Functional studies of RNA-binding properties of the Escherichia coli RNA chaperone ProQ

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Structural and functional research of interactions between small RNAs and RNA-binding proteins takes an important place in studies of gene expression regulation processes in all living organisms. For over two decades the only two proteins, CsrA and Hfq, have been known as RNA chaperones in bacteria. Recent studies have shown that FinO domain containing proteins seems to be another important class of bacterial RNA chaperones. ProQ protein, a FinO family member, was originally identified as an osmoregulatory factor required for optimal expression of the proline channel protein ProP. However, ProQ has now emerged to function as a sRNA binding protein in Salmonella and Escherichia coli. A similar role is predicted for proteins containing ProQ/FinO domain from various bacteria.

ProQ from Escherichia coli is a monomeric protein. It adopts an elongated structure with two domains separated by a disordered linker region. The N-terminal domain of ProQ (NTD), spanning residues 1-121, is composed of a ProQ/FinO domain and shares 35% sequence identity with its paralogs. C-terminal domain (CTD) is structurally related to Tudor-like domains commonly found in eukaryotic chromatin regulators. N- and C-terminal domains may interact with target RNA independently or cooperatively, depending on context.

The aim of our investigation is to study interactions of E. coli ProQ as well as its isolated domains with potential sRNA targets in the cell. We have identified a number of sRNAs that bind to ProQ and have measured the affinity of the protein to the RNAs. Based on these data significant differences in the RNA binding properties of the N-terminal and C-terminal domains of ProQ have been revealed. Using hydroxyl radical footprinting we have also identified protein-binding sites in the sRNAs.

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