Characterization of C-terminal structure of MinC and its implication in evolution of bacterial cell division

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Abstract

Bacterial cells have a fundamental need to divide by binary fission through accurate spatial and temporal regulation of septum formation, producing two daughter cells of equal size [1]. Proper cell division at the mid-site of Gram-negative bacteria reflects stringent regulation by the min system (MinC, MinD and MinE) [2]. Herein we solved the crystal structure of the C-terminal domain of MinC from Escherichia coli (EcMinCCTD). EcMinCCTD forms a dimer between the two β-sheets in each subunit, as observed in the Thermotoga maritima MinCCTD structure (TmMinCCTD). However, both EcMinCCTD and TmMinCCTD lack an α-helix (helix3) at their C-terminal tail, in comparison to Aquifex aerolicu MinCCTD (AaMinCCTD) which forms an extra interaction interface with MinD. By fusing helix3 to the C-terminus of EcMinC, we studied its effect on cell morphology and cell growth, revealing that Aahelix3 impaired normal cell division in E. coli. Furthermore, results of a co-pelleting assay and binding free energy calculation suggested that Aahelix3 plays an essential role in AaMinCD complex formation, under the circumstance of lacking MinE in A. aerolicu. Combining these results with sequence analysis of MinC and MinD in different organisms, we propose an evolutionary relationship to rationalize different mechanisms in cell division positioning in various organisms.

Reference