

STUDYING DNA METHYLATION VARIATION IN THE REFERENCE *BRASSICA. RAPA* LINE R-O-18

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Epigenetics:

- is the study of heritable changes in gene function that occur without a change in the DNA sequence.

DNA methylation:

- involves addition of methyl groups to cytosine residues
- can cause transcriptional gene silencing
- regulates gene expression

Aim of project:

To study the relationship between variation in methylation status of the *Brassica* 'A' genome and phenotypic plasticity at key stages of development.

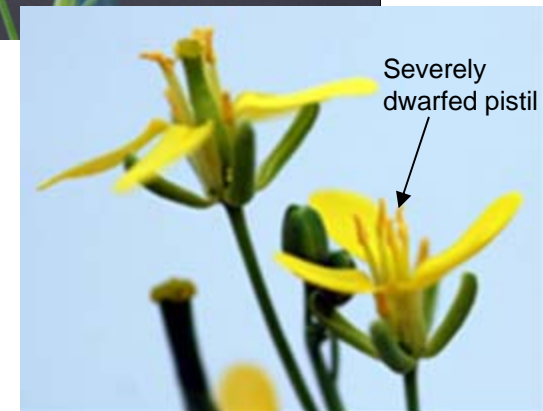
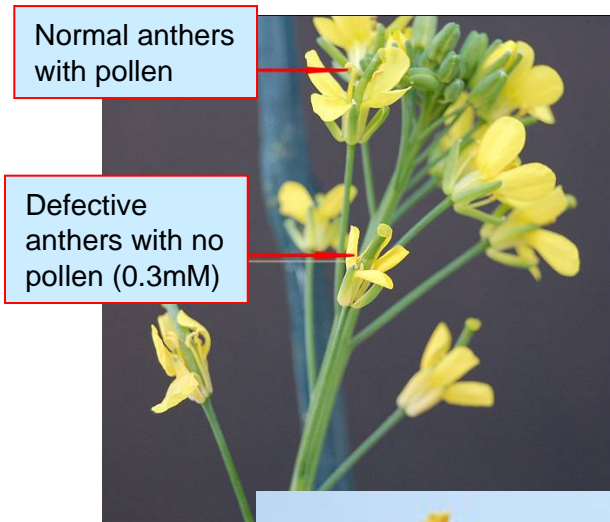
APPROACHES:

- Determine sensitivity of phenotype to variations in DNA methylation in *Brassica* 'A' genome (currently being sequenced).
 - A stochastically hypomethylated “E1” population was established *via* seed treatment with 5-Azacytidine.
 - Dosage response studies were carried out prior to establishing the population.
 - A total of 1000 “E2” lines is being established to serve as a platform for genetic and genomic analyses



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APPROACHES:

Determine the genome-wide distribution and organisation of DNA methylation.

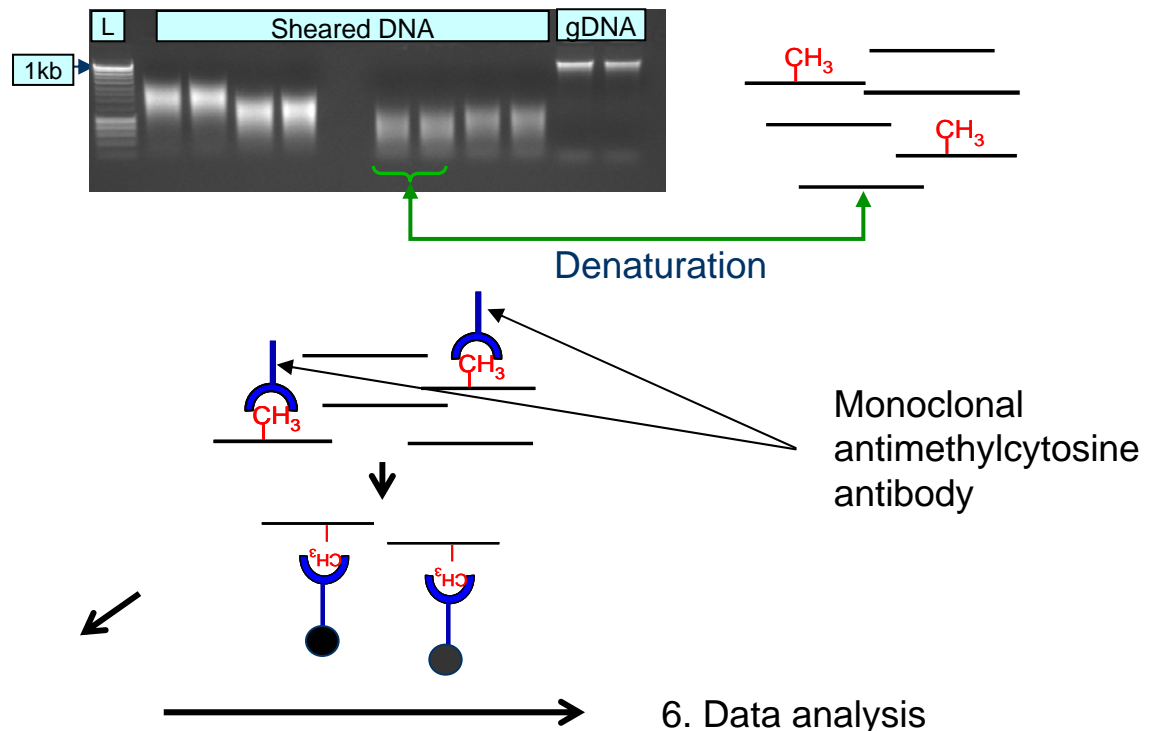
1. Genomic DNA is sheared into small molecular weight fragments

2. Fragmented DNA (350-600bp) is denatured

3. Immuno selection of methylcytosines with an antibody

4. Immunoprecipitation of captured fragments

5. Hybridisation onto *B. rapa* BAC arrays



APPROACHES:

- Analyse tissue-specific variations in DNA methylation during development under normal and stressed conditions.

THANK YOU