Mitteilungen Klosterneuburg 54 (2004): 33-42

Genotyping apricots *(Prunus armeniaca)* by SSR markers

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Apricots are the most important stone fruit for the Austrian market. Besides fresh market, juice, jam and spirit industries process huge amounts of apricots. Quality of products are even dependent on local climate and cultivar identity. As the identification of cultivars by horticultural and morphological parameters is time consuming and lacks reliability, a genetically based system would provide an advantage. With the help of 12 SSR markers developed from a peach (Prunus persica L.) library the genotype of 88 cultivars of apricot was analysed. The discrimination power of these SSR markers enabled us to get an individual profile for each true cultivar. Even sports of a cultivar could be detected by applying these SSR markers. The genetic heterozygosity was estimated by defining the proximity matrix and a dendrogramm was drawn. It could be confirmed that 'Ungarische Beste' and 'Klosterneuburger Marille' are the same cultivar. Genetic differences within these samples show that variations within the cultivar have already taken place.
Key words: apricot, cultivar identification, SSR marker, 'Ungarische Beste', 'Klosterneuburger Marille'

Genetische Analyse von Marillen (Prunus armeniaca) mittels SSR Markern. *Marillen sind die wichtigste Steinobstfrucht am österreichischen Markt. Neben dem Frischverzehr werden große Mengen als Saft, Marmelade und Spirituosen verarbeitet. Die Qualität der Produkte hängt vom lokalen Klima und der Sorte ab. Da die Identifizierung der Sorten durch gartenbauliche und morphologische Parameter sehr zeitaufwändig und unsicher ist, wäre ein genetisches Identifizierungssystem ein bedeutender Vorteil. Mittels 12 SSR Markern, welche aus dem Pfirsichgenom entwickelt wurden, konnte für 88 Marillengenotypen eine genetische Analyse angestellt werden. Das Unterscheidungspotenzial mit SSR Markern ermöglichte ein eigenständiges Profil für alle echten Sorten. Darüber hinaus konnten Mutanten einer Sorte ebenfalls mittels SSR Markern erkannt werden. Die genetische Heterozygotie wurde mittels Nachbarschafts-Matrix abgeschätzt. Es konnte bestätigt werden, dass 'Ungarische Beste' und 'Klosterneuburger Marille' identisch sind. Genetische Unterschiede innerhalb dieser Proben ließen die Variabilität dieser Sorte erkennen.*
Schlagwörter: Marille, Sortenidentifizierung, SSR Marker, 'Ungarische Beste', 'Klosterneuburger Marille'

Analyse génétique d'abricots (Prunus armeniaca) à l'aide de marqueurs SSR. *Les abricots sont les fruits à noyau les plus importants sur le marché autrichien. Les fruits ne sont pas seulement mangés à l'état frais, mais de grandes quantités sont également transformées en jus, confiture et eaux-de-vie. La qualité des produits dépend du climat local et de la variété. Comme l'identification des variétés à l'aide de paramètres horticoles et morphologiques est très incertaine et demande beaucoup de temps, un système d'identification génétique présenterait un grand avantage. Une analyse génétique de 88 génotypes d'abricots a pu être effectuée à l'aide de 12 marqueurs SSR développés sur la base du génome des pêches. Le potentiel de différenciation des marqueurs SSR a permis d'établir un profil propre à chaque variété originale. En outre, des mutants d'une variété ont également pu être reconnus au moyen des marqueurs SSR. L'hétérozygotie génétique a été estimée à l'aide de la matrice de voisinage. Il a été possible de confirmer que 'Ungarische Beste' et 'Klosterneuburger Marille' sont identiques. Les différences génétiques au sein de ces échantillons ont laissé apparaître la variabilité de cette variété.*
Mots clés : abricot, identification des variétés, marqueurs SSR, 'Ungarische Beste', 'Klosterneuburger Marille'

Apricot is a member of the family Rosaceae and originated from Manchuria in China. The transfer to Europe occurred via Armenia. The Greeks brought them to Europe and the Romans spread them over the continent. Finally today *Prunus armeniaca* has spread to all temperate zones of Austria (Wurm et al., 2002). Close related other Prunus species or *P. armeniaca* subspecies are not cultivated in this area. From the morphology of apricots it was concluded that the European cultivars are genetically close together (Löschnig und Passecker, 1954). The main criteria to form three clusters of the European apricots is the cold demand during winter. Most traditional cultivars in Austria belong to the group with need of medium cold demand.

