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of the  
TOMATO GENETICS COOPERATIVE

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FOREWORD

The Tomato Genetics Cooperative is a group of researchers who share an interest in tomato genetics, and who have organized informally for the purpose of exchanging information, germplasm, and genetic stocks. The Report of the TGC is published annually and, in addition to reports of work in progress by members, it contains updates on materials available and of the tomato linkage maps. The research reports include work on such diverse topics as new traits or mutants isolated, new cultivars or germplasm developed, interspecific transfer of traits, studies of gene function or control and tissue culture.

As of June 1, 1994 TGC membership stood at 420 from 45 different countries. Requests for membership (\$5.00 {US} per year) should be sent to Rich Zobel, 1017 Bradfield Hall, Cornell University, Ithaca NY 14853-1901. Suggestions for improvement or additions to the reports are always welcome.

Submission for the next report can be sent either to R. Zobel or M. Mutschler anytime before February 1, 1995 (submissions may be made on IBM or MacIntosh compatible discs with an included hard copy). Names for new mutants, clones, and RFLPs should be submitted to the nomenclature committee c/o R. Zobel, in advance of publication.

Requests for seed stocks should be addressed to the respective suppliers (p).

COVER FIGURE: Integration of the classical and RFLP maps of Chromosome 3. See p 8.

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## **EDITORIAL NOTE**

In the normal progression of things, changes in family size, sudden sabbatic opportunities (read: directed temporary change of location and job responsibilities) happen to most of us. When these take us away from our normal working environment, they can disrupt ongoing activities. This is especially so when one does not have an efficient technical staff person to oversee projects like the TGC Reports. We apologize for any inconvenience our situations may have caused.

**For future reference, articles for the TGC Reports are normally requested for February first. On the other hand, we will accept reports at any time during the year, and insert them into the next volume. As most of you have noticed, the reports do not come out immediately after the stated deadline - we need time to edit, organize, and formalize the full TGC Reports. We will accept reports (and changes to submitted reports) up until the day the TGC Reports go to press. This is facilitated if the reports are submitted on computer disk.**

Rich Zobel, College Park / Greenbelt, MD

## RESEARCH NOTES

*Dominance of Lapageria (Lpg) is reversed in crosses with Lycopersicon pennellii.*

**Balint-Kurtl, P.J., Jones, D.A. and Jones, J.D.G.**

The Sainsbury Laboratory at the John Innes Centre

Rick (1964) reported *Lapageria (Lpg)* as an incompletely dominant morphological marker causing, among other things, reduced trichome size and number and reduced viability. Although this is true for crosses involving *L. esculentum*, we have observed that *Lpg* is completely recessive when crossed to *L. pennellii*.

A *L. esculentum* plant heterozygous for *Lpg* was crossed to *L. pennellii*. Of the resulting 30 progeny none showed any features associated with the *Lpg* phenotype. Three of these F<sub>1</sub> plants were crossed back to *L. esculentum* plants wild type at the *Lpg* locus. The progeny of one cross segregated 8:16 *Lpg*:wild type (fitting a 1:1 ratio). F<sub>2</sub> progenies from these same three F<sub>1</sub> plants were also examined. The same plant that gave *Lpg* progeny when test-crossed, produced 6:83 *Lpg*:wild type progeny in the F<sub>2</sub>. The low number of *Lpg* individuals here is presumably due to segregation distortion in this region previously as observed among F<sub>2</sub> progeny from *L. esculentum* x *L. pennellii* crosses (Chetelat and de Verna 1991). The other 2 F<sub>1</sub> plants gave no *Lpg* F<sub>2</sub> progeny out of a total 51 plants.

