

## Natural variation in gene regulatory networks

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Understanding the causal relationship between genotype and phenotype is a major objective in biology. Genome-wide association studies (GWAS), which aim to identify genetic polymorphisms responsible for trait variation, are considered a standard tool to gain insights into trait architecture. This method has been successfully used in many different species to elucidate trait architecture. Here I will highlight that for traits involved in adaptation to the local environment, results may depend on where you sample, and sampling across a wide range of environments may decrease the power of GWAS. The reason is increased genetic heterogeneity for those traits: the regulation of flowering time, for example, is influenced by distinct genetic effects in different local populations. This highlights the prevalence of local adaptation. Furthermore, using gene expression as a molecular phenotype, we show that some genes are globally affected by shared variants, while others are affected by variants specific to sub-populations. These results illustrate that conclusions about genetic architecture can be extremely sensitive to sampling. We can identify gene regulatory networks that have been realized differently in different natural accessions, highlighting the extent of adaptive evolution within *Arabidopsis thaliana*. Last, I will highlight that even within the same plant, gene regulatory networks will differ across cell types.