*Correspondence

GENETIC IDENTITY OF RASPBERRY 'POLANA' PLANTLINGS EXAMINED USING MICROSATELLITE MARKERS

Fuad Gaši^{1*}, Adnan Hodžić¹, Mirza Hadžiavdić¹, Mirsad Kurtović¹, Jasmin Grahić¹, Lejla Lasić², Belma Kalamujić Stroil², Naris Pojskić²

¹University of Sarajevo, Faculty of Agriculture and Food Sciences, Sarajevo, Bosnia and Herzegovina ²University of Sarajevo, Institute for Genetic Engineering and Biotechnology (INGEB), Sarajevo, B&H

Abstract

Raspberry cultivars are clonally propagated and therefore all plants E-mail: belonging to a single cultivar represent the same genotype. Cultivar fudo01@yahoo.com integrity of raspberry plantlings placed on the market in Bosnia and Received Herzegovina (B&H) is based on examining of morphological traits, which January, 2017 is not a reliable tool for genetic identification. In this study plantlings Accepted declared as cultivar 'Polana' were genotyped using seven microsatellites, in April, 2017 order to gain preliminary insight into the genetic integrity of raspberry Published plantlings marketed in B&H. Plant tissue (leaves) from 10 raspberry plants June, 2017 were randomly sampled from a batch of plantlings sold by major fruit Copyright: ©2017 nursery in Bosnia and Herzegovina. Along with these samples, four Genetics & Applications, The reference cultivars with confirmed identity ('Polka', 'Autumn Bliss', Official Publication of 'Heritage' and 'Polana') were also included in the study. Seven primer pairs the Institute for amplified 31 alleles, or on average 4.4 alleles per locus. UPGMA cluster Genetic Engineering analysis, based on the Jaccard similarity coefficient, revealed that among and Biotechnology, University of Sarajevo the ten samples declared as 'Polana' plantlings only five were genetically identical to any of the other samples. The cluster analyses also exposed that none of the ten samples declared as 'Polana' seedlings were in fact identical or even closely related to the 'Polana' reference cultivar or any of the other Short communication reference cultivars. These findings clearly show that the genetic identity of primocane raspberry plantlings, currently sold in Bosnia and Herzegovina, needs to be tested using objective and reliable methods rather than simple morphologic observation.

Key words: cultivar integrity, morphological traits, DNA

Introduction

Red raspberry (*Rubus idaeus*), along with strawberry, represents the most commercially important berry fruit currently cultivated in Bosnia and Herzegovina (B&H). Raspberry cultivars are clonally propagated and therefore all plants belonging to a single cultivar possess an identical genetic makeup (same genotype). In order for raspberry plantlings to be placed on the market in B&H, they must be supervised during the nursery production in order to ensure the cultivar integrity. However, this supervision is based on examining morphological traits,

which are oftentimes not a reliable tool for the verification of genetic identity. Unlike morphological traits, microsatellite DNA markers have proven to be an excellent tool for examining the cultivar integrity among raspberry genotypes (Fernandez-Fernandez et al., 2011). A number of different microsatellites or SSRs (Simple Sequence Repeats) have been developed for R. idaeus (Graham et al., 2002; Castillo et al., 2010) and are available for this purpose. Microsatellite markers have previously been used in genetic studies of several fruit crops in Bosnia: apple (Gasi et al., 2010; Gasi et al., 2013a, Gasi et al., 2013d), pear (Gasi et al., 2013b), plum (Halapija-Kazija et al., 2014) and cherry (Gasi et al., 2013c). However, until now SSRs have not been used for genetic analyses of berry fruits in this country.

