# What is the project?

Introduction 000

### Main question: How do *cis*-regulatory elements evolve in plants?

- Cis meaning same
  - in this case elements on the same DNA strand
- i.e. how do non-coding elements on the same DNA strand affect gene expression?

## What are *cis*-regulatory elements?

#### Cis-regulatory elements

Introduction

 They are usually enhancers and promoters that control development and physiology by regulating gene expression.



Figure 1: Example promoter containing cis-regulatory elements. Cis-elements can be repeated more than once (purple) and can recruit different transcription factors (blue/red), all driving the same gene (green)

<sup>&</sup>lt;sup>1</sup>Wittkopp and Kalay (2012)

Introduction

#### Gene expression / phenotypic variation

- For most of the twentieth century, evolution of protein-coding sequences was commonly thought to be primarily (if not solely) responsible for phenotypic evolution
- Whereas more recent studies show that mutations which affect the function of these sequences contribute to phenotypic diversity within and between species
  - Many studies imply divergent cis-regulatory activity in phenotypic evolution <sup>2</sup>

<sup>2</sup>Carroll (2008)

# How can you study the evolution of *cis*-regulatory elements, in plants?

#### **Materials**

- Start with a little known plant: Arabidopsis thaliana
  - Has an extremely well covered genome, as well as transcription factor database
- Will later move towards Nicotiana benthamiana, to evaluate how transferable work on model systems are to others'

# Plants Arabidopsis thaliana Nicotiana tabacum

Figure 2: Example of Arabidopsis and Nicotiana

## Promoter study

#### Procedure to evaluate?

First choose two types of promoters to study:

The most constitutively expressed and Nitrogen-responsive

For each promoter type:

- Identify motifs where TFs bind, check if any TFs are commonly used
- Determine whether any patterns or similarities are present in groups/types of TFs
- 3 Incorporate nucleosome occupancy data (whether DNA is wrapped around a nucleosome or is open)
- Verify hypothesis in lab