

## Genomic and metabolic profiling of sialic (nonulosonic) acids

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Sialic acids (Sias) are nonulosonic acid sugars prominently displayed on cell surfaces of higher animals and occasionally mimicked by bacterial pathogens utilizing homologous biosynthetic pathways. In mammals, sialic acids are found on all mucosal surfaces in terminal positions of glycoproteins and glycolipids. More than a dozen microbial species are known to synthesize or scavenge sialic acids in order to shield their surfaces from host innate immune processes. We are interested in the evolution and structure of bacterial sialic acids and related nonulosonic acids and their impact on microbial interactions with animal hosts. We recently examined the genomes of ~1000 sequenced microbes and found that biosynthetic pathways for nonulosonic acids are far more widely distributed than previously realized. We used phylogenetic analysis, validated by targeted biochemistry, to predict nonulosonic acid types (i.e. neuraminic, legionaminic, or pseudaminic acids) expressed by various organisms. *Vibrio* species were well represented among the bacteria identified by genomic and phylogenetic approaches to encode nonulosonic acid biosynthetic (NAB) gene clusters. Here we confirm that many *Vibrio* species express di-*N*-acetylated nonulosonic acids. Using *Vibrio vulnificus* as a model system, we have used in-frame deletion and biochemical analysis to define the genetic basis of the nonulosonic acid synthase. Integrated phylogenetic and biochemical analyses of natural isolates define a relationship between specific alleles of NAB genes, specific genotypes of *V. vulnificus*, and different levels of nonulosonic acid expression. We suggest that sialic acid-like molecules expressed by certain *V. vulnificus* may impact host-microbe associations in multiple contexts, including virulence in humans.