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Genetic Differentiation of Apricot (*Prunus armeniaca* L.) Cultivars with SSR Markers

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Summary

A total of 44 apricot genotypes belonging to germplasm collection of Corvinus University (Budapest, Hungary), BOKU University (IOG, Vienna) and the Research Centre for Agriculture and Forestry Laimburg (Italy) were screened with 10 microsatellite primer pairs previously developed in apricot. All primers produced polymorphic amplification patterns, revealing 85 different alleles. The mean number of alleles per locus was 8.5. Out of them, 21 alleles occurred only once in the investigated samples. The observed heterozygosity for individual loci ranged from 0.9545 to 0.3182 with an average of 0.6604. A UPGMA dendrogram based on Nei's genetic distance divided the cultivars into two groups that reflect their geographic origin, one with genotypes originating from Europe and the other with genotypes from Central Asia. Implications of these data for the use of SSR markers as a tool for fingerprinting cultivars in breeder's right protection, but also in assisting breeding and selection programmes in apricot are discussed.

Key words. apricot – genetic diversity – microsatellites – pedigree – stone fruits – UPGMA

Introduction

Apricots (*P. armeniaca* L., *Rosaceae*, 2n=16) are grown in temperate and subtropical zones over large areas around the world, mostly in the Mediterranean Basin, North America and Asia, being the third economically most important stone fruit crops after peach and plum (OECD 2002). The world wide apricot industry produces 2.3 millions of tons of fruit per year. More than 55 % of the world's apricot production is restricted to Mediterranean climates; in fact Mediterranean countries like Turkey, Spain, Italy, France, Greece, together with countries like Iran, Pakistan, Ukraine, China, and USA account for 80 % of the world production (FAOSTAT 2004).

Apricot originates from Manchuria (China) and was transferred to Europe via Asia through Armenia. The Greeks introduced it to Europe and the Romans spread it over the continent. The Asian cultivars are the oldest with the richest variation. Most of the cultivars are self-incompatible; fruits are small to medium and ripen over a long period. From morphology and physiology of genetically closely related European cultivars it was concluded that they originated from a few Asian ancestors, having thus the lowest variation. They show lower chilling requirements and only a short ripening time (LÖSCHNIG and PASSECKER 1954; ZOHARY and SPIEGEL ROY 1975; MEHLENBACHER et al. 1991).

There are some limiting factors for the expansion of apricot production. These include a reduced choice of agronomically interesting and adapted varieties; a limited market value of semi-domesticated cultivars and poor adaptability of cultivars out of their native area. In addition, the most important problem for the apricot cultivars is frost damage during blooming, pathogens like Plum Box Virus (PPV) and European Stone Fruit Yellows (ESFY) (LAIMER 2003). Molecular markers may be a valuable help in this situation in several respects: Firstly, they can facilitate the detection of false identification. Secondly, genetic markers have the potential to identify "essentially derived" varieties. While essentially derived varieties are phenotypically different from their "parent", they should be genotypically almost identical. Development of a proper program to characterize different germplasm is necessary. There is a high potential of genetic markers for cultivar identification and breeder's rights protection in apricot. Simple sequence repeats (SSRs or microsatellites) are hypervariable single-locus markers that have previously been shown to be highly informative in varietal identification and genetic diversity (MORGANTE and OLIVIERI 1993; POWELL et al. 1996; FOSSATI et al. 2003). Genetic diversity and phylogenetic analysis of apricots was discussed using peach microsatellites loci (HORMAZA 2002; ROMERO et al. 2003; ZHEBENTYAYEVA et al. 2003). Taking advantage of the high polymorphism level of homologous SSRs, we have used microsatellites recently developed in apricot (LOPES et al. 2002; HAGEN et al. 2004; MESSINA et al. 2004; MAGHULY et al. 2005, 2006) to determine genetic relationships among apricot cultivars from different geographic origins and to identify individual accessions among a representative set of commercially available apricot varieties as useful information for setting breeding strategies on apricot. In the alpine valley of Vinschgau (Northern Italy), apricot production has a long tradition. 'Vinschger Marille' is a local cultivar appreciat-

