Title: Whole genome microarray data of chronic wound debridement prior to application of dermal skin substitutes

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Study Objective: Clinical consensus is that debridement is necessary for successful application of dermal skin substitutes (DSS). The aim here was to identify commonly expressed genes associated with wound healing in untreated acute wounds, chronic wounds (without a dermal skin substitute) and chronic wounds treated with wound debridement followed by application of DermaPure®.

Study Info / Design: For the first time, three data sets of whole genome microarray data generated from 3 studies were evaluated:

1. Acute wound (sequential biopsies) in human skin
2. Chronic wounds (sequential biopsies without dermal skin substitute) in human skin
3. Chronic wounds (sequential biopsies with DermaPure®) in human skin

Cutaneous biopsies were taken at two time points from untreated acute and chronic wounds and from chronic wounds treated with DermaPure® following debridement.

Results and Conclusion:

Over a 14-Day Period:
1. Acute Wounds – Over 13,000 genes had a fold change ratio of >1.01
2. Chronic Wounds without DermaPure – Over 21,000 genes had a fold change ratio of <1.01

Over a 42-Day Period:
3. Chronic Wounds with DermaPure – Over 12,000 genes had a fold change ratio of >1.01

Further analysis identified 2,120 genes to have a fold change ratio of greater than 1.01 in acute wounds and chronic wounds treated with DermaPure® and a subsequent fold change ratio of less than 1.01 in chronic wounds.

Based on biological process information available in Qlucore; novel genes were identified based on wound healing processes of proliferation, migration, differentiation, angiogenesis, extracellular matrix organization and apoptosis.

Specifically, microarray analysis identified significant differences (p<0.05) when comparing untreated chronic wounds to chronic wounds treated with DSS (DermaPure®).

Related to:
- Proliferation (HIPK2, LGR4, FGFR1, SRRT), migration (RHOC, PRPF40A, FGFR1)
- Differentiation (TCF4, COL13A1, GNPTAB, HUWE1, FGFR1)
- Angiogenesis (HIPK2, CASP8)
- Extracellular matrix organization (VWA1)
- Apoptosis (BBC3, HIPK2, KLFL1, PSM3, MSFD10, TOP2A, MLH1, CASP8, PDIA3, XAF1)

Chronic wounds treated with DSS (DermaPure®) exhibited similar expression levels compared to untreated acute wounds.
Chronic wounds treated with debridement followed by DermaPure® resemble untreated acute wounds at a genomic level.

These novel findings strengthen the recommendation to transform a chronic wound into an acute wounds supported by application of DermaPure®.