

Weekly Colloquium

Tuesday, 2/6/2018, 12:30pm, Billings Building – Rosedale Conference Room

“Biomechanical forces regulate gene transcription in mammalian neurons”

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Abstract:

The development of meter-long axons within peripheral nerves and white matter tracts is a remarkable yet unresolved biological process. Following the formation of synaptic connections, and the cessation of growth cone extension, mitotic tissues continue to expand between the proximal and distal segments of spanning axons. Such expansion conceivably applies temporary biomechanical stretch to local axons, which acts to regulate concomitant neuronal growth. While stretch is a known stimulus of neuron growth, the underlying molecular mechanisms are unknown. My primary research aims are to decipher the biological processes underlying long axon growth, and to discover methods of re-activating those mechanisms in order to support regeneration. My secondary aims are to develop methods of guiding new regenerative growth to the proper targets through the design of novel biomaterial scaffolds that may be implanted at sites of injury.

Publications:

Loverde J.R., Soteropoulos, P., Pfister, B.J. (2018). Biomechanical regulation of 496 genes in DRG neurons: A paradigm for the development of meter-long axons. (In-Preparation).

Loverde J.R., Pfister B.J. (2015). Developmental axon stretch stimulates neuron growth while maintaining normal electrical activity, intracellular calcium flux, and somatic morphology. *Front Cell Neurosci* 9:308.

Loverde J.R., Tolentino R.E., Pfister B.J. (2011). Axon stretch growth: the mechanotransduction of neuronal growth. *J Vis Exp*.

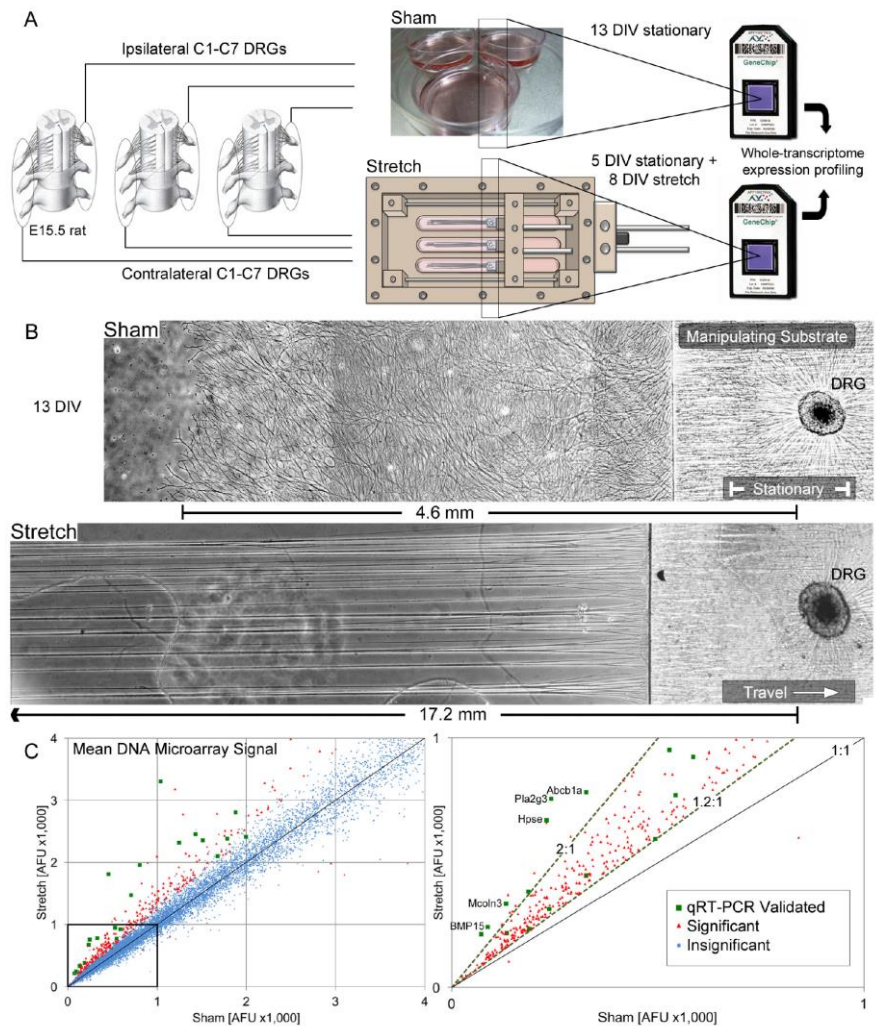


Fig. Overview of experiment conditions and gene expression analysis. (A) Biologically paired ipsilateral and contralateral cervical DRG explants from E15.5 rat pups were seeded onto Aclar substrates within experimental and control cultures. (B) Representative growth of stretch-grown and sham cultures following 13 DIV at the time of RNA isolation (See Fig. S1 for full view). (C) Whole-transcriptome analysis using Affymetrix GeneChip Rat Gene 1.0 ST Arrays. Left: The average signal intensity of stretch and sham microarrays $\leq 4,000$ fluorescence units (actual range was 5 to 24,000). Right: High-fold changes were determined by a normalized average microarray fluorescence ratio $\geq 2:1$ in stretch:sham cultures (≥ 2.0 -fold). Lower-fold changes were determined as having a minimum ratio of 1.2:1 fluorescence units (≥ 1.2 -fold). Blue circles and red triangles indicate insignificant and significant genes, respectively, while green squares indicate significant genes validated by qRT-PCR.