PROJECT SUMMARY
Healthcare-associated (HA) *Staphylococcus aureus* infections are declining but remain common. Conversely, rates of community-associated infections have not decreased due to the inadequacy of mechanisms to control transmission in a community setting. Hispanic Americans have a lower risk of infection than non-Hispanic whites, while American Indians face an increased risk for infections. The underlying causes of this disparity are unknown. Our long term objective is to use risk-based information founded upon empirical evidence of transmission to inform intervention strategies that reduce *S. aureus* transmission in the community. Our immediate goals are to determine whether national trends are reflected within different ethnic groups in Yuma, Arizona vis à vis infection rates and asymptomatic carriage. We will also determine if clinical strains are representative of community-carriage strains and not due to the emergence of a few, highly fit lineages. Given the broad differences in social interactions due to travel and residency patterns among ethnic groups, we also aim to determine the role that social relationships and interactions have on *S. aureus* transmission, either as risk or protective factors. The rationale is that we will gain an understanding of underlying causes of this health disparity and gain further insights into important components of *S. aureus* transmission: community carriage, pathogen genotypes, and the impact of social interactions.

Specific Aim #1. We will characterize *S. aureus* infection and carriage rates and compare circulating pathogen genotypes with those associated with disease isolated from local clinical specimens across full- and part-time resident groups, and across Hispanic and Non-Hispanic White ethnic groups. Whole genomes from community sampling will be phylogenetically compared to those from clinical samples to determine if the diversity of clinical pathogen genotypes is representative of community genotypes. We expect to find evidence that pathogen populations do not differ among these groups, suggesting that pathogen genotypes do not explain ethnic based disparities in *S. aureus* infections.

Specific Aim #2. We will determine and test social network- and social determinants-based risk factors for transmission of *S. aureus*. While enrolling participants, we will collect data that will define local social “contact” groups. We will use social determinants of health and social network variables (both ego-centric and relational) to determine the extent to which social relationships can contribute to understanding *S. aureus* transmission by 1) asking participants questions designed to quantify physical contact within a social group, 2) characterizing their nasal, pharyngeal, and hand microbiome as independent estimators of contact and social proximity resulting in transmission of commensal species, 3) and by comparing the evolutionary relatedness of *S. aureus* positive samples with the measured or estimated level of contact among participants.