Journal of Plant Breeding and Crop Science Vol. 4(2), pp. 25-31, 30 January, 2012
Available online at http://www.academicjournals.org/JPBCS
DOI: 10.5897/JPBCS11.090
ISSN 2006-9758 © 2012 Academic Journals

Full Length Research Paper

Cross-species amplification of 349 melon (*Cucumis melo* L.) microsatellites in gherkin (*Cucumis anguria* L.)

Yuichi Matsumoto[1]*, Nobuyoshi Watanabe[2] and Tsutomu Kuboyama[2]

[1]United Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology, Fuchu, Tokyo 183-8509, Japan.
[2]College of Agriculture, Ibaraki University, Inashiki, Ibaraki 300-0393, Japan.

Accepted 20 January, 2012

Gherkin (*Cucumis anguria* L.), also known as West Indian gherkin, burr gherkin, and maxixe, is mainly cultivated and consumed in India, Brazil, and the United States. Marker-assisted selection (MAS) is a highly desirable tool for gherkin breeding, because gherkin cultivation generally requires time, labor, and space. However, few DNA markers for gherkin have been reported. Cross-species amplification of 349 melon (*Cucumis melo* L.) microsatellite primer pairs was tested on three gherkin accessions. After polymerase chain reaction optimization, 149 (42.7%) microsatellite primer pairs successfully amplified all accessions. Of the amplified primer pairs, 41 (27.5%), 64 (43.0%), and 70 (47%) showed polymorphisms between the accessions PI 147065 and PI 320052, PI 147065 and PI 364475, and PI 320052 and PI 364475, respectively. The remaining 206 primer pairs did not amplify any of the three accessions. In the polymorphic primer pairs, the correlation coefficient between repeat number and polymorphic information content values was low; therefore, it seemed unnecessary to consider it for application of repeat numbers in gherkins. Current polymorphic microsatellite primer pairs would be useful for genetic analysis, landmarks in linkage studies, studying genome structure, MAS and evolutionary ecology of Cucurbitaceae.

Key words: West Indian gherkin, *Cucumis* spp., simple sequence repeat (SSR), polymorphism, breeding.

INTRODUCTION

Gherkin (*Cucumis anguria* L.) is also known as West Indian gherkin, burr gherkin, or maxixe and, like melon, belongs to the subgenus *Melo* (*Cucumis melo* L.) (Kirkbride, 1993). It is mainly cultivated and consumed in India, Brazil, and the United States (Mangan et al., 2008). The fruits are either boiled, fried, stewed, or used fresh in salads and are a valuable source of vitamins and minerals (Resende, 1998). Recent studies have reported the susceptibility of gherkin plants to pathogens causing diseases in melon or cucumber (*C. sativus* L.) plants, such as mosaic virus (Srinivasulu et al., 2010), streak virus (Krishnareddy et al., 2003), powdery mildew (Lebeda, 1984), and fusarium wilt (Matsumoto et al., 2011). Although new cultivars have been developed by cross breeding (Modolo and Costa, 2004), none of these cultivars have resistance against the previous mentioned pathogens. For suitable cultivation, it is necessary to breed cultivars resistant to these diseases. Molecular genetics technologies such as marker-assisted selection (MAS) could be highly desirable tools for gherkin breeding, because gherkin cultivation generally requires time, labor, and space. However, only few DNA markers are available for gherkins (Chung et al., 2006; Levi et al., 2005); these include loci for producing bitter fruit: *Bt* (Koch and Costa, 1991), loci that control fruit spaniness: *S* and *P* (Koch and Costa, 1991), and loci that controls the resistance to Cucumber green mottle mosaic virus: *Cgm* (den Nijs, 1982).