The main production is located in the eastern federal states of Niederösterreich and Burgenland. Centres of growing are the Wachau valley along the Danube, the Weinviertel region, especially Poysdorf, and Kittsee in Burgenland. The yield fluctuates due to the early blooming and the frequently resulting freezing damages. The volume of yearly harvest varies between 10 and 20 tonnes per ha. A quite large part of the production takes place in home gardens.

Different cultivars are evaluated for different usage. Whereas 'Ungarische Beste' and 'Klosterneuburger Marille' are mainly used for direct consumption or industrial processing of jam, juice or spirits, newer cultivars are used for the fresh market. The differentiation of these cultivars is not simple and a cause for wrong identification. In the past their common genetic identity was under discussion.

Recently introduced cultivars like 'Bergeron', 'Goldrich' and others are used for delivering to different market places and supermarkets. Due to the different suitabilities cultivar identification is necessary. Pomological methods for identification of cultivars are not precise enough and are the source of errors. Especially the identification of scions or woody material is limited and not reliable.

Molecular markers and their use for genotyping have revolutionised plant breeding and identification of cultivars (Rafalski and Scott, 1993; Thomas et al., 1993; Sosinski et al., 2000). Especially microsatellite markers have been approved for their usefulness in characterization of genotypes and the identification of cultivars. Identity can be confirmed if the genetic profile of an individual concurs with all alleles from a cultivar of the database data (Thomas et al., 1993). Comparability of the allele length allows to reproduce results independent from equipment and lab. Perfect SSR (Simple Sequence Repeats) markers are inherited in a codominant pattern and segregation according to Mendel. Several non perfect SSR markers show any other kind of heritage. Usually by the incidence of three alleles the formation of chimeric structures is indicated (Franks et al., 2002). As no SSR markers were developed from apricot we used SSR markers from peach (Cipriani, 1999). These markers were already amplified in different Prunus species as cherry, plum, apricot, almond, nectarine and peach. Nevertheless it was not clear if the SSR markers will provide high polymorphism suitable to enable us to identify cultivars of apricot or not.

Material and methods

Leaf material was gained by the collection of the Höhere Bundeslehranstalt und Bundesamt für Wein- und Obstbau (Federal College and Research Institute for Viticulture and Pomology) Klosterneuburg, by the apricot orchard of the Universität für Bodenkultur (University of Natural Resources and Applied Life Sciences) Vienna, by the private nursery Robert Schreiber in Poysdorf (Lower Austria), by the Hungarian collection of the Fruit Culture Research Institute (non-profit company), Cegléd. Lists of used cultivars are shown in table 1.

Preparation of DNA was performed according to a protocol already used for grapevine (Regner et al., 1998). Only young leaves resulted in high quality DNA with good performance for PCR analysis. Leaf samples were harvested only in April and May.

Following loci from peach genome were used as markers to characterize apricots: UDP96-003, UDP96-008, UDP96-015, UDP96-018, UDP96-019, UDP98-021, UDP98-024, UDP97-402, UDP97-403, UDP98-407, UDP98-410 and UDP98-412 (Testolin et al., 2000).

The amplification of the SSR loci was performed by following our general protocol but by applying specific annealing conditions. The general PCR protocol applied for these studies was 2 min denaturation at 94 °C and 35 cycles with annealing phase for 30 sec (temperature between 45 °C and 55 °C) and denaturation for 15 sec. at 92 °C. The annealing temperature for each locus was set according to the original protocol (Testolin et al., 2000). A final extension of the fragments was performed at 72 °C for 5 min. Due to the different size range of the involved loci multiplex PCR was feasible. At least the alleles of three loci were separated on one sequencing gel.

