

Cucumber Germplasm: Isozyme Genetic Stocks W6743, W6744, W6745

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A series of cucumber (*Cucumis sativus* L. var. *sativus*) populations (W6743, W6744, W6745) containing alternate alleles (allozymes) for 20 enzyme coding loci were released in Sept. 1995 by the U.S. Dept. of Agriculture (USDA), Agricultural Research Service. Lines within each population have been created through backcrossing and self-pollination to incorporate allozymes into three genetic backgrounds: European glasshouse, U.S. processing, and U.S. market types. Lines within each population are heterogeneous at specific isozyme or morphological loci and homozygous at others. These genetic stocks could be used for genetic marker research (e.g., linkage assessment, genetic drift detection) or in breeding programs (the incorporation of unique allelic constructs into elite lines) as a tool for varietal purity assessment and plant variety protection.

Origin

Allelic variation was initially observed in a survey of elite publicly released processing cucumber lines and plant introductions present in the U.S. cucumber collection (USDA Regional Plant Introduction Station, Ames, Iowa) in adenylate kinase (AK), fructose diphosphatase (FDP), glucosephosphate isomerase (GPI), glutathione reductase (GR), glycerate dehydrogenase (G2DH), isocitrate dehydrogenase (IDH), malate dehydrogenase (MDH), manosephosphate isomerase (MPI), peptidase with glycyl-leucine (PEP-GL), peptidase with leucyl-alanine (PEP-LA), peptidase with phenylalanyl-proline (PEP-PAP), peroxidase (PER), phosphoglucomutase (PGM), 6-phosphogluconate dehydrogenase (PGD), and shikimate dehydrogenase (SKDH)

(Knerr et al., 1989, 1994). Some allozymes of enzymes (e.g., G2DH, IDH, MPI, PGD, PEP-LA, SKDH) were not present in elite lines and were recovered from exotic germplasm [e.g., *C. sativus* var. *hardwickii* (R) Alef.; PI 183967 and PI 215589; Table 1]. The inheritance of allozymes for these enzymes conforms to Mendelian expectations, and the linkage relationships among these allozymes and between allozymes and some economically important morphological loci have been characterized (Table 2; Knerr and Staub, 1992; Meglic, 1994).

Crosses were made among elite lines, and between elite lines and exotic germplasm to incorporate rare allozymes into adapted germplasm. Lines (>F₄) were developed and used to determine the inheritance of the isozyme banding patterns resolvable in 15 enzyme systems using horizontal starch gel electrophoresis. These lines (5 to 10) were crossed to a European line (F₃; European glasshouse type) derived from the intermating of three proprietary glasshouse lines from Numhems Zaden BV, De Ruiter Zonen BV, and Nickerson Zwaan, BV, Poinsette 76 (U.S. market type), and GY14 (U.S. processing type). These three lines were used as recurrent parents during backcrossing in which cross progeny heterozygous for isozyme loci were identified and used as parents. After four backcrosses, lines were selfed twice and selected for alternate allozymes at each of 20 loci (*Ak-2*, *Ak-3*, *Fdp-1*, *Fdp-2*, *Gpi-1*, *Gr-1*, *G2dh*, *Idh*, *Mdh-1*, *Mdh-2*, *Mdh-3*, *Mpi-1*, *Mpi-2*, *Pep-gl*, *Pep-la*, *Pep-pap*, *Per*, *Pgm*, *Pgd-1*, and *Skdh*) and uniformity in the three genetic backgrounds. This resulted in the production of six European glasshouse (W6743), 11 U.S. processing (W6744), and eight U.S. market-type (W6745) lines that were homozygous for alternate alleles [e.g., *Ak-2* (11) and (22)] at specific loci (Table 3).

Description

Although these BC4S2 lines are distinct and can be placed into broad classifications according to potential horticultural utility, they are not phenotypically uniform within a specific type classification (Table 3). Lines within a specific type vary in skin texture (smooth or warty) and mature fruit color (green to orange) and length : diameter ratio (L : D), depending

on genetic background. Lines derived using European germplasm as recurrent parents tend to be smooth-skinned, relatively long, and fine-spined. Lines derived from backcrossing to U.S. processing and market lines vary in spine color (black or white) and some segregate for skin texture attributes (i.e., warts and spine thickness) and exhibit a range in L : D (2.0 to 4.8). This lack of uniformity could be due to pleiotrophic effects or linkages between allozymes and morphological traits (Meglic, 1994).

Availability

Limited seed of these genetic stocks are available upon written request to J.E.S.

