training, the CU-Net will evaluate a second set of independent images (N=100) to determine performance accuracy. Three specialized raters will establish the reliability and feasibility of CU-Net compared to conventional 2D and 3D ovarian ultrasound image analysis methods. RESULTS/ANTICIPATED RESULTS: The labeled training dataset of ovarian ultrasound images is expected to successfully train the CU-Net and allow for accurate identification of the ovary and the total number of antral follicles in the second testing set of ultrasound images. When compared to conventional 2D and 3D ultrasound image analysis methods, CU-Net is expected to have similar accuracy when compared to the gold-standard method (2D-Offline with Grid) and outperform other approaches, such as 2D-Real Time and 3D volume software (VOCAL and Sono-AVC). However, CU-Net is anticipated to be the fastest and most reliable method across users, supporting its clinical feasibility. DISCUSSION/SIGNIFICANCE: This study will immediately translate to providing a standardized platform that can improve the accuracy, reliability, and time demand required for the evaluation of ovarian ultrasounds across users and clinical and research settings.

Post-transcriptional regulation of the MiaA prenyl transferase by the small RNA CsrB in Escherichia coli (E. coli)

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OBJECTIVES/GOALS: MiaA is a highly conserved prenyl transferase that catalyzes synthesis of the i6A37 tRNA modification in E. coli. While transcriptional regulation of MiaA is well characterized, there is no information on the MiaA post-transcriptional regulation. The aim of this study is to characterize the post-transcriptional regulation of the MiaA gene in E. coli. METHODS/ STUDY POPULATION: To characterize the post-transcriptional regulation of miaA, we executed a targeted genetic screen of an E. coli small RNA library on a miaA-lacZ translational reporter fusion strain to identify small RNAs (sRNAs) that modulate MiaA translation or transcription termination. We also measured MiaA mRNA levels and miaA-lacZ activity in the absence or over-expression of candidate sRNA regulators of MiaA. We also measured MiaA mRNA levels in the absence of RNaseE and PNPase, two enzymes involved in mRNA turnover. Finally, we measured the ability of purified recombinant CsrA to bind to the MiaA mRNA transcript in vitro. RESULTS/ANTICIPATED RESULTS: We identified the carbon sensing sRNA CsrB and its cognate protein interaction partner CsrA, as potential post-transcriptional regulators of MiaA. Over-expression of CsrB fully repressed miaA-lacZ activity and MiaA mRNA levels. The absence of CsrA resulted in a defective miaA-lacZ activity and a 10-fold decrease in MiaA mRNA levels. We also identified an increase in the MiaA mRNA half-life particularly in the absence of RNaseE. Our results demonstrate an additional layer of regulation for the miaA operon by the CsrA/CsrB protein-sRNA system.

DISCUSSION/SIGNIFICANCE: MiaA is a highly conserved bacterial protein. Our data may represent phenomena in an array of bacteria that could be targeted by novel antibiotics. The human MiaA homologue, TRIT1, plays a role in mitochondrial disorders. We anticipate that information garnered from MiaA studies will elucidate TRIT1 function and its role in mitochondrial disorders.

Workforce Development

Contemporary Research Challenges

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Empowering the Participant Voice (EPV): Participant Feedback to Improve the Clinical Research Enterprise Rhonda G. Kost¹, Joseph Andrews², Ranee Chatterjee³, Alex Cheng⁴,

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OBJECTIVES/GOALS: Six CTSA sites formed a collaboration to DEVELOP, DEMONSTRATE, AND DISSEMINATE new infrastructure to streamline collection and analysis of research participant feedback, using the Research Participant Perception Survey (RPPS), common standards, and customized REDCap-based tools, to improve the clinical research enterprise. METHODS/STUDY POPULATION: DEVELOP charter, consensus approach, core survey, deployment standards, data-use agreements; define meta-data, system requirements for the infrastructure, use-cases. Engage stakeholders for broad institutional and community input. Build RPPS/REDCap project, visual analytics Dashboard External Module, and Program Dashboard module for evaluation. Configure to use with Multilingual Module. DEMONSTRATE by implementing site-based use cases that reflect local priorities and span diverse populations, testing different methods of survey deployment (REDCap, patient portal, SMS) to showcase utility and flexibility. Generate data for local and inter-institutional benchmarking. Refine, then DISSEMINATE new infrastructure across the Consortium and REDCap community for broader testing and uptake. RESULTS/ANTICIPATED RESULTS: The project team refined the RPPS survey for inclusivity and mode of informed consent; defined standards for survey timing, sampling, and study metadata; configured the data dictionary in English and Spanish for use with the multi-lingual module ; developed tools for project evaluation. Stakeholder engagement identified themes of anticipated value and fears about feedback. We designed an Ata-Glance Dashboard to display survey results with detailed analytics and filters. A REDCap application programming interface will send de-identified site data to the EPV Consortium Database to support benchmarking. Full implementation began November 2021 and will scale in 2022. Dissemination to Consortium and REDCap users is ongoing through presentations and a project website (www.Rockefeller.edu/research/epv). DISCUSSION/SIGNIFICANCE: Direct feedback from representative populations about their experiences in research is essential to understand and resolve barriers to broad participation in research. Streamlined RPPS/REDCap infrastructure provides a platform for local and national benchmarking, and collection of actionable data to improve clinical research.