polyploid citrus. DNAs from haploids *Citrus clementina* and *Citrus maxima* were mixed at different proportions to test the accuracy of the technique for quantitative analysis. All analyzed 7 SNPs provided clear clustering related with allele doses. DNA mixes at intermediary proportions revealed high correlation coefficients between observed and expected data (mean = 0.9796; sd = 0.0094). For all SNPs, separated cluster analyses and ANOVA from mixed DNA data formed all expected homogeneous groups, with correct assignation for practically all samples. Moreover, two triploid populations were easily genotyped and results were in agreement with expected segregations. KASPar technology is a routine and a cost-effective technique to assess the allele doses at the DNA level, which is especially interesting in citrus triploid breeding programs. Moreover, it could be also used to correlate genomic and transcriptomic doses in allele specific expression analyses.

S02P04

The parentage analysis contributes to the validation of high throughput SNP genotype calls of citrus

Fujii H.[1], Nonaka K.[1], Kita M.[1], Shimada T.[1], Endo T.[1], Kuniga T.[2], Ikoma Y.[1], and Omura M.[3]

[1]NARO Institute of Fruit Tree Science (NIFTS), Japan; [2]NARO Western Region Agricultural Research Center (NARO/WARC), Japan; and [3]Shizuoka University, Faculty of Agriculture, Japan. hfujii@affrc.go.jp

High-throughput genotyping is an important breeding tool to provide genome wide genotyping of germplasm for breeding and the selection of markers through linkage mapping. However, the validation system for genotyping calls from the automatic analysis has not been adequately developed to apply the high-throughput genotyping system in a practical fashion, because the marker data sets derived from DNA markers often contain missing or questionable genotype calls. Therefore, the objective of this study was to develop validation procedures using SNP data sets from a previously developed 384 multiplexed SNP array, named *CitSGA-1*, for the genotyping of *Citrus* cultivars. For this purpose, we initially used the manufacture's criterion that included: (1) the call frequency scores (over 0.9) for SNPs and (2) the GC10 and GC50 scores of samples. Thereafter, the following validation procedures were investigated: (3) removal of monomorphic SNPs genotype calls, (4) removal of No Call SNPs, and (5) removal of SNPs with discrepancies in the parentage analysis. In these procedures, the parentage analysis could detect the genetic discrepancy between parents and progeny in the reliable criteria. The obtained reliable SNP types were also tested for the reproducibility of calls by the replicated genotyping of accessions on the same SNPs. The results confirm these the validation procedures, which include the design of samples for parentage assays and the replicates necessary to obtain the reliability of large genotype calls.

S02P05

Comparative values of SSRs, SNPs and InDels for citrus genetic diversity analysis

Ollitrault P.[1], Garcia-Lor A.[2], Terol J.[3], Curk F.[4], Ollitrault F.[2], Talon M.[3], and Navarro L.[2]

[1]Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), BIOS, France; [2]Instituto Valenciano de Investigaciones Agrarias (IVIA), Centro de Protección Vegetal y Biotecnología, Spain; [3]Instituto Valenciano de Investigaciones Agrarias (IVIA), Centro de Genómica, Spain; and [4]Institut National de la Recherche Agronomique (INRA), GAP, France.
patrick.ollitrault @cirad.fr

SSRs have long been considered as almost ideal markers for genetic diversity analysis. With the increasing availability of sequencing data, SNPs and InDels become major classes of codominant markers with genome wide coverage. We have analyzed the respective values of SSRs, InDels, and SNPs for intra and interspecific *Citrus* genetic diversity analysis. Moreover, we have compared the diversity structure revealed by markers mined in a single heterozygous genotype (the clementine) and markers mined in a large interspecific survey. A random set of 25 markers was selected for each marker class to genotype 48 citrus accessions. SSRs were the most polymorphic markers at the intraspecific level allowing complete varietal differentiation within basic taxa (*Citrus reticulata*, *Citrus maxima*, *Citrus medica*). However, SSRs gave the lowest values for interspecific differentiation, followed by SNPs and InDels, that displayed low intraspecific variability but high interspecific differentiation. A clear effect of the discovery panel was observed for SNPs and InDels. The ascertainment biases associated with the clementine heterozygosity mining resulted mainly in an over estimation of within *C. reticulata* diversity and an underestimation of the interspecific differentiation. Therefore SSRs are very useful for intraspecific structure analysis while SNPs and InDels mined in large discovery panel will be more powerful to decipher the interspecific mosaic structure of secondary cultivated species.