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Systems Biology in Prokaryote –Eukaryote Symbiosis: Single-Crystal Spectroscopy Correlated with X-ray Crystallography and Other Complementary Methods

Thursday, 5 July 2012 13:00 (30 minutes)

We are creating a multidisciplinary, high throughput pipeline for the structural and biophysical analysis of macromolecules involved in bacterial N2-fixation in plants. Sinorhizobium meliloti 1021 and WSM419 are free-living or N2-fixing microbes. But, they only fix N2 under symbiotic, microaerobic conditions within root nodules of legumes such as alfalfa and its diploid model, Medicago truncatula. The genome sequences of S. meliloti and M. truncatula are known. Scientists from BNL, WA State Univ. (M. Kahn et al), Pacific Northwest National Lab (M. Lipton et al), Stanford Univ. (S. Long et al), the City Univ. of New York (H. Chen et al) and the NY Structural Genomics Research Consortium (S. Almo et al) collaborate to better understand this symbiotic relationship. The initial S. meliloti targets include annotated genes to proteins that bind either iron (˜144 ORFs), heme (63 ORFs), copper (28 ORFs), or is an oxidoreductase (535 ORFs). They are being characterized by small/wide angle X-ray scattering and by X-ray crystallography that is often correlated with single-crystal spectroscopy. In complementary studies, whole root nodules have been analyzed by mass-tag metabolomic and microproteomic analysis, as well as by microprobe X-ray fluorescence. Together these results provide the identity and relative abundance of bacterial and plant proteins, as well as the total distribution of first row transition metals in N2-fixing root nodules.
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