Revised List of Miscellaneous Stocks

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This list of approx. 1,560 miscellaneous genetic stocks is a revision of the previous one issued in TGC 53 (2003). Extinct, obsolete, or faulty accessions have been dropped. New accessions that have been added to the list include a group of 'provisional mutants' originating from various sources. These are mostly morphological traits detected in M2's and later generations from mutagenesis populations. Most are probably monogenic characters, with a few containing multiple mutant loci per line. Also, several new and useful linkage tester stocks, each containing two or more morphological markers on a single chromosome, have been acquired. The new tester stocks represent chromosomes 1, 7, 10 and 11.

We attempt to maintain all listed accessions in adequate seed supply for distribution. However, some stocks, such as certain multiple marker combinations, aneuploids, or prebreds, are weak and require special cultural care; consequently, seed supplies may at times be too low to permit distribution.

Names and phenotypic classes of individual mutations are given in the last Monogenic Stock List (TGC 55); other pertinent data are presented in previous TGC Reports, as cited below. More detailed information on these stocks are available at our website (http://tgrc.ucdavis.edu), including genotype, phenotype, origin, and recommendations for growth and reproduction.

see also:
Wild Species Stocks (1,131 accessions total) are listed in TGC 54 (2004)
Monogenic Stocks (994 accessions total) are listed in TGC 55 (2005)

Types of Stocks on this List

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1. CULTIVARS AND LANDRACES

1.1. Modern and Vintage Cultivars (198)

We maintain the following set of cultivars, inbreds, and breeding lines for various purposes, mainly as isogenic (or nearly isogenic) stocks for specific mutants, standards for genetic comparison, sources of disease resistances, or other purposes. Marglobe is considered the standard for tomato gene (mutant) nomenclature. Most lines have been maintained by selfing for many generations.

Accession	Cultivar
LA0818	A-1
LA0516	Ace
LA2838A	Ailsa Craig
LA2529	Alcobaca
LA2463	Allround
LA1995	Angela
LA3244	Antimold-B
LA3527	Apex 1000
LA0657	Beaverlodge
LA2973	Big Rainbow
LA2972	Big Yellow Red Ctr.
LA4347	B-L-35
LA1499	Break O'Day
LA0198	Cal 255
LA2414	Cal Ace
LA1439	Calmart
LA3316	Campbell 24
LA3317	Campbell 28
LA3228	Canary Export
LA2374	Caro Red
LA2400	Castlemart
LA3121	Chico Grande
LA4285	CLN2264F
LA4286	CLN2264G
LA3213	Columbian
LA0533	Condine Red
LA0817	CP-2
LA3247	Craigella
LA1162	Cuba Plum
LA1219	Dwarf San Marzano
LA0313	Dwarf Stone
LA3245	E.S.1
LA4024	E-6203
LA3238	Earliana
LA2006	Earlinorth
LA0266	Earlipak
LA3010	Earlipak
LA0517	Early Santa Clara
LA2711	Edkawi
LA3800	Fargo Self-pruning
LA3024	Fireball
LA3840	FLA 7060
LA3242	Flora-Dade
LA4026	Florida 7481
LA4025	Florida 7547

Accession	Cultivar
LA3030	Gardener
LA2969	Georgia Streak
LA2802	Globonnie
LA4011	GT
LA3231	Gulf State Market
LA0314	Hardin Miniature
LA3202	Hawaii 7997
LA3856	Hawaii 7998
LA4345	Heinz 1706-BG
LA0806	High Crimson
LA3237	Homestead 24
LA3320	Hotset
LA3144	Hunt 100
LA2805	Indehiscent Currant
LA3201	IRB 301
LA1089	John Baer
LA1131	Kallio's Alaskan Dwarf
LA0025	King Humbert #1
LA3240	Kokomo
LA3526	L04012
LA0505	Laketa
LA3203	Large Plum
LA3118	Laurica
LA0791	Long John
LA0534	Lukullus
LA3475	M-82
LA3120	Malintka 101
LA3007	Manapal
LA2451	Manapal
LA0502	Marglobe
LA1504	Marmande
LA0278	Marzano Grande
LA3151	Mecline
LA0011	Michigan State Forcing
LA3911	Micro-Tom
LA2825	Mobaci
LA2824	Moboglan
LA3152	Moboline
LA2821	Mobox
LA2830	Mocimor
LA3471	Mogeor
LA2828	Momor
LA2829	Momor Verte
LA2818	Monalbo
LA2706	Moneymaker

Accession	Cultivar
LA2819	Monita
LA2713	Montfavet 167
LA2714	Montfavet 168
LA2827	Moperou
LA2822	Mossol
LA2820	Motabo
LA2826	Motaci
LA2823	Motelle
LA3472	Movione
LA2661	Nagcarlang
LA3845	NC EBR-5
LA3846	NC EBR-6
LA3847	NC HS-1
LA3625	NC265-1 (93)-3-3
LA3802	New Hampshire Victor
LA2009	New Yorker
LA3321	Ohio 7663
LA1088	Ohio Globe A
LA2447	Ontario 717
LA2449	Ontario 7517
LA2396	Ontario 7710
LA2448	Ontario 7818
LA2970	Orange, Red Ctr.
LA2376	Pan American
LA0012	Pearson
LA0020	Pennheart
LA3528	Peto 95-43
LA3243	Platense
LA3312	Platense
LA3125	Pomodorini Napolitan
LA2715	Porphyre
LA3820	Potentate
LA3903	Primabel
LA0089	Prince Borghese
LA3233	Pritchard
LA3229	Prospero
LA2446	Purdue 135
LA2377	Purple Calabash
LA2378	Purple Smudge
LA0337	Red Cherry
LA0276	Red Top VF
LA3129	Rehovot 13
LA2356	Rey de Los Tempranos
LA0535	Rheinlands Ruhm
LA3343	Rio Grande

Accession	Cultivar
LA3145	Rockingham
LA0503	Roumanian Sweet
LA3214	Rowpac
LA2088	Royal Red Cherry
LA3215	Roza
LA1090	Rutgers
LA2662	Saladette
LA3216	Saladmaster
LA3008	San Marzano
LA0180	San Marzano (autodiploid)
2-297	San Marzano (autodiploid)
LA1021	Santa Cruz
LA2413	Severianin
LA2912	Short Red Cherry
LA3234	Sioux
LA3221	Slender Pear
LA3632	Start 24
LA0030	Stemless Pennorange
LA2443	Stirling Castle
LA1091	Stokesdale
LA1506	Stone
LA0164	Sutton's Best of All
LA2399	T-5
LA2590	T-9
LA0154	Tiny Tim
LA1714	UC-134
LA3130	UC-204C
LA1706	UC-82
LA2937	UC-MR20
LA2938	UC-N28
LA2939	UC-T338
LA2940	UC-TR44
LA2941	UC-TR51
LA0021	Uniform Globe
LA2445	V-121
LA0745	V-9 Red Top
LA3246	Vagabond
LA3905	Vantage
LA3122	Vendor
LA2911	Vendor (Tm-2^a)
LA2968	Vendor (Tm-2a)
LA2971	Verna Orange
LA2444	Vetomold K10
LA0744	VF-11
LA1023	VF-13L

Accession	Cultivar
LA1507	VF-145 21-4
LA0816	VF-145 22-8
LA1222	VF145 78-79
LA0742	VF-34
LA0490	VF-36
LA0743	VF-6
LA2086	VFN Hi Sugar
LA0815	VFN-14
LA1022	VFN-8

Accession	Cultivar
LA1221	VFNT Cherry
LA3630	Vrbikanske nizke
LA3465	Walter
LA0279	Webb Special
LA2464A	White Beauty
2-473	Yellow Cherry
LA2804	Yellow Currant
LA2357	Yellow Peach
LA3148	Zemer Kau

1.2. Latin American Cultivars (226)

This collection of Latin-American cultivars has been assembled from various sources but principally from our collecting trips, often at local markets. With a few exceptions they are indigenous in the sense that they are not recently introduced lines. Many of them are extinct in the source region, having been replaced by modern cultivars.

