**Defining “ribosome heterogeneity” by quantitative proteomics**

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While translational regulation is an important aspect of gene expression control, the ribosome itself is traditionally seen as a rather static machine. However, recent evidence suggests that the composition of the ribosome can vary in terms of ribosomal proteins (r-proteins), associated factors or post-translational modifications. It has therefore been suggested that different types of ribosomes can recognize and preferentially translate specific classes of mRNAs. However, to what extent such ribosome heterogeneity exists in cells remains elusive. Here, we used a quantitative proteomic approach to systematically characterize the composition of the ribosomes. First, our approach allowed us to accurately quantify the abundance of r-proteins across the different subunits, monosomes and polysomes. We observed stable stoichiometry of r-protein composition between monosomes and polysomes in HEK293, HeLa and mESC cells, challenging previous findings. Second, we identified a high-confident set of 112 monosome and/or polysome associated factors and characterized their biochemical and functional features. Lastly, we provide evidence that phosphorylation of one r-protein during mitosis inhibits polysome formation and regulates translation of a specific subset of mRNAs. Together, our results provide a detailed map of ribosome heterogeneity across subunits, monosomes and polysomes and suggests that phosphorylation of specific r-proteins is involved in translational control during the cell cycle.