World Academy of Science, Engineering and Technology
International Journal of Biological and Ecological Engineering
Vol:17, No:03, 2023

Characterization of the Queuine Salvage Pathway From Bacteria in the Human Parasite Entamoeba Histolytica

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Abstract : Queuosine (Q) is a naturally occurring modified nucleoside that occurs in the first position of transfer RNA anticodons such as Asp, Asn, His, and Tyr. As eukaryotes lack pathways to synthesize queuine, the nucleobase of queuosine, they must obtain it from their diet or gut microbiota. Our previous work investigated the effects of queuine on the physiology of the eukaryotic parasite Entamoeba histolytica and defined the enzyme EhTGT responsible for its incorporation into tRNA. To our best knowledge, it is unknown how E. histolytica salvages Q from gut bacteria. We used N-acryloyl-3-aminophenylboronic acid (APB) PAGE analysis to demonstrate that E. histolytica trophozoites can salvage queuine from Q or E. coli K12 but not from the modified E. coli QueC strain, which cannot produce queuine. Next, we examined the role of EhDUF2419, a protein with homology to DNA glycosylase, as a queuine salvage enzyme in E. histolytica. When EhDUF2419 expression is silenced, it inhibits Q's conversion to queuine, resulting in a decrease in Q-tRNA levels. We also observed that Q protects control trophozoites from oxidative stress (OS), but not siEhDUF2419 trophozoites. Overall, our data reveal that EhDUF2419 is central for the salvaging of queuine from bacteria and for the resistance of the parasite to OS.

Keywords : entamoeba histolytica,epitranscriptomics, gut microbiota, queuine, queuosine, response to oxidative stress, tRNA modification.
Conference Title : ICRNAB 2023 : International Conference on RNA Biology
Conference Location : Madrid, Spain
Conference Dates : March 20-21, 2023