# Methods and Approaches Used to Study Knockout Arabidopsis Plants

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### Methods of Gene Discovery

Conceptually there are two methods:

Forward Genetics: Hunt for observed mutations in the phenotype in the genome.

Reverse Genetics: Mutate a specific part of the genome and observe the effect on the phenotype.

#### Reverse Genetics

- Most genomes of model and commercially important organisms have been sequenced.
- Many genes, especially more complex regulatory sequences, produce no obvious phenotype or produce variable phenotypes.
- Advantages of forward genetics negligible in model organisms

#### Mechanisms of Reverse Genetics

- "Knockout" (KO) a gene and observe the resulting phenotype from its absence
- "Knockdown" by limiting its expression and observe the resulting phenotype
- Over-express a gene my modifying its regulatory sequences and observe the resulting phenotype

### Overview of our Experiment

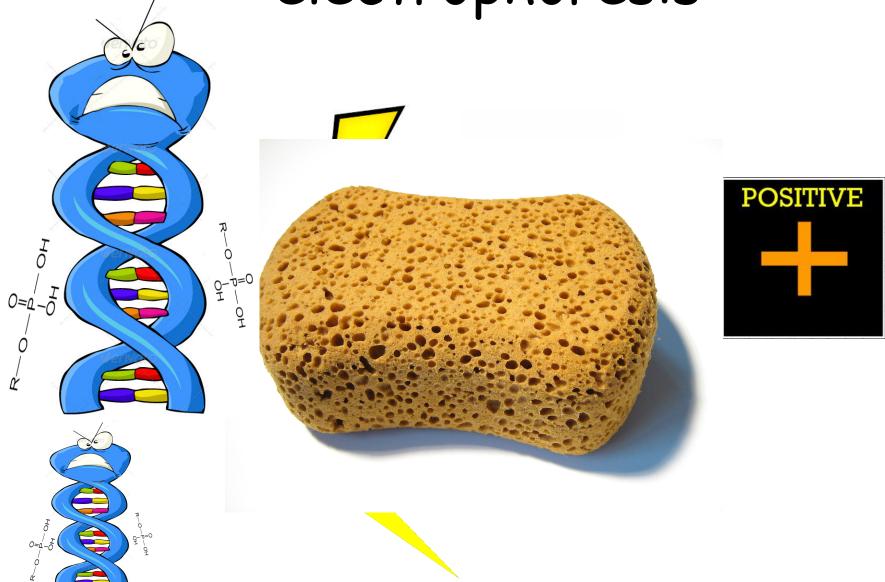
- Arabidopsis Thaliana are modified via a T-DNA from Agrobactium. T-DNA "knockout" a gene.
- Plants are screened for mutants using PCR primers specific to the T-DNA and the inhibited gene.
- Phenotype of mutant plants are compared to known wild-type plants.

# The differences illuminate the gene's function!



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Gol electrophoresis



#### Materials

- Agarose powder
  - Many pores; more powder=more accurate
- Tris Acetate EDTA buffer
  - pH 8.0, cations
- SYBR Safe
  - interchelates with DNA, fluoresces under UV light
- Loading dye
  - · Weighs down DNA solution
- Ladder

### Spectophotometry

 DNA exposed to UV light---->DNA absorbs UV light---->Less light is measured by photo-detector



### Why does DNA absorb UV light?

 Structure of purines and pyrimidines makes them absorb photons

#### Beer-Lambert Law

- How do we find the concentration of DNA from light absorbance?
- Beer-Lambert Law establishes a linear relationship between absorbance and concentration of material that absorbs
- Absorbance=epsilon\*path length\*concentration
  - Path length=1.1 mm
- That's why we always start NanoDrop with TE buffer blank with known concentration

### Bringing it all together

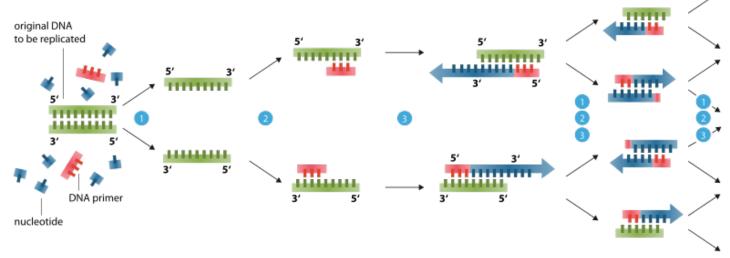
gDNA isolation is process of isolating genomic DNA from rest of plant Gel electrophoresis and spectophometry are used to verify this process.

#### What's next?

- How do we identify plants with the T-DNA?
- How do we determine the genotype of the plants?
- How do we determine where the T-DNA is inserted?
- How do we know where the gene is expressed?

