Review of: "The CGA Codon Decoding through Arg-tRNA^ICG Supply Governed by Tad2/Tad3 in Saccharomyces cerevisiae"

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Potential competing interests: No potential competing interests to declare.

In this paper, the authors indicated that an additional supply of $tRNA^{Arg}$(ACG) genes in *Saccharomyces cerevisiae*, which produce $tRNA^{Arg}$(ICG), recovered the product level of the encoding protein from the luc-reporter with consecutive CGA codons. These results suggest that the product reduction is due to inefficient decoding and deficiency in the tRNA supply. Furthermore, they examined the ratios of the mature $tRNA^{Arg}$(ICG) and the precursor $tRNA^{Arg}$(ACG) for wild type and some strains with modified expression levels of the anticodon first adenosine deamination enzymes, Tad2/Tad3, and concluded that the ratios are related to the expression levels of these deamination enzymes. The authors propose the concept of “anticodonome” which is a set of total anticodons of tRNAs that function in the ribosome for the decoding of whole genetic codes in an organism, and the present results are considered somehow to contribute to the establishment of the concept. Their approaches are scientifically sound and the results coming from the different sources are consistent. But this paper would be better with further proper modifications.

The relationship between the $tRNA^{Arg}$(I(G)CG)/$tRNA^{Arg}$(ACG) ratio in *S. cerevisiae* strains (less than 30%) and its evolutionary meaning would be very interesting point, and I would like to see some discussion on it. In addition, expression levels of Tad2/Tad3 are closely related to the ratios, but from a general reader's point of view, I would also like to see some structural information (summary) about Tad2/Tad3 (structural similarities and differences etc.) in their paper, although reference #14 would show it. And although the authors used tad3 ts strain, how about the result using tad2 ts strain? if it is available, I would like to see the result. Finally, regarding sequence analysis, ideally, the authors should conduct NGS analysis and increase the numbers of data before the final discussion, if the situation allows.

Following is minor remarks. (1) “arginyl-$tRNA^{ACG}$ (or Arg-tRNA(ACG))” etc. can generally be considered “arginine-charged tRNA”, so it should be written as, e.g., “$tRNA^{Arg}$(ACG)” and so on. (2) The numbering of supplementary figures is wrong. S1 and S2 would be reversed.