Accessions	Location
Bolivia	
LA0172	Santa Cruz
LA2699	Coroica
LA2871	Chamaca
LA2873	Lote Pablo Luna #2
LA2874	Playa Ancha
Brazil	
LA1021	Santa Cruz
Chile	
LA0466	Hacienda Rosario
LA0467	Lluta Valley
LA0468	Iquique
Colombia	
LA0356 - LA0358	Buenaventura
LA1539	Cali to Popayan
Costa Rica	
LA1215	
LA3453A - LA3453D	Turrialba
Cuba	
LA1162	
Ecuador	
LA0126	Quito mercado
LA0292	Santa Cruz
LA0408 - LA0410	Guayaquil
LA0415	Daular
LA0416	Puna
LA0423	Wreck Bay: Cristobal
LA1224	Puyo
LA1238	Viche
LA1239 - LA1241	Esmeraldas
LA1244	Coop Carmela
LA1249	Loja
LA1250	Loja

Accessions	Location
LA1251	Loja
LA2094	El Naranjo
LA2132	Chuchumbetza
LA2381 - LA2384	Malacatos
LA3126	Malacatos
LA3624	Santa Rosa
El Salvador	
LA1210	San Salvador
LA1211	San Salvador
Guatemala	
LA1460	Antigua
Honduras	
LA0147	Tegucigalpa mercado
LA0148	Tegucigalpa mercado
Mexico	
LA0146	Mexico City mercado
LA1218	Vera Cruz
LA1459	Huachinango
LA1462	Merida
LA1544	Xol Laguna
LA1564	Culiacan
LA1565	Val. nacionale
LA1566	Val. nacionale
LA1567	Sinaloa
LA1568	Yucatan
LA1702	Sinaloa
LA1703	Rio Tamesi
LA1704	Rio Tamesi
LA1994	
LA2083	Guaco, Culiacan
LA2084	Comala, Culiacan
Nicaragua	
LA1212	

Accessions	Location
LA1213	
Panama	
LA1216	
LA1217	
Peru	
LA1570	Cerro Azul
LA0113	Hacienda Calera
LA0116	Chiclayo mercado
LA0117	Piura mercado
LA0125D	Trujillo mercado
LA0131H	Arequipa mercado
LA0134C	Ayacucho mercado
LA0393 - LA0396	Chiclayo
LA0401 - LA0405	Piura
LA0457	Tacna mercado
LA0472	Tacna
LA0473	Calana
LA0477	Chincha
LA0478	Chincha
LA0721	Chiclayo
LA1313	Convento de Sivia
LA1315	Ayna
LA1390	La Molina
LA1397	Iquitos
LA1398	Iquitos
LA1650	Fundo Bogotalla
LA1655	Tarapoto
LA1669	Jahuay
LA1698	Kradolfer Chacra
LA1701	Trujillo
LA1976A	Calana

Accessions	Location
LA1976B	Calana
LA1976C	Calana
LA1988	Iquitos
LA2207 - LA2212	Bajo Naranjillo
LA2213 - LA2220	Nueva Cajamarca
LA2221 - LA2235	Moyobamba mercado
LA2237 - LA2244	La Habana
LA2245 - LA2253	Soritor
LA2254 - LA2257	Puerto Moyobamba
LA2258	Fundo Conovista
LA2259A-2259D	Moyobamba mercado
LA2260 - LA2264	La Huarpia
LA2265 - LA2268	Casaria de Pacaisapa
LA2269 - LA2276	Km 57 from Tarapoto
LA2278 - LA2282	Tabalosas
LA2283 - LA2307	Tarapoto mercado
LA2309 - LA2311	Punto Santa Cruz
LA2316	Sargento
LA2622	Mangual Pucallpa
LA2623	Pucalepillo Pucallpa
LA2676	San Juan del Oro
LA2841	Chinuna
LA2842	Santa Rita
LA2843	Moyobamba mercado
LA2844	Shanhao
LA2845	Moyobamba mercado
LA3222 - LA3226	San Isidro mercado
LA3646	Puente Tincoj

2. PREBRED STOCKS

2.1. Introgression Lines (ILs)

2.1.1. *L. pennellii* ILs (76)

The following group of introgression lines (ILs) was developed by Eshed & Zamir (Euphytica 79:175-179, 1994; TGC 49:26-30). Each IL (except IL8-1) is homozygous for a single introgression from *L. pennellii* (LA0716) in the background of *L. esculentum* cv. M-82 (LA3475). The entire *L. pennellii* genome is thereby represented by overlapping introgressions in a group of 50 lines. An additional 26 sublines provide increased mapping resolution in some regions. The IL # indicates the *L. pennellii* chromosome and introgressed segment number in each.

Access.	Line
LA4028	IL1-1
LA4029	IL1-1-2
LA4030	IL1-1-3
LA4031	IL1-2
LA4032	IL1-3
LA4033	IL1-4
LA4034	IL1-4-18

Access.	Line
LA4035	IL2-1
LA4036	IL2-1-1
LAA4037	IL2-2
LA4038	IL2-3
LA4039	IL2-4
LA4040	IL2-5
LA4041	IL2-6

Access.	Line
LA4042	IL2-6-5
LA4043	IL3-1
LA4044	IL3-2
LA3488	IL3-3
LA4046	IL3-4
LA4047	IL3-5
LA4048	IL4-1

Access.	Line
LA4049	IL4-1-1
LA4050	IL4-2
LA4051	IL4-3
LA4052	IL4-3-2
LA4053	IL4-4
LA4054	IL5-1
LA4055	IL5-2
LA4056	IL5-3
LA4057	IL5-4
LA4058	IL5-5
LA4059	IL6-1
LA4060	IL6-2
LA4061	IL6-2-2
LA4062	IL6-3
LA4063	IL6-4
LA4064	IL7-1
LA4065	IL7-2
LA4066	IL7-3
LA4067	IL7-4

Access.	Line
LA4068	IL7-4-1
LA4069	IL7-5
LA4070	IL7-5-5
LA4071	IL8-1
LA4072	IL8-1-1
LA4073	IL8-1-5
LA4074	IL8-2
LA4075	IL8-2-1
LA4076	IL8-3
LA4077	IL8-3-1
LA4078	IL9-1
LA4079	IL9-1-2
LA4080	IL9-1-3
LA4081	IL9-2
LA4082	IL9-2-5
LA4083	IL9-2-6
LA4084	IL9-3
LA4085	IL9-3-1
LA4086	IL9-3-2

Access.	Line
LA4087	IL10-1
LA4088	IL10-1-1
LA4089	IL10-2
LA4090	IL10-2-2
LA4091	IL10-3
LA4092	IL11-1
LA4093	IL11-2
LA4094	IL11-3
LA4095	IL11-4
LA4096	IL11-4-1
LA4097	IL12-1
LA4098	IL12-1-1
LA4099	IL12-2
LA4100	IL12-3
LA4101	IL12-3-1
LA4102	IL12-4
LA4103	IL12-4-1

2.1.2. *L. hirsutum* ILs (98)

The following group of introgression lines represent the genome of *L. hirsutum* (LA1777) in the background of *L. esculentum* cv. E-6203 (LA4024) via homozygous chromosome segments (Monforte & Tanksley, Genome 43:803-813; 2000). The first 57 lines (LA3913 - LA3969) represent approximately 85% of the donor genome, while the remaining 41 lines (LA3970 - LA4010) contain different introgressions, mostly derivatives of the first group. Unlike the *L. pennellii* ILs above, each *L. hirsutum* line may contain more than one introgression, representing one to several chromosomes, as indicated below.

Access.	Line	Chr.
LA3913	TA1258	1
LA3914	TA523	1
LA3915	TA1229	1
LA3916	TA1223	1
LA3917	TA1535	1
LA3918	TA1127	1
LA3919	TA1128	1
LA3920	TA1536	1
LA3921	TA1105	2
LA3922	TA1266	2
LA3923	TA1537	2
LA3924	TA1538	2
LA3925	TA1111	3
LA3926	TA1276	3
LA3927	TA1277	3
LA3928	TA1540	3
LA3929	TA1541	3
LA3930	TA1133	4
LA3931	TA1280	4
LA3932	TA1562	4

Access.	Line	Chr.
LA3933	TA1542	4
LA3934	TA1459	4
LA3935	TA517	4
LA3936	TA1475	4
LA3937	TA1473	4
LA3938	TA1287	5
LA3939	TA1293	5
LA3940	TA1112	5
LA3941	TA1543	5
LA3942	TA1117	5
LA3943	TA1544	5
LA3944	TA1539	6
LA3945	TA1545	6
LA3946	TA1546	6
LA3947	TA1559	6
LA3948	TA1303	7
LA3949	TA1304	7
LA3950	TA1547	7
LA3951	TA1312	7
LA3952	TA1315	8

Access.	Line	Chr.
LA3953	TA1316	8
LA3954	TA1548	8
LA3955	TA1320	8
LA3956	TA1324	9
LA3957	TA1325	9
LA3958	TA1330	9
LA3959	TA1331	9
LA3960	TA1550	10
LA3961	TA1551	10
LA3962	TA1552	10
LA3963	TA1337	10
LA3964	TA1339	10
LA3965	TA1555	11
LA3966	TA1554	11
LA3967	TA1342	11
LA3968	TA1350	12
LA3969	TA1121	12
LA3970	TA1219	1
LA3971	TA1218	2
LA3972	TA1173	2

