



## BiRC Seminar – open to all

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**Time:** Tuesday 26 January 2016, 14:15 - 15:00

**Venue:** BiRC, C. F. Møller's Allé 8, Building 1110-223

**Title:** Epigenetic variation in Arabidopsis

### **Abstract:**

Epigenome modulation in response to the environment potentially provides a mechanism for organisms to adapt, both within and between generations. However, neither the extent to which this occurs, nor the molecular mechanisms involved are known. We investigated expression and DNA methylation variation in Swedish Arabidopsis thaliana accessions grown at two different temperatures.

Environmental effects on DNA methylation were limited to transposons, where CHH methylation was found to increase with temperature. Genome-wide association mapping revealed that the extensive CHH methylation variation was strongly associated with genetic variants in both cis and trans, including a major trans-association close to the DNA methyltransferase CMT2. Unlike CHH methylation, CpG gene body methylation (GBM) on the coding region of genes was not affected by growth temperature, but was instead strongly correlated with the latitude of origin. Accessions from colder regions had higher levels of GBM for a significant fraction of the genome, and this was correlated with elevated transcription levels for the genes affected. Genome-wide association mapping revealed that this effect was largely due to trans-acting loci, a significant fraction of which showed evidence of local adaptation.

In general, genetic variation appeared to have a much greater effect on expression variation than methylation variation, although expression at around 60 loci showed clear evidence of being affected by methylation variation independently of genetic variation. Statistical analysis suggested that methylation affects expression more frequently than the other way around.

Our findings constitute the first direct link between DNA methylation and adaptation to the environment, and provide a basis for further dissecting how environmentally driven and genetically determined epigenetic variation interact and influence organismal fitness.

**After the seminar there will be beer/soda and chips in the lunch room!**