Table 1. List of cultivars studied, and their five main fruit traits: 1) Colour: LO = light orange; DO = dark-orange; Y = yellow; O = orange; RO = red-orange; 2) Consistency: F = firm; S = soft; MF = middle-firm; SK = sweet-kernel; 3) Taste of kernel: BK = bitter-kernel; 4) Size: EL = extrem-large; VL = very large; L = large; M = medium; SM = small; 5) Taste of the fruit flesh: SE = sweet; B = bitter; A = acidic, T = tasty. Compatibility: SI = Self-incompatible; SC = Self-Compatible; Origin: CA = Central Asia; IC = Irano-Caucasian; EE = East-Europe; WE = West-Europe; NA = North America. CIV = Consorzio Italiano Vivaisti.

Cultivar	Pedigree or cultivar group according to morpho-logical characteristics	Origin of samples	Country of origin	Fruit traits	Ripening time	Compati-bility.	References
'Ananasnij ciurpinskij'	–	Hungary	Ukraine (EE)	LO, MF, SK, M, SE	middle	SC	Pedryc et al. (pers. comm.)
'Bergeron'	Unknown seedling, Lyon , France	Hungary	Lyon, France 1920 (WE)	O, F, SK, M, T	late	SC	Lichou et al. 1998, 2003; Broznik and Kallay 2000
'Ceglédi óriás'	"Giant" group	Hungary	Hungary 1953 (EE)	DO, MF, SK, L, T	early	SI	Broznik and Kallay 2000
'Erevan'	Local variety in Armenia	Hungary	Armenia (IC)	LO, F, SK, L, SE	early	SC	Romero et al. 2003; Löschning and Passecker 1954
'Gulkin' (4 accessions)	Seedling	Pakistan	Pakistan (CA)	O, F, SK, S, SE	early	SI?	Thompson (pers. comm.)
'Hunza' (3 accessions)	Seedling	Pakistan	Pakistan (CA)	O, F, SK, S, SE	early	SI?	Thompson (pers. comm.)
'Karim Abad' (5 accessions)	Seedling	Pakistan	Pakistan (CA)	O, F, SK, S, SE	early	SI?	Thompson (pers. comm.)
'Kech-psar' 1445	Local variety in middle Asia	Hungary	Central-Asia, 1930 Kostina (CA)	Y, F, SK, M, –	very late	SI	Mehlenbacher et al. 1991
'Luizet' 343	Seedling, Lyon, France	Italy	France, 1838 (WE)	LO, F, SK, M, SE	early	SC	Lichou et al. 1998; Löschning and Passecker 1954
'M2000 m' (Pakistan)	Seedling	Pakistan	Pakistan (CA)	–	–	SI?	Fliri (pers. comm.)
'Magyar kajszi' C. 235	Hungarian Best	Hungary	Hungary (EE)	DO, F, SK, M, T	middle	SC	Broznik and Kallay 2000
'Moniqui'	–	Hungary	Spain (WE)	Y, S, BK, VL, SE	middle	SI	Lichou et al. 1998
'Orangered' ('Bahrt')	Lasgerdi Mashhadi x NJA2	Austria	USA (NA)	DO, MF, SK, L, –	early	SI	Lichou et al. 1998, 2003; Pedryc et al. (pers. comm.)
'San Castrese'	–	Italy	Italy (WE)	DO, F, –, L, –	late-middle	SC	Lichou et al. 1998
'Shalakh'	Local variety in Armenia	Hungary	Armenia (IC)	LO, F, SK, L, SE	early	SC	Romero et al. 2003; Löschning and Passecker 1954
'Vinschger Marille' (20 accessions)	Old local variety Val Venosta	South Tyrol	Italy (WE)	LO, MF, SK, M, SE	late	SC	Strada et al. 1989
'Zard' 2407	–	Hungary	Central-Asia (CA)	Y,S, –, SM, –	middle	SI	Pedryc et al. (pers. comm.)

ed for its fine aroma and ideal ratio of sugar to acids. It suffered severely from PPV infections in the early 1970ies (Giunchedi et al. 2002), which reduced drastically the number of trees. Recently, efforts are being made to revitalize apricot as a crop. In the frame of these activities 19 accessions of 'Vinschger Marille' have been selected from healthy trees that in future might be used as donor clones. These clones represent the core samples of this study.

