The Largest Ag-Genomics Meeting in the World.
PLANT & ANIMAL GENOME CONFERENCE XXVI
www.intlpag.org January 13 - 17, 2018 San Diego, CA

P0668: Construction of High Density Apricot (*Prunus armeniaca* L.) Linkage Map using SNPs Detected by Genotyping-by-Sequencing (GBS)

Several genetic linkage maps were constructed for the apricot (*Prunus armeniaca* L.) genome, using amplified fragment length polymorphisms (AFLPs) and simple sequence repeat (SSR) markers. Genotyping by sequencing (GBS) is a cost-effective alternative for developing thousands SNP markers useful for linkage map construction. In this report we present the first sequence-based genetic map in apricot. A saturated linkage map was developed from an apricot F1 population of 138 individuals, derived from the intra-specific cross of the cultivars 'Moniqui' and 'Paviot' (MxP). Due to contrast parental phenotypes, this cross segregates for several important agronomical characters such as self-compatibility, graft compatibility tendency and fruit color. The parents and individual progeny genotypes were generated at the Apek1 restriction sites. Raw unidirectional reads were processed using Stacks v1.35. Filtered reads were aligned to Peach v2.0 and analysis of distribution along peach scaffolds was performed. Two parental maps as well as consensus map were constructed for downstream applications. The resulting genetic maps composed of eight linkage groups were aligned to other *Prunus* saturated linkage maps. The MxP apricot maps presented here provides a valuable set of sequence-based SNPs useful for identification of quantitative trait loci (QTLs) and further analysis of the genetics of relevant morphological traits in apricot.

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