

**Project Title:** Characterization of key regulators of *Pseudomonas aeruginosa* virulence  
呼吸道病原細菌毒力關鍵調控因子的研究

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Transcription factors (TFs) significantly regulate transcription, mediating multiple biological pathways and events in eukaryotes and prokaryotes. The Gram-negative bacterium *Pseudomonas aeruginosa* is the primary human opportunistic pathogen that grows in a ubiquitous environment. *P. aeruginosa* tends to cause infection among burn victims, patients with cystic fibrosis, and individuals hospitalised for long periods.

To profile the whole TF-DNA binding landscapes and construct a comprehensive regulatory network of *P. aeruginosa*, the team performed ChIP-seq experiments of 158 TFs, which are short of TFs binding sites (TFBSs) information. Since the binding information of 158 TFs was acquired, the team planned to investigate their potential function on virulence-related pathways and pathogenesis of *P. aeruginosa*. An enrichment analysis was performed to define the term master regulator, which might play an important role in regulating a specific pathway by hypergeometric test (BH-adjusted  $P < 0.05$ ). The team primarily focused on the promoter region of TF-binding profiles on genes involved in 8 pathways, including QS, motility, biofilm production, antibiotic resistance, T6SS, T3SS, reactive oxygen species (ROS) resistance, and siderophores. Accordingly, 150 of 158 TFs bound at least one target gene associated with virulence, and 79 were identified as master regulators.

