Kamal Sharma et al., Agrotechnol 2014, 2:4
http://dx.doi.org/10.4172/2168-9881.S1.012

OMICS Group Conferences
Accelerating Scientific Discovery

3rd International Conference on
Agriculture & Horticulture
October 27-29, 2014 Hyderabad International Convention Centre, India

Determining of *S*-alleles in wild cherry population of Czech Republic

Kamal Sharma, Petr Sedlák, Jiří Korecký, Pavel Vejl and Josef Soukup
Czech University of Life Sciences, Czech Republic

Wild cherry (*Prunusavium* L.) is a valuable broadleaved tree. Wild cherry is a tolerant tree species allowing the establishment of mixed forest stands and is a relatively fast growing hardwood producing very high quality timber. In addition, a number of cultivars also have been developed for fruit production. For these reasons, the species has been the subject of numerous genetic studies, and much attention was focused on the preservation of its forest genetic resources. The self-incompatibility (S) genotypes of a collection of 50 Czech wild cherry accessions, were determined using polymerase chain reaction (PCR) methods of SRNase and SFB genes. PCR was done using conserved primers and fragments detection was carried out by capillary electrophoresis. The genotypes where the length of amplicon had similarity with other alleles were confirmed with the appropriate allele-specific primers for the known alleles. The incompatibility genotypes of all 50 accessions were determined. Fourteen S haplotypes were detected in all which were assigned to twelve incompatibility groups including group '0' of universal pollinator. Ten new incompatible group varieties were determined in this study and yet to assigned into the group. The wild cherry populations differed significantly with respect to allelic frequencies from sweet cherry cultivars; alleles S_1, S_3 and S_4, which are more frequent in sweet cherry, were less frequent in the wild cherry collections. S-haplotypes S_{14}, S_{16} and S_{22} were the most frequent and S_{18} was less frequent in wild populations of cherry in Czech Republic. The knowledge of the S genotypes will be useful for studying the gene flow within the orchards and these approaches should also be informative in wild populations diversity.

Keywords: *Prunusavium*, *S*-allele, *S-RNase*, *F-box*.

This study was Supported by the Ministry of Agriculture of Czech Republic Project NAZV No. QJ1210275 and project CIGA CULS No. 20144301 and by the European Social Fund in the Czech Republic, European Union, Ministry of Education Youth and Sports and OP Education for Competitiveness ESF/MEYS CZ.1.07/2.3.00/30.0040.

Biography

Kamal Sharma has completed his PhD from the Central Tuber Crops Research Institute, Trivandrum, India. At present he is researcher at Genetics and Breeding Department, Czech University of Life Science, Prague. He is studying sequential polymorphisms of self-incompatibility locus (S-locus) in cultivated and wild cherries (*Prunusavium* L.). He has published 26 research papers and abstracts at different conferences.

sharma@af.czu.cz