Material and Methods

Plant material and DNA extraction

44 apricot accessions were chosen to represent the European, Irano-Caucasian, Central Asian and North American cultivars with different origin kept at the germplasm collection of Corvinus University (Budapest, Hungary), BOKU University (IOG, Vienna), Research Centre for Agriculture and Forestry Laimburg (South Tyrol, Italy) and at the Consorzio Italiano Vivaisti (CIV, Ferrara, Italy) (Table 1). The plant material chosen for a comparison includes 19 accessions of 'Vinschger Marille', and 12 accessions of Central Asian seedling (five 'Karim Abad', four 'Gulkin', three 'Hunza') to highlight the contrast between highly selected and semi-domesticated cultivars.

Total genomic DNA was extracted from leaves using the DNeasy® Plant Mini Kit (QIAGEN) according to the supplier's instructions.

PCR amplification and data analysis

10 different primer combinations originally developed for apricot SSR loci (Lopes et al. 2002; Messina et al. 2004), which represent different regions of the apricot genome, were used for amplification of DNA from different apricot cultivars (Table 2). PCR amplifications were conducted in a total volume of 25 µl using 1x PCR buffer (provided by the manufacturer QIAGEN), 2 mM $MgCl_2$, 0.2 mM dNTPs, 4 pmol of each primer, 0.6 units Taq polymerase (QIAGEN HotStarTaq™ PCR), 20–30 ng of total genomic DNA. PCR-cycling conditions consisted of an initial denaturation step of 95 °C for 15 min, followed by 35 cycles of 50 s at 95 °C, 50 s at annealing temperature and 1 min at 72 °C. A final extension step of 10 min at 72 °C ended the cycle.

Table 2. Characteristics of the 10 SSRs studied.

Locus	Predicted length (bp)	Size range (bp)	Annealing temperature	Repeat type	References
ssrPaCITA7	211	186 – 224	60 °C	$(AG)_n$	Lopes et al. 2002
ssrPaCITA10	175	142 – 212	58 °C	$(CT)_n$	Lopes et al. 2002
ssrPaCITA19	114	98 – 148	60 °C	$(TC)_n$	Lopes et al. 2002
ssrPaCITA23	146	112 – 157	56 °C	$(AC)_n(AG)_n$	Lopes et al. 2002
ssrPaCITA27	262	224 – 266	58 °C	$(TC)_n(TA)_n(TG)_n$	Lopes et al. 2002
UDAp-407	188	118 – 162	58 °C	$(TC)_nTT(TC)_n$	Messina et al. 2004
UDAp-410	155	116 – 146	58 °C	$(AG)_n$	Messina et al. 2004
UDAp-414	174	150 – 214	58 °C	$(AG)_n$	Messina et al. 2004
UDAp-415	156	139 – 143	58 °C	$(GA)_n$	Messina et al. 2004
UDAp-420	175	154 – 262	58 °C	$(CT)_n$	Messina et al. 2004

Table 3. Variability parameters calculated for 10 SSR markers in 44 apricot cultivars.

