

SEMINAR

“The role of genetic & epigenetic variation in environmental adaptation of plants”

Dr. Manu Dubin

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11.00 - 12.30

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TPOC-3



SEMINAR ABSTRACT:

Rising temperatures and CO₂ levels along with altered precipitation patterns threaten both natural biodiversity and agriculture. Therefore, it is of critical importance to understand how plants will respond to these environmental changes and to develop crop varieties that are more resistant to extreme and unpredictable climates. In addition to genetic variation, epigenome modulation is thought to provide a mechanism for organisms to adapt, within and between generations. To investigate this potential mechanism Dr Dubin profiled variation of DNA methylation in populations of *A. thaliana* and found that accessions originating from colder climates show elevated CpG gene body methylation (gbM). This variation in methylation levels appears to be under strong selection and was mapped using GWAS and F2 populations to loci encoding histones or proteins involved in chromatin remodeling. At least some of these variants seem to be associated with altered temperature dependent gene expression patterns.

In order to determine the relevance of these findings to other plant species, whole-genome bisulfite sequencing was done on a worldwide panel of landrace and elite Barley cultivars. In this species gbM levels were also correlated with temperature minima (Spearman's Rho = 0.44), suggesting the relationship between gbM and temperature is likely widespread in plants. In contrast with *A. thaliana*, gbM makes only a minor contribution to overall DNA methylation variation in barley, with most of the variation instead occurring on transposons (TEs) which are significantly more abundant in this species. While TE methylation levels were also correlated with climate variables, the pattern was quite distinct from gbM: TE methylation correlated with short term (e.g. daily) temperature fluctuations. TE methylation levels were also inversely correlated with their copy number: plants from locations with high levels of daily temperature fluctuations having both lower levels of DNA methylation and a higher TE copy number, possibly due to heat-stress induced TE activation. Interestingly, TE copy number, which is the major driver of genome size variation in barley also showed some correlations with agronomic yield related traits such as 1000 kernel weight (Spearman's Rho = 0.30).

Given that TEs are often not linked with neighbouring genetic markers such as SNPs, they potentially represent an overlooked source of variation, which could be beneficially exploited in commercial breeding programs.

SPEAKER

INTRODUCTION:

Following undergraduate degrees in organic chemistry (University of Canterbury, New Zealand) and biochemistry (University of Sydney, Australia), Dr Manu Dubin did his masters at the Zoological Station in Naples Italy and then his PhD at the University of Kassel in Germany working on epigenetic regulation and nuclear organisation in the social amoeba *Dictyostelium discoideum*. In 2010 he moved to the Gregor Mendel institute in Vienna working on the role of DNA methylation in local adaptation in *Arabidopsis thaliana*. In 2015 Manu joined Bayer CropSciences as a visiting scientist working on genome and epigenome engineering. Since 2018 he has been at the University of Lille in France working on the role of small RNAs in the regulation of self-incompatibility and the role of DNA methylation and transposons in adaptation to climate and heavy metal tolerance.