Access.	Line	Chr.
LA3975	TA1629	3
LA3976	TA1138	4
LA3977	TA1467	4
LA3978	TA1468	4
LA3979	TA1630	4
LA3980	TA1290	5
LA3981	TA1116	5
LA3983	TA1631	5
LA3984	TA1632	5
LA3985	TA1306	7
LA3986	TA1309	7
LA3988	TA1318	8

Access.	Line	Chr.
LA3989	TA1319	8
LA3990	TA1560	8
LA3991	TA1326	9
LA3993	TA1549	10
LA3994	TA1635	10
LA3995	TA1553	11
LA3996	TA1120	11
LA3997	TA1563	1, 10
LA3998	TA1637	1, 11, 12
LA3999	TA1638	1, 12
LA4000	TA1557	1, 4

Access.	Line	Chr.
LA4001	TA1644	1, 7, 12
LA4002	TA1645	1, 8, 12
LA4003	TA1648	2, 11
LA4004	TA1649	2, 3, 6
LA4005	TA1652	3, 5
LA4006	TA1654	4, 10, 11
LA4007	TA1655	4, 12
LA4008	TA1656	5, 6, 9
LA4009	TA1564	5, 7, 10
LA4010	TA1561	8, 12

2.1.3. *S. lycopersicoides* IL (99)

The following group of ILs have been bred from *S. lycopersicoides* into the background of *L. esculentum* cv. VF36. These lines represent ~96% of the donor genome and are described in the following publications: Canady et al., 2005, Genome 48: 685-697; Rick et al. 1988 Theor. Appl. Genet. 76: 647-655. While some lines are available in the homozygous condition, many others are associated with sterility and must be maintained via heterozygotes. Marker analysis is required to identify heterozygous progeny. Seed of some lines may be limited or temporarily unavailable.

Acc.	Line	Chr.s
LA3344	*Mdh-1*	3
LA3345	*Dia-3*	9
LA3668	*Abg*	10
LA3866	LS1-1	1
LA3867	LS11-9	1
LA3869	LS42-4	2
LA3870	LS38-10	2
LA3871	LS41-3	2
LA3874	LS20-9	3
LA3875	LS24-14	4, 12
LA3876	LS29-1	8
LA3878	LS24-6	5
LA3879	LS1-5	5, 11
LA3882	LS43-14	2, 6
LA3883	LS48-6	7, 11
LA3886	LS48-5	7
LA3889	LS41-13	8
LA3892	LS48-2	11
LA3893	LS16-6	5, 12
LA3906	*Wa*, *Dl*	8
LA4230	LS15-2H	1
LA4231	LS15-2B	1
LA4232	LS11-11A	1
LA4233	LS20-9	1
LA4234	LS21-2	1
LA4235	LS10-2	1
LA4236	LS49-8A	2
LA4237	LS40-8	2

Acc.	Line	Chr.s
LA4238	LS5-1	2
LA4239	LS41-20	2
LA4240	LS1-13	3
LA4241	LS40-2	3
LA4242	LS14-8	3
LA4243	LS1-3	3
LA4244	LS10-9	4
LA4245	LS10-11A	4
LA4246	LS49-8B	4
LA4247	LS12-9	4
LA4248	LS11-6	5
LA4249	LS9-1	5
LA4250	LS49-8C	5
LA4251	LS49-3	5
LA4252	LS32-11	5
LA4253	LS11-11B	6
LA4254	LS32-14	6
LA4255	LS38-5	6
LA4256	LS9-22	6
LA4257	LS46-3	7
LA4258	LS19-7	7
LA4259	LS32-4	7
LA4260	SL-7F	7
LA4261	LS8-11	7
LA4262	LS20-16	8
LA4263	LS46-6A	8
LA4264	LS9-26A	8
LA4265	LS9-26B	8

Acc.	Line	Chr.s
LA4266	SL-8A	8
LA4267	LS16-10	8
LA4268	LS14-7	9
LA4269	LS12-2	9
LA4270	LS10-6	9
LA4271	LS49-5	9
LA4272	LS41-11	9
LA4273	LS12-8	10
LA4274	LS4-14	10
LA4275	SL-10	10
LA4276	LS12-12	10
LA4277	LS24-11	11
LA4278	LS3-2	11
LA4279	LS19-11	11
LA4280	LS1-5	11, 5
LA4281	LS13-13	12
LA4282	LS45-7	12
LA4283	LS8-9	12
LA4284	LS9-13	12
LA4293	LS5-8	1
LA4294	LS15-2AD	1
LA4295	LS15-2A	1
LA4296	LS15-2AA	1
LA4297	LS15-2AAA	1
LA4298	LS15-2BA	1
LA4299	LS4-9	5

Acc.	Line	Chr.s
LA4300	LS9-7B	5, 6
LA4301	SL-7A	7
LA4302	SL-7C	7
LA4303	SL-7D	7
LA4304	LS8-11A	7
LA4305	LS9-26C	7, 8

Acc.	Line	Chr.s
LA4306	LS46-6	8
LA4307	SL-8	8
LA4308	LS32-10	9
LA4309	LS10-6D	9
LA4310	LS19-10A	11
LA4311	LS14-2	12

Acc.	Line	Chr.s
LA4312	LS45-7C	12
LA4313	LS8-12A	12
LA4314	LS12-9B	4, 10
LA4315	SL-7	7

2.2. Backcross Recombinant Inbreds (99).

The following group of backcross recombinant inbred lines originated from the cross *L. esculentum* × *L. pimpinellifolium* (Doganlar et al. Genome 45: 1189-1202, 2002). The result of 2 BC's and at least 6 generations of inbreeding via single seed descent, the lines are highly homozygous (residual heterozygosity ~3%). The population has been genotyped at 127 marker loci, and the corresponding maps, map files, and QTL data are available from the Solanaceae Genome Network (www.sgn.cornell.edu). This set of 99 lines has been selected for optimum mapping resolution using the MapPop software, and provide a permanent, high resolution mapping population.

LA4139 through LA4229	BC-RIs
LA4024	*L. esculentum* parent (E-6203)
LA1589	*L. pimpinellifolium* parent

2.3. Alien Substitution Lines (7)

In the course of his study of segregation and recombination in *L. esculentum* x *L. pennellii* hybrids, Rick (Genetics 26:753-768, 1969; Biol. Zbl. 91:209-220, 1971) progressively backcrossed certain chromosomes of *L. pennellii* LA0716 into *L. esculentum*. Selected heterozygotes of later generations were selfed and subsequent progenies free of *esculentum* markers were selected as the substitution lines. The chromosome 6 substitution (LA3142) was further selected with RFLP markers to eliminate residual heterozygosity (Weide et al., Genetics 135:1175-1186, 1993). The mutant loci used to select each substitution are indicated.

LA	Chrom.	Marker Loci
2091	1	*au, dgt, inv, scf*
1639	2	*Me, aw, m, d*
1640	3	*sy, bls, sf*
3469	4	*clau, ful, ra, e, su*^{3}

LA	Chrom.	Marker Loci
3142	6	*yv, ndw, m-2, c*
1642	8	*l, bu, dl, al*
1643	11	*j, hl, a*

2.4. Monosomic Alien Addition Lines (10)

In the following group of monosomic additions (MA), each line contains a single extra chromosome from *S. lycopersicoides* LA1964 added to the *L. esculentum* genome (Chetelat et al., Genome 41:40-50, 1998). Intactness of the *S. lycopersicoides* chromosomes in these stocks has been tested with a limited number of markers, hence some may be recombinant. For example, our stock of MA-8 lacks *S. lycopersicoides* markers distal to TG330 on the long arm. Furthermore, we were unable to maintain MA-1 and MA-6, both of which are now extinct.

Like other types of trisomics, progeny of the monosomic additions include both diploids and trisomics, the proportion of which varies between each chromosome group. Identification of monosomic additions in each generation is facilitated by their phenotypic resemblance to the corresponding primary trisomic. Therefore, the guidelines of Rick (TGC 37:60-61, 1987) for identifying trisomics in the seedling stage are useful for selecting monosomic additions as well. To further simplify this process, we have backcrossed some

of the monosomic additions into the background of multiple marker stocks for the corresponding chromosomes. In this configuration, diploids are more easily distinguished from trisomics by the expression of recessive mutant alleles in the former, and dominant wild type in the latter. For example, in our stock of MA-2, the 2n progeny would have the phenotype *wv-aa-d*, whereas 2n+1 plants would be wild type at these marker loci (as well showing the expected trisomic syndrome). In addition, some monosomic additions carry dominant morphological markers that can be used to distinguish them from 2n progeny. The marker genotypes of 2n+1 vs 2n progeny are listed below for each chromosome.

