

A peer-reviewed version of this preprint was published in PeerJ on 16 January 2018.

[View the peer-reviewed version](https://doi.org/10.7717/peerj.4286) (peerj.com/articles/4286), which is the preferred citable publication unless you specifically need to cite this preprint.

Quandt EM, Traverse CC, Ochman H. 2018. Local genic base composition impacts protein production and cellular fitness. PeerJ 6:e4286 <https://doi.org/10.7717/peerj.4286>

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Selection on translation rate impacts genic base composition

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Abstract: The maintenance of a G+C content that is higher than the mutational input to a genome supports the view that selection serves to increase G+C contents in many bacteria. Recent experimental evidence from *Escherichia coli* has demonstrated that selection for increasing G+C content operates at the level of translation, but the precise mechanism by which this occurs is unknown. To determine the substrate of selection, we asked whether selection on G+C content acts across all sites within a gene or was confined to particular nucleotide positions or genic regions. We systematically altered the G+C contents of the GFP gene and assayed the effects of each variant on cellular fitness. The fitness differences were attributable to the base compositional variation in the terminal portion of the gene: increasing G+C content produced more stable mRNA secondary structures, which, in turn, slowed translation rate and allowed proper protein folding. We show that purifying selection against A and T mutations results from their tendency to increase the rate of translation and perturb the dynamics of protein folding.

Disclosure of Interest: None Declared

Keywords: None