

Genes Differentially Expressed in Persons with Chronic SCI with Neuropathic Pain

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Objectives: Pain affects most individuals with SCI, is often refractory to treatment, and negatively affects quality of life. Previously, we analyzed blood gene expression in individuals with chronic SCI (N=31) compared to ablebodied (AB, N=26) individuals. Most participants with SCI reported 2 major, simultaneous pain types (nociceptive, neuropathic). Here, we analyzed blood differential gene expression by worst pain type ranked by participants with SCI.

Design: Prospective, observational study

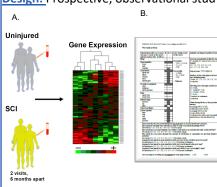
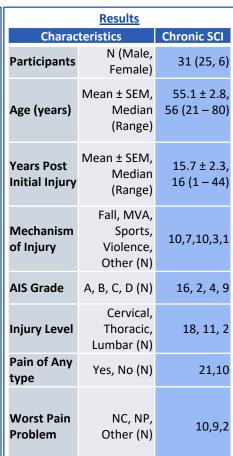
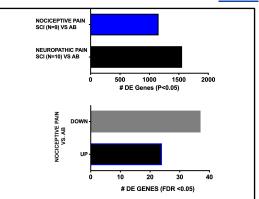


FIG. 1: A. Experimental design. B. The International SCI Basic Pain Data Set.^{6,7}.

NC=Nociceptive NP=Neuropathic



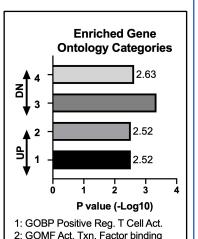
Results



*DE GENES (FDR < 0.05)

FIG. 2 With a Benjanimi-Hochberg false discovery rate (FDR) of 0.05, there were 37 down- and 24 up-regulated differentially expressed (DE) genes in participants with NC as worst pain type. There were no differentially expressed genes with FDR < 0.05 comparing AB to persons with SCI who ranked NP as worst pain type or between SCI participants who ranked either pain type as

their worst.



3: GOBP Pre. GPI anchor in ER mbe 4: GOMF Rec. Tyr Kinase binding

FIG 3. Gene Ontology (GO) Analysis of DE genes FDR < 0.05

Conclusions

T-Cells should be further investigated in nociceptive pain after SCI

References

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