Microsatellite DNA markers are the genetic markers of choice in mammalian and many plant species because of their abundance, high degree of polymorphism, and suitability for automation (Weber and May, 1989). Micro-satellite markers have several advantages over other

*Corresponding author. E-mail: yu-matsumoto@agri.pref.ibaraki.jp. Tel: +81 299 45 8330. Fax: +81 299 45 8351.

molecular markers, and hence, are more reliable for DNA fingerprinting. They show co-dominant inheritance, have large number of alleles per locus, and are abundant in genomes. In addition, the use of microsatellites is based on polymerase chain reaction (PCR) method, which is a simple technique and requires only small amount of DNA. However, novel microsatellites often have to be isolated before they can be used for each species, which generally demands considerable time and high costs. Recently, it has been widely accepted that microsatellites isolated from the source genome can be transferred to different individuals of the same species or the same genus (Barbará et al., 2007). For example, cross-species amplification is prevalent in *Brassica* (Szewc-McFadden et al., 1996), *Actinidia* (Weising et al., 1996), and *Prunus* (Downey and Iezzoni, 2000).

In the family Cucurbitaceae, the cross-species application was mainly reported in major crops such as melon, cucumber, pumpkin (*Cucurbita maxima* Duchesne), and watermelon (*Citrullus lanatus* [Thunb.] Matsum and Nakai) (Danin-Poleg et al., 2000; Chiba et al., 2003; Fukino et al., 2007) but not in gherkin. To date, many microsatellite linkage maps have been constructed and reported in melons (Danin-Poleg et al., 2001; Joobeur et al., 2004; Ritschel et al., 2004; Gonzalo et al., 2005; Fukino et al., 2007). If melon microsatellite markers are useful and commonly mapped in gherkins, they would be also suitable as anchor markers for studies on synteny. In this study, we attempted to transfer microsatellite primers derived from melon to gherkins, and assess the amplification and polymorphism between three accessions of gherkin.

MATERIALS AND METHODS

Plant materials and microsatellite markers

Three accessions of gherkin, PI 147065, PI 320052, and PI 364475, collected from Brazil, Ethiopia, and South Africa, respectively, were used in this study. These seeds were obtained from the Germplasm Resources Laboratory (USDA, Agricultural Research Service, Beltsville, Maryland, USA). A total of 349 microsatellite primers derived from melon (Danin-Poleg et al., 2001; Chiba et al., 2003; Joobeur et al., 2004; Ritschel et al., 2004; Gonzalo et al., 2005; Fukino et al., 2007) were used for PCR amplification in gherkins (Tables 1 and 2).

Polymerase chain reaction (PCR) amplification

Total genomic DNA was extracted from leaves of each plant using DNeasy Plant Mini Kit (Qiagen Inc., Valencia, CA, USA). The extracted DNA was diluted to a final concentration of 30 to 50 ng μL^{-1} prior to PCR. Amplifications were performed in 10 µL volumes containing 30 to 50 ng of genomic DNA, 0.25 µM of each primer, and 5 µL of 2× Go Taq PCR MasterMix (Promega Co., Madison, WI, USA) using the following conditions: 94°C for 3 min followed by 35 cycles of 30 s at 94°C, 1 min at 55°C, 1 min at 72°C, and a final extension step of 5 min at 72°C. The PCR products were labeled using post-PCR labeling (Kukita and Hayashi, 2002) and separated and detected using an ABI prism 3100/xl genetic analyzer (Applied Biosystems Inc., Foster City, CA, USA) with each capillary containing 1 µL of PCR product, 0.1 µL GeneScan-500 LIZ Size Standard (Applied Biosystems), and 8.9 µL of HiDi formamide (Applied Biosystems) that was denatured at 95°C for 5 min. The sizes of the fragments were estimated using the Gene Scan Software (Applied Biosystems).

Calculation of polymorphic information content (PIC) values

The information values of microsatellites were determined using their PIC values, which were calculated using version 1.0 of the Marker Tool Kit (Fujii et al., 2008). The PIC values were also used for the calculation of the correlation coefficient between repeat number and PIC values.

