Crops and climate change

Expose an animal to uncomfortable heat and it will up and leave; for plants, however, this is not an option. Dr Silje Veie Veiseth discusses how her work is revealing the epigenetic mechanisms underpinning a plant’s acclimation to climate change.

**What interests you most about plant epigenetics?**

Since I first learned about histone modifications during my bachelor’s degree, I’ve been intrigued by the subject. It’s fascinating to think that a dynamic process can change the way our genes are expressed, meaning our phenotype is not only determined by the DNA sequence.

Plants are especially interesting; it has been shown that they have evolved several epigenetic mechanisms to adapt to their environment, as plants cannot move around like animals. Keeping transposable elements (TEs) silenced is an important part of the epigenetic regulation of the genome, as these elements could otherwise move around and cause detrimental mutations. TEs can be activated under heat stress, and so, given the progression of global warming, we must learn how important crop plants respond to higher temperatures now more than ever before.

**Your present project focuses on the function of a specific group of histone-modifying enzymes, HKMTases. Could you outline the main objectives of this investigation?**

Our aim is to contribute to the understanding of plant responses and adaptation to heat stress by focusing on the control of TE activity. DNA methylation has been studied extensively in relation to TE control, but less so in relation to the roles of HKMTases. My project will address this gap in the literature by exploring the role of SUVR4, a specific HKMTase, in chromatin regulation.

**How does your approach to TE control aim to improve stress adaptation in plants?**

We have observed that overexpression of SUVR4 leads to increased suppression of transcriptional activity, and so we’re investigating whether SUVR4 can play a role in the resetting of TE suppression after stress release. We know that heat stress can activate transposons, including TEs that SUVR4 represses. One hypothesis of SUVR4 activity posits that the protein represses potentially damaging transposon mobility during heat stress. This theory may be commercialised in the future, as crop plants overexpressing SUVR4 would be more tolerant to the heat.

**What difficulties have you met with in your research, and how have you overcome them?**

I would say that the biggest challenge has been to cope with the fact that most experiments in the lab will not necessarily run smoothly. Oftentimes, you do a lot of work and have nothing to show for it, no results worthy of report. The best way to overcome this is simply to be patient, and do the protocol one (or, more likely, several) more time(s).

**You will soon be collaborating with Sir David Baulcombe at the University of Cambridge, UK; how do you predict this will benefit your project?**

Sir David Baulcombe is a highly respected scientist, well known to the plant research community, and co-discoverer of the gene silencing pathway of plants. A central focus of my project is whether my main gene of interest, SUVR4, plays a role in this silencing pathway. Working in Baulcombe’s lab will surely benefit my project, but also stands to benefit me personally, as I’ll learn to collaborate with new people in a foreign country. Additionally, for future grant proposals, a collaboration with Sir David Baulcombe will make my CV stand out from the rest.

**Can you highlight any unanswered questions in your field that you hope to solve in the future?**

In Arabidopsis (a model organism for plant biology), there have been contradictory reports on the histone modification trimethylation of H3K9, and whether it is associated with the activation or repression of genes. We identified SUVR4 as the first enzyme to produce this mark in Arabidopsis. By further exploring the role of SUVR4, I hope to clarify the biological outcome of the H3K9 trimethylation mark. Hopefully my future work will add to our understanding of how plants are affected by transposons in an increasingly warm climate.
The epigenetic mechanisms of plants

As global warming progresses, plants suffer increasingly from heat stress. Plant biologists at the University of Oslo, Norway, are determining the epigenetic factors that enable a plant’s adaptation to rising temperatures – and might one day be manipulated to produce heat-resistant crops.

CLIMATE CHANGE REPRESENTS a serious issue in all spheres – especially agriculture, the industry on which humankind’s sustenance depends. In lieu of legs with which to flee the heat, plants possess an unrivalled ability to acclimatise to increasing temperatures. It is by virtue of their dynamic genomes that plants adapt to climate change, though the precise mechanistic basis of this genomic reshuffling is yet to be delineated in full.

Making fruitful strides in the field of plant epigenetics, Dr Silje Vee Veiseth at the University of Oslo is studying the exemplar species Arabidopsis thaliana in order to determine the mechanisms underlying plant adaptation to hotter climes.

KEY MATERIALS AND METHODS

A. thaliana, commonly known as thale cress, is the standard model organism for plant biologists. Being the first plant to have its entire genome sequenced, A. thaliana is one of the most thoroughly documented species in its kingdom. Results obtained from Arabidopsis, such as those authored by Veiseth, are not limited to this particular species, and may be generalised quite freely due to conservation of most cellular mechanisms not only in plants, but also in other taxa. The SET domain genes Veiseth is studying are highly conserved, from yeast via plants to animals.