In this study, genetic identity of plantlings declared as cultivar 'Polana' were genotyped using microsatellites, in order to gain preliminary insight into the genetic integrity of raspberry plantlings marketed in Bosnia and Herzegovina. and Doyle, 1987). All of the sampled plants were declared by the nursery to be the plantlings derived from the primocane raspberry cultivar 'Polana'. Along with these samples, four reference cultivars with confirmed identity ('Polka', 'Autumn Bliss', 'Heritage' and 'Polana') were also included in the study. Seven primer pairs (Table used for SSR 1) amplifications have previously been published by Castillo et al. (2010). Polymerase chain reaction (PCR) amplification of SSR sequences was performed in a Veriti TM Thermal Cycler (Applied Biosystems, Foster City, CA) using fluorescently labelled primers. All PCR amplifications were performed as described in Castillo et al. (2010). The detection of SSR products was conducted on ABI 310 automated sequencer (Applied Biosystems). PCR product $(1 \ \mu L)$ was added to a master mix containing 9 μ L of deionized formamide and 0.5 μ L GeneScan-350 Rox size-standard (Applied Biosystems). Samples were heated at 95 °C for 5 min and immediately cooled down on ice. SSR profiles were scored using GeneMapper

SSR marker	forward primer	reverse primer						
RhM001	GGTTCGGATAGTTAATCCTCCC	CCAACTGTTGTAAATGCAGGAA						
RhM003	CCATCTCCAATTCAGTTCTTCC	AGCAGAATCGGTTCTTACAAGC						
RiM019	ATTCAAGAGCTTAACTGTGGGC	CAATATGCCATCCACAGAGAAA						
RhM023	CGACAACGACAATTCTCACATT	GTTATCAAGCGATCCTGCAGTT						
RhM011	AAAGACAAGGCGTCCACAAC	GGTTATGCTTTGATTAGGCTGG						
RhM043	GGACACGGTTCTAACTATGGCT	ATTGTCGCTCCAACGAAGATT						
RiM015	CGACACCGATCAGAGCTAATTC	ATAGTTGCATTGGCAGGCTTAT						

Table 1. Seven SSR markers developed by Castillo et al. (2010), used in this study

Materials and methods

Plant tissue (leaves) from 10 raspberry plants, randomly sampled from a batch of plantlings sold by a major fruit nursery in Bosnia and Herzegovina, were used for the isolation of genomic DNA applying CTAB method (Doyle Software ID v3.2 (Applied Biosystems). UPGMA cluster analysis, based on Jaccard similarity coefficient, was calculated using the obtained SSR data, in NTSYS software (Rohlf, 1993) and visualized by MEGA 5 software (Molecular Evolutionary Genetics Analysis), (Tamura et al., 2011).

Results and discussion

Seven primer pairs amplified 31 alleles (Table 2), or on average 4.4 alleles per locus, among all the 14 analysed raspberry samples. Higher values for the average alleles per locus (7.9), among the same SSR loci, have been published by Castillo et al. (2010). However, in that study 48 different raspberry genotypes were examined. Overall, the seven primer pairs used in our research provided sufficient variation for clear distinction among four reference cultivars.

The same cluster analyses revealed that among the ten samples declared as 'Polana' plantlings, only five were genetically identical to any of the other samples. Considering that raspberry plantlings are clonally propagated, all true offspring should share the same SSR profile. The cluster analyses also revealed that none of the ten samples declared as 'Polana' plantlings were in fact identical or even closely related to 'Polana' reference cultivar or any of the other

Table 2. SSR profiles (allele sizes expressed in base pairs) of 10 raspberry plants, declared as plantlings of the cultivar 'Polana', and four reference cultivars, obtained through the analyses of seven SSR loci.

Genotypes	RhN	1001	RhN	RhM003 RiM019		RhM023		RhM011		RhM043		RiM015		
'Polka'	239	241	202	202	180	182	195	195	289	291	371	373	351	351
'Autumn Bliss'	227	229	191	193	182	217	187	195	279	279	373	373	349	351
'Heritage'	227	236	193	202	180	182	187	195	281	291	371	371	349	351
'Polana' ref.	236	236	200	202	182	195	187	195	281	281	371	373	351	351
Sample 1	227	236	200	202	174	182	187	195	279	279	373	373	349	351
Sample 2	227	236	195	202	170	178	187	195	285	285	373	373	349	359
Sample 3	227	236	200	202	174	182	187	195	279	279	373	373	349	351
Sample 4	227	236	200	202	174	182	187	195	279	279	373	373	349	349
Sample 5	227	236	200	202	182	182	187	195	279	279	373	373	349	351
Sample 6	227	236	200	204	180	182	187	195	285	285	373	373	349	349
Sample 7	227	236	191	193	174	182	187	195	279	279	373	373	349	351
Sample 8	227	236	191	193	174	182	187	195	279	279	373	373	349	351
Sample 9	227	236	191	193	174	182	187	195	279	279	373	373	349	351
Sample 10	227	236	200	202	182	182	187	195	279	279	373	373	335	339

