



Genome wide selection in *Citrus* breeding

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ABSTRACT. Genome wide selection (GWS) is essential for the genetic improvement of perennial species such as *Citrus* because of its ability to increase gain per unit time and to enable the efficient selection of characteristics with low heritability. This study assessed GWS efficiency in a population of *Citrus* and compared it with selection based on phenotypic data. A total of 180 individual trees from a cross between Pera sweet orange (*Citrus sinensis* Osbeck) and Murcott tangor (*Citrus sinensis* Osbeck x *Citrus reticulata* Blanco) were evaluated for 10 characteristics related to fruit quality. The hybrids were genotyped using 5287 DArT_seq™ (diversity arrays technology) molecular markers and their effects on phenotypes were predicted using the random regression - best linear unbiased predictor (rr-BLUP) method. The predictive ability, prediction bias, and accuracy of GWS were estimated to verify

its effectiveness for phenotype prediction. The proportion of genetic variance explained by the markers was also computed. The heritability of the traits, as determined by markers, was 16-28%. The predictive ability of these markers ranged from 0.53 to 0.64, and the regression coefficients between predicted and observed phenotypes were close to unity. Over 35% of the genetic variance was accounted for by the markers. Accuracy estimates with GWS were lower than those obtained by phenotypic analysis; however, GWS was superior in terms of genetic gain per unit time. Thus, GWS may be useful for *Citrus* breeding as it can predict phenotypes early and accurately, and reduce the length of the selection cycle. This study demonstrates the feasibility of genomic selection in *Citrus*.

Key words: Molecular markers; DarT_seq; Linkage disequilibrium; Early selection; Selective accuracy