#### PCR

What is PCR?



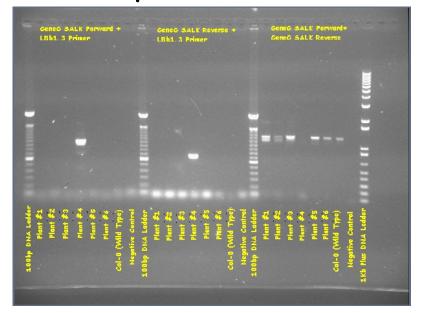
- What do we need in a PCR?
  - DNA template, 10x Ex Taq Buffer, dNTP mix,
    Primers, Ex Taq DNA Polymerase
  - Thermocycler

### Genotyping

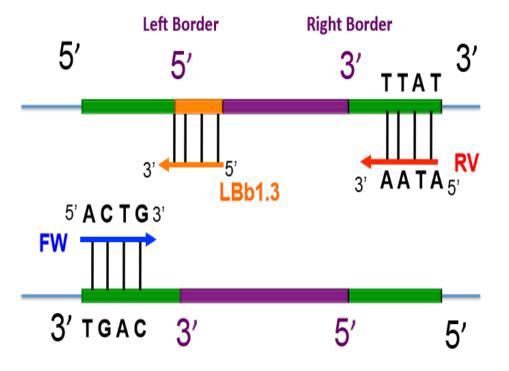
- Primers
  - Binds specifically to gene of interest and T-DNA
- Gel electrophoresis

- Visualize the PCR products in different

reactions

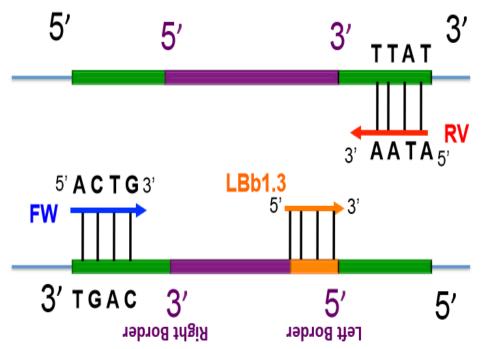


# What happens if T-DNA is present in the forward orientation?



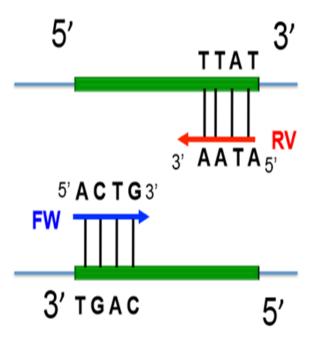
A PCR product is formed between the gene-specific forward and left border primers.

# What happens if T-DNA is present in the reverse orientation?



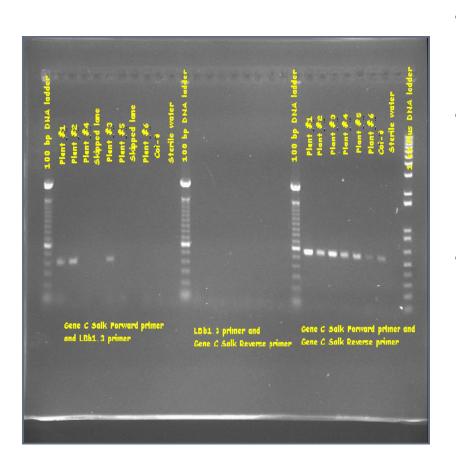
A PCR product is formed between the gene-specific reverse and left border primers.

# What happens if no T-DNA is present?



A PCR product is formed between the gene-specific forward and gene-specific reverse primers.

# How do we interpret gel electrophoresis results?



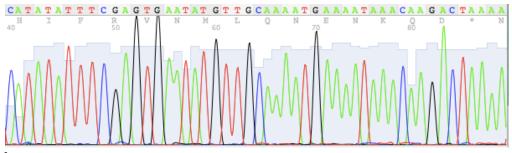
- Product in FW+RV only: WT
- Product in FW/RV +LBb1.3: homozygous for T-DNA
- Product in FW+RV and FW/RV+LBb1.3: heterozygous for T-DNA

#### PCR Purification/Gel Extraction

- Purify DNA fragments from primers, nucleotides, polymerases, salts
- DNA binds to QIAquick column membrane while impurities are washed away with buffer solutions
- Purified DNA eluted from column with addition of elution buffer

### Sanger Sequencing

Fluorescently labeled terminator ddNTPs used



- Helps determine:
  - Sequence of DNA
  - Location and structure of gene
  - Location of T-DNA insert
  - But how?

