Introduction

Sweet cherry is one of the most labor-intensive fruit crops due to hand harvesting. Successful mechanical or mechanically-assisted sweet cherry harvest requires a low retention force between the fruit and pedicel. To enable the adoption of future harvest technologies, it is necessary to identify genotypes that combine low pedicel-fruit retention force with excellent fruit quality. Experiments were conducted during 2009, 2010, and 2011, at the Washington State University Irrigated Agriculture Research and Extension Center, Prosser, USA. A total of 19 cultivars and 12 F1 seedlings in 2009, 29 cultivars and 19 F1 seedlings in 2010, and 29 cultivars only in 2011 were assessed.

Objectives

The study was designed to characterize the PFRF of current commercial sweet cherry cultivars and F1 seedlings, and determine the relationship between PFRF and fruit quality.

Results & Discussion

• The frequency of PFRF in sweet cherry cultivars and F1 seedlings displayed continuous distribution (Fig.1), suggesting that PFRF is a quantitative trait. F1 seedlings had lower PFRF than commercial cultivars (P<0.0001) suggesting that average PFRF can be reduced by breeding.

• Correlations between PFRF and fruit quality attributes were generally low (correlation coefficients of -0.106 to 0.103), suggesting that PFRF has minimal influence on fruit quality.

• In 2010 and 2011, significant differences for PFRF exist among varieties and between years, as well as for the interaction between variety x year (p<0.0001) (Fig.3, Table1). This highlights the importance of both genetics and environment on PFRF. Correlation between PFRF in 2010 and 2011 was low (R2=0.486) (Fig.2) which supports the significant G X E data.

• Sweet cherry cultivars and F1 seedlings (4.10.5-31, in particular, which is a cross between Lapins x Chelan) with low PFRF have been identified as candidates for further testing while we will continue to improve on PFRF through breeding.

Future Research

• Standardize phenotyping for PFRF
• Determine association between PFRF and gene markers to facilitate developing a MAB strategy to increase breeding efficiency

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