https://www.sciencedirect.com/science/article/abs/pii/S0003986114003488

Molecular network including eIF1AX, RPS7, and 14-3-3γ regulates protein translation and cell proliferation in bovine mammary epithelial cells

Cuiping Yu,Chaochao Luo,BoQu, Nagam Khudhair, Xinyu Gu,Yanli Zang, Chunmei Wang, Na Zhang, Qingzhang Li, Xuejun Gao

Abstract

14-3-3γ, an isoform of the 14-3-3 protein family, was proved to be a positive regulator of mTOR pathway. Here, we analyzed the function of 14-3-3γ in protein synthesis using bovine mammary epithelial cells (BMECs). We found that 14-3-3γ interacted with eIF1AX and RPS7 by 14-3-3γ coimmunoprecipitation (CoIP) and matrix-assisted laser desorption/ionization-time-of-flight/time-of-flight (MALDI-TOF/TOF) peptide mass fingerprinting analysis. These interactions of 14-3-3γ with eIF1AX and RPS7 were further confirmed by colocalization and fluorescence resonance energy transfer (FRET) analysis. We also found that methionine could promote protein synthesis and trigger the protein expression levels of 14-3-3γ, eIF1AX and RPS7. Analysis of overexpression and inhibition of 14-3-3γ confirmed that it positively affected the protein expression levels of eIF1AX, RPS7, Stat5 and mTOR pathway to promote protein synthesis and cell proliferation in BMECs. We further showed that overexpression of eIF1AX and RPS7 also triggered protein translation and cell proliferation. From these results, we conclude that molecular network including eIF1AX, RPS7, and 14-3-3γ regulates protein translation and cell proliferation in BMECs.