Histology Core News

Confocal Update

Following reports of users suffering through “fatal” errors during data collection, the confocal system has been serviced and software updated. It should now be fully functional again. Please pay attention to signage in the room regarding startup/shutdown procedures and note the following:

- Do not save your images and/or data to the desktop or anywhere on the C drive.
- Save all images/data into the D drive, into your personal flash drive, or onto Box.
- Images, data and folders currently on the desktop will be deleted on 6/28/2018. Please ensure you have saved your images before this date.

Recordings of the Summer Educational Series talks are available on the MRC website.

http://www.musculoskeletalcore.wustl.edu/content/Calendar/3020/Summer-Educational-Series.aspx

P30 Renewal Submitted

Thank you to everyone that contributed to the P30 submission! The MRC P30 has a resource community of over 80 Principle Investigators and supports the following Cores:

**Administrative Core**
- Pilot & Feasibility Grant Program which has awarded over $700K over the past 9 years to 20 PIs.
- Avioli seminar series & Summer Educational Series
- Annual MRC symposium with 7 travel awards
- Biostatistics resource
- Mouse genetic models database

**Histology and Morphometry**
- Histological sample processing, sectioning, staining
- Bioquant morphometry system
- Leica confocal microscope

**Musculoskeletal Animal Models**
- Osteoarthritis models
- Inflammatory bone loss and rheumatoid arthritis models
- Functional MSK assessment for small animals

**Structure and Strength Core**
- X-ray and microCT imaging
- Mechanical testing
Research in the Hirbe lab is focused on better understanding the biology of sarcomas, rare tumors of bone and soft tissue. There are over 100 different types of sarcomas all with a different underlying biology. We aim to utilize genomic information from patient sarcoma samples coupled with mouse models to better understand the development and progression of these cancers. Based on identification of mutated DNA repair pathways in a number of sarcomas (MPNSTs, rhabdomyosarcomas, pleomorphic sarcomas, and osteosarcomas), there is an ongoing project aimed at evaluation of therapies targeting this defect for treatment of bone and soft tissue sarcomas.

Approximately 13% of individuals with NF1 will develop MPNSTs during young adulthood. Currently, there are no predictive biological markers of disease progression, few therapeutic options, and dismal survival. Leveraging whole exome sequencing methods, we have identified several genes mutated in MPNSTs that may play a role in progression of these tumors. One of these genes, SPTBN2, codes for the protein, β-III-spectrin, which we found to be overexpressed in over 90% of MPNSTs. Further, knockdown of β-III-spectrin leads to increased cell death and decreased tumor growth in vitro and in vivo. We believe this is partially mediated through disruption of the plasma membrane and mis-localization of glutamate transporters and receptors such as EAAT4 and mGluR1, respectively. Current work in the lab is focused on better understanding this mechanism.

We also have a special interest in better understanding the development and spread of a particular soft tissue sarcoma, the malignant peripheral nerve sheath tumor (MPNST), an aggressive soft tissue sarcoma that occurs at an increased frequency in patients with the Neurofibromatosis Type 1 (NF1) tumor predisposition syndrome.

Come see us or email us to learn more!  
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