Locus	Number of putative alleles	Effective alleles per locus (Ne)	Observed heterozygosity (Ho)	Expected heterozygosity (He)	Inbreeding coefficient (F_{ST})	Gene flow (Nm)
ssrPaCITA7	12 (A–L)	5.0286	0.8636	0.8103	0.4610	0.2923
ssrPaCITA10	10 (A–J)	2.7977	0.3182	0.6499	0.7524	0.0823
ssrPaCITA19	7 (A–G)	3.9835	0.8864	0.7576	0.4083	0.3623
ssrPaCITA23	6 (A–F)	4.0375	0.8182	0.7610	0.4562	0.2980
ssrPaCITA27	6 (A–F)	4.3712	0.5814	0.7803	0.6365	0.1428
UDAp-407	13 (A–M)	3.8954	0.3636	0.7518	0.7554	0.0810
UDAp-410	10 (A–J)	3.8566	0.9545	0.7492	0.3556	0.4529
UDAp-414	9 (A–I)	4.7220	0.6818	0.7973	0.5675	0.1905
UDAp-415	6 (A–F)	3.1790	0.7500	0.6933	0.4529	0.3020
UDAp-420	6 (A–F)	2.8471	0.3864	0.6562	0.7022	0.1060
Mean	8.5000	3.8718	0.6604	0.7407	0.5505	0.2042
St. Dev.	2.6771	0.7479	0.2354	0.0559	–	–

