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Physiological functions of the CreBC two-component regulatory system in *Stenotrophomonas maltophilia*

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Stenotrophomonas maltophilia occurs naturally in a variety of habitats and harbors at least 43 sets of two-component regulatory systems (TCSs) to respond environmental conditions. The CreBC TCS is a conserved regulatory system found in *Escherichia coli*, *Aeromonas* spp., *Pseudomonas aeruginosa* and *S. maltophilia*. The physiologic roles of CreBC TCS in bacterial growth, morphology, secreted protease activity and swimming were assessed. We constructed creB, creC and creBC in-frame deletion mutants KJΔCreB, KJΔCreC and KJΔBC in *S. maltophilia* KJ and compared the behaviors of wild type and mutant strains in a variety of assays. Single knockout mutants KJΔCreB or KJΔCreC and the double mutant (KJΔBC) displayed wild type patterns of growth and morphology. Compared to that in wild-type KJ, secreted protease activity in KJΔCreB was unchanged; however, secreted protease activity was significantly reduced in KJΔCreC and KJΔBC. This finding suggested that CreC can be cognate with an unidentified response regulator and governs secreted protease activity. Single gene inactivation of either creB or creC in *S. maltophilia* KJ resulted in mutants with enhanced swimming motility and this phenotype was augmented in the double mutant KJΔBC. To elucidate the underlying regulatory circuit responsible for ΔcreBC-mediated swimming enhancement, morphological observation of the flagella was performed. Most KJΔBC cells had flagella numbers and morphology similar to those of wild-type KJ cells, ruling out the possibility that enhanced swimming motility in KJΔBC was due to altered flagella morphology. The exact mechanism responsible for the ΔcreBC-mediated swimming enhancement is still unclear.

Biography

Tsuey-Ching Yang is a Professor of National Yang-Ming University, Taiwan. She has published more than 50 papers in reputed journals.

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