RESULTS AND DISCUSSION

Of the 349 primer pairs tested, 149 (42.7%) showed positive PCR amplification in all three accessions. From those, 77 (51.7%) were polymorphic in two or three accessions (Table 1). For each polymorphic locus, the number of observed alleles per locus ranged from two to six with an average of 2.33, and their PIC values ranged from 0.35 to 0.81. The primer pair showing the largest number of alleles was CMMS4-3, showing polymorphisms in all three accessions. Of the amplified primer pairs, the number of polymorphic primer pairs between two accessions, namely, PI 147065 and PI 320052, PI 147065 and PI 364475, and PI 320052 and PI 364475 was 41 (27.5%), 64 (43.0%), and 70 (47.0%), respectively (Table 1). The remaining 206 primer pairs did not amplify in all three accessions (Table 2).

Fukino et al. (2007) reported that the correlation coefficient between repeat number and PIC values in melon and simple sequence repeat (SSR) markers with ten or more motif repeats are more efficient for detecting polymorphisms. However, in *Brassica* and melon, no correlation has been reported between the degree of polymorphism and the number of repeats (Danin-Poleg et al., 2001; Suwabe et al., 2002). In the present study, the correlation coefficient between the repeat number and PIC was low (0.11). Therefore, it was not necessary to consider the repeat number when applying this technique to gherkins.

In Cucurbitaceae, some DNA markers are transferable to other species. Danin-Poleg et al. (2000) and Fukino et al. (2007) reported the conservation of microsatellite loci between melon and cucumber. Furthermore, Chiba et al. (2003) reported the application of melon microsatellite markers to 9 species of Cucurbitaceae, cucumber, pumpkin (*Cucurbita moschata* L., *C. maxima* L., *Cucurbita pepo* L.), watermelon (*Citrullus lanatus* [Thunb.] Matsum. and Nakai), bottle gourd (*Lagenaria siceraria* [Mol.] Standl.), ash gourd (*Benincasa hispida* [Thunb.] Cogn.), bitter melon (*Momordica charantia* L.), and snake gourd (*Trichosanthes cucumeroides* [Ser.] Maxim.), many of which were applicable to bitter melon, cucumber, and pumpkin. However, no cross-species

Table 1. Microsatellite markers successful amplified sizes of PCR products and polymorphism in three accessions of gherkin.

