Posted 7 July 2025
Max Planck Unit for the Science of Pathogens, Berlin, Germany

A new translation factor joins the fray

Researchers discover a protein facilitating translation of specific amino acid sequences

Dmitry Ignatov, Emmanuelle Charpentier and her group at the Max Planck Unit for the Science of Pathogens have demonstrated that a newly identified protein in bacteria acts as a translation factor necessary for the efficient synthesis of proteins with proline-rich motifs. The findings have been published in the journal *Nature Communications*.

The fast and efficient synthesis of proteins is essential for the survival of all organisms. Ribosomes can synthesize polypeptides containing almost any combination of amino acids. However, the amino acid proline has a distinctive chemical structure that makes it difficult for peptide bonds to form between consecutive prolines. In bacteria, two specific proteins, EF-P and YfmR, have been shown to interact with ribosomes and assist in the formation of peptide bonds between consecutive prolines.

"Surprisingly, there is another factor that facilitates the synthesis of proteins containing polyproline motifs," says Prof. Emmanuelle Charpentier, the lead author of the study, Director of the Max Planck Unit for the Science of Pathogens and Honorary Professor at Humboldt-Universität zu Berlin.

Using mass spectrometry-based proteomics, the researchers identified proteins that interact with RNA in the pathogenic bacterium *Streptococcus pyogenes*. Many of these proteins interact with ribosomal RNA and represent ribosomal proteins and translation factors. The researchers focused on YebC, a protein of unknown function whose homologs are present in most bacterial species and mitochondria. They showed that YebC interacts with 23S ribosomal RNA near the peptidyl transferase center, suggesting that it plays an important role in forming peptide bonds. Further experiments showed that YebC facilitates the formation of peptide bonds between consecutive prolines.

This study improves our understanding of protein synthesis. Additionally, the application of YebC in the field of biotechnology could be explored: the protein could be employed to incorporate unnatural amino acids into proteins synthesized *in vitro*.

"Ribosomes interact with multiple proteins that modulate their activity," says Dmitry Ignatov, the first author and co-leader of the study, and post-doctoral researcher in Emmanuelle Charpentier's laboratory at the Max Planck Unit for the Science of Pathogens. "Our study discovers a new translation factor that is required in a fairly specific context."

"The mechanism of YebC activity remains to be elucidated," says Dmitry Ignatov. "Additionally, it is unclear why bacterial ribosomes require three different factors to translate the polyproline motifs. Further research is necessary to understand the interplay between EF-P, YfmR and YebC."

About the authors

Prof. Emmanuelle Charpentier is Director of the Max Planck Unit for the Science of Pathogens and Honorary Professor at the Institute of Biology, Humboldt-Universität zu Berlin. Her research focuses on understanding RNA- and protein-mediated regulation in the human pathogen *Streptococcus pyogenes*. Dmitry Ignatov is a post-doctoral researcher in Emmanuelle Charpentier's laboratory, working on proteins interacting with ribosomes.

The full study is published under the title "RNA-binding protein YebC enhances translation of proline-rich amino acid stretches in bacteria" in *Nature Communications*.

Publication

Dmitriy Ignatov [1], Vivekanandan Shanmuganathan [# 1], Rina Ahmed-Begrich [# 1], Kathirvel Alagesan [1], Karin Hahnke [1], Chu Wang [1], Kathrin Krause [1], Fabián A Cornejo [1], Kristin Funke [2], Marc Erhardt [1,2], Christian Karl Frese [1 3], Emmanuelle Charpentier [1,2]. **RNA-binding protein YebC enhances translation of proline-rich amino acid stretches in bacteria.** *Nature Communications* (2025) DOI: 10.1038/s41467-025-60687-4

[1]Max Planck Unit for the Science of Pathogens, Berlin, Germany.
[2]Institute of Biology, Humboldt-Universität zu Berlin, Berlin, Germany.
[3]Bayer AG, Wuppertal, Germany.
[4]Max Planck Unit for the Science of Pathogens, Berlin, Germany.
[#] These authors contributed equally

*Correspondence to: research@emmanuelle-charpentier.org

Further Information

https://www.mpusp.mpg.de

Contact

Prof. Emmanuelle Charpentier
Max Planck Unit for the Science of Pathogens
Charitéplatz 1
10117 Berlin
research@emmanuelle-charpentier.org

Dmitry Ignatov
Prof. Emmanuelle Charpentier's Laboratory
Max Planck Unit for the Science of Pathogens
Charitéplatz 1
10117 Berlin
ignatov@mpusp.mpg.de