

# Spotlight on Science

## Understanding Epigenetic Mechanisms in Endosperm Development



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### What is the key focus of your research project?

I belong to a group interested in the genetic and epigenetic mechanisms that control seed development. Our particular focus is to understand the developmental role of the endosperm, a nourishing tissue produced inside the seeds of most flowering plants after fertilization. The endosperm plays the role of supporting embryo growth, similar to what occurs with the placenta in mammals. My work in Claudia Köhler's group has focused on identifying epigenetic modifications during early stages of endosperm development, which required us to set up a method for purification of early endosperm which would allow to generate tissue-specific epigenome profiles.

### Why focus on plant endosperm?

The endosperm is essential for embryo development; defects in endosperm development result in embryo failure and seed abortion. One of the peculiarities that make the endosperm a very attractive tissue to study is that some genes are expressed in a

parent-of-origin specific fashion, meaning that either only the maternal or the paternal alleles of a particular gene are expressed. This epigenetic phenomenon is referred to as genomic imprinting. My main interest is to decipher the nature of the inherited imprint and to decipher the role of imprinted genes for endosperm development.

### What tools are you using to study the genomic imprinting?

I work with the model plant *Arabidopsis thaliana*, a well-known organism with a high quality annotated reference genome. Previous RNA expression studies in the group have determined which genes are imprinted in *Arabidopsis*. Because genomic imprinting is mainly controlled by DNA and histone methylation we have been studying these marks at a genome-wide level by generation of parental-specific DNA and histone methylation profiles using bisulfite-sequencing and chromatin immunoprecipitation (ChIP) sequencing, respectively.

### How has NuGEN enabled your research?

Working with a model plant like *Arabidopsis* has its benefits; however, it generates only very small seeds and a small endosperm with few nuclei. Additionally, to trace the parent-of-origin of epigenetic modifications we do

manual pollinations of defined parental plants, which is a laborious procedure resulting in limited amounts of material. For this reason the use of NuGEN's Ultralow systems for library preparation was a great help. With NuGEN's technical support we were able to set up the preparation of DNA methylation libraries using Ovation® Ultralow Methyl-Seq Library Systems and ChIP libraries with Ovation® Ultralow Library Systems V2 even with small amounts of starting material.

### And the final goal of this study?

Now that we have generated parent-of-origin specific endosperm epigenetic profiles I would like to understand the cross-talk among the different epigenetic marks and their effect on the regulation of endosperm development. Understanding of endosperm function in seed development is of great value for the crop breeders. Seeds of cereals like rice, wheat or maize are filled with endosperm, the tissue that we consume and that forms the major staple food worldwide. I am therefore convinced that a basic understanding of endosperm development by understanding the underlying epigenetic mechanisms holds great potential for future applications.