RFLP analysis of the 24 test cross plants segregating for *Lpg* showed that *Lpg* cosegregated with the RFLP marker TG310 located on chromosome 1 (Tanksley et al. 1992). The fact that no plants gave RFLP data inconsistent with their phenotypes and the absence of a modified segregation ratio in the test cross indicates that the locus in *L. pennellii* responsible for masking the *Lpg* phenotype in the F<sub>1</sub> is at or near the *Lpg* locus. Thus it seems likely that the *L. pennellii* gene at the *Lpg* locus is dominant over the *Lpg* mutation. It also seems likely that *Lpg* is a loss of function mutation and that its dominance in *L. esculentum* may be due to haplo-insufficiency of the wild type allele.

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Chetelat and de Verna (1991) Expression of unilateral incompatibility in pollen of *Lycopersicon pennellii* is determined by major loci on chromosomes 1,6 and 10. *Theor. Appl. Genet.* 82:704-712

Rick C. M. (1964) Inheritance and linkage relations of *Lapageria (Lpg)* TGC report 14:24-25

Tanksley et al. (1993) High density molecular linkage maps of the tomato and potato genomes. *Genetics* 132:1141-1160

The cloned tomato anionic peroxidase genes TAP1 and TAP2 correspond to the linked isozymes Prx-2 and Prx-3.

**Balint-Kurti,**

**P. J.**

The Sainsbury Laboratory at the John Innes Centre

Roberts and Kolattukudy (1989) cloned two highly homologous tomato anionic peroxidase genes, TAP1 and TAP2. These genes were found on the same genomic clone separated by about 1.5 kb. RFLP analysis using pTAP3.7 (a clone carrying the TAP2 gene) identified a *Hind*III polymorphism between *L. esculentum* and *L. pennellii* DNA. A population of 42 RFLP-characterized *L. esculentum* x *L. pennellii* F<sub>2</sub> plants provided by Steve Tanksley (Cornell) was then used to map TAP2 (and therefore TAP1) to chromosome 2 (see Figure 1) using the MAPMAKER computer (Lander 1987). This position is very close to that reported for the two anionic peroxidase isozymes *Prx-2* and *Prx-3* (Tanksley et al. 1993) which are reported to be 0.14 cM from each other (Rick et al. 1979). It is therefore very likely that TAP1 and TAP2 correspond to *Prx-2* and *Prx-3* although it is not clear which is which.

This result also gives some information on the relationship between physical and genetic distance in this region of the genome. It leads to an estimate of 10.7 kb per cM, which is very different to the calculated average for the tomato genome of 750 kb per cM (Tanksley et al. 1993). Near the *Tm-2a* region, on chromosome 9, 1 cM has been shown to correspond to almost 4 megabases (Ganal et al. 1989) while physical mapping in the *L<sub>2</sub>* region on chromosome 11 has shown that 1 cM corresponds to approximately 43 kb (Segal et al. 1992). It should be emphasized that the genetic distance data used to calculate all these ratios came from separate crosses involving different parents in each case.

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- Tanksley et al. (1993) High density molecular linkage maps of the tomato and potato genomes. *Genetics* 132:1141-1160.

