

Iron Response Element-mRNA Binding to Iron Response Protein: Metal Ion Sensing

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Abstract : Cellular iron homeostasis is accomplished by the coordinated regulated expression of iron uptake, storage, and export. Iron regulate the translation of ferritin and mitochondrial aconitase iron responsive element (IRE)-mRNA by interaction with an iron regulatory protein (IRPs). Iron increases protein biosynthesis encoded in iron responsive element. The noncoding structure IRE-mRNA, approximately 30-nt, folds into a stem loop to control synthesis of proteins in iron trafficking, cell cycling, and nervous system function. Fluorescence anisotropy measurements showed the presence of one binding site on IRP1 for ferritin and mitochondrial aconitase IRE-mRNA. Scatchard analysis revealed the binding affinity (K_a) and average binding sites (n) for ferritin and mitochondrial aconitase IRE-mRNA were $68.7 \times 10^6 \text{ M}^{-1}$ and $9.2 \times 10^6 \text{ M}^{-1}$, respectively. In order to understand the relative importance of equilibrium and stability, we further report the contribution of electrostatic interactions in the overall binding of two IRE-mRNA with IRP1. The fluorescence quenching of IRP1 protein was measured at different ionic strengths. The binding affinity of IRE-mRNA to IRP1 decreases with increasing ionic strength, but the number of binding sites was independent of ionic strength. Such results indicate a differential contribution of electrostatics to the interaction of IRE-mRNA with IRP1, possibly related to helix bending or stem interactions and an overall conformational change. Selective destabilization of ferritin and mitochondrial aconitase RNA/protein complexes as reported here explain in part the quantitative differences in signal response to iron in vivo and indicate possible new regulatory interactions.

Keywords : IRE-mRNA, IRP1, binding, ionic strength

Conference Title : ICRNAB 2019 : International Conference on RNA Biology

Conference Location : Madrid, Spain

Conference Dates : March 26-27, 2019