St. Dev.: Standard Deviation

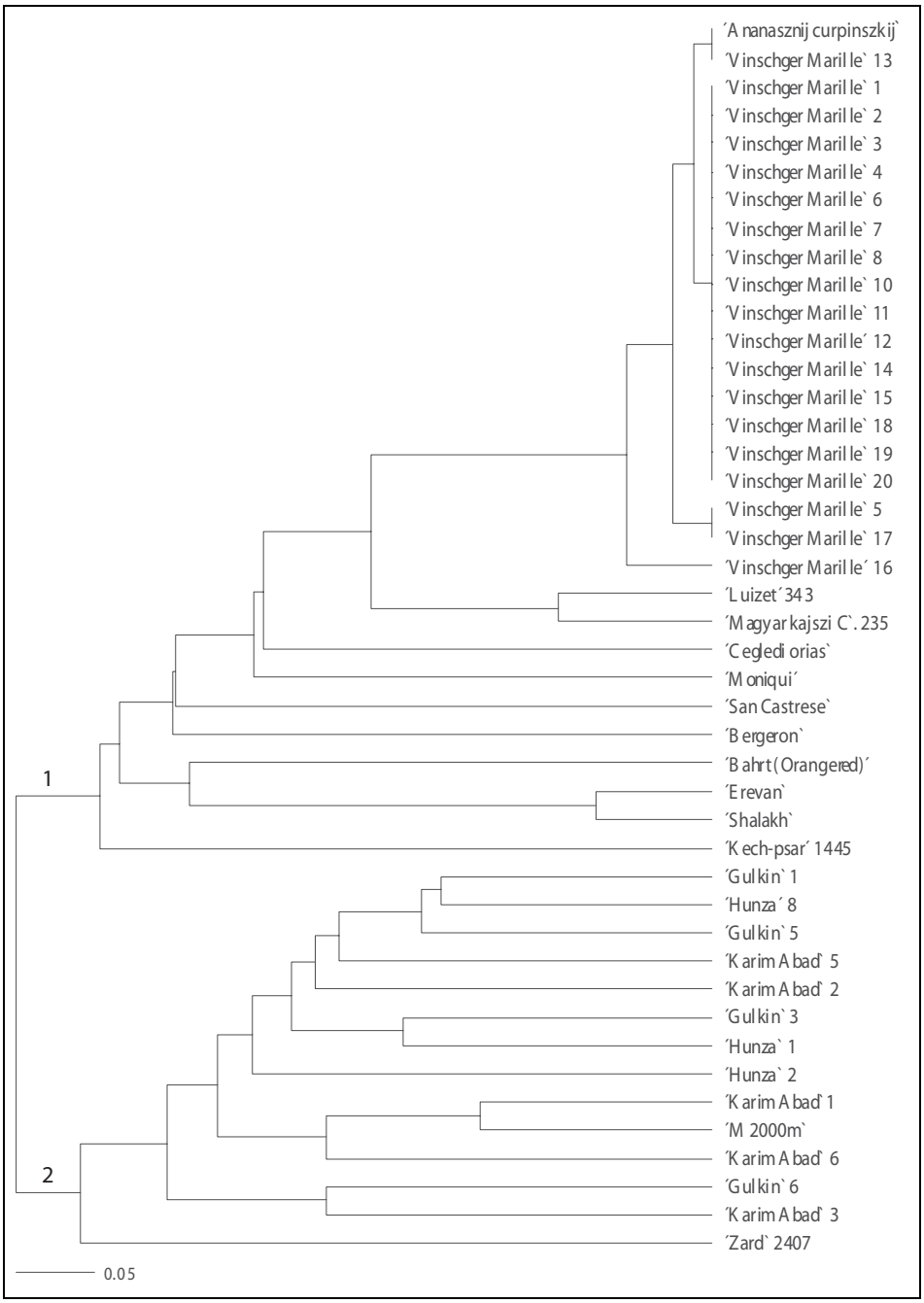


Fig. 1. UPGMA dendrogram for 44 apricot cultivars based on genetic distance.

Fluorescently labelled microsatellite fragments were analysed on an ABI 3100 capillary sequencer. Fragment sizing was performed using the ABI Genotyper software.

For each of the defined loci, SSR allelic composition was determined in 44 accessions. Putative alleles were indicated in alphabetical order (A for smallest fragment, etc.). The program POPGENE (version 1.32; YEH and BOYLE 1997; http://cc.oulu.fi/~jaspi/popgen/popgen.htm") was used to calculate allele frequencies at each locus, number of alleles, inbreeding coefficient (F_{ST}), gene flow (Nm) estimated from using the formula

$$Nm=0.25(1/F_{ST}-1)$$

(where N is the effective population size and m is the fraction of migrants per generation) by NEI (1978). Observed (H_o) and expected (H_e) heterozygosity were measured as described by LEVENE (1949), and NEI (1973). Pairwise genetic distances among the 44 apricot accessions were carried out, using the program PAUP version 4.

Results

Repeatable amplification was obtained for 10 polymorphic microsatellite primer pairs tested in the identification of the 44 apricot genotypes. The number of alleles per lo-

cus ranged from 6 to 13 alleles. Observed heterozygosity ranged from 0.3182 to 0.9545 for loci ssrPaCITA10 and UDAp-410 respectively, the mean observed heterozygosity being 0.6604. Altogether, 85 alleles were identified in the set of accessions with an average of 8.5 alleles per locus (Table 3). The mean of observed heterozygosity (H_o) was lower than the mean of expected heterozygosity (H_e).

Out of the 85 different alleles detected in all individuals, 21 alleles occurred only once in the investigated samples. They were found in apricots that originate from different eco-geographic groups, regions or with compatibility characteristics: 'Karim Abad' 6 and 'Hunza' 1 (at locus ssrPaCITA 10); 'Luizet' (at locus ssrPaCITA 19); 'Zard', 'Bahrt' and 'Bergeron' (at locus ssrPaCITA 7); 'Erevan', 'Hunza' 2, 'Karim Abad' 1 and 'Kech-psar' (at locus UDAp-407); 'Moniqui' and 'Kech-psar' (at Locus UDAp-415); 'Gulkin' 1 and 'San Castrese' (at locus UDAp-410); 'Gulkin' 5, and 'Bahrt' (at locus UDAp-414).

F_{ST} values ranged from 0.3556 (UDAp-410) to 0.7554 (UDAp-407) with an average of 0.5505. The gene flow Nm estimated from F_{ST} in locus UDAp-407 was estimated at 0.0810, a five times lower value than 0.4529 for locus UDAp-410 (Table 3).

UPGMA cluster analysis obtained from 10 SSR markers resulted in a dendrogram of genetic relationships that grouped cultivars in agreements with their geographic regions producing two main clusters (Fig. 1). The first contained all European cultivars along with Irano-Caucasian cultivars ('Erevan' and 'Shalakh') and one North American cultivar ('Orangered'), a descendant of the Iranian apricot cultivar 'Lasgerdi Mashhadi' (Lichou et al. 1998, 2003). The second included 14 out of 15 analysed Asian cultivars. Cluster 2 gathers only self- incompatible Asian accessions (Table 1, Fig. 1).