LA	Chrom.	2n+1	2n
3454	MA-2	*+-+-+*	*wv-aa-d*
3455	MA-3	*+-+-+*	*sy-bls-sf*
3456	MA-4	*+*	*+*
3457	MA-5	*+*	*obv*
3459	MA-7	*Bco-+-+*	*+-var-not*

LA	Chrom.	2n+1	2n
3460	MA-8	*Wa*	*+*
3461	MA-9	*+*	*+*
3462	MA-10	*Abg-+-+-+-+*	*+-u-t-nd-ag*
3463	MA-11	*+*	*+*
3464	MA-12	*+*	*+*

2.5. Other Prebreds (13). This group of prebreds contain selected morphological traits bred into cultivated tomato from related wild species. Some traits may be simply inherited, others likely involve multiple genetic loci. Also included are two interspecific hybrids useful for various purposes.

2.5.1. High soluble solids derivatives of *L chmielewskii*. Bred from LA1028 into the background of VF145-7879 (Rick, 1974, Hilgardia 42:493-510).

LA1500
LA1501
LA1502
LA1503
LA1563.

2.5.2. Monogenic and provisional mutants from *L. cheesmanii* (Rick, Econ. Bot. 21: 171-184, 1967).

LA1015 *h*, 'cps' (compressed fruit = reduced L/W ratio)
LA1016 *dps,* 'yg' (yellow green leaves)
LA1017 *ptb*, 'Ppc' (pachypericarp = thick-walled fruit)
LA1018 *ptb, u^G, Od, h,* dark buds (anthocyanin in bud calyces), bitter fruit
LA1019 'Ppc', thick calyx, firm fruit

2.5.3. Exserted stigmas from *L. pimpinellifolium*. Bred from LA1585 (Rick TGC 33:13-14, 1983):

LA2380

2.5.4. Interspecific hybrids.

LA3857 *L. esculentum* cv. VF36 × *S. lycopersicoides* LA2951, relatively male-fertile F_1 hybrid (clonally propagated).

LA4135 *L. esculentum* cv. VF36 × *L. pennellii* LA0716; useful as a rootstock for maintenance of *S. sitiens, S. juglandifolium,* and *S. ochranthum*.

3. STRESS TOLERANT STOCKS (50+)

We receive many requests for stocks with tolerances to environmental stresses (abiotic or biotic). Therefore, we chose this group of mostly wild species accessions based

on our observations of plants in their native habitats and/or reports in the literature. If TGC members know of other accessions which should be added to this group, we would be grateful for the information and seed samples to accession in the TGRC.

3.1. Drought tolerance

L. pennellii (general feature): LA0716, and others
L. chilense (esp. coastal sites): LA1958, LA1959, LA1972, and others
S. sitiens (general feature): LA1974, LA2876, LA4105, and others

3.2. Flooding tolerance

L. esculentum var. *cerasiforme* (wet tropics): LA1421, and others
S. juglandifolium, *S. ochranthum* (probably a general feature): LA2120, LA2682

3.3. High temperature tolerance

L. esculentum cv.s Nagcarlang (LA2661), Saladette (LA2662), Malintka-101 (LA3120), Hotset (LA3320)

3.4. Chilling tolerance

L. hirsutum (from high altitudes): LA1363, LA1393, LA1777, LA1778
L. chilense (from high altitudes): LA1969, LA1971, LA4117A
S. lycopersicoides (from high altitudes): LA1964, LA2408, LA2781

3.5. Aluminum tolerance

L. esculentum var. *cerasiforme* LA2710 (suspected)

3.6. Salinity and/or alkalinity tolerance

L. cheesmanii (from littoral habitats): LA1401, LA1508, LA3124, LA3909
L. chilense: LA1930, LA1932, LA1958, LA2747, LA2748, LA2880, LA2931
L. esculentum cv. Edkawi LA2711
L. esculentum var. *cerasiforme*: LA1310, LA2079 - LA2081, LA4133
L. pennellii: LA0716, LA1809, LA1926, LA1940, LA2656
L. peruvianum: LA0462, LA1278, LA2744
L. pimpinellifolium LA1579

3.7. Arthropod resistance

L. hirsutum, esp. *f. glabratum*: LA0407 and many others
L. pennellii: LA0716, and others

4. CYTOGENETIC STOCKS

4.1. Translocations (37)

The following group of translocation stocks have been assembled from the collections of their originators - D.W. Barton, C.D. Clayberg, B.S. Gill, G.R. Stringham, B. Snoad, and G. Khush. As far as we know, they are all homozygous for the indicated structural changes. They are described by Gill *et al*. (TGC 23: 17-18; TGC 24:10-12). Accessions with an asterisk comprise the tester set.

Accession	Chrom.s
*LA1115	T9-12
*LA1119	T3-8
*LA1120	T6-12
*LA1876	T1-2*

Accession	Chrom.s
*LA1885	T5-7*
*LA1898	T2-10a*
*LA1899	T6-11*
*LA1903	T4-7*

Accession	Chrom.s
LA1049	T1-9
LA1116	T1-11
LA1117	T5-7

Accession	Chrom.s
LA1118	T7-11
LA1121	T4-9
LA1122	T2-9
LA1123	T2-9
LA1124	T3-9
LA1125	T5-7
LA1126	T7-9
LA1127	T3-5
LA1129	T3-9

Accession	Chrom.s
LA1877	T2-4
LA1878	T2-7
LA1879	T2-9
LA1880	T2-11
LA1881	T2-12
LA1882	T12-3 or -8
LA1883	T3-7
LA1884	2 IV T3-8,9-12
LA1886	T12-3 or 8

Accession	Chrom.s
LA1892	2 IV T9-12, ?-?
LA1894	T2-9a
LA1895	T2-9b
LA1896	T1-12
LA1897	T7-11?
LA1902	T2- ?
LA1904	T2-9d
LA1905	T1-3 or 8
LA1906	T2-10b

4.2. Trisomics (35)

The following series of trisomics contain various kinds of extra chromosomes. Since the extras are transmitted irregularly, each stock necessarily produce a majority of diploid progeny, the remainder aneuploid. Primary trisomics yield mostly 2n and 2n+1, and rarely tetrasomics (2n+2). Telotrisomics yield telos and an occasional rare tetratelosomic. Secondary, tertiary, and compensating trisomics transmit other trisomic types as expected. Because transmission is irregular and reproduction of stocks requires much labor, our stocks are limited. In requesting our aneuploids, researchers are asked to keep these points in mind. To assist in the identification of primary trisomics at the seedling stage, the key features of each have been summarized by Rick (TGC 37:60-61, 1987). Additional 2n+1 stocks are listed under Monosomic Alien Additions.

Accession	Genotype
Primary trisomics	
delta-10	Triplo-1
delta-06	Triplo-2
delta-08	Triplo-3
delta-02	Triplo-4
delta-04	Triplo-5
delta-12	Triplo-6
delta-07	Triplo-7
delta-03	Triplo-8
delta-05	Triplo-9
delta-01	Triplo-10
delta-40	Triplo-11
delta-09	Triplo-12
Telo-trisomics	
delta-14	2n + 3S
delta-17	2n + 3L
delta-21	2n + 4L
delta-20	2n + 7L
delta-19	2n + 8L
delta-35	2n + 10S

Accession	Genotype
Secondary trisomics	
delta-44	2n + 2S·2S
delta-43	2n + 5L·5L
delta-36	2n + 7S·7S
delta-26	2n + 9S·9S
delta-31	2n + 9L·9L
delta-28	2n + 10L·10L
delta-41	2n + 11L·11L
delta-29	2n + 12L·12L
Tertiary trisomics	
delta-18	2n + 2L·10L
delta-16	2n + 4L·10L
delta-39	2n + 5L·7S
delta-15	2n + 7S·11L
delta-25	2n + 9L·12L
delta-23	2n + 1L·11L
Compensating trisomics	
delta-32	2n - 3S·3L + 3S + 3L·3L
delta-33	2n - 3S·3L + 3S·3S + 3L·3L
delta-34	2n - 7S·7L + 7S·7S + 7L·7L

4.3. Autotetraploids (17)

We are currently maintaining only the following group of tetraploids. Whereas we formerly stocked many more lines, their rapid deterioration, low seed yields, and lack of demand required that we prune them to a smaller group of more frequently used genotypes. All are *L. esculentum* unless otherwise noted, and arose from either induced or spontaneous chromosome doubling.