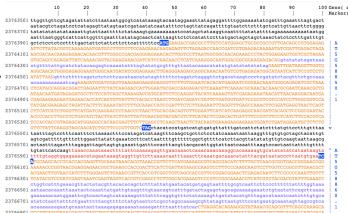


#### Bioinformatics

	> <u>AT5G58</u>		chr5:23763445-23763944 FORWARD LENGTH=500 Length = 500	
Score = 646 bits (326), Expect = 0.0 Identities = 442/500 (88%) Strand = Plus / Plus				
	Query:	112	aagtggtttttactaaatatggatattattattttgtaattgatttctatattcttttgg	171
	Sbjct:	1	aagtggtttttactaaatatggatattattattttgtaattgatttctatattcttttgg	60
	-			
	Query:	172	ttgttcgtagatattatcttaataatggcgtcatataaagtacaataggaaattatagag	231
	Sbjct:	61	ttgttcgtagatattatcttaataatggcgtcatataaagtacaataggaaattatagag	120
	Query:	232	gattttggaaaaatatcgatttgaaatttagtgactaatacgtctagatcctcatagagt	291
	Sbjct:	121	gattttggaaaaatatcgatttgaaatttagtgactaatacgtctagatcctcatagagt	180
	Query:	292	tatagtaatcgataatatcaatatttcctagttatcagattttgtaatcttctttgctca	351
	Sbjct:	181	tatagtaatcgataatatcaatatttcctagttatcagattttgtaatcttctttgctca	240

#### TAIR BLAST

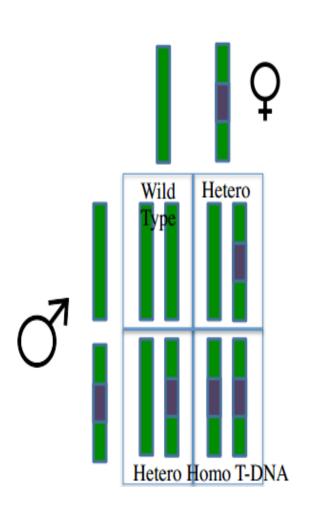
- Aligns query sequence with Arabidopsis genome database
- Look up additional information about the gene
- SeedGeneNetwork
  - Look up information about when and where the gene of Interest is expressed



# How do we observe and analyze phenotypes?

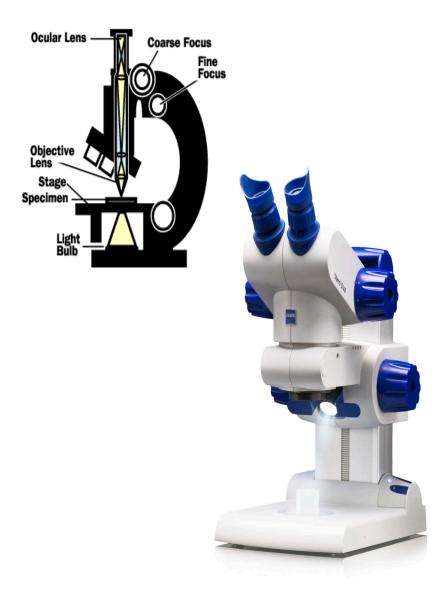
- Use <u>light microscopy</u> to get a cursory view of seed phenotype, that is its colour and shape, and to prepare seeds for Nomarski microscopy.
- Use <u>Nomarski microscopy</u> to observe seed phenotype at a greater detail, looking at tissues including the embryo and the suspensor.
- If any potential mutants were found, analyze the results with a <u>chi-squared test</u>.
- Observe and take measurements of mature plant <u>stems</u>, <u>leaves</u>, <u>flowers</u> and <u>roots</u>.

### What do we expect to observe?

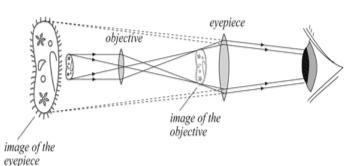


- Given a heterozygous parental line, one would expect on average \(\frac{1}{4}\) seeds to be wild type, \(\frac{1}{2}\) heterozygous and \(\frac{1}{4}\) homozygous.
- If the mutation is embryo lethal, we would expect a 3:1 ratio of green to white seeds.

### What is light microscopy?



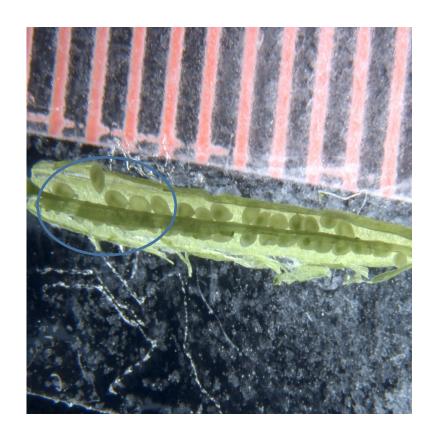
- Light, emitted by the light bulb, illuminates the specimen.
- The image is brought into focus within the microscope tube, which is then magnified by the ocular lens.
- We can adjust magnification, focus and brightness of the light source as desired to obtain better images.