Marker name[1]	PCR product (bp)			Number of alleles	Polymorphism[2]	PIC value
	PI 147065	PI 320052	PI 364475			
CMACC146	124/124	124/124	126/126	2	b,c	0.35
CMAGN52	108/116	108/116	106/118	4	b,c	0.67
CMAGN68	161/161	163/163	163/163	2	a,b	0.35
CMAGN73	124/124	124/124	122/122	2	b,c	0.35
CMAT35	111/111	111/111	111/111	1		0
CMATN22	155/155	155/155	155/155	1		0
CMATN90	126/126	126/126	126/126	1		0
CMBR1	127/127	127/127	115/115	2	b,c	0.35
CMBR3	176/176	180/180	180/180	2	a,b	0.35
CMBR8	102/102	102/102	102/102	1		0
CMBR13	188/188	188/188	188/188	1		0
CMBR14	111/115	111/115	113/117	4	b,c	0.67
CMBR15	160/160	160/160	183/183	2	b,c	0.35
CMBR21	174/179	174/179	174/179	2		0.38
CMBR23	138/138	138/138	126/126	2	b,c	0.35
CMBR26	100/100	100/100	100/100	1		0
CMBR31	171/171	304/304	327/327	3	a,b,c	0.59
CMBR34	147/147	149/149	147/147	2	a,c	0.35
CMBR39	133/133	133/133	133/133	1		0
CMBR41	125/125	125/125	125/125	1		0
CMBR42	95/95	95/95	95/95	1		0
CMBR44	124/124	124/124	122/122	2	b,c	0.35
CMBR49	132/132	130/130	132/132	2	a,c	0.35
CMBR54	102/102	102/102	104/104	2	b,c	0.35
CMBR56	134/134	134/134	124/124	2	b,c	0.35
CMBR61	132/132	132/132	130/130	2	b,c	0.35
CMBR64	124/124	124/124	124/124	1		0
CMBR69	124/124	110/110	114/114	3	a,b,c	0.59
CMBR70	132/132	132/132	132/132	1		0
CMBR71	95/95	95/95	85/85	2	b,c	0.35
CMBR83	107/107	107/107	107/107	1		0
CMBR89	131/131	131/131	129/129	2	b,c	0.35
CMBR91	118/118	118/118	118/118	1		0
CMBR100	114/114	114/114	104/104	2	b,c	0.35
CMBR109	116/116	116/116	116/116	1		0
CMBR111	106/106	106/106	106/106	1		0
CMBR116	222/222	216/216	212/212	3	a,b,c	0.59
CMBR124	166/166	166/166	166/166	1		0
CMBR134	236/236	236/236	206/206	2	b,c	0.35
CMBR135	124/124	140/140	140/140	2	a,b	0.35
CMBR153	168/168	168/168	168/168	1		0
CMCCA145	131/131	137/137	137/137	2	a,b	0.35
CMCT160a	89/89	89/89	89/89	1		0
CMCT44	87/87	87/87	85/85	2	b,c	0.35
CMCTN2	164/164	164/164	164/164	1		0
CMCTN7	110/110	124/124	104/104	3	a,b,c	0.59
CMCTN86	167/167	174/174	174/174	2	a,b	0.35
CMCTT144	181/181	181/181	184/184	2	b,c	0.35
CMGA104	112/112	114/114	110/110	3	a,b,c	0.59
CMGA165	117/117	113/113	115/115	3	a,b,c	0.59
CMGA172	124/124	122/122	124/124	2	a,c	0.35
CMGAN3	203/203	197/197	199/199	3	a,b,c	0.59

Table 1. Cont.

CMGAN12	148/148	148/148	146/146	2	b,c	0.35
CMGAN21	133/133	133/133	133/133	1		0
CMGAN25	169/169	169/169	169/169	1		0
CMGT108	170/170	170/170	170/170	1		0
CMMS3-2	427/427	427/427	427/427	1		0
CMMS4-3	158/164	161/167	156/162	6	a,b,c	0.81
CMMS33-1	372/372	374/374	379/379	3	a,b,c	0.59
CMMS33-2	282/282	282/282	282/282	1		0
CMMS34-6	138/138	138/138	138/138	1		0
CMMS34-8	181/181	101/101	151/151	3	a,b,c	0.59
CMN01_01	180/180	180/180	180/180	1		0
CMN01_02	235/235	235/235	233/233	2	b,c	0.35
CMN01_35b	123/123	123/123	123/123	1		0
CMN01_54	208/208	208/208	208/208	1		0
CMN01_55	187/187	187/187	187/187	1		0
CMN01_74	188/188	188/188	188/188	1		0
CMN01_88	112/112	112/112	118/118	2	b,c	0.35
CMN04_03	182/182	182/182	184/184	2	b,c	0.35
CMN04_09	269/269	269/269	269/269	1		0
CMN04_16	157/157	157/157	157/157	1		0
CMN04_21	190/190	190/190	188/188	2	b,c	0.35
CMN04_27	304/304	319/319	307/307	3	a,b,c	0.59
CMN04_37b	203/203	211/211	203/203	2	a,c	0.35
CMN04_67	114/114	114/114	110/110	2	b,c	0.35
CMN04_89	215/215	215/215	215/215	1		0
CMN05_08	237/237	237/237	245/245	2	b,c	0.35
CMN05_13	235/235	235/235	235/235	1		0
CMN05_17	250/250	250/250	250/250	1		0
CMN05_60	170/170	170/170	170/170	1		0
CMN05_69	146/146	144/144	148/148	3	a,b,c	0.59
CMN05_73	155/155	153/153	155/155	2	a,c	0.35
CMN05_75	180/180	180/180	180/180	1		0
CMN05_77	235/235	235/235	233/233	2	b,c	0.35
CMN05_79	200/200	200/200	200/200	1		0
CMN05_87	168/168	168/168	168/168	1		0
CMN05_89	239/239	239/239	239/239	1		0
CMN06_19	132/132	132/132	130/130	2	b,c	0.35
CMN06_41A	124/124	124/124	124/124	1		0
CMN06_49	181/181	181/181	181/181	1		0
CMN06_60B	125/125	125/125	113/113	2	b,c	0.35
CMN07_19	102/102	102/102	102/102	1		0
CMN07_32	250/250	250/250	254/254	2	b,c	0.35
CMN07_95	206/206	206/206	206/206	1		0
CMN09_22	102/102	102/102	102/102	1		0
CMN21_25	211/211	211/211	213/213	2	b,c	0.35
CMN21_29	252/252	252/252	252/252	1		0
CMN21_33	233/233	233/233	240/240	2	b,c	0.35
CMN21_42	223/223	217/217	212/212	3	a,b,c	0.59
CMN21_55	166/166	166/166	166/166	1		0
CMN21_85	206/206	206/206	206/206	1		0
CMN21_87	219/219	219/219	219/219	1		0
CMN21_88	265/265	265/265	255/255	2	b,c	0.35