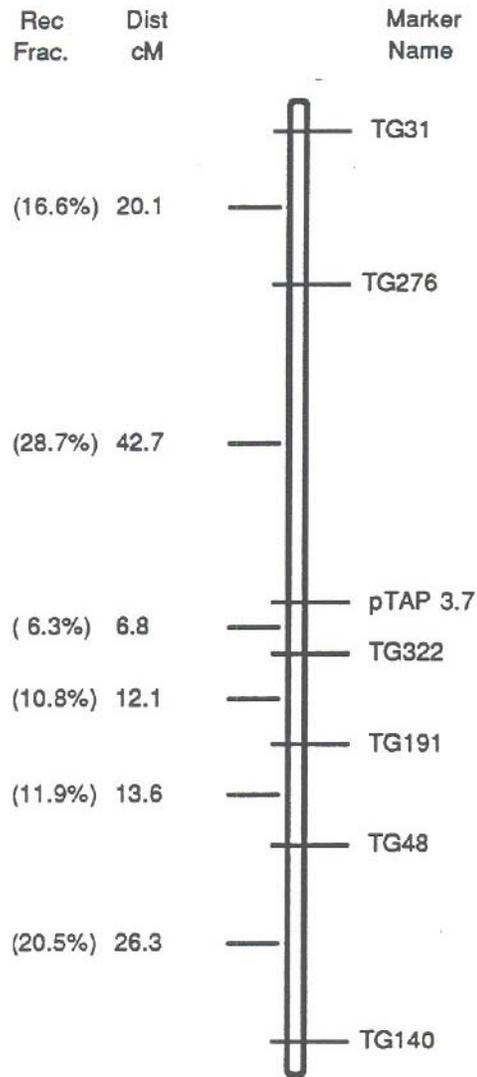


Figure 1 The position of pTAP3.7 on chromosome 2. This is approximately the same position as that given for Prx-2 and -3 (Tanksley, et al. 1993).

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The tomato *Alternaria* stem canker (*Asc*) locus confers resistance to the fungal pathogen *Alternaria alternata* f. sp. *lycopersici* and is linked to *sf* (*solanifolia*) on chromosome 3L (Witsenboer et al., 1989). Using molecular markers from Tanksley et al. (1992), we recently introduced *Asc* on the RFLP map (will be published elsewhere). The chromosomal position of *Asc* on the RFLP map, however, showed to be different from the predicted location on the integrated map (Koornneef et al., 1993). In order to correctly place *Asc* on the integrated map, three-point crosses are required. To this end, a chromosome 3 tester was selected containing the markers *sy* (*sunny*), *bls* (*baby lea syndrome*), *asc* and *sf* from an F<sub>2</sub> between LA 1004 and LA 1182. Subsequently, this tester-3 was crossed to ET570 which harbors a T-DNA in a Moneymaker background. This T-DNA was localized on the end of chromosome 3L by RFLP mapping and encodes resistance to kanamycin (*Km*) (K. Theres, pers. comm.). The resulting F<sub>2</sub> segregated for 5 loci in coupling phase: *sy*, *bls*, *Asc*, *sf* and *Km*. For *Asc* detached leaflet assays were performed (Witsenboer et al., 1989). *Km* was scored following spraying with kanamycin (Weide et al., 1989). All markers segregated in a 3:1 fashion. Recombinant fractions were calculated using JOINMAP (Stam, 1993) (Table 1). The *Asc* locus mapped between *bls* and *sf* (Figure 1). *Km* mapped distal to *sf* and consequently, the ET570 T-DNA is presently the most distal marker on the classical map of 3L.

Because *Asc* and ET570 now have been mapped on the classical map and the RFLP map, integration of the maps is possible. To construct an integrated map, linkage data of different markers have been used: classical markers (references in Koornneef et al., 1993), RFLP markers (Tanksley et al. 1992), and data combining both classic and RFLP markers (Figure 1). In addition to the *Asc* and ET570 linkage analyses that combine RFLP and classical markers, RFLP mapping data were included of *sy*, *r* and *sf* (Koornneef et al., 1993) and of *r* (Chetelat et al., 1993). The limitation of the classical map is that the markers were not all mapped relative to each other. Because most markers were mapped to *sy* and *sf* or to *r* (the backbones of the classical map), we used these to construct the integrated map. Although *pdc* has only been shown to be linked to *sy*, the marker was incorporated because it is the most distal marker on 3S. All recombination values and map positions were calculated using the computer program JOINMAP (version 1.3) with a LOD score of 3.0 for linkage groups, a LOD 0.05 for mapping, end Kosambi's mapping function (Stam, 1993). From figure 1 it is apparent that the integrated map of the long arm of chromosome 3 allows alignment of markers from different maps. In order to align markers on 3S, additional classical markers (e.g. *pdc*, *cn*, *sy*, *wf*) should be linked to RFLP markers. We would like to thank K. Theres for making available ET570 seeds and RFLP data, C. Rick for the gift of marker lines, M. Koornneef, R. Chetelat and S. Tanksley for exchanging linkage data, and P. Stam for developing and sharing the JOINMAP computer package.

