

competencies relate to the Joint Task Force for Clinical Translational Research Professionals Competencies. **METHODS/STUDY POPULATION:** Team science competencies for clinical research professionals are poorly defined. The JTF Clinical Trial Competencies lack sufficient emphasis on team science, though it is briefly included in two JTF competency domains: Leadership & Professionalism, and Communication & Teamwork. The competencies primarily focus on tasks related to clinical research and basic knowledge of product development; however, a conceptual model for applying the competencies using a team science lens is needed. Currently, the JTF competency figure is often thought of as sequential, given the competencies are numbered, creating the misconception that the last competencies are less important. We support a new figure showing the permeability of team science across competencies and the connectedness and equality of the competencies. **RESULTS/ANTICIPATED RESULTS:** Our anticipated results are to show the integral nature of team science in clinical research professional communities of practice. Once complete, we will have identified measurable team science competency-based skills essential for clinical research professionals at various levels of expertise. Understanding the multi-dimensional team science competencies will inform targeted team science education and training for clinical research professionals. Our revised competency framework provides an improved team science conceptual model for clinical translational science. **DISCUSSION/SIGNIFICANCE:** Our work will define team science competencies as related to clinical research professionals at all experience levels. The interdependence of teams across clinical trial activities necessitates a consideration of an improved conceptual framework for clinical translational team science competencies.

Workforce Development

219

Analyzing the NJ ACTS Education and Offering Inventory to Assess Training across the CTSA Consortium

Ebanks¹, Yasheca T¹, Hassan¹, Sohaib¹, Del Prado¹, Justine¹, Ebanks¹ and Yasheca T¹

¹The School of Health Professions at Rutgers University

OBJECTIVES/GOALS: The New Jersey Alliance for Clinical and Translational Science (NJ ACTS) interest in developing a comprehensive education and training program for enhancing the quality, efficacy, and safety of the clinical research enterprise led to the release of a survey distributed nationwide to assess initiatives in the translational science workforce. **METHODS/STUDY POPULATION:** Twenty-one hubs responded to the survey and data was exported from REDCap to Excel. Respondent demographics were categorized to formalize roles and data was categorically divided into sections based on training type (engagement, basic, postgraduate etc...) utilizing conditional formatting. The limitation in this survey was a branching logic defect aligned with questions on competency tool usage and the roles that they play which led to only six hubs having the advantage to respond to all questions. **RESULTS/ANTICIPATED RESULTS:** Summary findings showed that the majority of respondents for the survey (30%) were the Director of Operations'. Further; the Joint Task Force (JTF) domain Scientific Concepts and Research Design' was the most preferred Hard Skill (81%) while the least preferred was Investigational Product Development and Regulation' (29%). In spite of only six hubs receiving the short competency assessment; 50% of those hubs stated

they would utilize 'In House Assessment Tools' and 83% stated they used the tools to 'Develop Personalized Training Plans'. The assessment of this Inventory was indeed necessary to identify trends in available trainings across the CTSA consortium. **DISCUSSION/SIGNIFICANCE:** The internal cross training catalogue will help to develop an infrastructure for the NJ ACTS community to work along with other CTSA hubs while creating comprehensive clinical research training initiatives and programs.

Valued Approaches

Biostatistics, Epidemiology, and Research Design

224

Ends of Endemics: Capturing Viral UTRs in Clinically Relevant Arbovirus Samples[†]

Victoria Morris¹, Y Zhou¹, R Yun¹, J Thompson², B Khan³, B Bolling¹, SC Weaver¹ and AL Routh¹

¹University of Texas Medical Branch, ²Dow University of Public Health, Pakistan and ³Texas Department of State Health Services Arbovirus Laboratory

OBJECTIVES/GOALS: Whole-genome viral sequencing is vital to inform public health and study evolution. Arboviruses evolve in vectors, reservoir hosts, and humans, and require surveillance at all points. We developed a new rigorous method of sequencing that captures whole viral genomes in field-collected and clinical samples. **METHODS/STUDY POPULATION:** ClickSeq is a novel method of Next Generation Sequencing (NGS) library synthesis using azido-nucleotides to terminate reverse transcription. The cDNA generated can be ligated to sequencing and indexing primers at room temperature using copper (Cu I) and vitamin C. With this approach, we designed primers located ~250 bp apart along the genomes of the arboviruses Chikungunya 37797, Zika Dakar, Yellow Fever Asibi, Dengue serotype 2, West Nile 385-99, and St. Louis Encephalitis Virus (SLEV) clade II. We tested this method with varying viral titers: lab-infected mosquito pools, field-collected mosquito pools from a Texas West Nile and SLEV outbreak, and patient isolates from a Pakistani CHIKV outbreak. The cDNA was sequenced in the UTMB NGS Core and aligned using bowtie. **RESULTS/ANTICIPATED RESULTS:** The use of a single protocol to capture whole viral genomes including UTRs for multiple viruses from different sample collection styles is ideal for arboviruses. Primers for multiple viruses were pooled and used to sequence mosquito pools. The Tiled ClickSeq method captured whole viral genomes without the need for host depletion. UTRs were captured even when the viral strain used for primer design differed from the resulting strain. Discreet variants were captured in both the hypervariable nsP3 region and the UTR in the patient isolates from the CHIKV outbreak compared to the 2017 outbreak. Texas WNV and SLEV outbreaks are now defined from the 2020 outbreak and can be further tracked to update public health measures and understand viral evolution. **DISCUSSION/SIGNIFICANCE:** UTRs impact both human and mosquito fitness, leading to further outbreaks. Tiled ClickSeq aims to capture whole viral genomes with a method and cost that can be implemented by public health researchers to understand disease evolution as it happens to update both public health and basic virology to the effects of evolution on arboviruses.