Poster Presentation

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Structural Basis for the Novel Bidirectional Activity of the nanoRNase NrnA

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NanoRNA are RNA molecules 5 nt or less that are generated during several fundamental biological processes, including abortive transcription and RNA turnover. NanoRNA may play a role in the priming of transcription initiation. Degradation of nanoRNA is executed by two distinct families of nanoRNases. In E. coli and higher eukaryotes, Oligoribonuclease, a 3'-5' exoribonuclease from the DEDD family, is responsible for nanoRNA decay. However, orn homologs are missing from the vast majority of bacterial and archaeal genomes, including the Firmicute B. subtilis. NanoRNase A (NrnA), a DHH family phosphodiesterase in B. subtilis, is the founding member of the second class of nanoRNases, and is widespread in organisms lacking orn. NrnA was originally identified as a 3'→5' exonuclease, but we show biochemically that this enzyme is bidirectional, degrading 2-5 nucleotide long RNA oligomers from the 3' end, and longer RNA substrates from the 5' end. We have determined the crystal structure of Bacillus subtilis NrnA, which reveals a dynamic bi-lobal architecture, with the catalytic DHH domain linked to the substrate binding DHHA1 domain via an extended linker. While this arrangement is similar to the structure of RecJ, a 5'→3' DHH family DNase, NrnA has gained an extended substrate-binding patch that is likely responsible for its 3'→5' activity.

Keywords: Exonuclease, RNA Degradation, pAp phosphatase