

**MAPPING QUANTITATIVE TRAIT LOCI FOR REPEATED ORDINAL SCORES ON RASPBERRY RIPENING**

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Many of the traits of interest to fruit breeders are assessed visually using a categorical scale, and this poses challenges for genetic analysis. In an experiment to identify quantitative trait loci (QTLs) for raspberry ripening, 188 genotypes from a cross between raspberry varieties Latham and Glen Moy were grown in a randomised block experiment and ripening was scored repeatedly through the growing season from May to July by assessors using an ordered categorical scale. Principal coordinate analysis of the raspberry plots, based on a city-block similarity coefficient, was used to summarise the ripening profiles. The first principal coordinate had particularly high correlations with the early assessments, while the second coordinate was positively correlated with the late assessments and negatively correlated with the early assessment. An analysis of variance showed that both of these coordinates had significant variation among genotypes ( $p < 0.001$ ), with heritabilities of 44% and 35% respectively.

The principal coordinates were related to genetic marker data on the raspberry linkage map to locate QTLs by interval mapping. Three regions were identified as significantly affecting each principal coordinate. The most significant markers from each region were investigated using a repeated measures analysis of the assessor scores, which confirmed that three QTLs for early ripening and three for late ripening had been detected.