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The ribosome as novel target for stress-induced small regulatory RNAs.

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Small non-protein-coding RNA (ncRNA) molecules represent major contributors to regulatory networks in controlling gene expression in a highly efficient manner. All of the recently discovered regulatory ncRNAs that act on translation (*e.g.* microRNAs, siRNAs or antisense RNAs) target the mRNA rather than the ribosome.
To address the question, whether small ncRNA regulators exist that are capable of modulating the rate of protein production by directly interacting with the ribosome, we have analyzed the small ncRNA interactomes of ribosomes. Deep-sequencing and subsequent bioinformatics analyses revealed thousands of putative ribosome-associated ncRNAs in various model organisms (1,2). For a subset of these ncRNA candidates we have gathered experimental evidence that they associate with ribosomes in a stress-dependent manner and are capable of regulating gene expression by fine-tuning the rate of protein biosynthesis (3,4). Many of the investigated ribosome-bound small ncRNA appear to be processing products from larger functional RNAs, such as tRNAs (2,3) or mRNAs (3). Post-transcriptional cleavage of RNA molecules to generate smaller fragments is a widespread mechanism that enlarges the structural and functional complexity of cellular RNomes.
Our data reveal the ribosome as a target for small regulatory ncRNAs and demonstrate the existence of a yet unknown mechanism of translation regulation. Ribosome-associated ncRNAs (rancRNAs) are found in all domains of life and represent a prevalent but so far largely unexplored class of regulatory molecules (5). Future work on the small ncRNA interactomes of ribosomes in a variety of model systems will allow deeper insight into the conservation and functional repertoire of this emerging class of regulatory ncRNA molecules.

References

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