Journal of Applied Biology & Biotechnology Vol. 4 (02), pp. 038-045, March-April, 2016
Available online at http://www.jabonline.in
DOI: 10.7324/JABB.2016.40206

Predicted interaction of human Ribosomal Protein S15 with Fragile X Mental Retardation Protein

Edmund Ui-Hang Sim[1*], Xiang-Ru Ma[1], Stella Li-Li Chan[1], Choon-Weng Lee[2], Kumaran Narayanan[3,4]

[1]Department of Molecular Biology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia. [2]Institute of Biological Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia. [3]School of Science, Monash University, Bandar Sunway, 46150 Selangor, Malaysia. [4]Department of Genetics and Genomics Sciences, Mount Sinai School of Medicine New York, NY10029, USA.

ARTICLE INFO

Article history:
Received on: 12/01/2016
Revised on: 06/03/2016
Accepted on: 28/03/2016
Available online: 21/04/2016

Key words:
Ribosomal protein S15, FMRP, protein interaction, functional prediction, molecular docking

ABSTRACT

In addition to the central role of ribosome biogenesis, the human ribosomal protein S15 (RPS15) has extra-ribosomal roles that include its association with a congenital disease and a few types of cancer. However, current knowledge of its functions in the context of extra-ribosomal activities remains fragmented. An approach to gain insights into the interaction between RPS15 and possible protein partners is via Bioinformatics strategies. Based on the sequence-to-structure-to-function paradigm, structural data of a protein can be computationally analysed to derive logical interacting partners. This method can include three-dimensional model construction, structural neighbour prediction, and molecular docking analysis. By using this approach, we have constructed RPS15 3D-structural models that have allowed the prediction of 23 structural neighbours. Of these, two that are from human origin were further analysed and only one have logical prospect of binary protein-protein interactions. Further analysis of this structural neighbour revealed 7 candidate docking partners. From these, our molecular docking analysis demonstrated two most logical dock models of interactions between RPS15 with two different domains of the Fragile X Mental Retardation Protein 1 (FMRP1) protein. Hence, we have provided *in silico* evidence of *de novo* protein-protein interaction between RPS15 and the Fragile X Mental Retardation Protein 1 (FMRP1).

1. INTRODUCTION

Human ribosomal protein, S15 (RPS15) is a component of the 40S ribosome subunit, and is a member of the S19P family of ribosomal proteins. The *RPS15* gene was originally identified as *RIG*, a human homologue of *rig* (rat insulinoma gene) [1, 2]. Analysis of *RIG* in human insulinoma tissues revealed elevated expression in tumors relative to normal pancreatic or regenerating islets [3]. Similar observation of activated expression in cancer tissues has also been explained for human esophageal and colon cancers [4]. The mammalian *RPS15* gene sequence shows high homology (>88%) among different species, and the encoded protein is also highly conserved among mammalian species by having similarity in several functional domains, namely the two cyclic adenosine monophosphate (cAMP) and cyclic guanosine monophosphate (cGMP)-dependent kinase phosphorylation, one ribosomal protein S19 signature, 4 N-myristoylation, and 5 casein kinase C phosphorylation sites [5]. During the processing of yeast pre-40S subunit, RPS15 has been shown to interact or bind directly with ribosome assembly factors such as the low temperature viability (Ltv1), and RIght Open reading frame kinase 2 (RioK2 or Rio2) proteins [6]. In the case of Rio family of protein kinases, depletion or reduction of RPS15 significantly decreased the level of human RioK2 and -K3 [7], suggesting direct interaction between RPS15 and these factors during 40S ribosome biogenesis. Besides its involvement in ribosome biogenesis, the association of RPS15 with diseases has been reported, albeit of mechanism(s) that is largely undefined. For example, like many other RP genes, RPS15 has been suspected to be associated with Diamond Blackfan Anemia (DBA) [8].

** Corresponding Author*
Dr. Edmund Ui-Hang Sim, Department of Molecular Biology Faculty of Resource Science and Technology, Universiti Malaysia Sarawak 94300 Kota Samarahan Malaysia. Tel: +60-82-583199 and/or -583041 Fax: +60-82-583160, E-mail: uhsim@frst.unimas.my