Yield of DNA fragments was estimated by running an

Table 1:
List of involved apricot cultivars (Klosterneuburg = Höhere Bundeslehranstalt und Bundesamt für Wein- und Obstbau; Poysdorf = Baumschule Robert Schreiber; BOKU = Universität für Bodenkultur; Marchegg = Reiserschnittgarten der Landeslandwirtschaftskammer Niederöstereich)

Nr.	Code	Cultivar	Nr.	Code	Cultivar
M1	131/01/005 Klosterneuburg	Frühe v. Hinterholzer	M44	Magyar kajszi C602 Genbank	Ungarische Beste
M2	131/01/009 Klosterneuburg	Klosterneuburger Marille Higatsberger	M45	Magyar kajszi C555 Genbank	Ungarische Beste
M3	131/01/012 Klosterneuburg	Klosterneuburger Marille Hinterholzer	M47	NLK 2 Marchegg	Wahre Große Frühe
M4	131/01/017 Klosterneuburg	Klosterneuburger Marille Standard	M48	BOKU M4	Ungarische Beste Redl
M5	131/01/020 Klosterneuburg	Kecskemeter Rosenaprikose	M49	Magyar kajszi C637 Genbank	Ungarische Beste
M6	131/01/028 Klosterneuburg	Ungarische Beste	M50	08207012 Klosterneuburg	Klosterneuburger Marille
M7	RS-8 Poysdorf	Perfektion	M51	NLK 1 Marchegg	Klosterneuburger Marille
M8	RS-25 Poysdorf	E1 Gm Dr. Jacob	M52	Magyar kajszi C1646 Halasto	Ungarische Beste
M9	RS-31 Poysdorf	Goldrich	M53	08201011 Klosterneuburg	Balogh 2
M10	RS-17 Poysdorf	Carmen	M54	BOKU M7	Klosterneuburger Marille Roiss
M11	RS-9 Poysdorf	Polonais	M55	Magyar kajszi C592 Genbank	Ungarische Beste
M12	RS-10 Poysdorf	Fantasme	M56	Gönci magyar kajszi Halasto	Ungarische Beste
M13	RS-18 Poysdorf	Early Blush	M57	G. magyar kajszi Üzemi tabla	Ungarische Beste
M14	RS-2 Poysdorf	Hargrand	M58	082 03 019 Klosterneuburg	Klosterneuburger Marille
M15	RS-15 Poysdorf	Harrogem	M59	082 03 027 Klosterneuburg	Klosterneuburger Marille
M16	RS-1 Poysdorf	Ivresse	M60	082 07 019 Klosterneuburg	Klosterneuburger Standard
M17	RS-22 Poysdorf	Brevira	M61	082 02 019 Klosterneuburg	Klosterneuburger Marille
M18	RS-20 Poysdorf	Gönci magyar kajszi	M62	082 06 010 v	Klosterneuburger Marille
M19	RS-14 Poysdorf	Lejuna	M63	BOKU M2	Kremser Rosenmarille
M20	RS-31 Poysdorf	Goldrich	M64	BOKU M1	Aprikose von Buda
M21	RS-3 Poysdorf	Bergarouge	M65	082 05 019 v	Klosterneuburger Marille
M22	RS-16 Poysdorf	Orangered	M66	082 02 011 Klosterneuburg	Klosterneuburger Marille
M23	RS-24 Poysdorf	Virosia	M67	082 01 002 Klosterneuburg	Balogh 1
M24	RS-5 Poysdorf	Klosterneuburger Klon 3	M68	082 05 003 Klosterneuburg	Ungarische Beste
M25	RS-28 Poysdorf	Klosterneuburger Typ Schreiber	M69	082 04 034 Klosterneuburg	Klosterneuburger Marille
M26	RS-12 Poysdorf	Kesckemeter Rosenaprikose	M70	082 06 018 Klosterneuburg	Klosterneuburger Marille
M27	RS-19 Poysdorf	Aurora	M71	082 05 011 Klosterneuburg	Klosterneuburger Marille
M28	RS-11 Poysdorf	Rouge Tardif Delbard	M72	BOKU M3	Klosterneuburger Marille Tulln
M29	RS-4 Poysdorf	Harval	M73	BOKU M5	Marille Küppers
M30	RS-30 Poysdorf	Aurora Fertility	M74	082 03 003 Klosterneuburg	Klosterneuburger Marille
M31	RS-27 Poysdorf	Bergeron Klon INFEL 660	M75	082 01 019 Klosterneuburg	Nagy 1
M32	RS-26 Poysdorf	Tardicot	M76	082 01 027 Klosterneuburg	Nagy 2
M33	RS-13 Poysdorf	Veharda	M77	BOKU M6	Kecskemeter (Späte Marille Häbling)
M34	RS-23 Poysdorf	Kuresia	M78	082 04 027 Klosterneuburg	Klosterneuburger Marille
M35	RS-29 Poysdorf	Pui-sha-sin	M79	082 02 036 Klosterneuburg	Klosterneuburger Marille
M36	RS-21 Poysdorf	Magyar kajszi C. 235	M80	082 04 019 Klosterneuburg	Frühmarille
M37	RS-32 Poysdorf	Jumbo Cot	M81	082 01 033 Klosterneuburg	Klosterneuburger Marille II
M38	RS-7 Poysdorf	Velkepavlovicka LE 12-2	M82	082 05 035 Klosterneuburg	Klosterneuburger Marille
M39	RS-6 Poysdorf	Ungarische Beste	M83	082 04 003 Klosterneuburg	Klosterneuburger Marille
M40	Magyar kajszi C235 Halasto	Ungarische Beste	M84	082 02 003 Klosterneuburg	Nagy 4
M41	Magyar kajszi C501 Genbank	Ungarische Beste	M85	082 03 011 Klosterneuburg	Klosterneuburger Marille
M42	NLK 3 Marchegg	Ungarische Beste	M86	082 07 001 Klosterneuburg	Ungarische Beste
M43	NLK 4 Marchegg	Ungarische Beste	M87	082 02 026 Klosterneuburg	Ungarische Beste
			M88	082 05 027 Klosterneuburg	Klosterneuburger Marille

