The Role of Ribosomal RNA Modifications in Ribosome Biogenesis

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Ribosome biogenesis is critical for cell proliferation and survival as ribosomes catalyze the synthesis of proteins, and regulation of protein synthesis is crucial for control of gene expression in cells. A critical step in ribosome production is the processing and chemical modification of ribosomal RNAs (rRNAs). The majority of modifications being 2'-O methylations and pseudouridylations, which are guided by classes of non-coding RNAs: box C/D small nucleolar RNAs (snoRNAs) and box H/ACA snoRNAs, respectively. Given that rRNA modifications and r-proteins help to stabilize the structure and guide the folding of the ribosome, and dysregulation of these components can impair the production of proteins and lead to disease, it is important to uncover more about their precise contributions to ribosome biogenesis. To this end, it is hypothesized that rRNA modifications, especially pseudouridylations, facilitate the binding of r-proteins to the rRNA because of the increase in hydrogen bond potential in the modified pseudouridine provides. Previously published databases and softwares were used to construct 1D and 2D maps of mature yeast rRNA, and a self-developed Python script was coded to analyze the distribution and proximities of the r-proteins and modification sites. The results reveal that most snoRNA binding and modifications occur in "hotspots" of the rRNA and suggests that snoRNA binding regions, along with their corresponding modifications, particularly pseudouridylations, may directly influence r-protein incorporation as 38.78% of all pseudouridylations and 20.37% of all 2'-O methylations directly overlap with an r-protein binding site, contradicting previously held beliefs in RNA science.

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