

Genetic analysis of flavour and texture in potato

Glenn Bryan¹, David Lloyd¹, Sanjeev Kumar Sharma¹, Mark Taylor², Christine Hackett³, Ian Nevison³, John Bradshaw

¹Genetics Programme, SCRI, Invergowrie, Dundee, UK

²Plant Products and Food Quality Programme, SCRI, Invergowrie, Dundee, UK

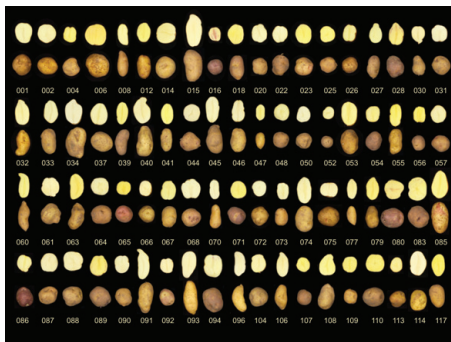
³Biomathematics and Statistics Scotland (BioSS), SCRI, Invergowrie, Dundee, UK

Introduction

Potato flavour and texture are traits of increasing importance as drivers of consumer choice. Previous efforts to identify genetic factors influencing such traits have suffered from a lack of variation among commercial varieties. We have expanded the phenotypic variability by use of our unique population of long-day adapted diploid *Solanum phureja* clones, known to possess strong flavours as well as unusual textural properties.

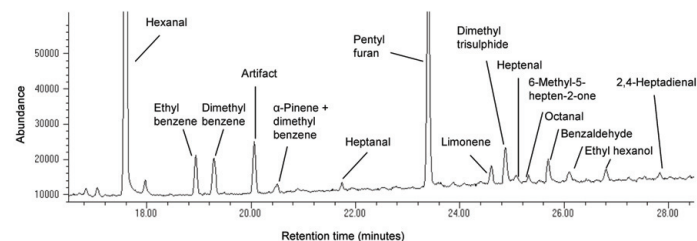
Population development

Hybrid clones resulting from an initial cross between diploid *S. tuberosum* clone 2DH40 and *S. phureja* clone DB337(33) (the variety Mayan Gold) were used in backcrosses to both parents. One of the four hybrid populations (FT.4) was taken forward for genetical studies of sensory and volatile characteristics of potato. A sample of tubers from different clones of the FT.4 population is shown in the figure below.



Volatile profiling

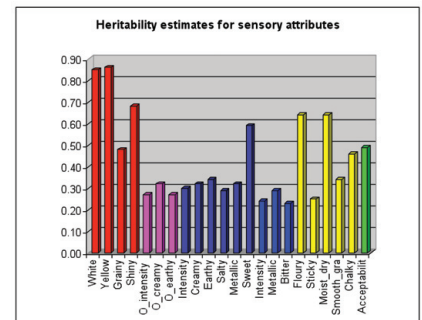
We established a method for entrainment of volatile compounds released from cooked potato tubers. We added fixed amounts of non-intrinsic standards (2-Pentanone and β -Ionone) to the sample matrix to allow more accurate peak quantification. Peaks on the GC-MS chromatograms were assigned by correlating retention times and mass spectra with those of known standards. A total of 41 volatile compounds were quantified and normalised against the β -Ionone peak. These values were calculated for a total of 114 samples from the FT.4 backcross population, plus controls.



The figure above shows a representative section of ATD-GC/MS total ion chromatogram trace of cooked phureja/tuberosum hybrid potato tubers, showing a number of flavour-related volatile organic compounds.

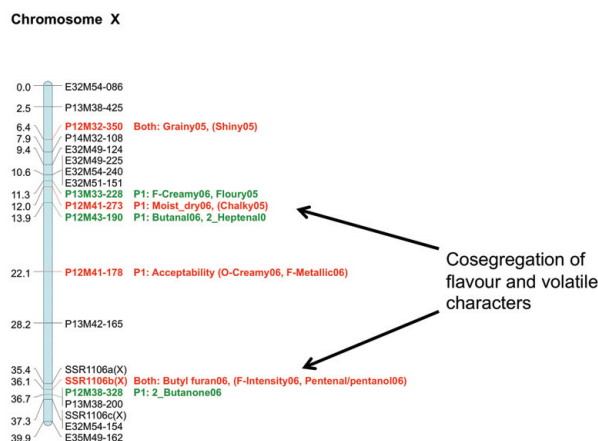
Sensory analysis of cooked potatoes

Sensory data for 119 individuals of the FT.4 population were generated, and a joint analysis of the sensory data gathered over two years was performed. A palette of 22 sensory traits grouped into 5 modalities were used. Variance components for the different sources of variation in the combined analysis of adjusted means of clones were used to compute 'broad-sense' heritabilities. Encouragingly, 18 of 22 sensory attributes showed a significant ($P < 0.05$) difference among the clones tested.



QTL analysis of volatile and sensory profiles

The FT.4 population was subjected to linkage analysis, resulting in a genetic map of ~250 markers (AFLPs and SSRs) which has identified the expected twelve chromosomes. The phenotypic data (sensory, volatiles) were subjected to a Kruskal-Wallis QTL analysis, with putative QTLs located on all twelve linkage groups. A permutation test was carried out to establish levels of significance for this population. Significant clustering of QTLs between sensory and volatile suggests possible causative linkages that require further work. For example chromosome X contains several significant QTL effects, with two examples of QTLs for sensory traits and volatile components mapping to the same region.



Cosegregation of flavour and volatile characters

Summary

It has been possible, for the first time, to identify QTLs for sensory and textural characters in potato. Interestingly QTLs for some volatile components of cooked potatoes co-segregate with flavour QTLs. This analysis paves the way for candidate gene and other functional studies. We are currently analyzing other traits, such as texture and 'umami' on the FT.4 population.