Table 2:
Alleles and their frequency

96-003		Frequency	Confidence 95 %
93	3	0.075	0.173
95	5	0.125	0.235
98	1	0.0025	0.104
99	17	0.425	0.554
107	1	0.025	0.104
109	4	0.1	0.205
111	9	0.225	0.348
96-019			
155	1	0.02	0.088
160	1	0.02	0.088
162	2	0.041	0.118
163	5	0.104	0.198
168	30	0.625	0.73
197	1	0.02	0.088
201	1	0.02	0.088
202	1	0.02	0.088
212	8	0.145	0.248
97-402			
122	1	0.019	0.083
123	12	0.39	0.327
126	3	0.058	0.111
128	2	0.039	0.102
129	7	0.137	0.234
130	1	0.019	0.083
131	3	0.058	0.111
135	9	0.176	0.279
146	22	0.411	0.526
98- 012			
88	11	0.2	0.292
94	1	0.018	0.074
100	3	0.054	0.124
107	7	0.127	0.211
109	9	0.163	0.292
114	6	0.109	0.211
115	3	0.054	0.124
116	2	0.036	0.1

Table 2 (continued):
Alleles and their frequency

98-021		Frequency	Confidence 95 %
84	1	0.019	0.083
104	1	0.019	0.083
105	12	0.235	0.344
106	4	0.083	0.211
107	3	0.061	0.138
108	2	0.04	0.11
125	1	0.019	0.083
126	1	0.019	0.083
127	3	0.061	0.138
129	10	0.204	0.301
130	3	0.061	0.138
131	3	0.061	0.138
141	1	0.019	0.083
143	2	0.04	0.11
157	2	0.04	0.11
98-024			
75	1	0.02	0.086
84	1	0,02	0.086
86	1	0,02	0.086
87	9	0,187	0.29
90	32	0,666	0.754
92	1	0,02	0.086
95	1	0,02	0.086
96	3	0,065	0.143

aliquot of the sample on a 2 % agarose gel stained with ethidium bromide. The samples were denaturated by heating up with formamide and loaded together with a size standard (Genescan 350 Tamra, Appl. Biosystems, Warrington, GB) to a 6 % polyacrylamid gel. Detection of the SSR fragments labelled with the fluorescent dyes 6FAM, TET and HEX (Applied Biosystems) was carried out by an automated sequencer (ABI 373, Perkin-Elmer, Vienna). Labelling with these different fluorescent colouring agents facilitated the application of multiplex PCR.

The calculation of the SSR based heterozygosity index was performed by using a software program designed

for multivariate analysis and identification of nematodes (TIEFENBRUNNER et al., 2002). The data were calculated according to Microstat (http://hpgl.stanford.edu/projects/microstat) with a square frame method.

