The transcriptional regulator YdgT interacts with the bacterial replication machinery

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The DNA polymerase III (pol III) holoenzyme, formed by two catalytic cores and seven accessory proteins, is the replicative enzyme in *Escherichia coli*. Whiting the catalytic core, the α subunit contains the 5'-3' DNA polymerase activity, while ε is the 3'-5' proofreading exonuclease. The ε subunit consists of two domains: the N-terminal domain (ε186) binds θ and contains the exonuclease activity, while the C-terminal domain is required for binding to the α subunit. The function of θ is still uncertain and bacteria lacking this subunit do not show a clear phenotype. It has been proposed that its interaction with ε186 could stabilize the exonuclease subunit.[1]

Here we report that simultaneous deletion in *E. coli* of the genes encoding θ and YdgT leads to a significant decreased in the growth rate of the cells under high osmolarity conditions. YdgT is a member of the Hha/YmoA family of proteins found in enteric bacteria. The most relevant feature of these proteins is their ability to interact with members of the H-NS family forming a regulatory complex that oligomerises on the DNA molecule repressing the transcription of many environmentally regulated genes.[2]

Using NMR, we have found that YdgT is able to interact with ε186, even in the presence of θ, suggesting that YdgT is a multifunctional protein that is not only involved in the regulation of gene transcription but also in DNA replication.

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[2] Madrid, C.; Balsalobre, C.; García, J.; Juárez, A., *Mol. Microbiol.*, **2006**, *63*, 7-14.