



**PhD position available: Effects of polyploidization on the wheat methylome-transcriptome complex**

**Supervisors:** Peter Civan (CRCN INRAE, <https://www.researchgate.net/profile/Peter-Civan>), Jerome Salse (DR1 INRAE, [https://www.researchgate.net/profile/Jerome\\_Salse](https://www.researchgate.net/profile/Jerome_Salse))

**Period:** Starting before the end of 2021 until 2024

**Application:** please send your CV and letter of support to [peter.civan@inrae.fr](mailto:peter.civan@inrae.fr) and [jerome.salse@inrae.fr](mailto:jerome.salse@inrae.fr)

**Laboratory:** INRAE-UCA UMR 1095 GDEC, Génétique, Diversité et Ecophysiologie des Céréales, PaleoEVO team (<http://bit.ly/PaleoEvo>), 5 chemin de Beaulieu, 63000 Clermont-Ferrand

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### **Project description**

Wheat is one of the most important crops globally, forming a crucial part of human diet. Bread wheat has a polyploid genome resulting from ancient hybridization between its diploid and tetraploid progenitors some 10K years ago. Understanding the genetic consequences of polyploidization on the wheat genome, transcriptome, and ultimately phenotype, can have crucial implications for utilization of genetic diversity in breeding. The seminal polyploidization of bread wheat evolution can be recreated in experimental settings, producing synthetic/nascent polyploids, which are not simply a sum total of the parental genomes, but are modified by various genetic and epigenetic changes, including sequence elimination, transcriptomic changes and epigenetic modifications. Although some of these changes are reproducible and similar to the ones found in natural polyploid wheats, their systematic, genome-wide characterisation is lacking. Moreover, the mechanistic basis of these changes remains poorly understood, and it is unclear whether they are necessary for proper functioning and fertility of the nascent polyploids, or mere (potentially deleterious) byproducts of the polyploidization process.

The best described consequence of polyploidization in wheat is the re-programming of its transcriptome, also called expression partitioning. Transcriptomic studies have shown that homoeolog silencing is pervasive in bread wheat, with 27.6%-45% of homoeologous groups having one or two gene copies silenced. A portion of these changes is established immediately after polyploidization and can be studied in synthetic allohexploids. Although there are several possibilities how transcriptional reprogramming can be achieved (e.g., gene loss, TE insertion in gene's vicinity; position effect due to translocation), mounting evidence suggests that DNA methylation (i.e. cytosine methylation) is the primary mechanism of polyploidy-induced reprogramming that ensures its heritability. Despite the obvious importance of gene expression (de)regulation in polyploid crops, virtually no studies have examined on the genome-wide scale the possible links between gene expression changes and DNA methylation patterns in nascent wheat polyploids.

This projects aims to provide gene-based (but genome-wide) exploration of these processes. Building on existing transcriptomic data collected from families of nascent synthetic allohexaploids where 'binary DEGs' have been identified (differentially expressed genes showing no transcription in the synthetic wheat despite robust transcription in the parents), the PhD candidate will first explore gene losses and aneuploidy as the potential causes of such patterns. Subsequently, the core of the project will focus on links between cytosine methylation and altered expression. These will be explored through methylome sequencing (Illumina) of amplicon libraries (homoeolog-specific) constructed from the binary DEGs. Various gene partitions (UTRs, exons, introns), sequence contexts (CpG, CHG, CHH), crossing schemes, tissues and generation will be examined to provide a detailed assessment of methylation changes in respect to altered transcription in polyploids. These changes will be evaluated in the context of wheat diversity and agronomically important traits, with the aim to inform future breeding efforts.

### **Required skills and qualifications:**

- MSc degree in molecular genetics, or similar (required)

- wet-lab experience with DNA extractions, PCR, etc. (required)
- experience with primer design and DNA methylation analysis (beneficial)
- bioinformatics: experience with command-line interface, R, scripting, next-generation sequencing data (beneficial)
- proficient use of English (required)
- scientific curiosity, strong motivation to learn new methods and deliver the outlined goals
- ability to work independently, but also as an integrated part of a team

**Select publications from the group:**

Pont et al., Tracing the ancestry of modern bread wheats. *Nat Genet.* 2019, 51:905-911.

Pont and Salse, Wheat paleohistory created asymmetrical genomic evolution. *Curr Opin Plant Biol.* 2017, 36:29-37.

El Baidouri et al., Reconciling the evolutionary origin of bread wheat (*Triticum aestivum*). *New Phytol.* 2017, 213:1477-1486.

Murat et al., Reconstructing the genome of the most recent common ancestor of flowering plants. *Nat Genet.* 2017, 49:490-496.