DOCTORAL CANDIDATE:	Ivan Myhre Winje
DEGREE:	Philosophiae Doctor
FAKULTY:	Faculty of Mathematics and Natural Sciences
INSTITUTE:	Department of Bioscience
AREA OF EXPERTISE:	Muscle physiology
SUPERVISORS:	Kristian Gundersen, Leonardo Meza-Zepeda
DATE OF DISPUTATION:	June 15 2018

DISSERTATION TITLE: *Myonuclear identification and epigenetics in skeletal muscle*

SUMMARY:

Being the most abundant tissue in the human body, skeletal muscle serves important functions such as locomotion, energy and protein homeostasis. Although all muscles follow the same basic concept, different muscles are composed of muscle fibers that that vary in their metabolic and contractile properties. This allows the organism to fine-tune each muscle to its functional demand. During a lifetime the system is confronted as the organism experiences periods of exercise, disuse and disease, forcing the muscle fibers to adapt is functional characteristics and phenotype accordingly.

In response to exercise, the muscle obtains a more oxidative phenotype to meet the new energy demands. During muscle growth, the number of myonuclei increases and allows increased protein production. It has been demonstrated that myonuclei do not disappear during atrophic conditions such as disuse and de-training, providing a basic mechanism where the muscle can regain its previous strengths after periods of inactivity. Recent evidence points towards epigenetic mechanisms playing an important role in phenotypical adaptions. Although such mechanisms remains largely unexplored in skeletal muscle

Winje has investigated how myonuclei responds to cancer-induced atrophy and shown that myonuclei are not lost from muscle fibers following a 21% reduction in muscle volume. To study the epigenetic mechanisms behind phenotypical adaption, Winje has identified a protein that is selectively expressed on myonuclei, allowing enrichment and epigenetic characterization of myonuclei. In his work he shows that the phenotypical differences between oxidative and glycolytic muscle are reflected in the epigenome.