Results and Discussion

12 SSR markers from a genomic peach library (REGNER et al., 1998) were used to characterize 88 genotypes of apricot. Two of the markers (UDP96-018 and UDP97-403) were monomorph in our selection of apricots and therefore were excluded from further studies. The markers UDP96-015, UDP 98-407 and UDP98-410 could not be stabilized by adaptation trials. Alleles could not be reproduced all the time. Therefore we decided to neglect these markers. Another phenomenon was the very frequent incidence of null alleles in all other loci. Despite several trials some loci do not result in an allelic profile. Others allowed us only to amplify at least one allele. It is supposed that mutations in the annealing side happen more frequently in apricot. The highest information content is gained by locus UDP98-412 because of the even distribution of the frequencies of the 9 found alleles (Table 2). On the other side at the locus UDP-008 only 3 alleles occur in 90% of the cultivars. The bad frequency distribution pattern reduces the information content of the locus.

The probability of identity (PI) represents the chance that two randomly chosen cultivars show the same SSR profile (Table 3). With increasing number of loci the probability that two randomly chosen cultivars are identical decreases. By using the seven SSRs of our study the probability (PI) that two different cultivars share the same genetic profile is only 2,8 $x10^{-6}$. That means the same profile of different true cultivars can be excluded. Characterization of cultivars with seven SSR loci enables us to differentiate all of them (Table 4). Even very closely related cultivars could be differentiated. For instance with the help of SSR genotyping the genetic differences of 'Early Blush' and 'Aurora' could be traced. It was supposed that both are the same cultivar but in our results they deviate at three SSR loci. Another open question was the origin of 'Fantasme'. According to our results the derivation from 'Bergeron' could not be confirmed (WURM et al., 2002). For the precise definition of heritages it would be necessary to analyse far more loci. Our experience of grapevine analysis is that less than 30 markers will not result into assured parentages (REGNER et al., 2001). The multivariate analysis and even the proximity matrix (Table 5) show that these cultivars are heterozygous. The discrimination power of the SSR marker is sufficient to characterize all individual genotypes (Fig. 1).

Table 3
Probability of identification

Locus	Heterozygosity expected	Estimated from null alleles	Probability of identity (PI)
96-003	0.736	-0.151	0.171
96-008	0.548	-0.291	0.309
96-019	0.573	-0.271	0.267
97-402	0.768	-0.131	0.124
98-021	0.871	-0.068	0.051
98-024	0.533	-0.303	0.31
98-012	0.843	-0.084	0.081
PI			$2.808x10^{-6}$

The most popular apricot cultivars of Austria are 'Ungarische Beste' and 'Klosterneuburger Marille'. Despite their slightly different horticultural description (Table 6) it is supposed that these cultivars are identical. As none of the sources could be excluded as not true to the type we involved several genotypes to clarify the origin of these cultivars (Table 7). The multivariate analysis shows that genotypes of 'Ungarische Beste' and Klosterneuburger are more or less identical. The dense occurrence in the centre of genetic profile indicates the