Accession	Genotype
2-095	cv. San Marzano
2-483	cv. Red Cherry
LA0457	cv. from Tacna mercado
LA0794	*ag, t^{v}*
LA1917	*L. chilense*
LA2335	*L. pimpinellifolium*
LA2337	cv. Stokesdale
LA2339	cv. Pearson
LA2340	*L. pimpinellifolium*
LA2342	cv. Danmark

Accession	Genotype
LA2343	cv. Waltham Fog
LA2581	*L. peruvianum*
LA2582	*L. peruvianum* var. *humifusum*
LA2583	*L. chilense*
LA2585	*L. pimpinellifolium*
LA2587	*L. esculentum* var. *cerasiforme*
LA3255	cv. Ailsa Craig

5. CYTOPLASMIC VARIANTS (3)

The following three lines are cytoplasmically-inherited chlorotic variants maintained by the TGRC and included in the miscellaneous group for want of better classification. They were induced by mutagens and are inherited in strictly maternal fashion. They are not transmitted by pollen but in reciprocal crosses -- no matter what male parents we have used -- the progeny are 100% variant.

LA1092 Uniform yellow, induced by fast neutrons in hybrid background (G.S. Khush)
LA1438 Light green, induced by X-rays in cv. Moneymaker (K. Kerkerk)
LA2979 Cyto-variegated, in cv. Glamour (R.W. Robinson)

6. GENETIC MARKER COMBINATIONS

6.1. Chromosome Marker Stocks (182)

This group consists of stocks in each of which has been assembled a series of marker genes for a single chromosome. In a few cases markers on other chromosomes are also present (listed in parentheses). Some of the more useful stocks have been combined with male steriles in order to make them useful for large scale test crossing. These stocks are listed below according to chromosome, and within each chromosome group by accession number. Asterisks indicate the preferred marker combination for each chromosome (i.e. that which provides the best map coverage).

Access.	Genotype
Chromosome 1	
LA0910	*per, inv*
LA0984	*scf, inv*
LA0985	*inv, per*
LA1003	*scf, inv, per*
LA1082	*era, um*
LA1107	*inv, co*
LA1108	*inv, dgt*
LA1169	*scf, dgt*
LA1173	*gas, co*
LA1184	*au^{tl}, dgt*
LA1185	*au^{tl}, scf, inv*

Access.	Genotype
LA1186	*au^{tl}, scf, inv, dgt*
LA1431	*au^{tl}, dgt*
LA1490	*au^{tl}, co, inv, dgt*
LA1492	*ms-32, bs*
LA1529*	*au^{tl}, co, scf, inv, dgt*
LA2354	*br, y (p, l)*
LA3209	*imb, irr, y*
LA3301	*fla, com^{in}*
LA3302	*imb, com^{in}*
LA3303	*imb, inv*
LA3305	*imb, Lpg*

Access.	Genotype
LA3306	*com^{in}, inv*
LA3307	*com^{in}, Lpg*
LA3346	*au, bs*
LA3347	*au, ms-32*
LA3348	*au, com*
LA3349	*au, imb*
LA3350	*au, br*
LA3351	*imb, Lpg/+*
LA3352	*imb, au, Lpg/+?*
Chromosome 2	
LA0271	*aw, O*
LA0286	*d, m*

Access.	Genotype
LA0310	*Wo^{m}, d*
LA0330	*bk, o, p, d, s* (*r, y*)
LA0342	*Wo^{m}, d* (*ms-17*)
LA0514	*aw, Wo^{m}, d*
LA0639	*Me, aw, d*
LA0650	*aw, d*
LA0715	*Wo^{m}, Me, aw, d*
LA0732	*suf, d*
LA0733	*Wo^{m}, d, ms-10*
LA0754	*aw, p, d, m, o*
LA0777	*dil, d*
LA0789	*Me, aw, d, m*
LA0790	*wv, Me, aw, d*
LA0986	*s, bk, Wo^{m}, o, aw, p, d*
LA1525	*aa, d*
LA1526	*are, wv, d*
LA1699	*Wo^{m}, bip*
LA1700*	*wv, aa, d*
LA3132	*Prx-2^{1}, ms-10, aa*
Chromosome 3	
LA0644	*r, wf*
LA0782	*sy, sf*
LA0877	*pau, r*
LA0880	*sf, div*
LA0987	*pli, con*
LA0988	*ru, sf*
LA1070	*ru, sf, cur*
LA1071	*sy, bls, sf*
LA1101	*cn, sy, sf*
LA1175	*bls, aut*
LA1430*	*sy, Ln, bls, sf*
Chromosome 4	
LA0774	*ful, e*
LA0885	*ful, e, su^{3}*
LA0886	*ful, ra, e*
LA0888	*ful, ven, e*
LA0889	*ra, su^{3}*
LA0890	*ra, ven*
LA0902	*ful, ra^{2}, e* (*ms-31*)
LA0915	*clau, ful*
LA0916	*clau, ra, su^{3}*
LA0917*	*clau, ful, ra, e, su^{3}*
LA0920	*ful, ra, e, su^{3}*
LA0989	*afl, ful*
LA0990	*cm, ful, e, su^{3}*
LA0992	*clau, ra, su^{3}* (*com*)
LA0993	*ra, si*
LA0994	*cm, ver*
LA1073	*clau, afl*
LA1074	*clau, ver*
LA1075	*ver, e, su^{3}*
LA1536	*clau, su^{3}, ra; icn*

Access.	Genotype
Chromosome 5	
LA0512	*mc, tf, wt, obv*
LA1188	*frg, tf*
LA3850*	*af, tf, obv*
Chromosome 6	
LA0336	*c, sp* (*a, y*)
LA0640	*yv, c*
LA0651	*m-2, c*
LA0773	*yv, m-2, c*
LA0802	*yv, m-2, c* (*ms-2*)
LA0879	*tl, yv*
LA1178	*yv, coa, c*
LA1189*	*pds, c*
LA1190	*pds, yv*
LA1489	*yv, ves-2, c*
LA1527	*d-2, c*
LA3805	*m-2, gib-1*
LA3806	*yv, Mi, B^{og}, sp, c*
LA3807	*tl, yv, c*
Chromosome 7	
LA0788	*La/+, deb*
LA0882	*La/+, deb, adp*
LA0923	*ig, La/+*
LA0924	*La/+, not*
LA1083	*ig, flc*
LA1103*	*var, not*
LA1104	*deb, not*
LA1172	*La/+, lg-5*
Chromosome 8	
LA0513	*l, bu, dl*
LA0712	*l, bu, dl; ms-2*
LA0776	*l, va^{virg}*
LA0897	*l, bu, dl, al*
LA0922	*bu, dl, spa*
LA0998	*l, bu, dl, Pn/+*
LA0999	*tp, dl*
LA1012	*dl, l*
LA1191	*spa, ae*
LA1442	*dl, glg, marm*
LA1666*	*l, bu, dl, ae*
Chromosome 9	
LA0883	*pum, ah*
LA0884	*wd, marm*
LA1000	*nv, ah*
LA1001	*pum, ah, marm*
LA1100	*ah, pla, marm*
LA1112	*marm, lut*
LA1176	*Crk, ah, marm*
LA3353*	*ah, marm, pct*
LA3841	*Tm-2^{a}, Frl, nv,* ™
Chromosome 10	
LA0158	*Xa/+, u, t* (*y*)

Access.	Genotype
LA0339	*ag, u*
LA0341	*h, ag* (*ms-2*)
LA0643	*u, l-2*
LA0649	*t^{v}, ag*
LA0711	*t^{v}, ag* (*ms-2*)
LA1002	*h, u, l-2, t, ag* (*pe, lg*)
LA1085	*h, res*
LA1086	*h, ten*
LA1110	*icn, ag*
LA1192	*hy, ag*
LA1487	*icn, t^{v}*
LA2493	*Xa-2, hy, h, ag*
LA2495	*Xa-2, h, ten, ag, al*
LA2496	*Xa-2, h, l-2, t*
LA2497	*hy, u, icn, h, ag*
LA2498	*u, Xa-3, h*
LA2499	*u, nor, t*
LA2500	*u, icn, h*
LA2501	*u, icn, h, ag*
LA2502	*u, h, auv, l-2, t^{v}*
LA2503	*u, h, l-2, t^{v}, ag*
LA2504*	*u, h, t, nd, ag*
LA2505	*u, l-2, t, ag, Xa*
LA2506	*ag, h, l-2, oli, t^{v}*
LA2507	*h, t, nd, ag*
LA2508	*h, t, ag, Xa*
LA2509	*oli, l-2, t^{v}, ag* (*wf*)
LA2591	*Xa-2, h, ag*
LA2592	*u, h, t, nd, ag*
LA2593	*u, auv, ag*
LA4341	*h, hy, u*
Chromosome 11	
LA0259	*hl, a*
LA0291	*hl, a* (*ms-2*)
LA0729	*neg, a*
LA0730	*a, pro*
LA0761	*a, hl, j*
LA0798	*a, hl, j* (*ms-2*)
LA0803	*hl, a, pro* (*ms-2*)
LA0881	*neg, hl, a*
LA0925*	*j, hl, a, f*
LA1102	*a, hl, tab*
LA1109	*j, hl, mnt*
LA1488	*neg, ini*
LA1786	*j, f, a, bi* (*c*)
LA2352	*j, f* (*p, c*)
LA2364	*j, a, f* (*y, wt, c, l, u*)
LA2489	*neg^{ne-2}, a*
LA4290	*a, bks*
LA4291	*a, bks^{2}*
LA4292	*j-2, up, wv-3*
LA4344	*a, mon*

Access.	Genotype
Chromosome 12	
LA1111	*fd, alb*

Access.	Genotype
LA1171	*yg-2^{aud}, fd*
LA1177*	*alb, mua*

6.2. Linkage Screening Testers (13)

The following set of linkage testers each combines two pairs of strategically situated markers on two different chromosomes (see TGC 22: 24). They are intended primarily for assigning new, unmapped markers to a chromosome. The more complete chromosome marker combinations (list 6.1 above) should be used for subsequent testing to delimit loci more accurately. Whereas six of these stocks should pretty well cover the tomato genome, we list below the entire series of the current available testers because alternative stocks differ in their usefulness, depending upon the phenotype of the new mutant to be located. The chromosomal location of each pair of markers is indicated in parentheses.