Table 1. Cont.

CMN22_09	177/177	177/177	177/177	1		0
CMN22_11	115/115	115/115	103/103	2	b,c	0.35
CMN22_85	207/207	207/207	213/213	2	b,c	0.35
CMN23_01	281/281	281/281	281/281	1		0
CMN23_06	271/271	271/271	271/271	1		0
CMN23_25	168/168	168/168	161/161	2	b,c	0.35
CMN23_42	125/125	125/125	127/127	2	b,c	0.35
CMN23_48	173/173	167/167	173/173	2	a,c	0.35
CMN53_05	227/227	227/227	227/227	1		0
CMN53_10	165/165	165/165	165/165	1		0
CMN53_28	113/113	113/113	113/113	1		0
CMN53_44	105/105	107/107	107/107	2	a,b	0.35
CMN53_46	248/248	243/243	248/248	2	a,c	0.35
CMN53_68A	261/261	261/261	261/261	1		0
CMN53_72A	107/107	111/111	107/107	2	a,c	0.35
CMN61_13	156/156	160/160	156/156	2	a,c	0.35
CMN61_14	172/172	172/172	172/172	1		0
CMN61_88	125/125	125/125	125/125	1		0
CMN62_03	164/164	164/164	164/164	1		0
CMN62_21	357/357	357/357	357/357	1		0
CMN62_40	180/180	180/180	180/180	1		0
CMN62_95	97/97	97/97	97/97	1		0
CSTA50	165/165	167/167	165/165	2	a,c	0.35
CMTAA166	173/173	166/166	173/173	2	a,c	0.35
CMTAAN100	181/181	174/174	181/181	2	a,c	0.35
CMTC13	182/182	182/182	182/182	1		0
CMTC158	176/176	176/176	176/176	1		0
CMTC168	183/183	183/183	183/183	1		0
CMTC51	261/261	258/258	261/261	2	a,c	0.35
CMTCC813	136/136	136/136	136/136	1		0
CMTCN1	122/122	122/122	150/150	2	b,c	0.35
CMTCN30	192/192	192/192	192/192	1		0
CMTCN56	106/106	106/106	114/114	2	b,c	0.35
CMTCN67	135/135	139/139	135/135	2	a,c	0.35
CSLHCPA	218/218	220/220	212/212	3	a,b,c	0.59
CSTCC813	130/130	135/135	135/135	2	a,b	0.35
SSR184	297/297	291/291	293/293	3	a,b,c	0.59
SSR303	355/355	348/348	353/353	3	a,b,c	0.59
TJ3	165/165	167/167	159/159	3	a,b,c	0.59
TJ10	118/118	136/136	138/138	3	a,b,c	0.59
TJ27	174/174	176/176	176/176	2	a,b	0.35
TJ29	126/126	126/126	126/126	1		0
TJ30	162/162	162/162	162/162	1		0
TJ31	190/190	194/194	192/192	3	a,b,c	0.59
TJ33	181/181	181/181	181/181	1		0

