Gene expression analysis of Traumeel®'s effects in inflammation[19]

Full title
Deep Sequencing Transcriptome Analysis of Murine Wound Healing: Effects of a Multicomponent, Multitarget Natural Product Therapy-Tr14

Experimental model
Partial-thickness dermal abrasion wound healing mouse model

Objective
To characterize gene expression changes during inflammation resulting from the treatment with Traumeel®

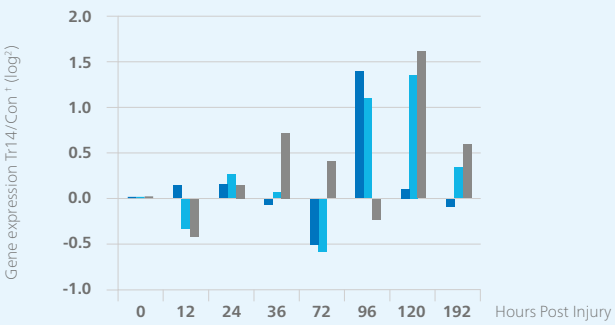
Method
Transcriptome analysis via single molecule sequencing

INTERVENTIONS

Traumeel®

Saline control and topical placebo

Gene expression changes during wound healing



p-values	12	24	36	72	96	120	192
Muscle	0.019	ns	0.016	0.035	0.0014	ns	0.049
Wounding	0.0001	0.002	ns	0.0015	0.0053	0.0053	0.0075
Cytokine	0.028	ns	0.043	ns	ns	0.0051	ns

Gene ontology categories:
- Muscle contraction
- Response to wounding
- Response to cytokine stimulus

— Traumeel® produced biologically significant changes in gene expression during wound healing, including well-known pathways, such as TGF-β, cytokine signaling, inflammation, wound contraction, collagen, and enzymes of the extracellular matrix.

— Traumeel® treatment reflects two general types of changes: (1) changes in the gene expression of the cells in injured tissue, and (2) the influx of new cell types into the wounded area.

— These signals may indicate effects upon resident fibroblasts and infiltrating immune cells and are consistent with known effects of Traumeel® on inflammation and pain.

— Traumeel® consistently regulated gene expression related to cell differentiation and cell motility suggesting an effect on the cellular state in the wound microenvironment, potentially increasing the repair capacity of the wound.

† Tr14= Traumeel®; Con = Control

St. Laurent G, Seilheimer B, Tackett M, et al. Deep Sequencing Transcriptome Analysis of Murine Wound Healing: Effects of a Multicomponent, Multitarget Natural Product Therapy-Tr14. Front Mol Biosci. 2017;4(AUG):1-12. doi:10.3389/fmolb.2017.00057