Veiseth employs a variety of molecular and genetic techniques to determine which genes and signalling molecules are involved in the complex physiological responses of plants. Chief among these techniques is chromatin immunoprecipitation (ChIP), an assay involving the use of antibodies to determine how specific proteins interact with the genome. Using ChIP, Veiseth can, for example, deduce the genetic targets of Arabidopsis’ histone lysine methyltransferases (HKMTases).

TRANSPOSONS

Otherwise known as transposable elements (TEs), transposons are repetitive DNA segments capable of moving around within the genome. These ‘jumping genes’ can affect how an organism’s DNA is spelled out, thus giving rise to mutations. The notorious bacterial phenomenon of antibiotic resistance may even involve TEs, supporting the notion that transposons may play an evolutionarily conserved role of modifying the genome in accordance with environmental changes.

A single transposon’s activity can mean the difference between a Chardonnay and a Cabernet grape, a considerable phenotypic transformation. Under agreeable environmental conditions, a number of complex mechanisms are at work to keep transposons dormant. However, when a plant experiences heat stress, certain transposons are actively expressed, affecting its development.

HKMTASES

In order to investigate how transposons are regulated in a genome in the context of temperature changes, Veiseth is using HKMTases. HKMTases are enzymes that catalyse the donation of methyl groups – small hydrocarbons – to the lysine residues of histones. These proteins are often likened to spools about which the DNA of eukaryotic cells is wound. By methylating histones, HKMTases modify the expression levels of specific genes, up- or down-regulating their translation into functional proteins.

Actively expressed and repressed genes occupy distinct compartments of the cell nucleus; the euchromatin and heterochromatin, respectively. Expressed transposons, however, translocate within the genome, inserting themselves into the genetic code to produce mutations. This mutagenic activity can destabilise the genome, potentially resulting in chromosome breakage – bad news for any organism. Transposons are

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EXPLORING THE EPIGENETIC MECHANISMS OF STRESS ADAPTATION IN PLANTS

OBJECTIVE
To use Arabidopsis histone lysine methyltransferases (HKMTases) as a tool to investigate how transposons are regulated in a genome and how this process can be affected by increasing temperatures.

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also found between actively expressed genes in euchromatin; it is here that the SUVR4 HKMTase operates.

SUVR4
Veiseth is presently unravelling SUVR4’s transposon-repressing effects. This HKMTase adds methyl groups to lysine 9 of histone H3 (H3K9). By use of an artificially over-expressed recombinant form of SUVR4, which fluoresces, Veiseth and colleagues demonstrated that upregulation of SUVR4 resulted in the trimethylated version of H3K9 being spread across the cell nucleus, as visualised under the microscope.

Subsequent ChIP experiments, together with other experiments, revealed this histone modification to suppress the activity of the affected transposons, SUVR4 therefore opposes the mutagenic activity of the TEs. Heat stress is known to activate certain transposons, and Veiseth postulates that SUVR4 serves to reset the repression of these transposons following release from heat stress, as part of an epigenetic defence mechanism.

It is important to emphasise that, whilst crops must be protected from the disadvantageous effects of unsuppressed transposons, these TEs are also key to the diversification of plant genomes, and may be exploited to develop more adaptable crops.

POST-TRANSLATIONAL MODIFICATION
In addition to the SET domain via which HKMTases catalyse methylation, most HKMTases contain further domains that enable them to respond to other post-translational modifications and cellular signals. The ligands that bind at these regulatory domains alter the activity of the enzyme, and thus constitute components of its regulatory pathway.

Veiseth’s group found SUVR4’s H3K9 trimethylation activity to be enhanced by the process of ubiquitination, which describes the post-translational (after the gene is translated into a protein) modification of adding ubiquitin, a regulatory protein aptly termed for its near omnipresence in eukaryotic tissues. SUVR4’s ubiquitin dependence hints at the nature of this HKMTase’s regulation, an area that Veiseth plans to elucidate. Given the existence of multiple cell signalling pathways governing transposon activity, some of which engage in cross-talk with one another, Veiseth’s goals are certainly ambitious.

Emphasising the extent of her ambition, Veiseth reports an early success – the first piece of the regulatory pathway puzzle: “So far this is only preliminary data, but pilot ChIP experiments indicate that the activity of SUVR4 on transposons is dependent on RNA polymerases”. RNA polymerases PolIV and PolV are involved in RNA-directed DNA methylation in Arabidopsis, a mechanism that acts to silence transposons. Gaining the understanding, and thus ability, to control plant adaptation means that Veiseth’s research has the potential to help salvage agriculture in the parched soils of tomorrow.