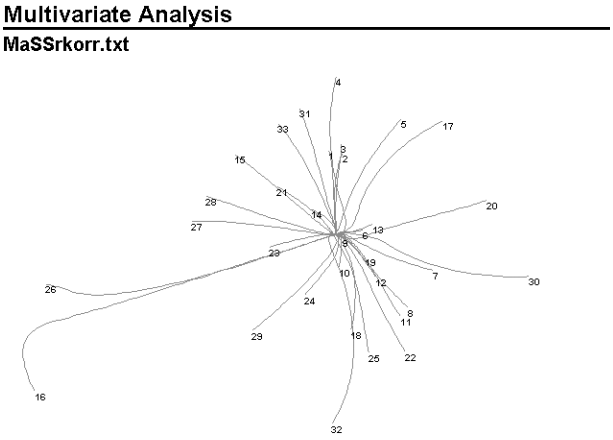

Fig. 1: Tree of the multivariate analysis

Table 4:
Alleles of the different cultivars

Nr.	Genotyp	96-003	96-008	96-019	97-402	98-021	98-024	98-012
1	Frühe v. Hinterholzer	99	133 137	168 212	129 146	105 130	90	88 118
2	Klosterneuburger Marille Higatsberger	99	133 137	168 212	129 146	105 130	90	88 100 118
4	Klosterneuburger Marille Standard	99	133 137	168 212	129 146	105	90	88 118
5	Kecskemeter Rosenaprikose	95 99	133 135	212	146	105	84 90	114 118
6	Ungarische Beste	99	121 133 135	168 212	129 146	105	90	88 118
7	Perfektion	95 99	133	168	131 146	126	90	107
8	E1 Gm Dr. Jacob	93 111	133	168 202	133 135 146	130	90	107 114
10	Carmen	93 111	133	168	133 135	108 157	90	109
11	Polonais	95 99	133	168	122 146	127	90	107 114
12	Fantasme	111	133	168	146	106 129	90	116 118
13	Early Blush	111	133	160 168	135 146	107 157	90	109
14	Hargrand	111	133	168			90	100 109
15	Harrogem	99	133	168	123 126	141	90	107
16	Ivresse	99	133 137	168	146	106 129	90	88 115
17	Brevira	99	133 137	162 168	129 146	106 127	75 90	107 118
18	Gönci magyar kajszi					84	90	88 100
19	Lejuna	95				105 143	90	88
20	Goldrich	99 111	133	168	131 135	107 129	90 96	109 114
21	Bergarouge		133	168	129 135	106	90	
22	Orangered			155 168		104 125	90	88 109
23	Virosia	99	133 137	168	129 146	131 143	87 90	88 107
27	Aurora	111	133	162 168	135 146	107	90 95	109
28	Rouge Tardif Delbard	99 111	133 137	168	146	106 129	87 90	114 118
29	Harval	99	133	168	123 131	129	87 90	109 114
30	Aurora Fertility	111	133	168	135 146	105 129	92 96	109
31	Bergeron	109	131 137	163 168 212	146	105 129	87 90	115 118
32	Tardicot	109	133 137	168 201	146	106 131	87 90	107 118
33	Veharda	109	133 137	168 212	146	105 129	87 90	116 118
34	Kuresia	95 99	122 133	163 168	126 146	127 129	87 90	109 114
35	Pui-sha-sin	93 98	133 135	163 168 197	126 135	105	86 90	94 109
36	Magyar kajszi C. 235	99	133 137	163 168 212	128 146	105	87 90	88 118
37	Jumbo Cot	109 107	133 135	163 168	130 135	108 129	90 96	109 115
38	Velkepavlovicka LE 12-2	99	133 137	168 212	128 146	105 131	87 90	88 118

Table 5:
Proximity matrix of the different cultivars (only M1 to M16 is shown)

	M1	M2	M4	M5	M6	M7	M8	M10	M11	M12	M13	M14	M15	M16
M1	0,0000	7,1110	6,2500	16,0000	14,6900	18,0600	21,0100	25,0000	18,0600	18,0600	25,0000	17,6400	16,0000	10,5600
M2		0,0000	7,1110	16,6700	16,0000	18,0600	21,0100	25,0000	18,0600	18,7800	25,0000	15,7300	16,0000	11,1100
M4			0,0000	12,2500	11,1100	18,0600	25,8400	25,0000	18,0600	18,0600	25,0000	17,6400	16,0000	10,5600
M5				0,0000	15,3400	25,0000	29,3400	36,0000	22,5600	22,5600	30,2500	31,3600	30,2500	22,5600
M6					0,0000	24,1700	27,5600	26,6900	24,1700	19,5100	26,6900	19,6500	26,6900	21,0100
M7						0,0000	14,6900	16,0000	7,5630	12,2500	18,0600	7,8400	6,2500	12,2500
M8							0,0000	14,6900	13,4400	15,3400	7,8400	16,0000	21,7800	28,4400
M10								0,0000	16,0000	12,2500	6,2500	1,9600	16,0000	20,2500
M11									0,0000	12,2500	18,0600	7,8400	9,0000	12,2500
M12										0,0000	9,0000	1,9600	16,0000	9,0000
M13											0,0000	1,9600	20,2500	20,2500
M14												0,0000	7,8400	12,2500
M15													0,0000	12,2500
M16														0,0000

Table 6:
Morphological description of apricot 'Ungarische Beste' and 'Klosterneuburger Marille'

