

A Sociogenomic Analysis of Chronic Wounds

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Background/Objective:

8.2 million US patients are affected with chronic wounds, with costs ranging from \$28.1-\$96.8 billion. Increasing healthcare costs, population age, and chronic condition incidences pose immense threats to the healthcare system and patients struck with the burden of chronic wounds. A sociogenomic approach to investigating mechanisms of chronic wound formation at the genomic level could provide a better understanding of how environmental factors and social demographics impact the development of such wounds. Our goal was to explore possible associations between outcomes of chronic wounds, healing status, genotype, gene expression, and the role of social demographics.

Experimental Design:

DNA and RNA were isolated from blood samples obtained from 51 patients with chronic wounds. Participant demographics and health information was collected for analysis. iPLEX® and MassARRAY® systems were used to genotype ten SNPs of seven genes involved in wound healing. Quantification of gene expression was performed via RT-qPCR. T-test analysis, ANOVA, and Fisher's Exact test were used for statistical analysis of results.

Results:

Significant relationships were discovered between increased *VDR* expression with heart disease, peripheral vascular disease (PVD), and hypercholesterolemia/hyperlipidemia. TT genotype of *rs1544410* present in vitamin D receptor (*VDR*) gene was associated with increased *VDR* expression as compared to CT genotype. Furthermore, increased methylenetetrahydrofolate reductase (*MTHFR*) gene expression was associated with PVD. Finally, the CC genotype of *rs2274976* present in *MTHFR* gene was associated with better wound outcome than the CT genotype.

Conclusion/Impact:

This study is one of the first known to investigate the impact of environmental factors and demographics on gene expression in patients with chronic wounds. Our results indicate social environment and genotype can play a significant role in patient gene expression and wound outcome. Future studies with larger sample sizes are warranted to investigate additional demographic data and expression of other genes involved in wound healing.

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