UPGMA cluster analysis, based on Jaccard similarity coefficient, revealed that among the reference cultivars, 'Heritage' and the reference 'Polana' samples clustered the closest (Figure 1). Similar findings have already been reported by Bassil et al. (2012). Also, considering that 'Heritage' is a parent of the cultivar 'Polana' this result was entirely expected.

reference cultivars. The obtained results indicate that investigated samples are at least in partgenerative offspring, which probably arose through spontaneous hybridization between unknown raspberry genotypes. These findings clearly show that the supervision of nursery production, based on morphological traits, does not guaranty cultivar integrity.



Figure 1. UPGMA cluster analyses of 10 raspberry plants, declared as plantlings of the cultivar 'Polana', and four reference cultivars

Conclusions

The genetic identity of primocane raspberry seedlings, currently sold in Bosnia and Herzegovina, needs to be tested using a more objective and reliable method than simple morphologic observation. The results of this study indicate that DNA markers are a necessary tool for this task, among which microsatellites can be considered as highly suitable.

References

- Bassil NV, Nyberg A, Hummer KE, Graham J, Dossett M, Finn CE (2012) A universal fingerprinting set for red raspberry. Acta Hortic 946:83–87.
- Castillo NRF, Reed BM, Graham J, Fernández-Fernández F, Bassil NV (2010) Microsatellite markers for raspberry and blackberry. J Am Soc Hortic Sci 135:271–278.
- Doyle JJ, Doyle JL (1987) A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochemical Bulletin 19, 11-15.
- Fernandez-Fernandez F, Antanaviciute L, Govan CL, Sargent DJ (2011) Development of a multiplexed microsatellite set for fingerprinting red raspberry (Rubus idaeus) germplasm and its

transferability to other Rubus species. Journal of Berry Research 177–187.

- Gasi F, Simon S, Pojskic N, Kurtovic M, Pejic I (2010) Genetic assessment of apple germplasm in Bosnia and Herzegovina using microsatellite and morphologic markers. Sci Hortic 126:164–171.
- Gasi F, Simon S, Pojskic N, Kurtovic M, Pejic I, Meland M, Kaiser C (2013a) Evaluation of apple (Malus x domestica) genetic resources in Bosnia and Herzegovina using microsatellite markers. Hort Sci 48:13–21.
- Gasi F, Kurtovic M, Kalamujic B, Pojskic N, Grahic J, Kasier C, Meland M (2013b) Assessment of European pear (Pyrus communis L.) genetic resources in Bosnia and Herzegovina using microsatellite markers. Sci Hort 157:74–83.
- Gaši F, Memić S, Kurtović M, Drkenda P, Memić S, Skender A, Šimon S. (2013c) Determining the identity of a promising new sour cherry cultivar using SSR markers. The Journal of Ege University Faculty of Agriculture 1: 53-56.
- Gasi F, Zulj Mihaljevic M, Simon S, Grahic J, Pojskic N., Kurtovic M., Nikolic D, Pejic I (2013d). Genetic structure of apple accessions maintained ex situ in Bosnia and Herzegovina examined by microsatellite markers. Genetika 45(2):467–478.
- Graham J, Smith K, Woodhead M, Russell J (2002) Development and use of simple sequence repeat SSR markers in Rubus species. Mol Ecol Notes 2:250–252.
- Halapija-Kazija D, Jelacic T, Vujevic P, Milinovic
 B, Cicek D, Bisko A, Pejic I, Simon S, Zulj
 Mihaljevic M, Pecina M, Nikolic D, Grahic J,
 Drkenda P, Gasi F (2014) Plum germplasm in
 Croatia and neighbouring countries assessed by
 microsatellites and DUS descriptors. Tree Genet
 Genom 10, 761–778.
- Rohlf FJ (1993) NTSysPC. Applied Biostatistics, New York, NY.
- Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S (2011) MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol 28, 2731– 2739.