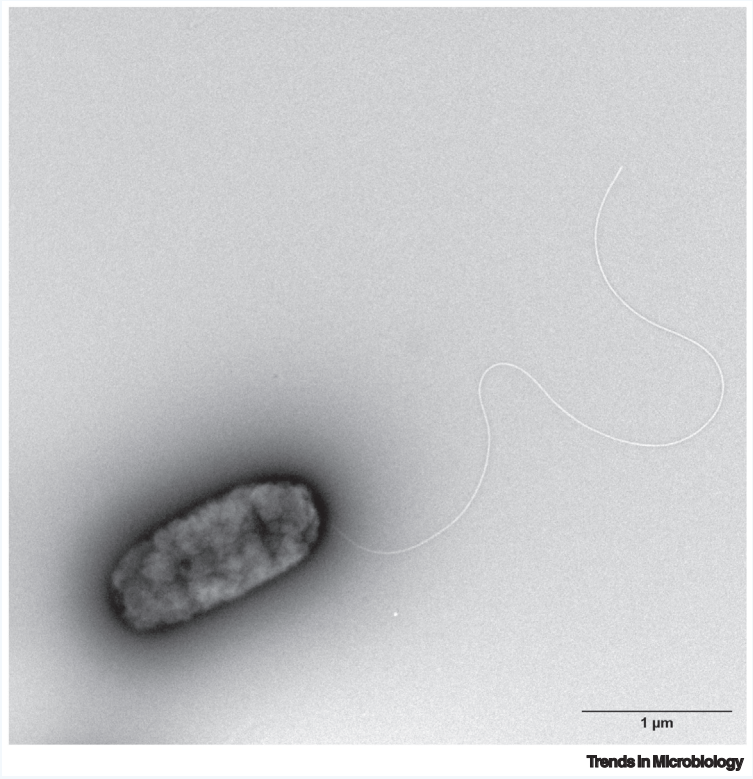
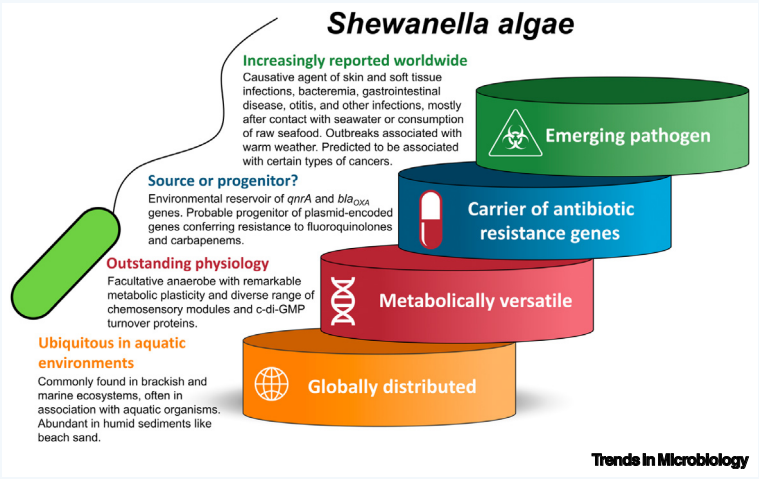


The facultative anaerobic, halophilic, mesophilic, rod-shaped, and Gram-negative bacterium *Shewanella algae* is widespread in marine and brackish ecosystems, where it can be isolated from water, sediments, or aquatic organisms such as algae, fish, or marine invertebrates. The ubiquity of *S. algae* and its ability to colonize niches outside and inside a living host is supported by a remarkably versatile physiology and metabolism, which includes the ability to use a broad array of alternative electron acceptors (AEAs) for respiration, a feature shared with other *Shewanella* species, alongside other metabolic traits. Unlike most *Shewanella* species, *S. algae* is an occasional human pathogen. The presence of virulence factors in *S. algae* genomes indicates its potential to adapt to a pathogenic lifestyle. Overall, the epidemiology and clinical manifestations of *S. algae* infections are similar to those of halophilic *Vibrio* species and may be influenced by global climate changes. Here I summarize the key genomic, taxonomic, metabolic, physiological, and epidemiological characteristics of this bacterial species.



KEY FACTS:

The genome of *S. algae* consists of a single chromosome of 4.8–5.2 Mbp, with a G+C content of 53%. Some strains carry plasmids. The reference genome for this species is CP068230.1.

