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Determine the role of codon usage in regulating protein expression, folding and function

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Codon-usage bias has been observed in almost all genomes and is thought to result from selection for efficient and accurate translation of highly expressed genes. Many genes exhibit little codon usage bias, which is thought to reflect a lack of selection for messenger RNA translation. Alternatively, however, non-optimal codon usage may be of biological importance. By taking the frequency gene in *Neurospora* as an example, optimization of its codon usage profile not only elevated the expression level but also altered its protein structure and function. With further biostatistics analysis, we found genome-wide correlations between codon choices and predicted protein secondary structures: Non-optimal codons are preferentially used in intrinsically disordered regions and more optimal codons are used in structured domains. These correlations are conserved in other eukaryotes. Taken together, our results suggest that codon choices and protein structures co-evolve to ensure proper protein folding. Our study also provides guidance towards the codon optimization strategy when expressing recombinant proteins: Protein folding and function should also be considered at the same time of improving the expression level.

Biography

Mian Zhou has completed her PhD from UT Southwestern Medical Center at Dallas in 2014. Presently she is an Associate Professor in East China University of Science and Technology in Shanghai, China. By working codon bias and recombinant protein expression in fungi, she has published several papers in *Nature and Molecular Microbiology*.

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