Access.	Genotype
LA0780	*yv, c* (chr 6)*; h, ag* (chr 10)
LA0781	*ful, e* (chr 4)*; neg, a* (chr 11)
LA0784	*ful, e* (chr 4)*; hl, a* (chr 11)
LA0982	*clau, e* (chr 4)*; hl, a* (chr 11)
LA0983	*l, dl* (chr 8)*; ah, marm* (chr 9)
LA1164	*var, not* (chr 7)*; ah, marm* (chr 9)
LA1166	*clau, su^{3}* (chr 4)*; icn, ag* (chr 10)

Access.	Genotype
LA1182	*sy, sf* (chr 3)*; alb, mua* (chr 12)
LA1441	*coa, c* (chr 6)*; hl, a* (chr 11)
LA1443	*scf, dgt* (chr 1)*; l, al* (chr 8)
LA1444	*wv, d* (chr 2)*; af, tf* (chr 5)
LA1491	*scf, dgt* (chr 1)*; spa, ae* (chr 8)
1665	*scf, dgt* (chr 1)*; l, ae* (chr 8)

6.3. Miscellaneous Marker Combinations (288)

The following list groups stocks in which various mutant genes have been combined for various purposes. A few of these items include linked genes, but are classified here because other linkage testers provide the same combinations or because they are more useful as markers of several chromosomes. Some multiple marker combinations that are of limited usefulness, difficult to maintain, and/or redundant with other genotypes, have been dropped from the current list.

Access.	Genotype
LA0013	*a, c, d, l, r, y*
LA0014	*al, d, dm, f, j, wt, h*
LA0052	*j, wt, br*
LA0085	*Wo, d, h*
LA0137	*dl, wd, gq*
LA0154	*u, d, sp, h*
LA0157	*d, m, p, r, y*
LA0158	*t, u, Xa, y*
LA0159	*a, e, mc, t, u, y, wf*
LA0169	*ps, wf, wt*
LA0189	*bl, cl-2*
LA0190	*wf, br, bk*
LA0215	*at, y, u*
LA0281	*e, t, u*
LA0296	*br, bk, wf*
LA0297	*tf, ug, Nr*
LA0299	*ag, rv*
LA0345	*ch, j-2*
LA0497	*ch, j-2, sf*
LA0499	*Od, sn, at, cm/+*

Access.	Genotype
LA0508	*gf, d, c, a, r, y*
LA0638	*ht, d, r*
LA0648	*rv, e, Wo, wf, j, h*
LA0719	*Jau, clau*
LA0727	*wv, d, c, r*
LA0728	*a, lut*
LA0759	*lg, vi, pe, t*
LA0760	*lg, vi*
LA0770	*clau, pa*
LA0775	*tf, h, au, +/d*
LA0801	*atv, slx*
LA0875	*hp, u, sp*
LA0876	*hp, sp*
LA0895	*tp, sp, u, Hr*
LA0907	*lut, pr*
LA0908	*per, var*
LA0909	*con, sf*
LA0912	*ht, su^{3}*
LA0913	*ful, su^{3}, ht*
LA0914	*com, ful*

Access.	Genotype
LA0991	*ful, e, com*
LA0995	*deb, um*
LA0996	*um, ig*
LA1018	*h, Od, ptb*
LA1038	*e, ht, su*
LA1072	*sy, sf, um*
LA1078	*ria, ves-2*
LA1079	*c, ves-2*
LA1105	*con, cur*
LA1106	*fsc, ah*
LA1163	*wv, d, tf*
LA1170	*cn, con*
LA1219	*d, u*
LA1663	*Ln, Wo^{m}*
LA1664	*hp, lp*
LA1783	*ad, sp*
LA1787	*Bk-2, en*
LA1789	*sl^{cs}, a*
LA1796	*Rs, d, h*
LA1804	*sr, sp, u*

Access.	Genotype
LA1805	*sr, y*
LA1806	*ti, y, wf, al, j*
LA2349	*p, d, r, wt, j, f*
LA2350	*y, ne, p, c, sp, a*
LA2351	*c, l, u, h*
LA2353	*y, wt, n*
LA2355	*sp, ug*
LA2360	*e, wt, l, u*
LA2363	*y, Wo, wt, c, t, j*
LA2369	*p, Tm-1*
LA2370	*wf, n, gs*
LA2372	*sp, fl*
LA2441	*d, m-2, mc, rvt, t, u*
LA2452	*B, f, gf, y*
LA2453	*Gr, u*
LA2454	*neg^{ne-2}, u*
LA2457	*u, so*
LA2458	*Pto, sp, u*
LA2461	*sp, stu, u*
LA2464	*aer-2, r, upg, y*
LA2465	*sp, u, v-2*
LA2466	*d, t, v-3*
LA2467	*pe, u, vi*
LA2473	*alb, c, gra, sft*
LA2477	*vo, cjf, wf, sp, l, u, h*
LA2478	*ae^{atr}, r, gs, h*
LA2486	*inc, pds, sp, u, t*
LA2490	*pdw, mc, pst, dl*
LA2492	*ti, wf, e, mc, u, a*
LA2524	*af, sd*
LA2526	*dp, sp, u*
LA2527	*l allele, sp, u*
LA2595	*br, d, dm, wt, al, h, j, f*
LA2597	*y, r, wf, mc, m-2, c, gs, gf, marm, h*
LA2797	*bu, j*
LA3128	*Ln, t, up*
LA3212	*tmf, d, sp, u*
LA3217	*glg, Pts*
LA3250	*t, u*
LA3251	*Del, y*
LA3252	*Del, t*
LA3254	*a, c, l, Ve*
LA3256	*at, t*
LA3257	*gf, gs, r*
LA3258	*u, Ve*
LA3261	*Del, gs*
LA3262	*Del, ug*
LA3267	*Cf-4, u*
LA3268	*Tm-2, nv, u*
LA3269	*Tm-1, u*
LA3271	*Cf-?, Tm-1, u*
LA3273	*Gp, Tm-2^2*
LA3274	*ah, Tm-2, nv, u*
LA3275	*ah, Gp, Tm-2^2*
LA3276	*Tm-1, u, Ve*
LA3279	*at, Del*
LA3284	*at, gf*
LA3286	*r, ug, y*
LA3287	*hp, r, ug*
LA3288	*hp, ug, y*
LA3289	*gf, r, y*
LA3290	*gf, hp, y*
LA3291	*at, hp, t*
LA3292	*Tm-2, u*
LA3294	*bl, d, u*
LA3297	*Tm-1, Tm-2, nv*
LA3299	*ep, u*
LA3311	*og^c, u*
LA3315	*sp, pst, u, j-2, up, vo*
LA3362	*gs, t*
LA3363	*at, gs*
LA3364	*gs, u*
LA3365	*gf, gs*
LA3366	*t, y*
LA3367	*hp, t*
LA3368	*hp, y*
LA3369	*at, y*
LA3370	*at, hp*
LA3371	*hp, u*
LA3372	*gs, y*
LA3373	*at, u*
LA3374	*u, y*
LA3375	*gs, r*
LA3376	*Del, hp*
LA3381	*r, y*
LA3382	*r, u*
LA3383	*gs, hp*
LA3384	*gf, y*
LA3385	*gs, Nr*
LA3386	*gf, t*
LA3387	*Nr, t*
LA3389	*Nr, y*
LA3390	*Nr, ug*
LA3391	*gf, hp*
LA3393	*r, t*
LA3394	*at, ug*
LA3395	*gs, hp, y*
LA3396	*at, u, y*
LA3397	*gs, t, y*
LA3398	*gs, hp ,t*
LA3399	*at, gs, hp*
LA3400	*at, hp, u*
LA3401	*at, gs, y*
LA3402	*hp, t, u*
LA3403	*gf, gs, u*
LA3404	*hp, u, y*
LA3405	*gs, hp, u*
LA3406	*at, hp, y*
LA3407	*gs, u, y*
LA3408	*t, u, y*
LA3409	*gs, t, u*
LA3410	*at, gs, u*
LA3411	*gs, r, u*
LA3412	*gf, gs, hp, u*
LA3413	*at, gf*
LA3414	*t, ug*
LA3415	*ug, y*
LA3416	*hp, ug*
LA3417	*r, ug*
LA3418	*gf, gs, ug*
LA3419	*at, gf, gs*
LA3420	*gf, ug*
LA3421	*Nr, u*
LA3422	*at, gs, ug*
LA3423	*gf, gs, hp, u, y*
LA3424	*gs, hp, u, y*
LA3425	*gf, gs, hp, t, u*
LA3426	*gs, hp, t, u*
LA3427	*gf, gs, t, u*
LA3428	*l, u, Ve*
LA3429	*Del, gs, hp*
LA3432	*Tm-1, Tm-2, nv, u*
LA3433	*ah, Tm-2, nv, u*
LA3437	*at, Nr*
LA3442	*de, dil, u*
LA3443	*cor, de, u*
LA3444	*cor, dil, u*
LA3445	*cor, pum, u*
LA3446	*cor, sp, u*
LA3447	*dil, sp, u*
LA3448	*in, u*
LA3449	*d, sp, u*
LA3450	*bls, sp, u*
LA3451	*bl, sp, u*
LA3540	*l, u*
LA3541	*gs, r, ug*
LA3542	*u, ug*
LA3543	*bls, o, u*
LA3545	*Del, u, y*
LA3546	*bls, Cf-?, u*
LA3547	*ah, u*
LA3548	*pum, u*
LA3549	*bls, Gp, Tm-2^2, u*
LA3557	*Del, gf*
LA3558	*gf, Nr*