Table 1. Sources of the less common allozymes in 15 cucumber enzymes.^z

Locus ^y	PI	Source
<i>Ak-2</i> (2)	279469	Japan
	279463	Japan
<i>Ak-3</i> (2)	169334	Turkey
	255937	Netherlands
<i>Fdp-1</i> (2)	169383	Turkey
	192940	People's Republic of China
<i>Fdp-2</i> (1)	137851	Iran
	164952	Turkey
<i>Gpi-1</i> (1)	200815	Burma
	422192	Hungary
<i>Gr-1</i> (1)	109275	Turkey
<i>G2dh</i> (1)	285606	Poland
<i>Idh</i> (1)	215589	India
	183967	India
<i>Mdh-1</i> (2)	171613	Turkey
	209064	United States
<i>Mdh-2</i> (1)	174164	Turkey
	357835	Yugoslavia
	419214	Hong Kong
	255236	Netherlands
<i>Mdh-3</i> (2)	267942	Japan
	432854	People's Republic of China
<i>Mpi-1</i> (2) ^x	176954	Turkey
	249562	Thailand
<i>Pep-gl</i> (1)	113334	People's Republic of China
<i>Pep-gl</i> (2)	212896	India
	137851	Iran
<i>Pep-la</i> (2)	212896	India
	169380	Turkey
<i>Pep-pap</i> (1)	354952	Denmark
	163213	India
<i>Per</i> (2)	188749	Egypt
	215589	India
<i>Pgm</i> (2)	171613	Turkey
	177364	Iraq
<i>Pgd-1</i> (1)	169380	Turkey
	222782	Turkey
<i>Pgd-1</i> (2)	188749	Egypt
	289698	Australia
<i>Skdh</i> (1) ^x	302443	Taiwan
	390952	Russia

^zSources are only given for the less common allele of a locus used based on previous studies by Knerr et al. (1989) and Knerr and Staub (1992). There is also a common allele in addition to each of those listed above.

^yEnzyme loci designation, where multiple loci of an enzyme exist, is distinguished by hyphenated numerals and alleles are enclosed in parentheses.

^zHeterogeneous population containing alternate homozygous and heterozygous genotypes.

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Table 3. Allozyme and morphological variation in genetic stocks of cucumber.

Identity	Allelic constitution of enzyme coding loci ²											
	Ak-2	Ak-3	Fdp-1	Fdp-2	Gpi-1	Gr-1	G2dh	Idh	Mdh-1	Mdh-2	Mdh-3	Mpi-1
<i>European greenhouse type</i>												
6743A	12	22	22	22	22	11	22	12	22	22	11	12
6743B	12	22	22	22	22	11	22	12	12	22	11	12
6743D	12	12	12	11	22	11	22	22	11	22	11	12
6743E	22	22	22	22	22	22	11	22	11	22	11	22
6743I	22	22	22	22	22	22	22	22	11	22	11	11
6743J	22	22	22	22	22	11	22	22	11	11	11	22
<i>U.S. processing type</i>												
6744C	12	12	22	11	22	11	22	12	11	22	11	22
6744F	22	12	12	11	22	11	22	22	22	22	11	22
6744G	22	12	11	22	11	11	22	22	12	22	12	22
6744H	22	12	12	11	22	11	22	22	12	22	22	22
6744I	11	22	22	22	12	11	22	22	11	22	22	22
6744K	11	22	22	11	11	11	22	22	11	22	12	22
6744L	11	22	22	11	11	11	22	22	11	22	22	22
6744M	11	22	22	11	22	11	22	22	11	11	11	22
6744P	12	11	11	11	22	11	22	22	11	22	11	11
6744S	12	12	12	11	22	11	22	22	11	22	11	12
6744T	11	12	12	11	22	11	22	22	11	22	11	12
<i>U.S. market type</i>												
6745A	22	22	11	22	22	11	12	22	12	22	12	11
6745D	22	22	12	22	22	12	22	22	11	22	11	11
6745E	12	22	12	22	22	11	22	22	11	11	22	12
6745F	11	22	11	22	22	11	22	22	11	22	12	11
6745G	11	22	11	22	22	11	22	22	11	22	22	11
6745H	12	22	12	22	22	11	22	22	11	12	12	12
6745J	12	12	22	11	22	11	22	12	11	22	22	22
6745K	11	12	11	11	22	11	22	11	11	22	12	11

²Allozymes that occur in highest frequency are given the mobility designation 100. All other alleles produce protein products with relative mobilities to allozyme 100 (mm) as follows: Ak-2(1)-98, Ak-3(1)-98, Fdp-1(1)-96, Gpi-1(1)-98, Gr-1(1)-97, G2dh(1)-94, Idh(1)-94, Mdh-1(2)-101.5, Mdh-2(1)-98, Mdh-4(2)-102, Mpi-1(1)-96, Mp-2(2)-103, Pep-gl(1)-98, Pep-la(1)-98, Pep-pap(1)-95, Per(2)-105, Pgm(2)-102.5, Pgd-1(1)-98, Skdh(1)-98.