Discussion

Microsatellites polymorphism

To a certain extent, cross transportability of the SSR markers among different plant species allowed using primers developed in a particular species for related taxa (Ciofi et al. 1998). Cross-species amplification of heterologous peach primers was extensively used in stone fruit (Hormaza 2002; Romero et al. 2003; Zhebentyayeva et al. 2003). A greater genetic distance usually implies a decreasing ability of primers to amplify certain loci, a lower amount of detected polymorphism, and a shortening of the length of microsatellites (Steinkellner et al. 1997; Hormaza 2002). Null alleles are common in cross-species amplifications and are presumably due to mutations in the primer binding sites (Ciofi et al. 1998).

The increase in the amount of polymorphisms detected has been confirmed in this study, since all homologous primer pairs produce highly polymorphic amplification patterns. The average number of alleles per locus was 8.5, which was higher than the 7.64 observed by Zhebentyayeva et al. (2003) in seventy-four native apricot accessions with 14 polymorphic SSRs, the 4.1 detected by Hormaza (2002), and the 3.1 described by Romero et al. (2003).

These differences are due to the fact, that all previous studies on genetic diversity of apricot used microsatellites developed in peach. The higher number of alleles in our study was obtained with ten SSRs, developed in apricot, and selected for their high level of polymorphism (Lopes et al. 2002; Messina et al. 2004). The ability of SSR markers to provide a unique genetic profile for individual genotypes is reflected by a high allele number and heterozygosity. In our study observed heterozygosity averaged over the 10 loci was 0.6604. This is higher than the mean value reported with peach SSRs by Romero et al. (2002) and Zhebentyayeva et al. (2003) in apricot (0.32 and 0.517, respectively).

The proportion of variance within a species that is due to populations' subdivision is represented by F_{ST}-values. According to Wright (1951), a F_{ST} value greater than 0.25 indicates high genetic differentiation (Hartl and Clark 1997). As the average of F_{ST} values was 0.5545 (Table 2), genetic differentiation is relatively high among accessions. In apricot, high levels of genetic differentiation could be explain by the mating system and low incidence of gene flow. Domestication may have occurred in Central Asia, through the natural association of wild and semi–wild forms and propagated seedlings, while in Europe the introduction of vegetative propagation and the selection of a few superior cultivars to a certain extent reduced genetic variability (Zohary and Hopf 1994). In fact, most of the Central Asian cultivars are known to be self-incompatible, while most European cultivars are self-compatible (Mehlenbacher et al. 1991). A high level of F_{ST} value indicates a low level of gene flow. Indeed, the gene flow estimated in this study was low as described by Nm (Table 3).

Apricot genetic diversity and relationships among accessions

The dendrogram generated from the UPGMA cluster analysis produced two clusters related to the geographical origin of the genotypes. All of the European cultivars analysed belong to cluster 1.

"Vinschger Marille" and 'Annanasnij ciurpinszkij' cluster together, indicating that they could have a common genetic background.

Based on their history, it has been suggested that the genetic basis of European apricot cultivars is rather narrow (Kostina 1969). 'Vinschger Marille' can be considered as a particularly suitable example confirming this hypothesis, since it reveals a very low degree of polymorphism across all accessions.

Interestingly, Hungarian Best 'Magyar kajszi' hybrids and the French cultivar 'Luizet' cluster together. Indeed it has been suggested, that the Central European cultivar 'Magyar kajszi' occurs in the pedigree of the latter (Faust et al. 1998, Hormaza 2002).

Hybrids of the Central Asian cultivar 'Shalakh' and 'Erevan' appear in cluster 1, together with 'Kech-psar' 1445, 'Orangered' with an Iranian ancestor and the European cultivars. In accordance with larger survey (Maghuly et al. 2005, 2006), these results confirm that European apricots contain germplasm of Asian origin. This is in agreement with the hypothesis, that apricots moved from China to Armenia (Central Asia) and finally were introduced to Europe by the Romans (70–60 BC) through Greece and Italy (Mehlenbacher et al. 1991; Faust et al. 1998; Oecd 2002).

