#048

Investigating genome dominance in *Brassica napus*

Hugh Woolfenden[1]

Rachel Wells[1]
Richard J Morris[1]

[1] John Innes Centre, Norwich, United Kingdom

Background:

Oil seed rape (OSR), or *Brassica napus*, is a commercially important crop due to its high oil content. *B. napus* is an allotetraploid species resulting from the hybridization of two diploid *Brassica* species: *B. rapa* and *B. oleracea*. It is not fully understood whether one progenitor genome is dominant over the other, and the interplay between the parental genomes remains a topic of research. Understanding genome dominance will help provide insight into parental genome interactions, and potentially, inform crop breeding strategies.

Objective:

Studying genome dominance in OSR has several objectives. Firstly, it helps to understand how polyploidisation has affected the expression of homoeologous genes. Secondly, it can provide insights into the genetic mechanisms underlying important traits, e.g., flowering time, and its subsequent impact on yield. Finally, this knowledge can be applied to develop new breeding strategies for improving crop productivity and quality.

Methods:

To investigate gene expression dominance in OSR, we selected several accessions based on their environmental requirements, i.e., Winter OSR, Semi-Winter OSR and Spring OSR. For example, Winter OSR accessions are dependent on vernalisation and thus require a prolonged period of cold to promote the onset of flowering. We sampled various tissues of each accession across development to facilitate a fine-grained analysis of genome dominance. To achieve this, we performed RNA sequencing (RNA-seq) on these samples, which were then processed using a bioinformatic pipeline to quantify gene expression. We separated the resulting data according to parental genomes and assessed genome dominance by computing gene expression bias between homoeologs over time and then compared the bias across tissues.

Results:

We will present results of how the A genome (from *B. rapa*) and the C genome (from *B. oleracea*) have changed their expression of homoeologous genes upon polyploidisation. We will examine gene expression dominance across development and in the tissues of several *B. napus* accessions. In addition, we will present how genome dominance changes between accessions that have different environmental requirements, e.g., Spring OSR vs. Winter OSR.

Conclusions:

This is the first study, to our knowledge, that describes genome dominance in *Brassica napus* on such a granular scale across tissues and development.