Poster Presentation

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Structure of a Novel Bacterial c-GMP Binding Protein

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cAMP is an important secondary messenger molecule widely distributed across all living kingdoms, whereas cGMP is generally considered to be restricted to eukaryotes. Recently, solid evidences for cGMP signaling in Rhodospirillum centenum have been provided, and it is proposed that cGMP could also be adapted to deliver messages to diverse outputs via unknown mechanisms. While the structures and functions of binding between cAMP and its receptor protein CRP have been well studied in the past, currently no structure of prokaryotic cGMP-binding protein complex is known. Here we report the first determination of a cGMP-receptor crystal structure from the plant pathogen Xanthomonas campestris (Xcc) to a resolution of 2.2 Å. The new cGMP receptor Xcc0249 is found to belong to the CRP/FNR family protein containing both a cyclic-Nucleotide Binding Domain (cNBD) and a GGDEF domains, and exhibits strong cGMP binding and diguanylate cyclase activities. Mutations of crucial amino acid residues responsible for cGMP binding to Xcc0249 are found to significantly reduce the biofilm formation and virulence in Xcc. Isothermal calorimetry (ITC) measurements demonstrate that Xcc0249 can bind preferentially to cGMP with a much stronger affinity (KD: 2.93E-7) than cAMP (KD: 1.79E-5). cGMP binding to Xcc0249 is also found to enhance the GGDEF diguanylate cyclase activity, implying a broader functional role of cGMP and a possible linkage between the cGMP and c-di-GMP interaction networks in bacteria. References

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