Cluster 2 includes 14 Asian accessions (seedlings from Pakistan) with a high variability of different alleles

(Fig. 1). The Pakistani practice of planting seeds from the best trees over an extended period of time has resulted in an high amount of variation (THOMPSON 1993).

In Asia, evolution of genetic basis of apricot germplasm occurred predominantly through natural seedling and may have preserved genetic diversity, while in Europe, clonal production through grafting and vegetative propagation has been practiced (HAGEN et al. 2002; ZHEBENTYAYEVA et al. 2003).

The fact that 10 polymorphic microsatellites loci were sufficient to distinguish among all selected varieties suggests that cultivar identification, whether as a means to control breeders right or mislabelling mistake, It is to be greatly assisted by the use of microsatellite markers (MAGHULY et al. 2005, 2006). Marker-assisted selection is a distinct possibility as a future development in apricot breeding. The short ripening period of European apricot cultivars (1– 2 months) compared to the 4,5 months of Central Asian germplasm is causing problems particularly at harvest in years with long winters and mild springs, when most cultivars ripen at the same time within a few weeks. Asian germplasm could therefore be used to extend the harvest period over several months.

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References

BROZNIK, S. and T. KALLAY 2000: Csonthejas gyümölcsfajtak. Agrarmarketing Centrum, Budapest, pp 127–154.

CIOFI, C., S.M. FUNK, T. COOTE, D. CHEESMAN, R.L. HAMMOND, I.J. SACCHERI and M.W. BRUFORD 1998: In: KARP, A., P.G. ISAAC and D.S. INGRAM (eds): Molecular Tools for Screening Biodiversity. Chapman & Hall, London, 413–417.

FAOSTAT 2004: Agriculture database. Web site: apps.fao.org/page/collections?subset=agriculture.

FAUST, M., D. SURÁNYI and F. NYUJTÖ 1998: Origin and dissemination of apricot. Hort. Rev. **22**, 225–266.

FOSSATI, T., F. GRASSI, F. SALA and S. CASTIGLIONE 2003: http://www.ingentaconnect.com/content/bsc/mecol/2003/00000012/00000008/art00002;jsessionid=5rh06t7551po5.victoria" options="\o 'Molecular analysis of natural populations of Populus nigra L. intermingled with cultivated hybrids'. Mol. Ecol. **12**, 2033–2043.

GIUNCHEDI, L., C. POGGI POLLINI and R. BISSANI 2002: Vaiolatura delle drupacee o sharka. Informatore Fitopatologico. Speciale Difesa Drupacee. **5**, 19–24.

HAGEN, S., B. KHADARI, P. LAMBERT and J.M. AUDERGON 2002: Genetic diversity in apricot revealed by AFLP markers: species and cultivar comparisons. Theor. Appl. Genet. **105**, 298–305.

HAGEN S., J. CHAIB, B. FADY, V. DECROOCQ, P. BOUCHET, P. LAMBERT and J.M. AUDERGON 2004: Genomic and cDNA microsatellites from apricot (*Prunus armeniaca* L.). Mol. Ecol. Notes **4**, 742–745.

HARTL, D.L. and A.G. CLARK 1997: Principles of population genetics. 2nd ed. Sinauer Associates, Sunderland

HORMAZA, J.I. 2002: Molecular characterization and similarity relationships among apricot (*Prunus armeniaca* L.) genotypes using simple sequence repeats. Theor. Appl. Genet. **104**, 321–328.

KOSTINA, K.F. 1969: The use of varietal resources of apricots for breeding. Trud. Nikit. Bot. Sada **40**, 45–63.

LAIMER, M. 2003: Detection and elimination of viruses and phytoplasmas from pome and stone fruit trees. Hort. Reviews **28**, 187–236.

LEVENE, H. 1949: On a matching problem in genetics. Ann. Math. Stat. **20**, 91–94.

LICHOU, J. 1998: Abricot. Ctifl, Paris, France.

LICHOU, J., M. JAY, P. VAYSSE and N. LESPINASSE 2003: Recognizing apricot varieties. Ctifl, Paris, France.