Despite diverse origins, *S. algae* strains belong to the same taxonomic subspecies (digital DNA–DNA hybridization >79%). Early studies showed similarity between clinical and environmental strains. The features that differentiate pathogenic (i.e., clinical) from potentially pathogenic (i.e., environmental) strains or lineages, if any, remain unclear.

Shewanella upenei and *Shewanella haliotis* are later heterotypic synonyms of *S. algae*. Some published *Shewanella* strains, like BrY, had been misidentified as *S. algae*. Clinical misidentification of *S. algae* as other bacteria was once common, but less frequent nowadays with improved automatic identification systems, matrix-assisted laser desorption/ionization-time-of-flight (MALDI-TOF), and the use of genome sequencing.

S. algae can be isolated from environmental sources using media such as Lygnby's iron agar supplemented with L-cysteine, which detects its H_2S-producing capacity. Enrichment cultures improve recovery.

S. algae is intrinsically resistant to fosfomycin and grows at 42°C and high NaCl concentrations, facilitating its selection and initial differentiation from other *Shewanella* species. Clinical isolation is also straightforward using standard microbiological procedures.

S. algae moves via a single, polar flagellum and can colonize surfaces through biofilm formation. Biofilm regulation by respiration of specific AEAs might support niche specialization.

Sequenced strains contain 28–31 chemoreceptors and 61–67 GGDEF, EAL, or HD-GYP domain-containing proteins, indicating extensive sensory capacities and representing about twice and three times, respectively the number of chemoreceptors and c-di-GMP turnover proteins of an average

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Declaration of interests

The author declares no competing interests.

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Outbreaks associated with warm weather episodes have been documented in the Western Baltic Sea region, concomitant with *Vibrio* outbreaks and with a comparable incidence. Outbreaks associated with warmer water conditions are likely to occur in other water bodies, reinforcing the need for adequate surveillance and reporting.

The abundance of *Shewanella* spp., including *S. algae*, in aquatic sediments, facilitated by its versatile energy metabolism, makes this redox-stratified niche a relevant environmental reservoir.

While an association between *S. algae* and cancer remains unclear, some evidence links *Shewanella* spp., presumably pathogenic species like *S. algae*, to certain malignancies, such as colorectal or prostate cancer. The presence of *Shewanella* has been associated with poor prognosis in gastric cancer. These findings warrant further investigation.

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TAXONOMY AND CLASSIFICATION:
KINGDOM: Bacteria
PHYLUM: Pseudomonadota
CLASS: Gammaproteobacteria
ORDER: Alteromonadales
FAMILY: Shewanellaceae
GENUS: *Shewanella*
SPECIES: *Shewanella algae*

bacterium. Overall, the type strain genome encodes 248 input domains, 226 of which are predicted to bind to small molecules.

S. algae is a natural reservoir and presumptive progenitor of *qnrA* genes found in enterobacterial plasmids, which confer fluoroquinolone resistance. It also carries chromosomal bla_{OXA} carbapenemases. Various acquired mobile genetic elements linked to antibiotic resistance or virulence have been identified in *S. algae* genomes.

Traditional allelic replacement strategies show limited efficiency in *S. algae*. More efficient and effortless gene-editing methods are needed.

DISEASE FACTS:
S. algae causes, primarily, skin and soft-tissue infections, bacteremia, otitis, or gastrointestinal disease after exposure to seawater or consumption of raw or undercooked seafood. Skin and soft tissue infections can occasionally be aggressive. Underlying pathologies predispose to infection, although cases in healthy individuals also occur. Infections affecting animals, such as fish and marine invertebrates, have also been documented.

Around 80% of *Shewanella* infections in humans are attributed to *S. algae*.

S. algae produces hemolysin, catalase, siderophores, and various exoenzymes that may contribute to its pathogenicity. Biofilm formation is thought to enhance adhesion to human tissues. Putative type VI secretion systems and related effector proteins have been predicted *in silico*.

S. algae was originally described as a tetrodotoxin (TTX) producer, but its ability to produce TTX at levels significant for foodborne intoxications remains uncertain, with some studies failing to reproduce this finding.

S. algae is tolerant to bile salts and can grow on thiosulphate–citrate–bile salts–sucrose (TCBS) agar, where it forms green colonies. Some strains have acquired urease operons. These features may contribute to gastrointestinal disease. In addition, putative virulence islands have been described, for example, but not exclusively, in enteritis isolates.

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