

Poster Presentation

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Degenerate Sequence Recognition by AdpA

J. Ohtsuka¹, M. Yao¹, K. Nagata¹, K. Miyazono¹, Y. Zhi¹, Y. Ohnishi², M. Tanokura¹

¹The University of Tokyo, Department of Applied Biological Chemistry, Graduate School of Agricultural and Life Sciences, Tokyo, Japan, ²The University of Tokyo, Department of Biotechnology, Graduate School of Agricultural and Life Sciences, Tokyo, Japan

AdpA is the central transcriptional factor in the A-factor regulatory cascade of *Streptomyces griseus* and activates hundreds of genes required for both secondary metabolism and morphological differentiation, leading to onset of streptomycin biosynthesis as well as aerial mycelium formation and sporulation. It has been shown that AdpA binds to over 500 operator regions with the loosely conserved consensus sequence, 5'-TGGCSNGWWY-3' (S: G or C; W: A or T; Y: T or C; and N: any nucleotide). However, it is still obscure how AdpA can control hundreds of genes. To reveal the molecular basis of the low nucleotide sequence specificity, we have determined the crystal structure of the complex of DNA-binding domain of AdpA and a 14-mer duplex DNA with two-nucleotide overhangs at 5'-ends at 2.95-Å resolution. The crystal structure and electrophoretic mobility-shift assays showed that only two arginine residues, Arg262 and Arg266, are involved in the sequence recognition and determine the nucleotide specificity/preference of continuous five base-pairs of positions 1–5 in the consensus sequence. These results partially explain how AdpA directly controls hundreds of genes.

[1] M.D. Yao, J. Ohtsuka, K. Nagata, et al., *J. Biol. Chem.* 2013, 288, 31019-31029

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