LOPES, M.S., K.M. SEFC, M. LAIMER and A.Da CÂMARA MACHADO 2002: Identification of microsatellite loci in apricot. Mol. Ecol. Notes **2**, 24–26.

LÖSCHNIG, H.J. and F. PASSECKER 1954: Die Marille (Aprikose) und ihre Kultur. Österreichischer Agrarverlag Wien, Austria.

MAGHULY, F., E.G. BORROTO FERNANDEZ, S. RUTHNER, A. PEDRYC and M. LAIMER 2005: Microsatellite variability in apricots (*Prunus armeniaca* L.) reflects their geographic origin and breeding history. Tree Genetics & Genomes **1**, 151–165.

MAGHULY, F., E.G. BORROTO FERNANDEZ, S. RUTHNER, G.D. BISZTRAY, A. PEDRYC and M. LAIMER 2006: Microsatellite characterisation of apricot (*Prunus armeniaca*) cultivars grown in Central Europe. Acta Hort. (In press).

MEHLENBACHER, S.A., V. COCIU and F. HOUGH 1991: Apricot (*Prunus*). In: MOORE, J.N. and R.J. BALLINGTON (eds): Genetic resource of temperate fruit and nut crops ISHS Wageningen, 65–107.

MESSINA, R., O. LAIN, M.T. MARRAZZO, G. CIPRIANI and R. TESTOLIN 2004: New set of microsatellite loci isolated in apricot. Mol. Ecol. Notes. **4**, 432–434.

MORGANTE, M. and A.M. OLIVIERI 1993: PCR-amplified microsatellites as markers in plant genetics. Plant J. **3**, 175–182.

NEI, M. 1973: Analysis of gene diversity in subdivided populations. P. Nat. Acad. Sci. USA. **70**, 3321–3323.

NEI, M. 1978: Estimation of average heterozygosity and genetic distance from a small number of individuals. Genetics. **89**, 583–590.

OECD 2002: Consensus Document on the Biology of *Prunus* sp. (Stone fruits): Series on Harmonization of Regulatory Oversights in Biotechnology Nr. **24**. http://www.olis.oecd.org/olis/2002doc.nsf/LinkTo/env-jm-mono.

POWELL, W., G.C. MACHRAY and J. PROVAN 1996: Polymorphism revealed by simple sequence repeats. Trends Plant Sci. **7**, 215–222.

ROMERO, C., A. PEDRYC, V. MUNOZ, G. LLACER and M.L. BADENES 2003: Genetic diversity of different apricot geographical groups determined by SSR markers. Genome. **46**, 244–252.

STEINKELLNER, H., C. LEXER, E. TURETSCHEK and J. GLÖSSL 1997: Conservation of $(GA)_n$ microsatellite loci between *Quercus* species. Mol. Ecol. **6**, 1189–1194

STRADA, G.D., F. PENNONE, C. FIDEGHELLI, F. MONASTRA and D. COBIANCHI 1989: Monografia di cultivar di albicocco. Istituto Sperimentale per la Frutticoltura, Roma.

THOMPSON, M.M. 1993: Exploration and exploitation of new fruit and nut germplasm. p. 155–160. In: JANICK, J. and J.E. SIMON (eds): New crops. Wiley, NewYork.

WRIGHT, S. 1951: The genetical structure of populations. Ann. Hum. Genet. **15**, 323–354.

YEH, F.C. and T.J.B. BOYLE 1997: Population genetic analysis of co-dominant and dominant markers and quantitative traits. Belg. J. Bot. **129**, 156–159.

ZHEBENTYAYEVA, T.N., G.L. REIGHARD, V.M. GORINA and A.G. ABBOTT 2003: Simple sequences repeat (SSR) analysis for assessment of genetic variability in apricot germplasm. Theor Appl Genet. **106**, 435–44.

ZOHARY, D. and P. SPIEGEL ROY 1975: Beginning of fruit growing in the Old World. Science. **187**, 319–327.

ZOHARY, D. and M. HOPF 1994: Domestication of plants in the Old World. 2nd ed. Clarendon Press, Oxford.

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