SCIENCE FOR THE BENEFIT OF HUMANITY

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A Novel Quantitative Method for tRNA-profiling

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Technology Summary

tRNAs are an essential component of the cellular translational machinery and its abundances vary widely across genomes, cell states and cell types. The variation in tRNA abundances has important implications for regulating protein expression and could be an indicator of disease vs normal states.

The field of tRNAs profiling is relatively untapped because quantifying tRNAs using cDNA-based approaches yield unpredictable biases and false measurements. tRNAs have extensive secondary and tertiary structures and post-transcriptional modifications that interfere with reverse-transcription and hybridization. Our scientists have designed a high throughput tRNA profiling method that relies on proprietary tRNA-specific probe development, hybridization, ligation, purification, Next-Generation Sequencing and subsequent quantification. This method obviates the need for reverse-transcription and provides a more realistic and precise measure of tRNA abundance. This technology is an effective tool to quantitate tRNA abundances, and could potentially provide a valuable indicator of disease progression.

Application

- A quantitative research tool for measuring global tRNA levels in diverse cell types and genomes.

Advantages

- A *reverse-transcription-free* method that is less susceptible to unpredictable biases
- High signal-to-noise ratio, achieved by purification of tagged tRNA
- High throughput, owing to (1) the design of a set of probes that hybridizes to all tRNAs, and (2) downstream Next-Generation Sequencing
- Broadly applicable method to different sequenced genomes, as this technology provides a computational pipeline for designing species-specific probes

Stage of Development

- A proof of concept has been implemented and tested on various human breast cancer cell lines. Evaluation of their global tRNA profiles revealed that certain tRNAs with particular anticodons are enriched in cells of a higher metastatic state.

Lead Inventors

- Drs. Sohail Tavazoie and Hani Goodarzi

Patent Information

- *Patent pending*

Reference

- Goodarzi *et al.* 2016. Modulated Expression of Specific tRNAs Drives Gene Expression and Cancer Progression.*Cell* 165:1416-27 DOI: http://dx.doi.org/10.1016/j.cell.2016.05.046
- http://newswire.rockefeller.edu/2016/06/02/researchers-uncover-how-silent-genetic-changes-drive-cancer/

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