Access.	Genotype
LA3559	*Del, gs, y*
LA3561	*gf, gs, hp, Nr, u*
LA3562	*gf, gs, u, y*
LA3563	*sp, u*
LA3585	*gf, u, ug*
LA3586	*t, u, ug*
LA3587	*r, u, ug*
LA3589	*u, ug, y*
LA3590	*Nr, gs, y*
LA3591	*Nr, u, y*
LA3593	*hp, u, ug*
LA3594	*gs, hp , ug*
LA3595	*gf, hp, ug*
LA3596	*hp, t, ug*
LA3597	*at, hp, ug*
LA3598	*r, t, ug*
LA3599	*at, t, ug*
LA3600	*t, ug, y*
LA3601	*gf, r, t*
LA3603	*at, gf, y*
LA3604	*hp, r, t*
LA3605	*at, ug, y*
LA3606	*r, t, y*
LA3607	*gs, hp, Nr*
LA3608	*hp, Nr, t*
LA3609	*hp, Nr, y*

Access.	Genotype
LA3615	d^x, *u*
LA3675	*hp, Nr, u*
LA3676	*gf, hp, t*
LA3677	*gf, hp, r*
LA3678	*Nr, u, ug*
LA3679	*gs, Nr, ug*
LA3680	*Nr, t, u*
LA3682	*gs, t, ug*
LA3683	*gs, ug, y*
LA3684	*Nr, t, y*
LA3686	*gs, Nr, t*
LA3688	*gf, gs, hp*
LA3689	*gs, hp, r*
LA3691	*r, u, y*
LA3692	*at, r, y*
LA3693	*g, t, u*
LA3694	*Del, gs, u*
LA3695	*Del, hp, t*
LA3697	*gs, r, t*
LA3698	*gs, r, y*
LA3699	*gf, u, y*
LA3700	*at, gf, u*
LA3701	*at, t, u*
LA3702	*gf, gs, y*
LA3703	*gf, hp , u*
LA3704	*at, gf, hp*

Access.	Genotype
LA3706	*at, gs, t*
LA3706	*Del, t, y*
LA3709	*Del, gf, gs, hp, u*
LA3741	*pum, u*
LA3742	*de, u*
LA3743	*cor, u*
LA3744	*sph, u*
LA3745	*bl, u*
LA3771	*hp,* B^c
LA3810	*hp, t*
LA3811	*gf, r*
LA3812	*bls, Tm, Tm-2, nv*
LA3815	*Del, t, ug*
LA3821	*dil, pum, u*
LA3823	*pum, sp, u*
LA3826	*mon, u*
LA3827	*dil, cor, sp, u*
LA3830	*ep,* B^c*, u*
LA3831	*gf, gs, r, y*
LA4136	*Rg-1, r*
LA4342	*oli, u, y*
LA4343	*gq, h*
LA4348	*yg-2,* c^{int}

7. Provisional mutants (107).

The following group of provisional mutants are listed here, rather than with the monogenic stocks because they have not been fully characterized. For some, a monogenic segregation has not been verified, for others complementation tests were either not performed or did not detect allelism with existing mutants of similar phenotype. Most of these lines resulted from mutagenesis experiments, the remainder occurring spontaneously. Genetic background is indicated, if known. More information on these stocks is available at our website.

Access.	Traits	Phenotype	Background
2-293	Snout	Fruits distorted, always snouted.	S. Marzano
2-305	Broad	Leaves broader and more divided than Pearson, internodes shortened; fruits elongate.	Pearson
2-473	Yellow fruit, pale corolla	Spontaneous mutant	Red Cherry
2-493	Purple tipped leaves, puny	Miniature plant, reduced fruit set, parthencocarpic fruit.	Peto 795
2-575	Poxed fruit	Pox marks in radial lines, in ripe fruit = yellow or necrotic.	PI 260395
2-585	Balloon	Short internodes, leaves dark green, acuminate, extremely plicate and veins prominent; leaves broad and wavy, highly divided; flowers small, poorly opened; mostly parthenocarpic fruit.	CP-2
2-621	Turbinate	Flowers semiturbinate, corolla wavy, anthers semi-dialytic.	VFN-8

Access.	Traits	Phenotype	Background
2-625	Prolific leaves	Leaves highly modified and proliferated, dark green.	VFN-8
2-629	Me-oid	Plant rank, most branches do not terminate, yet have sp gene; leaves ext. reduced with long terminal segment, laterals short and strongly recurved.	VFN-8
2-633	Hooded flowers	Corolla funneliform as a result of corolla segments being joing distally more than normal.	breeding line
2-643	Yellow green	Whole plant yellow green, moderate vigor, good fruit set. Similar to fy and yt genes.	VF36
3-003	yv-oid	Yellow green cots, very chlorotic leaves, later chlorosis is general, strong anthocyanin. In field, entirely normal.	VF36
3-055	Round cotelydons and leaves	Chlorotic interveinal regions, normal vigor, short round cots.	VF36
3-073	Abnormal flowers	Calyx and corolla segments enlarged; stamens deformed, dialytic and petaloid; pistil fasciated, distorted.	VF36
3-077	Dwarf	Slow, dwarf, broad recurved leaves, heavy stems, short internodes. Leaves dark green, strongly recurved at tips of all segments, not rugose. As brittle as hl.	VF36
3-082	Dwarf	Short stocky dwarf, recurved leaves. Leaves not rugose or stiff, but strongly recurved. Good expression at seedling stage.	VF36
3-083	Yellow virescent	Bright yellow virescent, paler later.	VF36
3-084	Yellow green	Leaves overall yellow green, becoming speckled green.	VF36
3-088	Light green, dark veins	Light green, miniature stature.	VF36
3-097	Yellow green	Yellow green, narrow leaves, entire margins.	VF36
3-098	Slow chlorotic	Slow chlorotic, yellow green leaves, not fully divided (clavate).	VF36
3-101	tl mimic	Probably an allele of tl, complete response to thiamine application.	VF36
3-106	Strong anthocyanin	Strong anthocyanin under leaf, slow slender and erect.	VF36
3-107	Bright yellow virescent	Bright yellow virescent leaves.	VF36
3-112	Crippled	Leaf rugose, rough, variegated dark green / grey green; older leaves deformed.	VF36
3-115	rv-oid	Overall light green leaves with dark veins; stunted, narrow segments.	VF36
3-118	Rugose recurved leaves	Leaves rugose, recurved; plant dwarfish, 2/3 size.	VF36
3-127	Bright yellow	Overall bright yellow, plant 2/3 size.	VF36
3-241-1	Yellow, anthocyanin	Overall yellow, anthocyanin on stem.	VF36
3-243	Long narrow	Long narrow twisted leaves, anthocyanin on stem. Entire, narrow segments, suggesting triplo-3., flowers with elongate parts.	VF36
3-303	Slow, narrow leaves	Very slow,(1/10), yellow green virescent, leaves narrow and acute, deep dark veins	Moneymaker

