Protein binding to a Distal PEA3 site is correlated with altered GAP-43 expression in DRG neurons.

<u>C.A. Laidlaw</u>, P.L. Andersen and D.J. Schreyer. Cameco MS Neuroscience Research Center, University of Saskatchewan, Saskatoon, Canada.

The growth associated protein GAP-43 is so-named because its expression is upregulated in neurons during development or regenerative axon growth. The 5'UTR of the GAP-43 gene contains three putative recognition sites for polyoma enhancer activator 3 (PEA3), an Ets family transcription factor. We have used electrophoretic mobility shift assays (EMSAs) to study weather protein binding to these sites may be involved in transcriptional regulation of GAP-43. Whole cell extracts were prepared from control dorsal root ganglia (DRG) or DRG that had been peripherally axotomized three days previously. One major band appeared on EMSA gels at which probe binding was specifically competed by cold probe. The intensity of this band was markedly increased in injured DRG, in correlation with increased GAP-43 expression. We then prepared adult DRG cultures and exposed them to medium conditioned by L8 muscle-like cells, a procedure previously found to repress GAP-43 expression. In these experiments, a higher molecular weight band appeared whose intensity was negatively coorelated with GAP-43 expression. We also examined nuclear extracts from RN46A neuron-like cell line. Undifferentiated RN46A cultures show a polygonal morphology, low GAP-43 expression, and low PEA3 probe binding on EMSAs. Differentiated RN46A cultures show neurite outgrowth, high GAP-43 expression and high PEA3 probe binding. These coorelative observations suggest that PEA3 proteins may be transcriptional regulators for GAP-43.

Supported by MRC Canada and Cameco MS Neuroscience research Center.