

W0299

**Structural Analysis of Dispersin B, a Biofilm-Releasing Glycosyl Hydrolase from the Periodontopathogen *Actinobacillus actinomycetemcomitans*.** C. Raganath<sup>1</sup>, N. Ramasubbu<sup>1</sup>, L.M. Thomas<sup>2</sup>, J.B. Kaplan<sup>1</sup>, <sup>1</sup>Dept. of Oral Biology, UMDNJ, Newark, NJ USA, <sup>2</sup>HHMI, Div. of Biology, California Inst. of Technology, Pasadena, CA USA.

Bacteria in a biofilm are enmeshed in a self-synthesized extracellular polysaccharide matrix that holds the bacteria together in a mass and firmly attaches the bacterial mass to the underlying surface. A major component of the extracellular polysaccharide matrix in several phylogenetically diverse bacteria is PGA, a linear polymer of N-acetylglucosamine residues in  $\beta(1,6)$ - linkage. PGA is produced by the gram-negative periodontopathogen *Actinobacillus actinomycetemcomitans* as well as by the gram-positive device-associated pathogen *Staphylococcus epidermidis*. We present the crystal structure (2.0Å) of dispersin B, a soluble glycosyl hydrolase that degrades PGA. Dispersin B crystallizes in the orthorhombic space group C222<sub>1</sub> with cell dimensions a = 41.02, b = 86.13, c = 185.77 Å. The core of the enzyme consists a  $(\beta/\alpha)_8$  barrel topology similar to other  $\beta$ -hexosaminidases but significant differences exist in the arrangement of loops in the vicinity of the active site. The location and interactions of the glycerol and acetate moieties in conjunction with the sequence analysis suggest that dispersin B cleaves  $\beta(1,6)$ -linked N-acetylglucosamine polymer using a catalytic machinery similar to other family 20 hexosaminidases which cleave  $\beta(1,4)$ -linked N-acetylglucosamine residues.

This project was supported by the USPHS Grant DE12585 (N.R.) and DE15124 (J.B.K.).