IRON(II) AND MAGNESIUM BINDING TO FULL-LENGTH LSU rRNA AND AN ANCESTRAL CORE.

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Introduction: RNA-cation interactions are crucial for the folding of large, globular RNA structures, as cations allow negatively-charged phosphate groups to pack closely together. In modern biology, Mg^{2+} is the divalent cation most commonly found interacting with RNA, but recent reports suggest that Fe(II) may have held a more prominent role in the proposed "RNA world". We are exploring the interactions between Fe(II) and a model resurrected ribosomal RNA as well as its parental large subunit rRNA in order to better understand the folding of large RNAs under simulated early earth conditions. The ribosome is universal to modern biology, and likely fostered a transition from an RNA-centric biology to a protein-based biology well before the last universal common ancestor. Comprehending the folding of the ribosome's RNA components is crucial to understanding the emergence of complex life on earth. We have used chemical footprinting techniques (SHAPE; Selective 2'-Hydroxyl Acylation analyzed by Primer Extension) to provide single-nucleotide resolution data on the structure of ribosomal RNA under plausible early earth conditions.

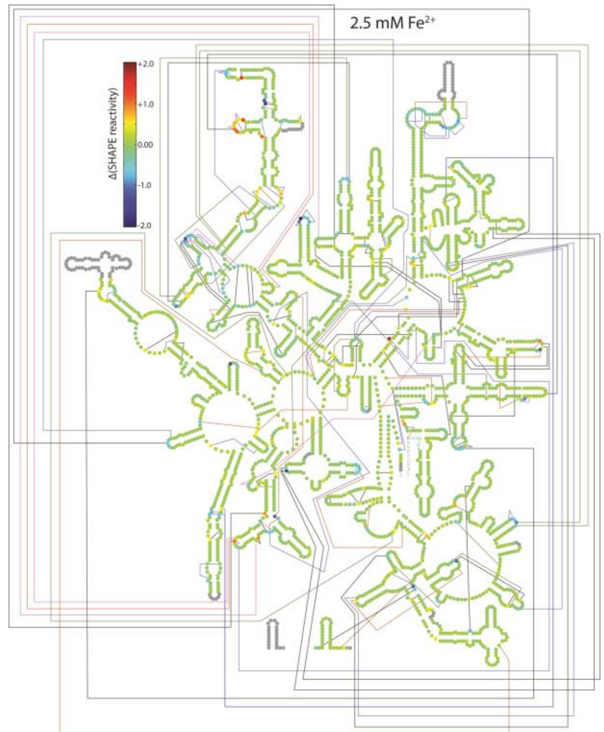

Figure: Fe^{2+}-induced changes in SHAPE reactivity can be attributed to formation of observed tertiary structures in the 23S rRNA. Comparison of SHAPE reactivities obtained in the presence and absence of 2.5 mM Fe^{2+}. Positive values indicate nucleotides with increased SHAPE reactivity in presence of 2.5 mM Fe^{2+}, while negative values denote decreased reactivity. Both samples contained 200 mM NaOAc, 50 mM NaHEPES, pH 8, and data was collected under anoxic conditions. Lines represent selected RNA-RNA tertiary contacts observed in the 23S crystal structure (PDB 2J01). Only those interactions that occur at or near (within one nt) a site that exhibits a significant Fe^{2+}-induced change in SHAPE reactivity are displayed. Interactions lines are colored as follows: Magenta; nt-Mg^{2+}-nt, grey; base-base, green; base-sugar, brown; base-phosphate, and blue; base-stacking interactions. Regions where crystal structure data are unavailable are shown as grey circles. Regions where SHAPE data is not available in one or both data sets (5' and 3' ends) are displayed as sequence only, not circles.