## Evolution of the Baltic Sea Shewanella

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The Genus Shewanella is comprised of 50 different named species which have been isolated from a variety of environments (mostly aquatic) including terrestrial subsurface and deep sea sediments, fresh and salt-waters, and creatures common to these environments including fish, squid, algae, oysters, sponge, mussels. Distinguishing characteristics of this genus include their unparalleled respiratory diversity and the capacity to thrive at low temperatures. There are currently 21 genomic sequences publically available for the Genus Shewanella, including four different S. baltica strains isolated from different depths within the Baltic Sea, providing an excellent opportunity to examine the genetic basis for their ability to occupy niches that vary dramatically in temperature, salinity, redox, and pressure. The orthology of predicted proteinencoding genes from each of the completed Shewanella genomes was initially conducted by protein-protein pair-wise reciprocal BLAST and subsequently refined by manual curation. Approximately half of each genome contributed to the core of conserved proteins present in all Shewanella, while between 76 and 82% of the proteins were conserved among the four S. baltica genomes. Two strains, S. denitrificans and S. baltica OS155 have the most genes absent from the Genus- and Species-specific conserved protein cores, respectively. Gene loss in S. denitrificans was predominated by single gene deletions often accompanied by breaks in genome synteny, while large deletions of gene loci accounted for nearly half of the S. baltica core proteins lost in OS155. Based on our current projection of gene functions in these two strains, it appears that the greatest impact of these mutational events was to reduce their respiratory versatility. Genes acquired by the Baltic Sea isolates include functions associated with defense against eukaryotes and phage suggesting that this is an important survival strategy for shewanellae inhabiting the Baltic Sea.