	Ungarische Beste	Klosterneuburger Marille
Shape	conical	conical
Origin	Hungary seedling selected by Glocker in Enyed (1868) several types available	supposed to be Hungary the Hungarian-originated trees were sold from 1862 to 1873 in Klosterneuburg and therefore the growers named them due to that location (LÖSCHNIG and PASSECKER (1954)
Maturation	early to middle, mid of July	middle to late, some days later than Ungarische Beste
Differences of size and shape	slightly smaller than Klosterneuburger Marille, small deviations from round shape, seam is weak and is interrupted, trace of pistil is brown and well formed, sinus of the leaf is shallow, some folds lips only little open	large sized, seam is interrupted on the underside and disappears at the peak of the pistil, not symmetrical round shaped, a little heightened; sinus of the leaf is deep and round and narrow; lips open
Fruit skin	slightly woolly	intensely woolly, dependent on weather conditions, more red than Ungarische Beste or even some red-brown pigments
Fruit	orange	orange with tendency to red
Stone	seed less bitter than Klosterneuburger Marille	

Table 7:
Alleles of different samples of 'Ungarische Beste' and 'Klosterneuburger Marille'

Nr	M 1		M 2			M 4			M 5			M 8			M 9		**M 12**		
Kl 1	99		133	137		168	212		129	146		105	130		90		88	118	
Kl 2	99		133	137		168	212		129	146		105	130		90		88	100	118
Kl 3	99		133	137		168	212		129	146		105	130		90		88	100	118
Kl 4	99		133	137		168	212		129	146		105			90		88	118	
U 6	99		133	135		168	212		129	146		105			90		88	118	
Kl 24	99		133	137		168			129	146		105	131		90		88	118	
Kl 25	95		133			162	168		135	146		108	127		87	90	107	109	
U 39	99		133	137		163	168	212	129	146		105	131		87	90	88	118	
U 42	99		133	137		168	212		129	146		101	105	131	87	90	88	118	
U 43	95		133	137		168	212		129	146		101	105	131	87	90	88	100	118
U 44	99					162	168	212	122	128	144	106			88	94	88		
U 45	95		133	137		168	212		129	146		101	105		87	90	88	118	
U 46	95		133	137		168	212		129	146		101	105	131	87	90	88	100	118
U 48	95		133	137		168	212		129	146		101	105	131	87	90	88	100	118
U 49	97	99	133	137		162	168	212	129	146		101	105	131	87	90	88	100	118
Kl 50						168	212		129	146		101	105		87	90	88	118	
Kl 51	99		133	137		168	212		129	146		101	105	131	87	90	88	100	118
U 53	99		133	137		168	212		129	146		101	105		87	90	88	118	
KL54	99		133	137		181			128	146		105	131		86	90	88	118	
U 55	99		133	137		162	168	212	128	146		105	131		86	90	88	118	
U 56						168									90		88		
U 57	99					168						106	125		90		88	107	118
Kl 58	99		133	137		168	212		129	146		101	105	131	87	90	88	118	
Kl 59	99		133	137		168	212		129	146		101	105	131	87	90	88	100	118
Kl 60	99	111	133	137		168			123	146		101	105		87	90	112		
Kl 61	99		133			168			126	131		131	155		87	90	107		
Kl 62	99		133	137		168	212		129	146		101	105	131	87	90	88	118	
Kl 63	99		133	137		168	212		129	146		101	105	131	87	90	88	118	
Kl 65	98		133	137		168	212		129	146		106	131		90		88	100	118
Kl 66	99		133	137		168	212		129	146		106	131		90		88	118	
U 67	99		133	137		168	212		129	146		105	131		90		88	118	
U 68	96	99	126	133	137	168	212		129	146		105	131		90		88	100	118
Kl 69	96	99	126	133	137	168	212		129	146		105	131		90		88	100	118
Kl 70	99		126	133	137	168	212		129	146		105	131		90		88	118	
Kl 71	99		133	137		168	212		129	146		105	131		90		88	118	
Kl 72	98		133	137		168	212		129	146		105	131		90		88	118	
Kl 73	99		133	137		168	212		129	146		105	131		90		88	118	
Kl 74	99		133	137		168	212		129	146		105	131		90		88	118	
U 75	99		133	137		168	212		129	146		105	131		90		88	118	

Table 7 (continued)