[1]References of primer sequences; 'CMMS': Chiba et al. (2003); 'SSR': Joobeur et al. (2004); 'CMBR': Ritschel et al. (2004); 'CMAGN', 'CMATN', 'CMCTN', 'CMGAN', 'CMTCN', and 'TJ' : Gonzalo et al. (2005); 'CMN': Fukino et al. (2007); the others: Danin-Poleg et al. (2001). [2]'a', 'b', and 'c' indicates polymorphism between PI 147065 and PI 320052, PI 147065 and PI 364475, and PI 320052 and PI 364475, respectively.

application has been reported, and only few DNA markers have been found in gherkin.

In this study, 149 microsatellite primer pairs were successfully amplified, and 77 primer pairs showed

Table 2. Name of unsuccessful amplified microsatellite markers in three accessions of gherkin.

Marker name[1]						
CMAGN32	CMBR136	CMBR82	CMMS22-2	CMN06_66	CMN22_15	CMN61_90
CMAGN33	CMBR137	CMBR84	CMMS24-3	CMN06_84	CMN22_16	CMN62_05
CMAGN61	CMBR140	CMBR88	CMMS30-3	CMN07_05	CMN22_17	CMN62_08
CMAGN68	CMBR148	CMBR9	CMMS33-2	CMN07_46	CMN22_22	CMN62_41
CMAGN75	CMBR149	CMBR90	CMMS34-8	CMN07_54	CMN22_23	CMN62_74
CMAGN79	CMBR150	CMBR92	CMMS35-1	CMN07_57	CMN22_27	CMN62_89
CMAT141	CMBR16	CMBR93	CMMS35-3	CMN07_70	CMN22_44	CMTA134a
CMATN22	CMBR17	CMBR94	CMMS35-4	CMN08_03B	CMN22_45	CMTA134b
CMBR6	CMBR18	CMBR95	CMMS36-2	CMN08_04	CMN22_54	CMTA170a
CMBR10	CMBR19	CMBR97	CMN01_03	CMN08_22	CMN22_93	CMTA170b
CMBR101	CMBR30	CMCT160a+b	CMN01_07	CMN08_40	CMN23_15	CMTC163
CMBR104	CMBR33	CMCT58	CMN01_15	CMN08_77	CMN23_43	CMTC47
CMBR105	CMBR35	CMCTN38	CMN01_34	CMN08_79	CMN23_64	CMTCN14
CMBR107	CMBR40	CMCTN4	CMN01_38	CMN08_90	CMN23_79	CMTCN18
CMBR110	CMBR43	CMCTN5	CMN01_48	CMN21_03	CMN53_19	CMTCN35
CMBR112	CMBR45	CMCTN53	CMN01_83	CMN21_04	CMN53_36	CMTCN50
CMBR113	CMBR47	CMCTN65	CMN01_86a	CMN21_06	CMN53_40	CMTCN6
CMBR114	CMBR48	CMGA104	CMN04_01	CMN21_09	CMN53_43	CMTCN8
CMBR115	CMBR50	CMGAN24	CMN04_03	CMN21_16	CMN54_48	CMTCN9
CMBR117	CMBR51	CMGAN80	CMN04_10	CMN21_17	CMN61_15	CSCCT571
CMBR119	CMBR53	CMMS1-3	CMN04_19	CMN21_34	CMN61_27	CSCTTT15b
CMBR121	CMBR60	CMMS1-7	CMN04_35	CMN21_37	CMN61_35	SSR411
CMBR123	CMBR63	CMMS2-3	CMN04_40	CMN21_41	CMN61_40A	TJ26
CMBR125	CMBR66	CMMS3-1	CMN04_66	CMN21_59	CMN61_44	TJ30
CMBR126	CMBR67	CMMS4	CMN04_79	CMN21_62	CMN61_61	
CMBR127	CMBR68	CMMS4-1	CMN05_82	CMN21_67	CMN61_63	
CMBR129	CMBR75	CMMS11-3	CMN06_08	CMN21_74	CMN61_64	
CMBR130	CMBR77	CMMS12-3	CMN06_25	CMN21_77	CMN61_65	
CMBR131	CMBR79	CMMS12-4	CMN06_57	CMN21_80	CMN61_70B	
CMBR132	CMBR81	CMMS15-4	CMN06_62	CMN21_82	CMN61_81	