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Table 1. Recombination percentages (Rec%) with standard deviation (SD) of markers in the F<sub>2</sub> derived from tester-3 x ET570.

|                        |   |   |            |   |           |
|------------------------|---|---|------------|---|-----------|
| <i>sy bls asc sf -</i> | + | + | <i>Asc</i> | + | <i>Km</i> |
| ----- X -----          |   |   |            |   |           |
| <i>sy bls asc sf -</i> | + | + | <i>Asc</i> | + | <i>Km</i> |

| Marker           | Rec% | SD  |
|------------------|------|-----|
| <i>Asc - sy</i>  | 33.4 | 3.7 |
| <i>Asc - bls</i> | 20.2 | 2.9 |
| <i>Asc - sf</i>  | 17.9 | 2.8 |
| <i>Asc - Km</i>  | 35.5 | 3.9 |
| <i>Km- sy</i>    | 45.8 | 4.3 |
| <i>Km- bls</i>   | 40.8 | 4.1 |
| <i>Km- sf</i>    | 20.8 | 3.1 |
| <i>sy - bls</i>  | 25.4 | 3.3 |
| <i>sy - sf</i>   | 42.7 | 4.2 |
| <i>bls - sf</i>  | 27.7 | 3.4 |

## CHROMOSOME 3

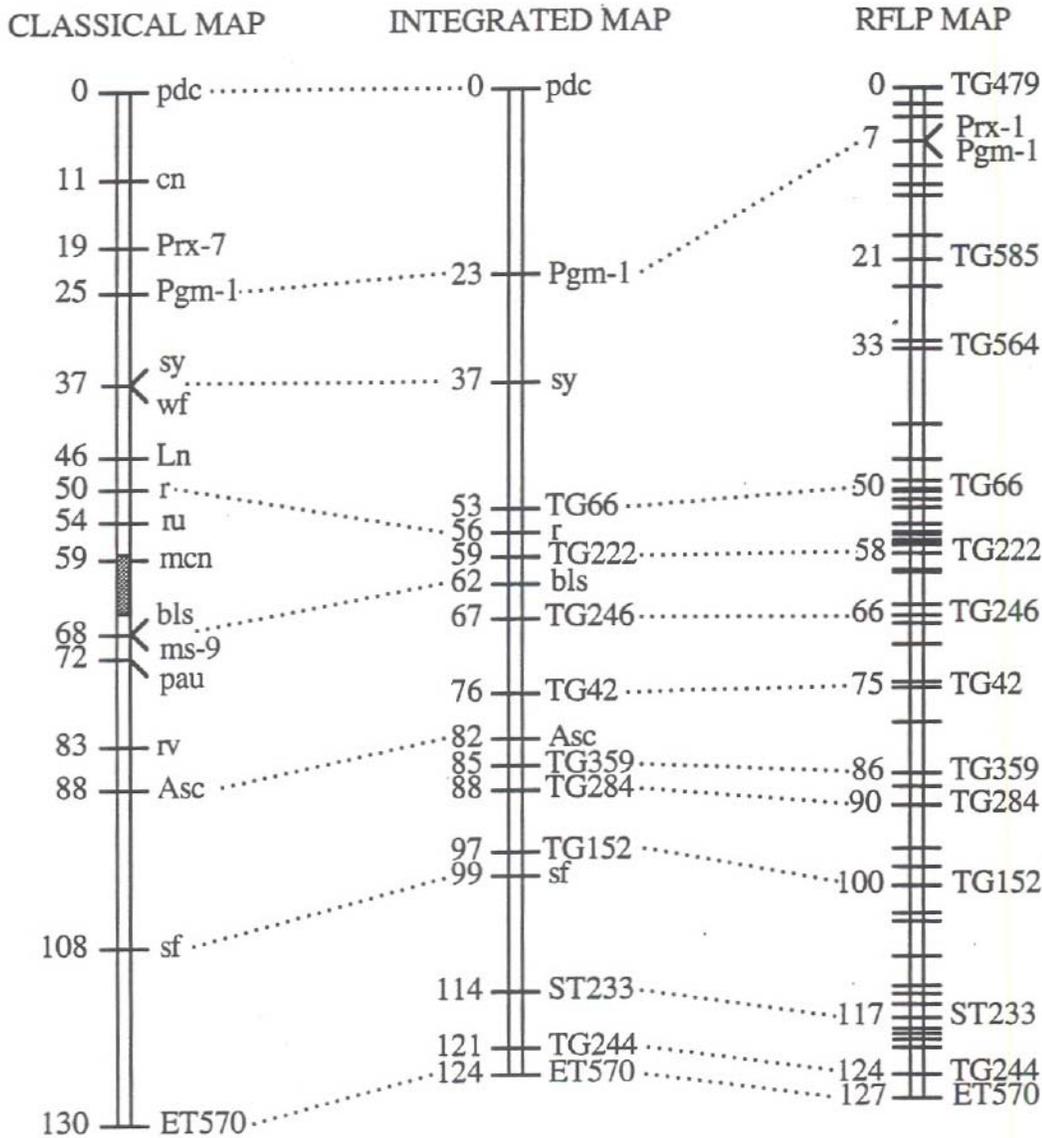


Figure 1. Different maps of tomato chromosome 3 (after Koornneef et al., 1993). The classical map has been constructed following the addition of *Asc* and *ET570* (see text) and the repositioning of *r* and *pau* by Koornneef et al. (1993). The RFLP map has been built by recomputing the segregation data of 94 markers (Tanksley et al., 1992) comprising 56 loci (horizontal lines, only some are tagged). The construction of the integrated map is described in the text. The positions of the markers are expressed in cM and are calculated using JOINMAP. The gray rectangle on the classical map represents the centromere.

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A study was made using plant material, derived from Platense, in order to assess their behavior under natural conditions of infection in the field. The plant used belonged to the Quilquil and Nuco varieties, which bear a plum-shaped fruit used industrially, and also the Uco Plata and Pitihue varieties, which bear salad fruits. Other accessions of interest were PE-4 and CIAPAN-20 belonging to *L. pimpinellifolium* and PI-126944 and PE-23 belonging to *L. peruvianum*. The susceptible variety used as a control was Rio Grande, used by industries to produce concentrated tomato, pastes, marketed by the Peto Seed Company.

