

Structural insights into the characteristic slow translocation in cold-adapted bacteria *Pseudoalteromonas haloplanktis*

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Global warming has accelerated the melting of glaciers and other permanently frozen environments at an alarming rate. This trend raises the chance of releasing previously unknown pathogenic bacteria, posing risks to both plant and animal life. Psychrophiles, bacteria adapted to cold environments, have evolved specialized features to endure low temperatures. However, the intricate molecular mechanisms governing key central cellular processes in these species remained poorly understood. To address this knowledge gap, we have reconstituted a minimal translation elongation system from psychrotolerant bacteria *Pseudoalteromonas haloplanktis*. Employing fast kinetics techniques, we discovered that the rate of tRNA translocation in *P. haloplanktis* is much slower than mesophilic bacteria *Escherichia coli*, a characteristic attributed to its ribosome. To obtain structural insights of the process, we have determined the cryo-electron microscopy (cryo-EM) structure of the *P. haloplanktis* 70S ribosome at a global resolution of 2.8 Å. This structural allows detailed comparison of the key functional sites as well as intersubunit interactions, yielding the possible structural reason for the slow translation in *P. haloplanktis*. Our study provides the first mechanistic and structural characterization of translation elongation in psychrophilic model bacteria and lays the ground for further investigations.