[1]References of primer sequences; 'CMMS': Chiba et al. (2003); 'SSR': Joobeur et al. (2004); 'CMBR': Ritschel et al. (2004); 'CMAGN', 'CMATN', 'CMCTN', 'CMGAN', 'CMTCN' and 'TJ' : Gonzalo et al. (2005); 'CMN': Fukino et al. (2007); the others: Danin-Poleg et al. (2001).

polymorphisms in gherkin. Specifically, polymorphisms were observed among PI 320052 and PI 364475 (Table 1). In our previous study, PI 320052 was resistance and PI 364475 was susceptible to *Fusarium oxysporum* f. sp. *melonis* race 1,2y (Matsumoto et al., 2011). Thus, these polymorphic microsatellite primer pairs could be useful for the genetic analysis of resistance. Furthermore, they could also be used as landmarks in linkage studies, for investigating genome structure, and in evolutionary ecology of Cucurbitaceae.

REFERENCES

Barbará T, Palma-Silva C, Paggi GM, Bered F, Fay MF, Lexer C (2007). Cross-species transfer of nuclear microsatellite markers: potential and limitations. Mol. Ecol., 16: 3759–3767.

Chiba N, Suwabe K, Nunome T, Hirai M (2003). Development of microsatellite markers in melon (*Cucumis melo* L.) and their application to major cucurbit crops. Breed. Sci., 53:21–27.

Chung SM, Staub JE, Chen JF (2006). Molecular phylogeny of *Cucumis* species as revealed by consensus chloroplast SSR marker length and sequence variation. Genome, 49: 219–229.

Danin-Poleg Y, Reis N, Baudracco-Arnas S, Pitrat M, Staub JE, Oliver M, Arus P, deViente CM, Katzir N (2000). Simple sequence repeats in *Cucumis* mapping and map merging. Genome, 43: 963–974.

Danin-Poleg Y, Reis N, Tzuri G, Katzir N (2001). Development and characterization of microsatellite markers in *Cucumis*. Theor. Appl. Genet., 102: 61–72.

den Nijs APM (1982). Inheritance of resistance to *cucumber green mottle virus* (CGMV) in *Cucumis anguria* L.. Cucurbit Genet. Coop. Rpt., 5: 56–57.

Downey SL, Iezzoni AF (2000). Polymorphic DNA markers in black cherry (*Prunus serotina*) are identified using sequences from sweet cherry, peach, and sour cherry. J. Amer. Soc. Hort. Sci., 125: 76–80.

Fujii H, Yamashita H, Shimada T, Endo T, Shimizu T, Yamamoto T (2008). Marker Tool Kit: an analysis program for data sets consist of DNA marker types obtained from various varieties. DNA Polymorphism, 16: 103–107.

Fukino N, Sakata Y, Kunihisa M, Matsumoto S (2007). Characterisation of novel simple sequence repeat (SSR) markers for melon (*Cucumis melo* L.) and their use for genotype identification. J. Hort. Sci. Biotech., 82: 330–334.

