Project title:	A genetic approach to improving post-harvest quality (HAPI)
Project number:	CP 150
Project leader:	Dr James Monaghan (HAU)
Report:	Annual report, June 2017
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Location of project:	Harper Adams University, University of Warwick, Reading University and industry partner sites.

Background

Minimal processing adds significant value to fresh produce, however, it also increases its perishability reducing shelf life and leading to waste of the produce and the resources used to grow it. This project is aimed at postharvest discolouration, a significant cause of quality loss in a wide range of fresh produce such as sliced apple, cut cabbage and lettuce. The main issue we are addressing is postharvest discolouration of lettuce in salad packs. UK lettuce production/imports are worth £240m farm gate but the retail value of UK processed salads is £800m. However, Tesco have recently reported that 68% of their salads are thrown away; the situation is similar for other retailers. There is therefore a need to improve postharvest quality to reduce waste and deliver consistently good quality products to consumers. Modified atmosphere packaging can provide control but once the pack is opened oxygen enters resulting in discolouration. Growing conditions also influence postharvest discolouration but are difficult to control in field crops. Breeding lettuce varieties with reduced propensity to discolour is a way to address the problem. To do this we need to understand the genetics and biochemistry of discolouration.

We are building on previous PhD research at University of Warwick which identified genetic factors controlling the amount of pinking and/or browning that developed on lettuce leaves in salad packs, 3 days after processing. However, we do not know what compounds or which genes are involved and we now intend to find this out through a multidisciplinary project involving three universities; Harper Adams, Reading and Warwick, a lettuce breeding company, a lettuce grower, a salads processor and AHDB Horticulture.

We have produced a set of experimental lettuce lines which we know show differences in the amount of pink or brown discolouration they produce. We have grown and processed these lettuces in a way that mimics commercial production. We assess the salad packs for the amount of discolouration developed over 3 days. We can then link this information to the plant's DNA profile to identify genetic factors for discolouration and DNA markers which can be used by plant breeders.

The same lettuces are also being analysed for compounds produced by a biochemical pathway called the phenylpropanoid pathway. This is thought to produce the pigments that cause discolouration. We know from other studies the genes which control the phenylpropanoid pathway and we have found the same genes in lettuce. We are studying how these genes behave in lettuce plants that produce a lot of discolouration and ones that do not discolour. We will also see how the genes behave under different growing conditions. We can link these gene expression patterns to the amount of pinking and browning to see which genes

are the key ones. Once we have done this we can look for naturally occurring versions of the genes which give a reduced discolouration.

The compounds produced by the phenylpropanoid pathway influence other things such as pest and disease resistance, taste etc. We do not want to reduce the amount of discolouration by breeding but end up with lettuce susceptible to pests or with poor taste. Therefore, we are assessing lines which show high discolouration or no discolouration for their resistance to aphids and mildew and for taste to see if there are any differences. There are some compounds produced by the pathway which are colourless but still provide some pest and disease resistance, so by knowing more about the genetics and biochemistry, breeders will be able to carry out smart breeding.

Project Objectives:

1. Increase understanding of the genetics of pinking and browning in lettuce
2. Determine the role of the phenylpropanoid (PP) pathway in lettuce discolouration
3. Determine whether non PP pathway genes have a role in lettuce discolouration
4. Test the robustness of a genetic approach to reducing discolouration.
5. Identify potential sources of beneficial alleles for key genes.
6. Assess the potential impact on pest and disease resistance and taste
7. Test the applicability of the findings from lettuce *to babyleaf*, cabbage and apple**.**

Key results to date include

- Demonstration of significant variation for post-harvest pinking and browning in a recombinant in-bred lettuce population derived from a cross between cultivars Saladin x Iceberg.
- Evidence to suggest that the symptoms of pinking and browning have different genetic controls.
- Significant quantitative trait loci (QTL) (specific groups of genes) have been identified for both pinking and browning phenotypes.
- Significant variability in both key gene sequences and metabolic activities associated with the biochemical pathways is thought to be involved.

- Environment has a key influence on the development of symptoms, and browning appears to be more sensitive to season than pinking. Warmer conditions during growth are correlated with an increase in browning of cut leaves post-harvest but this does not affect pinking rates.

Future planned work for 2017-18

- We are studying whether similar responses are seen in young and older leaves. This will make the work relevant to babyleaf lettuce crops.
- We will complete the molecular and biochemical analysis of the field samples from the field trials at HAU to clarify common and unique pathways involved in the two phenotypes and provide targets for breeding programmes.
- We are completing the analysis of the effect of environment across current and historic data sets where the same lines have been grown and post-harvest discolouration scored.
- We have screened a set of wild relatives and commercial lines for discolouration after processing; this material will allow breeders to identify 'lost' genes that may be used in new breeding material.