# What can we observe with a light microscope?

Observing a wild type silique with a light microscope

Observing a mutant silique with a light microscope

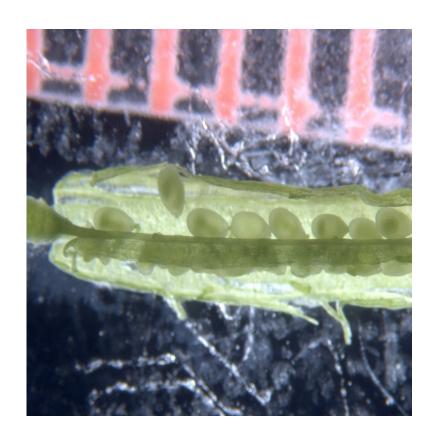


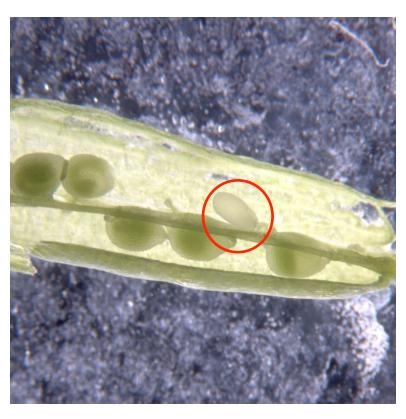


# What can we observe with a light microscope?

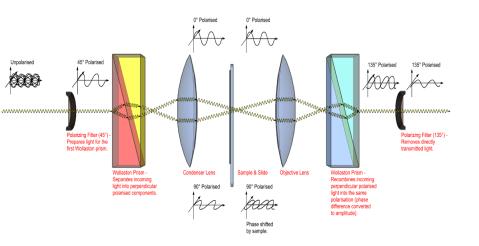
Taking a closer look at a wild type silique

Taking a closer look at a mutant silique





### What is Nomarski microscopy?



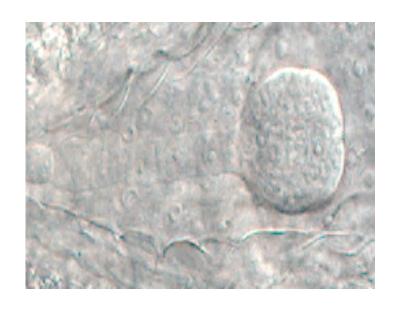


- Also known as differential interference microscopy.
- Light is <u>polarized</u> at 45°, then separated into <u>two coherent</u> <u>light waves</u> polarized at 0° and 90°, then focused onto the <u>sample 0.2 microns apart</u>.
- The rays experience <u>different</u> phase shifts as they travel through the sample, and are recombined to produce <u>wave</u> interference, making the ray brighter or darker. A second polarizing filter removes any light which did not experience phase shifts.

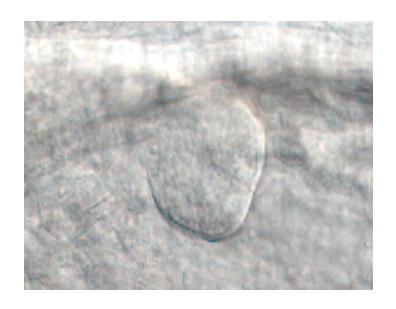
# What can we observe with a Nomarski microscope?

Observing a wild type seed with a Nomarski microscope

Observing a mutant seed with a Nomarski microscope



A globular stage embryo with normal phenotype.



A globular stage embryo with abnormal phenotype.

## How do we perform a chi-squared test?

- $X^2=\Sigma(O-E)^2/E$ , where  $X^2$  is the chi-squared test statistic, O is the observed frequency, and E is the expected frequency.
- Let our null hypothesis be that the expected ratio is 3:1 for green to white seeds, and calculate appropriate expected values.
- Compare the test statistic to a chi-squared distribution table and get a p-value, with 1 degree of freedom, as there are only two possible phenotypes.
- Reject the null hypothesis if the associated p-value is less than 0.05.
- · Otherwise, fail to reject the null hypothesis.

# What can we observe on mature plants?

- Stems: Height of main stem, thickness, number of branches.
- · Leaves: Shape, colour, length, size.
- Flowers: Sepals, petals, anthers, pistils.
- Roots: Length, number of branches.

### Measuring mature plants

Measuring main stem height

Measuring root length