To assure high levels of infection in field cultivation, transplanting was carried out on the 23 June in a plot, near peppers grown for paprika, that had been badly affected by the virus. The experimental design consisted of two repetitions, and each simple plot had a row of 5 plants, 40 cm between plants and with 1 m between each row. At the end of each simple plot, five plants belonging to the susceptible Rio Grande variety were planted to act as a control, in order to confirm the onset of the virus.

The disease was recorded based on symptoms and a later ELISA test, using TSWV-L as antiserum (LOEWE). The evolution of the vector population (*Frankliniella occidentalis*) was also followed with leaf and flower samples taken at 15 days intervals. It had already been noted that the epidemiological evolution of the disease was closely related to thrips populations in the plant matter assayed. The onset of the virus in the field was, in general, found in all the plants belonging to the Rio Grande variety, which confirmed the presence of the disease in the test plots.

The incidence of the disease related to marketable yield differed greatly depending on the plant variety (table 1). The marketable yield obtained from the industrially used Argentinean varieties, Quilquil and Nuco, exceeded 5 Kg/m<sup>2</sup>, which is satisfactory in agronomic terms. In contrast, the control plants did not produce any saleable harvest, given that all the fruits were infected by TSWV. Therefore, it has been demonstrated that the two former varieties can be cultivated in the Mediterranean coastal region despite the virus, whereas the latter, Rio Grande, a more susceptible variety is not useful.

