

“Characterization of 3’ untranslated regions for optimization of gene expression in yeast”

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In metabolic engineering it is often desirable to express several genes to achieve the desired product in the organism of choice. The main regulatory mechanism governing gene expression is the choice of promoter, i.e. in the step of transcription initiation. However, posttranscriptional processes such as mRNA stability and translation initiation are also major determinants for successful gene expression. Such processes are often mediated by the 3’ untranslated region (3’UTR) of the mRNA and the protein(s) binding to it. RNA binding proteins termed PUF-proteins are evolutionarily conserved and best characterized as posttranscriptional repressor. We have characterized PUF-protein dependent 3’ UTR regulation using COX17 3’UTR and PUF3 that is known to regulate COX17 mRNA in the yeast *Saccharomyces cerevisiae*. The upstream mechanisms influencing the activity of PUF3- protein were also investigated. Our result has confirmed that putative recognition sequences for Puf3 on COX 17 3’UTR are important for the binding of Puf3. Lack of the first 30 amino acids in the N- terminus, which are a potential phosphorylation site, made PUF3 to have less repression activity on its target mRNA. On the other hand the C-terminus of PUF 3 was shown less role other binding to transcripts. The N-terminal were sufficient for repression when linked to the MS2-domain, but that the carbon source dependent regulation is not mediated by the N-terminal of Puf3. Our results indicate care should be taken during any C-terminus tagging procedure, which can concomitantly replace important sequences in 3’ UTR and give incorrect conclusion on gene Expression.

Biography

Nebeyu Yosef has graduated from Addis Ababa University at 2006. He has been working as Instructor in Bethel Medical college for about four years. He is now graduate student in Chalmers University of Technology.