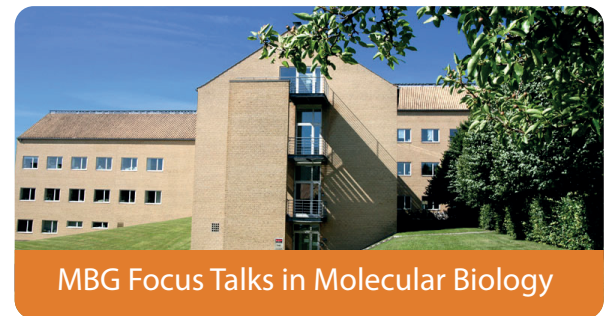


MBG FOCUS TALK

hosted by Stig Uggerhøj Andersen



Monday September 21st, 2015 at 11:15-12:00

Build. 3140 room 114 (Meeting room 5)

Senior scientist Andrew Griffiths

Forage Improvement Group, AgResearch, Palmerston North, New Zealand

White Clover: From Genomes to Grasslands

White clover (*Trifolium repens* L.) is a principal legume in temperate pastoral systems that produces high quality forage and fixes atmospheric nitrogen into plant available forms through bacterial (*Rhizobium*) symbiosis. At AgResearch in New Zealand there is a long history in clover and perennial ryegrass (*Lolium perenne*) cultivar development which has been augmented in recent years with the development of substantial genomic and genetic resources. As part of Pastoral Genomics, a New Zealand Industry: Government-funded research consortium, we have developed microsatellite markers, moderately dense clover genetic linkage maps and QTL populations to underpin marker-assisted selection for specific agronomic traits. This is being now being further progressed by developing Genotyping by Sequencing marker platforms to enable and test Genomic Selection strategies that align with our commercial breeding pipelines.

White clover has a relatively compact genome (≈ 1 Gb), but is an allogamous allopolyploid ($2n=4x=32$) which provides challenges for breeding and for developing a de novo reference genome using next generation sequencing platforms. Pastoral Genomics, in collaboration with researchers at Aarhus University, has sequenced white clover and its diploid progenitors (*T. occidentale* and of *T. pallescens*) to facilitate understanding and utilisation of these species. Final annotated assemblies of the three species provide insights into sequence assembly challenges and strategies in high-diversity polyploid species, and provide a greater understanding of the origin of white clover itself.

This seminar will provide an overview of major white clover programmes including: marker-assisted breeding; clover::Rhizobium interactions; and the latest insights from the clover reference genomes initiative.