Nr	M 1		M 2		M 4			M 5		M 8		M 9		M 12		
U 76	96		133	137	168	212		129	146	105	131	90		88	118	
Kl 78	99		133	137	168	212		129	146	105	131	90		88	118	
Kl 79	100		133	137	168	212		129	146	105	131	90		88	118	
Kl 81	99		133	137	168	212		129	146	105	131	90	147	88	118	
Kl 82	99		133	137	168	212		129	146	105	131	90	147	88	118	
Kl 83	99		133	137	168	212		129	146	105		90	147	88	118	
U 84	99		133	137	168	212		129	146	105	131	90	147	88	100	118
Kl 85	99		133	137	168	212		129	146	105	131	90	147	88	118	
U 86	99		133	137	168	212		129	146	105	131	90	147	88	118	
U 87	95	99	133	137	168			146		131		84	90	88		
Kl 88	95	99	133	137	162	168	212	128	148	106	131	84		88	118	

Table 8:
Genetic descriptor for identification of apricot characteristics: SSR marker : UDP 98-021
Primer sequence (TESTOLIN et al., 2000):
F: AACGAGCAATTGGCAGAATC
R: GAATATGAGACGGTCCAGAAGC

Relative base pair length Distance to allele N	Cultivar code of the allele	Example cultivar
N	GOE1	Gönci Magyar kajszi
N+20	OR1	Orangered
N+21	UN 1	Ungarische Beste
N+22	FA1	Fantasme
N+23	EB1	Early Blush
N+24	JC 1	Jombo Cot
N+41	OR 2	Orangered
N+42	PE 1	Perfektion
N+43	PO 1	Polonais
N+45	FA 2	Fantasme
N+46	F.H 2	Frühe von Hinterholzer
N+47	VI 1	Virosia
N+57	HA 1	Harrogem
N+59	LE 2	Lejuna
N+73	EB 2	Early Blush

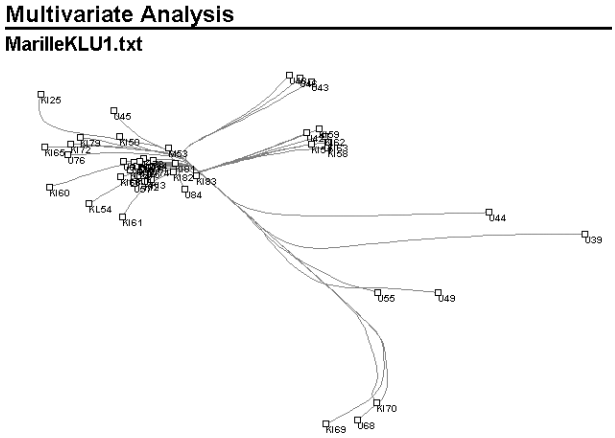

Fig. 2: Tree of the multivariate analysis of table 7

same identity. But both cultivars include even some deviating genotypes. Due to their vegetative propagation it can be supposed that these changes happened by mutations. Genotypes far away from the genetic centre of 'Klosterneuburger Marille' (Kl 69 and Kl 70) and 'Ungarische Beste' (U 49, U 55, U 44 and U 68) are supposed to have a misinterpreted identity. The main genotype of the cultivar is focused between U 84, Kl 50 and Kl 68. These genotypes can be regarded as true to type and represent more or less genetic identity.
The genetic profile of a cultivar gained by SSR analysis offers absolute allele length as a means of differentiation and identification. Trying to perform ring trials it

was not feasible to harmonize these absolute values by different labs for grapevine (This et al., 2004). The way to describe a cultivar is usually done with the help of descriptors. It would be in good agreement with the morphological description to use genetic loci as descriptors. These genetic descriptors could be based on the data gained in this study (Table 8). We propose for each SSR loci to use them as an allelic ladder based on alleles gained for a well known specific cultivar. A similar identification system was already established for grapevine. The advantage of this method is the better comparability of data and the tool for description of a crop cultivar. Even these values should be used to define genotypes of germplasm collection. For the comprehensive definition of a cultivar more genetic descriptors are demanded. Usually by using six suitable markers the probability of identity (PI) of different cultivars is small enough to characterize all true cultivars. We expect from the apricot community some more loci to establish this system. The proposed UDP 98-021 could function as the model descriptor for apricot identification.

Precise identification of apricot should not be any longer the mystery of only few experts without any possibility of analytical control.

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Received December 18, 2003