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Oral Communication Abstract – 6.09

UNLOCKING GENETIC DIVERSITY FOR PEACH FRUIT ACIDITY THROUGH GLOBAL GWAS AND GENOMIC PREDICTION-BASED SELECTION

DA SILVA LINGE C.*, BACCICHET I.*, CHIOZZOTTO R.*, GASIC K.**, FU W.**, BYRNE D.***, RAWANDOOZI Z.***, WORTHINGTON M.****, BASSI D.*, CIRILLI M.*, HARDNER C.*****, ROSSINI L.*

*) Department of Agricultural and Environmental Sciences (DISAA), University of Milan, Milan, Italy **) Department of Plant and Environmental Sciences, Clemson University, Clemson, SC, United States ***) Department of Horticultural Sciences, Texas A&M University, College Station, TX, United States ****) Department of Horticulture, University of Arkansas, Fayetteville, AR, United States ****) Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, Brisbane, QLD 4072, Australia

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Peach (*Prunus persica*) has been cultivated since ancient times, reaching a global production of 24.9 million tons in 2021. However, peach consumption remains stagnant, mainly due to inconsistent fruit taste recognized by consumers. To expedite the release of 'elite' varieties with improved taste, efficient strategies are needed to enhance traditional breeding selection approaches. Alongside sugar content, fruit acidity is a major determinant of taste that affects consumer preferences and, consequently, the trend in peach purchases. In this study, a unique large dataset comprising 3,074 individuals from several European (FruitBreedomics) and American (RosBREED) collections, as well as one ongoing breeding program (MAS.PES) were analyzed with the aim of genetically dissecting titratable acidity (TA) in peach. We conducted a genome-wide association study (GWAS) and implemented genomic prediction-based selection (GP) in order to: i) expand knowledge of the genetic architecture of acidity trait in peach; ii) provide reliable genomic information; and iii) facilitate rapid breeding

advancements to meet market demands. All materials were genotyped using the 9K SNP array and coupled with fruit acidity records (from 1993 to 2020). GWAS performed on 1,401 accessions using different models (MLM, FarmCPU and Blink) revealed significant associations with TA on chromosomes 1, 2, 5, 6, and 8. Stable associations were detected on chromosomes 1 and 7 5. Furthermore, the relationship between stable associations (detected in at least two models) and TA was validated within multi-progeny collections and breeding populations from MAS.PES and RosBREED programmes. A genomic prediction model was further implemented using a reference population containing 2,372 individuals. Acidity content data of full-sib offspring belonging to several crosses were used to validate the model. The results showed extremely promising prediction accuracy (0.88) and ability (up to 0.90), indicating the potential for large-scale 'on field' application.

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