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Fruit quality traits have a significant effect on consumer acceptance and subsequently on peach (*Prunus persica* L. Batsch) consumption. Pedigree-based analysis (PBA) using Visual FlexQTL software has been conducted on seven low to medium chill F_1 families along with the founders and parents. Phenotypic data were collected over two years at a high chill (Fowler, CA) and medium chill (College Station, TX) locations and genotyped using the 9K SNP Illumina array. The objectives of this study were to 1) identify QTL(s) associated with fruit quality traits; 2) estimate QTL genotypes for important breeding parents; 3) identify predictive single-nucleotide polymorphism (SNP) or haplotype alleles for desired QTL alleles; and 4) determine source of the alleles for three important fruit quality traits, namly blush (BL), soluble solids content (SSC), and titratable acidity (TA) through pedigree-based analysis (PBA) on Texas peach/nectarine germplasm. Our analysis detected one major QTL on the central part of LG4 for blush at interval 42 – 44 cM that explained about 20 % of the total phenotypic variance (PVE). A major QTL for TA co-localized with the major locus for low-acid fruit (*D*-locus) at the proximal end of LG5 at 0 - 0 cM. This QTL was consistent across all data sets, explaining about 60 % of the phenotypic variance. There was a QTL at the distal end of LG5 at 52 - 62 cM that was associated with both TA and SSC, which explained about 15 % of the phenotypic variance. In addition, haplotype analyses for these QTLs revealed unique SNP haplotypes that are associated with the predictive SNP marker(s) of desired QTL alleles along with their original sources. Our findings will help peach breeders develop new predictive DNA-based molecular marker tests that can be used routinely in marker-assisted breeding (MAB) for enhancing peach quality traits.

Specified Source(s) of Funding: RosBREED

Development and Evaluation of a 9K SNP Addition to the Peach Ipsc 9K SNP Array v1 *(Poster Board #242)*

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The IPSC 9K peach SNP array released by the international community has been a valuable tool in research and application. Even though majority of SNPs (84%) were polymorphic in the evaluation panels there were many genomic regions with low coverage, including those important for breeding. The existing peach array has been updated with 9K additional SNPs covering previously identified gaps and including recently identified SNPs important for breeding. SNPs (1,808,996) identified by sequencing 49 genomes of additional peach accessions were used as the main source of additional SNPs. Focal point strategy was used to select 8,971 SNPs within 40kb window from the 2,821 focal points distributed across the genome. Additional 129 SNPs were chosen to saturate either regions important for breeding or close the gaps larger than 100kb. The array was validated with 1,770 peach and 26 Prunus accessions (almond, plum, apricot, wild relatives). The add-on contained 7,862 SNPs evenly spread across 8 peach pseudo-molecules with only one SNP positioned on scaffold 13 covering 224.99Mbp of peach genome. The 9K add-on improved the 9K peach array by increasing the total number of usable SNPs by 7,206. The number of SNPs per chromosome increased on average by 50% with only on average 0.18% increase in total physical coverage. Number of gaps larger than 0.3 Mbp was reduced to 2 one on each chromosome 3 and 8. Overall genotyping efficiency in all material was >90% except in almond, 82%. Number of informative markers, assessed by ASSIsT software, were highest in peach 64% and lowest in almond 10%, with 61% of markers being informative in wild Prunus (12) and 35% in apricot (4) and 2 - 33% in Japanese and European plum, respectively. Among 36.2% discarded markers 33% were monomorphic and 30% shifted homozygous in material used. Those markers could be informative in different background raising total number of informative markers. Ann addition of new SNPs to array improved the density and usefulness of the array in Prunus species. The practical applications of new 16K Illumina SNP peach array will be discussed.

Specified Source(s) of Funding: USDA-NIFA-SCRI-RosBREED (2014-51181-22378)

Genome Wide Association Studies for Fruit and Leaf Resistance to Bacterial Spot [*Xanthomonas Arboricola* pv *Pruni* (*Xap*)] in Peach *(Poster Board #243)*

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Bacterial spot, caused by the bacterium *Xanthomonas arboricola* pv. *pruni* (*Xap*), causes premature defoliation, reduced vigor and productivity, and yield loss due to unmarketable fruit in peaches (*Prunus persica* (L.) Batsch) grown in humid regions around the world. The development of bacterial spot resistant peach cultivars could help to mitigate the environmental and health risks of bactericides applied for disease control while reducing input costs for growers. Because *Xap* pressure varies from year to year depending on environmental conditions and disease incidence is low in some important breeding sites, molecular markers associated with bacterial spot resistance can help breeders to develop resistant cultivars efficiently. Markers for fruit resistance to bacterial spot developed from quantitative trait