Our results concord with those obtained by researchers in Brazil and Argentina (Calvar and Sansinanea, 1988; Gallardo, 1992; Boiteux et al., 1993), as far as the native species are concerned, which would suggest that they possess a degree of field resistance against the different isolates of the virus present on the different continents. It is therefore, important to point out the behavior demonstrated by CIAPAN-20, which proved sensitive to artificial inoculations, but did not develop symptoms of the disease when cultivated under natural field conditions. We believe that the type of tolerance shown by this accession should be studied in greater depth, with a view to its possible use in breeding programs.

Table 1. The evolution of the percentage of plants with TSWV symptoms, and later confirmation using ELISA test during cultivation.

|                                      | 26-7 | 23-8 | 21-9 | 18-10 | 15-11 | (1) |
|--------------------------------------|------|------|------|-------|-------|-----|
| Quilquil                             | 0    | 2.3  | 2.3  | 7.1   | 9.5   | 5.8 |
| Nuco                                 | 0    | 5.0  | 11.6 | 13.3  | 18.3  | 5.1 |
| Uco Plata                            | 0    | 0.0  | 0.0  | 11.7  | 11.7  | 4.2 |
| Pitihué                              | 0    | 0.0  | 9.6  | 16.1  | 19.1  | 4.7 |
| <i>L. pimpinellifolium</i> PE-4      | 0    | 0.0  | 0.0  | 0.0   | 0.0   | --- |
| <i>L. pimpinellifolium</i> CIAPAN-20 | 0    | 0.0  | 0.0  | 0.0   | 0.0   | --- |
| <i>L. peruvianum</i> PI-126944       | 0    | 0.0  | 0.0  | 0.0   | 0.0   | --- |
| <i>L. peruvianum</i> PE-23           | 0    | 0.0  | 6.6  | 33.3  | 40.0  | --- |
| Rio Grande                           | 0    | 6.6  | 40.0 | 86.6  | 100.0 | --- |

(1) marketable yield

#### Acknowledgments

The authors gratefully acknowledge the cession of Argentinean varieties by Dello Calvar (INTA Alto Valle) utilized in this work. Likewise we are extremely grateful for the financial support provided by Instituto Nacional de Investigaciones Agrarias by means of the Projects N<sup>o</sup> SC93-183-C3-1 and SC93-184-C5-1 and to the Instituto Valenciano de Estudios e Investigacion. S. Rosello thanks the Conselleria de Cultura, Educacio i Ciencia de is Generalitat Valenciana for the grant of his scholarship.

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#### *Partial resistance loci for tomato bacterial wilt show differential race specificity*

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Bacterial wilt, caused by *Pseudomonas solanacearum*, is one of the most devastating diseases of tomato worldwide. While the molecular biology of pathogenicity is well-characterized in the bacterium (Boucher et al, 1992), little is known about resistance in the host. In part, this is due to the fact that resistance is multigenic and complex (Acosta et al. 1964). Recently, we utilized DNA markers, including restriction fragment length polymorphisms (RFLPs), to uncover major partial resistance loci for bacterial wilt in a highly resistant tomato genotype (L285) (Danesh, et al. 1994). These results were based on the disease responses of 71 individuals in an F<sub>2</sub> mapping population challenged with *P. solanacearum* isolate UW-364 (race 1. biovar 4). Three unlinked resistance loci of intermediate effect were identified in the mapping population. A locus on chromosome six controlled more than 50% of total variation in resistance, while two other resistance loci were found on chromosomes seven and ten. Notably, the locus on chromosome seven was

statistically significant only if plants were inoculated through shoots. If inoculated through roots, the chromosome seven locus was not significant.

Since these earlier studies were based on experiments with only one strain of *P. solanacearum*, an important question was whether the partial resistance loci provided varying levels of resistance to different *P. solanacearum* isolates. Therefore, cuttings from F<sub>2</sub> plants in the mapping population were inoculated with two other strains of the pathogen and the statistical significance for the resistance loci on chromosomes six and ten estimated for each strain. All three strains were Race 1, with UW-364 coming originally from China (L. Sequiera, U. Wisconsin) and the other two strains (PSS4 and PSS97) both coming from Taiwan (Jaw Feng, Asian Vegetable Research and Development Center). Moreover UW-364 and PSS4 were both isolated from tomato, while PSS97 was isolated from eggplant.