³Skin texture: Sm = smooth, W = warty, Seg = segregating; skin color: G = green, Y = yellow, O = orange; spine color: W = white, B = black, Seg = segregating.

⁴L : D = length : diameter ratio.

Table 2. Enzymes assayed using specific buffer systems that provided adequate resolution of isozyme loci observed in cucumber.

Enzyme	Abbreviation	E.C. designation ²	Buffer ³ system	No. loci ⁴
Adenylate kinase	AK	2.7.4.3	S-4	2
Fructose diphosphatase	FDP	3.1.3.11	A	2
Glucosephosphate isomerase	GPI	5.3.1.9	R	1
Glutathione reductase	GR	1.6.4.2	S-4	1
Glycerate dehydrogenase	G2DH	1.1.1.29	R	1
Isocitrate dehydrogenase	IDH	1.1.1.42	S-4	1
Malate dehydrogenase	MDH	1.1.1.37	S-4	3
Manosephosphate isomerase	MPI	5.3.1.8	S-4	2
Peptidase with glycyl-leucine	PEP-GL	3.4.13.11	A	2
Peptidase with leucyl-alanine	PEP-LA	3.4.13.11	M	1
Peptidase with phenylalanyl-proline	PEP-PAP	3.4.13.11	S-4	1
Peroxidase	PER	1.11.1.7	A	1
Phosphoglucomutase	PGM	5.4.2.2	R	1
6-phosphogluconate dehydrogenase	PGD	1.1.1.43	S-4	2
Shikimate dehydrogenase	SKDH	1.1.1.25	S-4	1

²Enzyme commission number.

³Buffers of Clayton and Tretiak (1972), Ridgway et al. (1970), and Selander et al. (1971), Markert and Faulhaber (1965) designated as C, R, and S or M, respectively.

⁴Loci designated by previous examination (Knerr and Staub, 1992) or during this survey using standard criteria and nomenclature (Richmond, 1972).

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Allelic constitution of enzyme coding loci ^z								Fruit characteristics ^y			
<i>Mpi-2</i>	<i>P-gl</i>	<i>P-la</i>	<i>P-pap</i>	<i>Per</i>	<i>Pgm</i>	<i>Pgd-1</i>	<i>Skdh</i>	Skin texture	Skin color	Spine color	L : D ratio ^x
<i>European greenhouse type</i>											
11	22	22	22	11	12	22	22	Seg	G-Y to Y-G	W	3.8:6.0
11	12	22	22	11	12	22	22	Seg	G-Y to Y-G	W	3.8:6.0
12	11	12	22	11	11	12	22	Sm	G-Y to Y	W	4.0:5.5
11	22	22	22	11	11	22	22	Sm	G-Y to Y	W	3.8:5.6
11	12	22	22	11	11	22	11	Sm	G to Y	W	5.8:6.0
11	11	22	22	11	22	22	22	Seg	Y	W	3.5:3.8
<i>U.S. processing type</i>											
22	12	22	22	22	12	22	22	W	G to O	W	2.8:3.0
22	22	22	22	11	11	22	22	W	G-Y to Y	W	3.2:4.0
22	22	12	22	11	11	22	12	W	Y to Y-G	W	3.0:4.5
22	22	22	22	11	11	22	11	W	Y to Y-G	W	2.8:3.5
22	12	22	11	11	11	22	22	W	Y to Y-G	W	2.5:3.3
22	22	22	11	11	11	22	22	Seg	Y	W	2.4:2.8
22	11	22	11	11	11	22	22	Seg	Y-G to Y	W	2.3:2.6
11	11	22	11	11	11	22	11	Seg	G-Y to Y	W	2.2:3.2
22	11	22	11	11	11	11	22	W	Y-G to Y	W	2.7:3.5
11	11	22	11	11	11	12	22	Seg	O	B	2.6:3.8
11	11	22	11	11	11	12	22	Seg	O to YG	B	2.0:3.5
<i>U.S. market type</i>											
12	11	22	22	11	12	22	22	Seg	O-Y to Y	Seg	3.5:4.3
11	12	22	22	11	11	22	12	Seg	O-Y to Y	Seg	3.8:4.3
11	11	22	22	11	12	12	22	Seg	G-Y to Y	W	3.3:3.8
11	11	22	22	11	12	11	22	Seg	G to Y	W	3.0:3.8
11	11	22	22	11	11	11	22	Seg	Y-G to Y	W	3.8:4.5
11	11	22	22	11	12	12	22	W	Y-G to Y	W	3.8:4.8
11	22	22	22	22	12	22	12	Seg	Y	B	3.0:3.8
22	11	22	22	11	22	22	11	Seg	O to Y	B	3.0:4.3