

templates, checklists, and interactive tools, along with a real-world simulation, to support COs in all stages of the research process. RESULTS/ANTICIPATED RESULTS: Focus groups and usability testing involving external community experts validated the toolkit's content and usability. Participants expressed enthusiasm and a sense of empowerment, indicating that the toolkit allows them to actively shape research processes and infuse their specific voices and needs into their partnerships. The toolkit is designed to support breaking down barriers like jargon and cultural adaptability to improve accessibility and open conversation. The impact of this Team Science focused toolkit is under evaluation. This presentation will showcase the toolkit, detail its collaborative development, and explore potential applications, ultimately offering a path to more equitable and valuable community-based research. DISCUSSION/SIGNIFICANCE: By providing COs with the resources and knowledge to participate as equal partners in research collaborations, it enhances self-advocacy, transparency, and equity. The toolkit has the potential to utilize Team Science to foster productive communication in community-academic research partnerships.

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### **Formative Findings from a Dissemination and Implementation (D&I) Study of TeamMAPPs, an Evidence-Based Team Science Curriculum Designed for CTSA Hubs**

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OBJECTIVES/GOALS: We are using ethnographic methods and Dissemination and Implementation (D&I) frameworks to study barriers and facilitators to implementing 'TeamMAPPs: Team Methods to Advance Processes and Performance in Science.' TeamMAPPs is an evidence-based Team Science curriculum deployed as five online modules and being implemented across CTSA hubs. METHODS/STUDY POPULATION: For this pre-implementation study, we used the Implementation Mapping framework to understand likely barriers and facilitators, with the aim of designing implementation strategies and long-term outcome measures. Data included field notes from a two-day train-the-trainer, one visit to a key implementing site, and 27 interviews. Participants were four TeamMAPPs conceptualizers, four module designers, and 15 implementers from seven implementing sites, each with a CTSA hub (four were interviewed twice). We coded transcripts using the Consolidated Framework for Implementation Research (CFIR) to identify contextual barriers and facilitators to D&I, the Reach, Effectiveness, Adoption, Implementation, and Maintenance (RE-AIM) D&I outcomes framework, and target competencies of TeamMAPPs. RESULTS/ANTICIPATED RESULTS: Priority D&I outcomes that emerged were adoption, reach, and effectiveness. Potential barriers/facilitators to "adoption" included institutional willingness to incentivize scientists to utilize TeamMAPPs, support for Team

Science at CTSA, and systems of rewards for scientists to undergo trainings. Anticipated barriers/facilitators for "reach" were closely tied to adoption, such as institutions' ability to persuade or require scientists to take trainings. Other issues relevant to reach included the time it takes to time to complete TeamMAPPs and potentially fraught intra-team dynamics arising if modules are implemented as a whole-team intervention. Anticipated barriers/facilitators for "effectiveness" included having adequate tools to assess actual impact. DISCUSSION/SIGNIFICANCE: TeamMAPPs has the potential to accelerate advances in translational sciences across the CTSA consortium. As this D&I study proceeds we will continue Implementation Mapping and use the Expert Recommendations for Implementing Change (ERIC) to develop bundles of implementer-informed strategies to the effectively deliver TeamMAPPs among CTSA.

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### **Multigenerational impacts on DNA methylation signatures in autism spectrum disorder**

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OBJECTIVES/GOALS: to investigate the potential impact of grand-parental factors and multigenerational epigenetic inheritance on the development of ASD METHODS/STUDY POPULATION: Our study recruited participants from the CHARGE (Child Autism Risks from Genetics and the Environment) study, including grandparents, parents, and children. A questionnaire was used to gather information about the participants' exposure to environmental factors. Saliva samples were collected from 349 participants. Newborn dried blood spots from probands and parents are still being collected from the California New born Registry. DNA was extracted from 349 saliva samples from 85 families and subjected to whole genome bisulfite sequencing (WGBS) to analyze DNA methylation. Sequence alignments and bioinformatic analyses will be performed using R packages called DMRichR and Comethyl. RESULTS/ANTICIPATED RESULTS: Sequence alignments and bioinformatic analyses are ongoing, utilizing DMRichR to identify individual genomic loci associated with ASD in each of the three generations and Comethyl to compare correlation patterns between methylation marks and selected variables, including grand parental exposures. New born blood spot collections of parents and probands are ongoing and will be used to identify potential ASD epigenomic signatures that are tissue and life-stage independent. DISCUSSION/SIGNIFICANCE: This research will provide new insights into the increased prevalence and underlying etiology of ASD that should pave the way for future research in the field. DNA Methylation signatures can help create molecular biomarkers which can be used together with behavioral clinical tests for diagnosis of ASD.