NIH-funded Research Based on the GRC and Local Collaboration Investigates how Genetics and the Environment Shape Chronic Wound Microbiomes

Funding:

"Patient Genetic Determinants of Chronic Wound Microbiome Composition," awarded to PI Caleb Phillips from the National Institutes of Health, $421,373, 2022-2025.

Project summary:

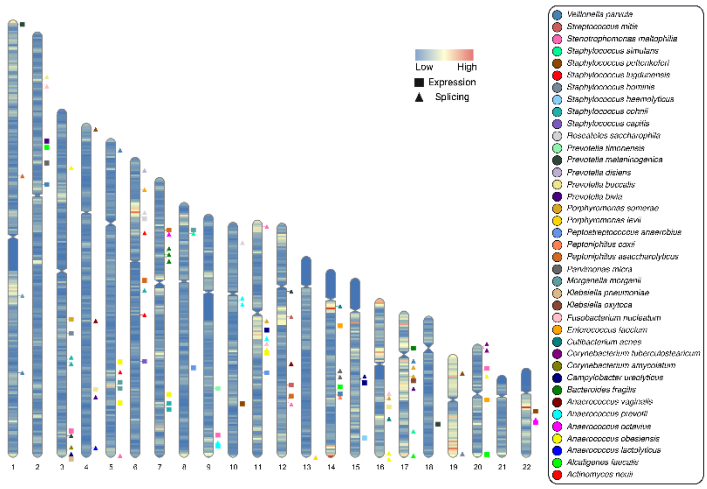
Millions of Americans from all walks of life suffer from chronic wounds. Chronic wounds are a major humanistic burden that lowers patient quality of life, increases mortality rates, and is an economic burden costing at least $3 billion annually. One reason that chronic wounds display poor healing is due to bioburden cause by microbes that live in the wound bed. It is widely known among physicians and researchers that chronic wound sufferers often differ in the microbes that colonize their wounds. However, why patients differ in species detected in their wounds, and how these differences relate to healing differences, is not very well understood. Over the past few years, an integrative research team has shed new light on this issue.

The research team consists of Dr. Caleb Phillips (TTU Curator of the NSRL's Genetic Resources Collection and Associate Professor in Biology), Dr. Craig Tipton (Director of Biostatistics, MicroGenDX), Dr. Todd Little (TTU Professor Educational Psychology), Dr. Nicole Phillips (University of North Texas Health Sciences Center), Dr. Joe Wolcott MD (Southwest Regional Wound Care Center), Dr. Kendra Rumbaugh (TTU Health Sciences Center), and graduate students Rebecca Gabrilska, Jake Ancira, and Khalid Omeir. For this research, the team is utilizing the Wolcott Wound Care Collection (~1,400 wound and tissue samples), a specialized collection of the NSRL's Genetic Resources Collection, that preserves and curates patient tissues for later study and discovery.

Findings to date include:

- There are hundreds of locations in the human genome where people differ, and those differences help explain why patients differ in the microbes in their chronic wounds.
- The microbes found in wounds sampled from thousands of people from across the United States differs depending on the climate (e.g., temperature and humidity) where people live.
- Differences in chronic wound microbes, as well as patient factors like smoking, explain a lot amount of differences in a person's healing time.

Taken together, these results inform how person-specific factors are consequential for chronic wound healing.



Chromosomal ideogram illustrating the 109 significant genes identified through two-cohort mbTWAS analysis. Each marker represents the mid-position of a significant gene on chromosomes directly to the left. Marker colors indicate the species to which genes were associated, and shapes indicate if the association was for a gene or intron retention. Chromosomal gene density is illustrated by banding. (R: RIdeogram).

Publications:

Tipton, C. D., R. Gabrilska, J. Ancira, C. Jarvis, L. Koenig, C. Wakeman, N. Van Gestel, R. D. Stevens, K. Rumbaugh, K. Ardon-Dryer, and C. D. Phillips. Submitted. Analysis of 9,241 North American wound specimens reveals six major microbiome community state types and meteorological associations. Nature Communications.

Omeir, K., J. Ancira, R. Gabrilska, C. D. Tipton, C. Miller, A. Noe, K. Subasinghe, M. Rowe, N. Phillips, J, Wolcott, and C. D. Phillips. Submitted. Heritable tissue-specific gene expression associates with chronic wound microbial species. Wound Repair and Regeneration.

Ancira J, Gabrilska R, Tipton CD, Miller C, Stickley Z, Omeir K, Wakeman C, Little T, Wolcott J, Phillips CD (resubmitted). A Structural equation model predicts chronic wound healing time using patient characteristics and wound microbiome composition. Wound Repair and Regeneration

Tipton, C. D., R. D. Wolcott, N. E. Sanford, C. Miller, G. Pathak, T. K. Silzer, J. Sun, D. Fleming, K. P. Rumbaugh, T. D. Little, N. Phillips, and C. D. Phillips. 2020. Patient genetics is linked to chronic wound microbiome composition and healing. PLoS Pathogens, journal.ppat.1008511.