Phosphostate of the ribosomal P-proteins

P-02.1-16

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The protein phosphorylation is the most common post-translational modification (PTM) which regulates protein activity. It can be responsible for on/off switching of their activity, can change the interaction pattern of proteins or can modulate their subcellular localization or dynamics. Phosphorylation has been described for many ribosomal proteins (RPs) found both within the 40S (12 proteins) and 60S (15 proteins) subunits. The phosphorylation is a dynamic process that can appear in different cell conditions like in mitosis as well as in response to external stress stimuli e.g. hypoxia. Growing evidence has shown an enormous potential of phosphorylation of ribosomal proteins as a regulatory mechanism turning the activity of the translational apparatus. For example, the recent report has revealed that translation can be regulated during mitosis by uL11 phosphorylation. Despite the advent of high-throughput analyses devoted to mapping PTM's of ribosomal proteins, the phosphostate and phosphorylation impact of ribosomal proteins are not described exhaustively. Among RPs that undergo phosphorylation are the P-stalk proteins, namely uL10 protein and P1-P2 proteins. They are responsible for the stimulation of translational GTPases activity during all stages of ribosomal action. Although it is known that the P-stalk proteins are phosphorylated by CK2 kinase. Here, using Pro-Q staining, the method which selectively detects protein phosphorylation, we show that many ribosomal proteins are phosphorylated. Moreover, to describe the detailed phosphostate of the P-stalk proteins in different conditions as well as in cell lines, we applied the Phos-tag technique. Our results indicate that the ribosomal P-proteins phosphostate is changing upon application of environment stimulus, which is consistent with the idea that they may provide another level of regulation for translational machinery.