Environmental signals can directly influence gene expression through epigenetic mechanisms, causing phenotypic changes that can be transmitted to progeny. In plants, this is in part achieved by small interfering RNAs (siRNA) which guide covalent modification of DNA, such as cytosine methylation, to specific targets including repetitive sequences and transposable elements. Environmental stress also leads to genome-wide DNA hypomethylation, misregulation of transposon-derived sequences and ultimately ‘genomic-shock’.

Although most stress-induced epigenetic modifications are not thought to be heritable, there is increasing evidence for the inheritance of novel environmentally-induced epigenetic states or ‘environmental epialleles’. Although the formation of environmental epialleles represents an important source of variation and a powerful driving force of adaptive evolution, the precise mechanism remains unclear.

The aim of my project is to identify environmental epialleles through computational methods. Analysis of Illumina sequencing data from temperature stressed maize plants sampled during stress and after a recovery period has so far revealed that a significant proportion of the maize genome is misregulated at both the genetic and epigenetic level. These findings indicate that plants continue to respond after exposure to stress and that this response is likely mediated by epigenetic mechanism(s), including siRNA-directed DNA modifications.