Summary

Rosaceae, usually referred to as the rose family, is the same family as apricots. It is a diploid species with eight pairs of chromosomes (2n=16), and it is distinguished by a significant amount of heterozygosity. However, the absence of a high-quality reference genome for the apricot has turned into a handicap that has significantly hampered our understanding of how the genetic background, evolutionary diversity, and demographic diversity of the apricot influence accessions of phenotype. The juvenility phase of apricots lasts only approximately 2-3 years, which is comparably short compared to the majority of other fruit tree species, which require 6–10 years.

Twenty randomly selected samples of different apricot genotypes were used in the investigation. As soon as possible after leaf collection, DNA was extracted using the Nucleospin Plant II micro kit. The ND-1000 NanoDrop Spectrophotometer was used to measure the extracted DNA concentrations, and if necessary, DNA was diluted to 20 ng/µl. This followed the amplification of DNA fragments by the touch down PCR technique in which the multiple primers(forward and reverse) were used for each sample, the primers used included AMPA-105, BPPCT 002, BPPCT 007, BPPCT 030, MA039a, PceGA25, UDP 98 410, samples were labelled i to xx (one to twenty).

In the study, agarose gel electrophoresis was used to analyze the quality and quantity of the DNA concentration before analyzing the PCR results. Both experiments made use of 1% TBE agarose gels, which were made using a 5x TBE stock solution.

The sizes of the alleles were determined using the ALFexpress® II DNA Analyzer (Amersham Bioscience), which employs a polyacrylamide gel electrophoresis technology to separate DNA fragments utilizing automated detection of fluorescently tagged DNA molecules.

After samples were separated on a 6% polyacrylamide gel, the fragment lengths were detected using an ALF. Unfortunately, not all samples were examined due to the university's closure; only 4 (AMPA-105, BPPCT 002, BPPCT 030 and PceGA025) of the 7 markers tested have been reviewed by ALF.

From the study, 23 different allele sizes were successfully detected with aforementioned 4 markers.

The SSR primers generated allele sizes in the range of 176 to 208 for AMPA-105, 170 to 194 for PceGa25,181 to223 for BPPCT002 and 138 to 150 for BPPCT030.

All the four markers that used in this study were viable to distinguish the genotypes from each other except in the case of Veecot and Gönci 83. From the study, mean of the different alleles (Na) was 5,75, mean of effective alleles (Ne) was 3,466; mean of observed heterozygosity (Ho) was 0,525 while the mean of expected heterozygosity (He) was 0.678. Regarding heterozygosity index 0.5 and above value suggest an ideal applicable marker to genotype Prunus species. Thus, all the analyzed 4 microsatellites are suitable for distinguishing them.

PceGa25 with the highest allele frequency (monomorphic) while AMPA-105 showed the lowest allele frequency hence highest degree of polymorphism and so considered the most ideal marker for distinguishing the twenty cultivars studied. For the expected heterozygosity (He) the range was between 0.5 and 0.55 while the observed heterozygosity (Ho) ranged from 0.584 to 0.825. According to the results, the mean value of the He was generally greater than that of the Ho.

There was a significant amount of genetic variability within the genotypes under study, evidenced by the low similarity values across the 20 Prunus genotypes. As a result, the SSR are a perfect marker for differentiating the 20 genotypes under investigation since they are highly informative, codominant, multi-allele genetic markers that are transferable between related species and experimentally repeatable.

The twenty Prunus genotypes could be distinguished by these markers (SSR), which in this investigation AMPA-105 showed the highest degree of polymorphism. Therefore, SSR markers can be utilized an important method of choice for revealing genetic variation and identifying slightly different genotypes in breeding program ideally by the MAS technique. The research will be a helpful source of knowledge for developing molecular markers for cold tolerance as well as understanding the genetic variations in cold tolerance within the apricot species.