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High-throughput phenotyping of an apple core-collection for the identification of genotypes with high water use efficiency

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Abstract

To detect genotypes (gt) with high water use efficiency (WUE) in apple (*Malus × Domestica Borkh.*), the morpho-physiological characteristics of a core-collection (CC) were evaluated in 2014. Four one-year-old clones for 193 gt of the CC were grown in pots under greenhouse conditions until they reached 20 leaves. Plants were then transferred into a phenotyping platform (PhenoArch). Plants were irrigated to maintain soil water content values of 1.4 g g^{-1} in order to avoid any water stress during 46 days. Pot weights were recorded twice a day and plant 3D pictures were taken every two days using high-throughput phenotyping technologies. With these data, we computed plant leaf area, biomass, transpiration, and WUE during the experiment. We also collected manually multiple morphological traits that could be related with WUE. For each trait, we tested nine mixed models to account for the spatial variability inside PhenoArch. The Best Linear Unbiased Predictors of genetic values were estimated by selecting the model with the lowest bayesian information criterion. Variance estimates of the selected models were used to estimate the broad-sense heritability (H^2) for each trait. H^2 ranged from 0.4 to 0.8. WUE had H^2 values of 0.7. The genetic values for selected traits were used to construct a Hierarchical Ascendant Classifications (HAC) of the CC. Six groups of gt with differences in plant morphology and WUE were distinguished. Results of this study will be used in genome wide association studies to relate phenotypic variations to genetic polymorphisms and to enable the introduction of WUE in apple breeding programs.