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# NEUROSCIENCES

SEMINAR SERIES

## Genetic dissection of spinal circuits processing mechanical pain

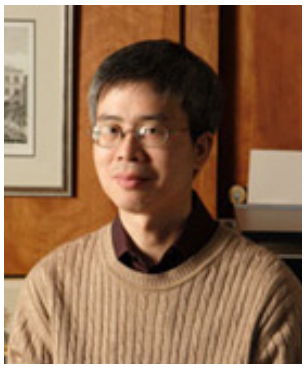
**Qiufu Ma, Ph.D.**
Professor, Department of Neurobiology
Harvard Medical School
Dana-Farber Cancer Institute
Boston, MA

**Monday, August 4th 2014**
**12:00-1:00 p.m.**

Alfond 106
UNE, Biddeford Campus

*Lunch will be provided*

Hosted by: Lei Lei, Ph.D.
Sponsored by: COBRE and CEN



Dr. Qiufu Ma received his Ph.D. from the University of California, Los Angeles, in 1994, and conducted postdoctoral training in developmental neurobiology at the California Institute of Technology, where he isolated a transcriptional factor that functions as a mammalian neuronal fate-determination factor. He joined the Dana-Farber Cancer Institute in 1999 and became a full professor in 2011.

His laboratory is currently interested in investigating the mechanisms underlying the formation of the pain circuitry. In mammals, painful/noxious sensory information is detected by a specialized group of sensory neurons called nociceptors. These neurons express a diverse array of ion channels and receptors that respond to noxious thermal, chemical and mechanical stimuli. Noxious sensory information is relayed through the dorsal horn of the spinal cord to the brain. A major goal of his research is to understand how distinct classes of nociceptors and spinal relay neurons are specified during development.

To address these questions, Dr. Ma's laboratory has taken a systematic approach to identify transcription factor (TF) genes expressed in the pain circuitry. TF genes are known to play central roles in cell type specification. In the mouse genome, about 1500 genes encode TFs that contain known DNA-binding motifs. In team together with Chuck Stiles lab, they have used in situ hybridization to map the spatial distribution of over 1200 TF genes in the developing mouse nervous system. By this systematic approach, they have gained a global view of TF genes expressed in nociceptors or pain relay neurons.