Access.	Traits	Phenotype	Background
3-305	La-mimic	Identical with La in all respects, except leaves more subdivided.	Moneymaker
3-307	Broad, grey green	Seedling dwarf, cotyledons and leaves broad, light grey green leaves very convex, deep veined. Mature plant normal size, leaves reduced, slightly chlorotic interveinally, bullate, few fruits set.	Moneymaker
3-309	Bunchy growth, mitten leaves	Seedling dwarf, (1/3 size) short internodes, leaves abbreviated, mitten shaped. Same phenotype in mature plant.	Moneymaker
3-311	Slow, rugose	Seedling extremely slow (1/20), leaves with fewer segments, very rugose, dark green.	Moneymaker
3-315	Glossy dwarf	Extreme dwarf (1/10 size), dark glossy green, like d^x.	Moneymaker
3-317	ra-oid	2/3 size, leaves rounded, convex,recurved, resembles rava. Flowers tiny, hooded, set few fruit.	Moneymaker
3-319	Striated, divided	1/3 size, cotyledons and leaves variably striated, leaves short, convex, recurved, well divided and variably deformed, leaves dark green, variably bullate, twisted and deformed flowers, very few fruit set.	Moneymaker
3-321	Narrow, dissected	Cotyledons narrow, small elliptical; leaves narrow, deeply serrated, surface irregular, turning grey-green, small flowers, scattered fruit set.	Moneymaker
3-323	Spirally coiled	1/3 size, cotyledons ext. narrow, leaves spirally coiled and large; plant gets all wrapped up in itself, leaves very dark green, rugose and dentate.	Moneymaker
3-325	Short, yv	Dwarf, short internodes (1/3), leaves and cotyledons broad, leaves slightly paler with deep veins. Mature plant (GH only): very short compact, yv like, extreme distinct.	Moneymaker
3-329	Bronzing	Dwarf (1/5 size), cotyledons and leaves large, leaves broad and convex, later bronzing interveinally, flowers tiny.	Moneymaker
3-331	Serrated leaves	Leaves extremely narrow, deeply serrated like acl. Mature plant 1/3 size, tiny dark green plicate leaves, dainty appearance, flowers hooded.	Moneymaker
3-335	Gold dust virescent	1/3 size, bright yellow virescent (gold dust), Narrow acute leaves with deep veins	Moneymaker
3-337	Glossy dwarf	Leaves short, smooth and glossy, compact (1/20 size) plant, delayed flowering.	Moneymaker
3-341	Dwarf	Dwarf stature (1/2 size), very short internodes, concave leaves, deep veins, interveinal chlorosis, leaf segments small and few, flowers small.	Moneymaker
3-403	Fimbriate leaves	Two plants with fimbriate leaves, like nv (from Epstein 516)	VF36
3-404	Speckled white	Fine white marginal speckling, nearly normal size.	VF36
3-405	Streaked virescent	2\3 size, streaked cotelydons, strong yellow green virescence.	VF36

Access.	Traits	Phenotype	Background
3-406	Streaked variegated	Large size, streaked and variegated, extremly irregular, like "crippled"	VF36
3-408	bu mimic	Early seedlings show bunch habit with extremely short internodes, almost rosette like; exceeds bu in compactness	VF36
3-411	Blue green; bushy roots	1/4 size, dark blue green, streaked anthocyanin of leaf undersides; bushy roots, dense growth of solely twisted lateral roots	VF36
3-423	ra-oid	Slender seedling with grey-green colour and recurved leaves. Slow (1/3 normal). Prominent silky hairs of type ra syndrome, like 3-318	VF36
3-424	Extreme dwarf	Extreme dwarf with type d syndrome; intermediate between dd and d:x in stature	VF36
3-434	d^cr like	Dwarf like allele of d:cr, except leaves are more obtuse, broader, and more ruffled	VF36
3-436	Overall yellow	Uniformly overall yellow like au and var.	VF36
3-441	Singed hairs	Nearly normal size, also hairless with less suppressed hairs above cotyledons, like singed	VF36
3-601	clau mimic	Resembles clausa, but F1 allele test shows not allelic.	VFNT Ch
3-612	wiry mimic	Resembles wiry, strong expression.	VFNT Ch
3-613	La mimic	Segregates as a dominant La mimic in M2. Also segregates for a dgt-like mutant.	VFNT Ch
3-614	pds-oid	Short, stocky, 1/4 size, light green, not much like pds.	VFNT Ch
3-617	Dwarf	Dwarf like, not allelic with d, linked to bip but not Wo.	VFNT Ch
3-618	mimic of a	Reduced anthocyanins.	VFNT Ch
3-619	wiry mimic		VFNT Ch
3-621	d mimic	Typical d syndrome, though more extreme, but not allelic with d.	VFNT Ch
3-622	d mimic	Typical d syndrome, but not allelic with d.	VFNT Ch
3-624B	Yellow virescent		VFNT Ch
LA0506	Triplo-8 mimic	Triplo-8 mimic, ex. 2-72. Maybe dominant deficiency transmitted through egg, not pollen.	S. Marzano
LA0652	calycine poxed	Spotting is pox. Calycine trait is allele of ch. Both spotting and calycine appear as dominants.	
LA0739	ag mimic	allele of ag?	
LA0765	Acute leaves	Acute leaves.	
LA0791	Long John	Originated from crosses among pear types. Elongate fruit shape segregates about 120 long : 48 + in F2's with wild type.	
LA0801	Pseudopolyploid		
LA0870	frizzled virescent		
LA0871	Calico		
LA1012	Mottled, chlorotic petiole	Also segregates for dl, l.	
LA1060	spl-oid	Derived from hg x (sy sf) F2; bright yellow interveinal areas, leaves strongly rolled and reducded especially at growing point.	
LA1065	Miniature	Derived from pic x (ag h, c yv) F2. Phenotype like	

Access.	Traits	Phenotype	Background
		rmt, leaves reduced and strongly plicate, 1/3 size plant.	
LA1066	Speckled	Speckled mutant derived from lutea, small darker colored seedling, tiny lighter colored specklings, closely resembles pun, probably allelic.	
LA1095	fy-oid	Low grade yg chlorophyll deficiency, uniform over plant; expr. stronger in field.	Rutgers
LA1098	Multiple inflor.	Proliferated and elongate inflorescence, in sp line.	
LA1144	ful mimic	Uniform strong yg, like ful.	Earlipak 7
LA1148	Light green	Light yellow green, normal vigor, poor expression in seedling.	VF145 7879
LA1149	Xanthoid	Bright yellow, stronger at growing point, segregates 2 normal, 1 Xanthoid, 1 chlorotic lethal.	
LA1154	pale virescent, twisted leaves	Pale virescent, twisted leaves; strongly chlorotic growing point, green at first, turning pale, almost whitish; extremely slow (1/10+ normal); twisted and distorted cotyledons.	
LA1160	Fused cotyledons	Cotyledons fused along the proximal part of the margins, net effect suggesting cot's of morning glory.	
LA1193	Yellow-sectored	Extremely stunted and sterile in field.	
LA1201	rv-oid		
LA1202	Dirty orange cherry		
LA1436	Withered cotyledons	Withered cotyledons, slow (1/3 size), compact seedling, strong yellow virescent, older leaves are strongly yellow green.	
LA1494	Adventitious roots		
LA1532	rv-oid	Clearly defined, useful seedling marker.	VF145-7879
LA1533	Purple stem	Incompletely dominant, Early seedlings not well distinguished, later moderately intense purpling, especially on leaf veins on undersides.	
LA1707	Short stature	Not true dwarf phenotype; good vigor and distinct in seedling stage.	VF145-7879
LA2018	Anthocyanin deficient	No anthocyanin at any stage.	Niagara
LA2019	Virescent tangerine mimic	Homozygous for phenotype exactly like t^v. Jointless, very firm fruit, determinate canning type vine, vigorous.	
LA2020	Dark green foliage	Dark geen foliage; fruit 10-12 locules, catfaced, yellow skin and red flesh.	
LA2021	Variegated yellow	Very slow and stunted; variegated yellow in large patches over most of the older foliage. Seedling: bright yellow green, the yellow spots turning to white.	
LA2358	Marginal leaf chlorosis		
LA2375	Lc- reduced locule	May not be monogenic, possibly pleiotropic effect of pear shape (ovate gene).	
LA2806	Incomplete anthocyanin	Grey green hypocotyl, similar to ai and pai, but darker. Spontaneous mutant.	Vis

Access.	Traits	Phenotype	Background
	mutant		
LA2817	lg mimic	lg mutant, possibly allelic	
LA2897	Virescent gold top		
LA2899	Wrinkled fruit		
LA3851	Virescent		R.Ruhm