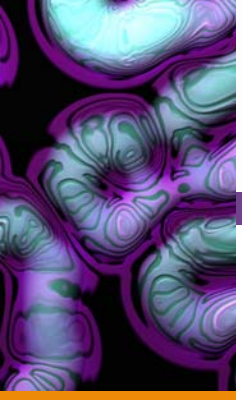

CENTER FOR INTEGRATED BIOSYSTEMS

Department of Animal, Dairy and Veterinary Sciences

Presents a joint seminar by

Dr. Jason White

School of Veterinary Science
The University of Melbourne

Matt McDonagh

Section Leader
Proteomics Primary Industries Research Victoria

Location: Merrill-Cazier Library room 154

June 12, 2007 from 3:30-4:30 PM

Seminar

Deconstructing the Callipyge Phenotype: A Functional Genomics Approach

The *callipyge* mutation in sheep results in significant skeletal muscle hypertrophy. The hypertrophy trait is inherited in a pattern described as polar over-dominance; the phenotype is only displayed in progeny that inherit the mutated allele from the paternal side. The hypertrophy is associated with fast glycolytic fibres with an associated decrease in the size and proportion of type 1 fibres. The causative SNP is in an imprinted region of ovine chromosome 18 and is surrounded by a number of protein coding regions including Dlk-1, peg-11 and GTL-2. We have used a functional genomics approach to try and delineate the mechanism(s) underlying the callipyge phenotype combining microarray analysis with proteomics and histological analysis. A number of candidate genes and pathways have been identified that are associated with the phenotype. This seminar will outline the approach and discuss some of the preliminary mechanistic data which has been generated.

Hosted by Dr. Noelle Cockett 797-2875

Refreshments will follow in the Biotechnology Building Lobby