

THE PEACH GENOME: A COMPARATIVE GENOMICS REFERENCE FOR IDENTIFICATION OF GENES CONTROLLING TRAITS OF IMPORTANCE IN FRUIT AND FOREST TREES

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With the advent of molecular marker based technologies in plant breeding, researchers in fruit and forest tree genetics have explored their application to genetically map and genotype key tree species genomes. Much of the evolution of these technologies within these tree species has gone on in parallel between the forest and fruit tree genetics research communities with little exploration of the interface between the two. Culminating with the completion of whole genome sequences for key tree species in particular peach (*Prunus persica* (L) Batsch), significant advances in gene discovery and our understanding of the gene networks underlying characters of importance for tree sustainability and improvement are coming to the forefront. Because there are a number of common breeding targets for fruit and forest trees, comparatively merging the genetics and genome sciences of each provides opportunities to significantly build our understanding of the fundamental biology of tree species while integrating marker assisted breeding approaches for fruit and forest tree improvement. The peach genome serves as a key tree genome in this regard. In this presentation a brief history of the development of the peach genome as a resource for tree genetics and genomics is presented and data from comparative genomics studies among forest and fruiting trees will be highlighted to demonstrate the importance of this genomics resource for integrating the forest and fruit tree genomics research communities into a common forum for the continued study and preservation of our tree resources.