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"Local Control of Pyoderma Gangrenosum"

Background: Pyoderma gangrenosum (PG) is a rare, non-infectious neutrophilic dermatosis that presents as painful, ulcerative, non-healing wounds. Pathergy, defined as hyperreactivity of the skin following minor trauma, is one of the hallmarks of PG. Currently, there is no consensus involving the diagnosis, treatment, and management of PG. A recent case report demonstrated that the use of a dehydrated human amnion/chorion membrane (dHACM) following surgical debridement in a single patient promoted wound healing. However, the physiologic mechanism underlying the effects of PG wound treatment with dHACM remains unknown.

Objective: The objective of this study is to characterize and compare PG wounds pre- and post- treatment with dHACM by identifying transcriptomes of select genes of genetic pathways.

Methods: This study is part of an ongoing clinical trial with a target enrollment of 20 patients. A pre-screening process is conducted on all potential subjects. The clinical portion of the study involves two operations: 1) debridement of the wound and treatment with dHACM until sufficient wound granulation is identified, followed by 2) split-thickness skin graft (STSG) coverage of the wound one week later. For the genomic analysis, wound samples are collected during each operation for total RNA isolation (RNeasy Mini Kit, Qiagen, Germantown, Maryland) and processed via real-time quantitative reverse transcriptase polymerase chain reaction (GENEWIZ, South Plainfield, NJ). Clinical outcome data on wound healing are collected during routine patient follow-up for 22 weeks post-operation.

Results: As of August 2022, a total of 2 subjects have been enrolled in the study. All subjects underwent treatment with dHACM, STSG, and were followed-up in clinic. The transcriptome data for each patient has been acquired and is under analysis. A third potentially eligible study candidate has been identified and is awaiting study enrollment.

Future Direction: Clinical outcomes are promising. Additional patient enrollment along with gene enrichment analysis, pathway analysis, and functional annotation of the transcriptomes are required to provide further insight into the treatment of PG with dHACM and its effects on local gene expression.