Gonzalo MJ, Oliver M, Garcia-Mas J, Monfort A, Dolcet-Sanjuan R, Katzir N, Arus P, Monforte AJ (2005). Simple-sequence repeat markers used in merging linkage maps of melon (*Cucumis melo* L.). Theor. Appl. Genet., 110: 802–811.

Joobeur T, King JJ, Nolin SJ, Thomas CE, Dean RA (2004). The Fusarium wilt resistance locus *Fom-2* of melon contains a single resistance gene with complex features. Plant J., 39: 283–297.

Kirkbride Jr JH (1993). Biosystematic monograph of the genus *Cucumis* (Cucurbitaceae). Parkway Publishers Boone North Carolina.

Koch PS, Costa CP (1991). Inheritance of plant and fruit characters in gherkin. Hort. Bras., 9: 73–77.

Krishnareddy M, Devaraj, Raman L, Jalali S, Samuel DK (2003). Outbreak of *Tobacco streak virus* Causing Necrosis of Cucumber (*Cucumis sativus*) and Gherkin (*Cucumis anguria*) in India. Plant Dis., 87: 1264.

Kukita Y, Hayashi K (2002). Multicolor post-PCR labeling of DNA fragments with fluorescent ddNTPs. Biotechniques, 33:502–506.

Lebeda A (1984). Screening of wild *Cucumis* species for resistance to cucumber powdery mildew (*Erysiphe cichoracearum* and *Sphaerotheca fuliginea*). Sci. Hort., 24: 241–249.

Levi A, Thomas CE, Simmons AM, Thies JA (2005). Analysis based on RAPD and ISSR markers reveals closer similarities among *Citrullus* and *Cucumis* species than with *Praecitrullus fistulosus* (Stocks) Pangalo. Genet. Res. Crop. Evol., 52: 465–472.

Mangan F, Mendonça R, Moreira M, Nunes S, Finger F, Barros Z, Galvão H, Almeida G, Silva RA, Anderson M (2008). Production and marketing of vegetables for the ethnic markets in the United States. Hort. Bras., 26: 6–14.

Matsumoto Y, Ogawara T, Miyagi M, Watanabe N, Kuboyama T (2011). Response of wild *Cucumis* species to inoculation with *Fusarium oxysporum* f. sp. *melonis* race 1,2y. J. Japan. Soc. Hort. Sci., 80: 414–419.

Modolo VA, Costa CP (2004). Gherkin elite line selection. Crop Breed. Appl. Biotech., 4: 63–67.

Resende GM (1998). Influence of planting dates on indian gherkin cultivar's yield. Hort. Bras., 16: 167–171.

Ritschel PS, Lins TC, Tristan L, Buso GSC, Buso JA, Ferreira ME (2004). Development of microsatellite markers from an enriched genomic library for genetic analysis of melon (*Cucumis melo* L.) BMC Plant Biol., 4: 9.

Srinivasulu M, Sarovar B, Johnson AA, Gopal DS (2010). Association of a potyvirus with mosaic disease of gherkin (*Cucumis anguria* L.) in India. Indian J. Microb., 50: 221–224.

Suwabe K, Iketani H, Nunome T, Kage T, Hirai M (2002). Isolation and characterization of microsatellites in *Brassica rapa* L. Theor. Appl. Genet., 104: 1092–1098.

Szewc-McFadden AK, Kresovich S, Bliek SM, Mitchell SE, McFerson JR (1996). Identification of polymorphic, conserved simple sequence repeats (SSRs) in cultivated *Brassica* species. Theor. Appl. Genet., 93: 534–538.

Weber JK, May PE (1989). Abundant class of human DNA polymorphisms which can be typed using the polymerase chain reaction. Amer. J. Hum. Genet., 44: 388–397.

Weising K, Fung RWM, Keeling DJ, Atkinson RG, Gardner RC (1996). Characterization of microsatellites from *Actinidia chinensis*. Mol. Breed., 2: 117–131.