

Using genomics approaches to understand mechanisms of response to complex environmental conditions in non-model plants

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Understanding how organisms are able to respond at different time scales is an essential component of deciphering the impact and long-term consequences of changing environment. Rapidly developing genomic tools for model plants grown in controlled conditions can now be used to examine the mechanisms of phenotypic response in a broad array of wild organisms and biologically relevant conditions.



Studies in wild settings allow for exploring how phenotypic variation is modulated by variation in gene expression resulting from sequence polymorphisms and regulatory mechanisms. While studies investigating adaptation have largely assumed that trait variation is based on sequence variation, we now know that non-genetic effects can result in heritable, novel phenotypes even without variation in DNA sequence and could therefore provide an unappreciated source of response. My lab group uses reduced representation bisulphite sequencing and transcriptomic approaches to explore the potential role of genetic and epigenetic processes in natural and controlled studies of native and invasive species like *Spartina alterniflora* and Japanese knotweed. We also leverage the power of the eudicot *Arabidopsis* and monocot *Brachypodium distyllum* model plant species to confirm our findings in these non-model plants. Combined these studies will enhance our understanding of how genetic and epigenetic variation interact in response to environment on different time scales, and ultimately contribute to adaptation.