Genetic, Metabolite and Phenotypic Determination of Friction Discolouration in Pear

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Munazza Saeed

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ABSTRACT

Friction discolouration (FD) of pears is a postharvest disorder responsible for significant consumer discontent in markets because of the unattractive appearance of the fruit surface. New Zealand pear breeders are aiming to develop novel pear varieties with consumer desired fruit characters (skin colour, flavour and storability), with reduced susceptibility to FD. Therefore understanding the genetic control of FD is essential to enable development of new pear cultivars using genomics-informed breeding. FD is influenced by agronomic and genetic factors. Previous research on this disorder has been limited to a small number of commercial cultivars and no study has been done to understand its genetic basis. Biochemical constituents (polyphenol oxidase activity, phenolic compounds and ascorbic acid concentration) and skin anatomy have been proposed to play important roles on FD susceptibility in a limited number of cultivars. The Plant and Food Research (PFR) breeding population with hundreds of closely related seedlings is an ideal resource to test whether these previously identified associations hold true across multiple genotypes.

In this study, 241 genotypes from two segregating populations (POP369 and POP356) derived from interspecific crosses between Asian (*Pyrus pyrifolia* Nakai and *P. bretschneideri* Rehd.) and European (*P. communis*) pears were used to identify biochemical and genetic factors associated with susceptibility to FD. In 2013, a small replicated trial involving eight genotypes was conducted. Large variability for FD and other variables was recorded. Four different trends were observed for genotypes for which multiple harvests were obtained in a single season. Most of the genotypes were consistently low or consistently high throughout the season, but a proportion (26.1 %) showed an increase in FD susceptibility during the season and a further 15.7 % showed a decreasing trend in susceptibility. Twenty genotypes had multiple harvests in each of 2011 and 2012, and 13 of these showed consistent trends from year to year. These results indicate a significant genetic component to FD but with additional influence from the stage of fruit maturity at harvest and external environmental conditions.

Single nucleotide polymorphism (SNP)-based linkage maps suitable for QTL analysis were developed for the parents of both populations. The maps for population

POP369 comprised 174 and 265 SNP markers for the male and female parent, respectively, while POP356 maps comprised 353 and 398 SNP markers for the male and female parent, respectively. Phenotypic data for 22 variables measured over two successive years (2011 and 2012) were used for quantitative trait locus (QTL) analysis. QTLs linked to phenotyped variables were identified, including QTLs for FD on linkage groups 2, 3, 7, 10 and 14. A number of stable QTLs across the years were detected for some aspects of fruit quality as well as potential risk factors for FD incidence.

Overall, no single underlying phenotypic variable (enzyme or substrate) appeared to act as a rate limiting factor to susceptibility of FD in both populations and in 2013 trial. However certain phenolics consistently appeared to have weak negative association with FD. This suggests a separate role from their typical concept of being a substrate. Identification of stable QTLs controlling firmness, PPO activity, and phenolic compound concentration have also provided future opportunities for identification of candidate genes by utilizing the reference genome sequences of ‘Bartlett’ and ‘Dangshansuli’ pears and syntenic apple ‘Golden Delicious’. This study also demonstrated that FD is controlled by multiple small effect QTLs and genomic selection could be employed to select elite genotypes with reduced susceptibility to FD, early in the breeding cycle.

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Dedicated To My Parents

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LIST OF ABBREVIATIONS

AsA	Ascorbic acid
cDNA	Complementary DNA
cM	Centi morgan
Conc.	Concentration
contig	Contiguous sequence
DA	Discriminant analysis
Da	Dalton
DNA	Deoxyribonulceic acid
FD	Friction discolouration
FMF	Find molecular features
GBS	Genotyping by sequencing
GEBV	Genomic estimated breeding value
GS	Genomic selection
GxE	Genetic x environment
HPLC	High performance liquid chromatography
LC-MS	Liquid chromatography mass spectrometry
LOD	Logarithm of odds
MAS	Marker assisted selection
NGS	Next generation sequencing
POP	Population
PPO	Polyphenol oxidase
QTL	Quantitative trait locus
RAD-seq	Restriction site associated sequencing
RAPD	Random amplified polymorphic DNA
RFLP	Restriction fragment length polymorphism
RNA	Ribonucleic acid
SNP	Single nucleotide polymorphism
Spp	Specie
SSR	Simple sequence repeat
TSS	Total soluble solids