The results (Table 1) clearly demonstrate that the partial resistance loci differ in their absolute and relative impact on resistance depending on *P. solanacearum* strain. Specifically, the partial resistance locus on chromosome six (near CT184) was highly dependent on *P. solanacearum* strain, showing the greatest resistance to UW-364, but little resistance to PSS4 and only modest resistance against PSS97. By contrast, the partial resistance locus on chromosome 10 (near TG225b and TG230) showed moderate levels of resistance to all three strains, although its greatest effect was also observed with UW-364.

Table 1. Statistical association between selected RFLP loci and bacterial wilt disease response for various strains of *P. solanacearum*

| LOCUS  | LOCATION | STRAIN         |        |                |        |                |        |
|--------|----------|----------------|--------|----------------|--------|----------------|--------|
|        |          | UW-364         |        | PSS4           |        | PSS97          |        |
|        |          | r <sup>2</sup> | p      | r <sup>2</sup> | p      | r <sup>2</sup> | p      |
| CT184  | Chrom 6  | 0.54           | 0.0001 | 0.06           | 0.0509 | 0.11           | 0.0100 |
| CT225b | Chrom 10 | 0.25           | 0.0001 | 0.14           | 0.0018 | 0.15           | 0.0011 |

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*Attractiveness of 'Allure' tomato, Lycopersicon esculentum to Colorado potato beetle, Leptinotarsa decimlineata.*

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Colorado potato beetles are an increasing problem with tomatoes. Both adults and larvae eat the leaves. Sometimes the fruits are nibbled enough to allow rots to enter. Potato beetles are attracted to the ornamental tomato 'Allure' which contains the wooly genet  $Wo^{mz}$ .

This attractiveness of the wooly gene was first noted in 1987 (Kerr, 1989) late in the season when the weather was cold. At first it was suggested that the beetles were just trying to find a place to keep their tarsi warm. This didn't seem to be a scientific explanation for cold-blooded insects. Besides, later observations indicated they were even more attracted in warm weather. Eigenbrode et al. (1993) have reported that  $Wo^{mz}$  is more susceptible to beet armyworm than most other tomatoes. It is probably that 'Allure' gives off an odor which people cannot detect.

In our 1993 trials (sprayed once for potato beetle control before records were taken) (Table 1) almost every beetle from 1 ha (2 1/2 acres) accumulated on four rows of 'Allure'. These rows were in different parts of the fields. Colorado potato beetles also fed on potatoes and eggplant but we do not have information on their relative attractiveness.

'Allure' was introduced as an ornamental tomato to be used primarily in home gardens. When Colorado potato beetles are controlled it produces a bushy plant *sp* about two feet in diameter. The plants are productive yielding small roundish fruits about two inches in diameter. The color is tangerine *t*. The attractive long whitish hairs of  $Wo^{mz}$  also produce "peach fuz" on the fruit. This cultivar also has the gene *alb* which gives ornamental white blotches and sectors in the leaves especially when the plants are young. The flavor is more spritely or acidic than most North American cultivars. However it is better than most of the tomatoes obtainable in Ontario in the winter.

It is expected that 'Allure' will find its main use as an ornamental for flower gardens or patios. It will be appreciated where insecticides are not used and as an IPM (integrated pest management) trap crop for concentrating Colorado potato beetles from a wide area.

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Kerr, E.A. 1989. Susceptibility to Colorado potato beetles in 'Wooly' tomatoes. TGC Report 39:20.  
Eigenbrode, S.D., J.T. Trumble and R.A. Jones. 1993. Resistance to beet armyworm, lemipterans and *Liriomyza* spp. in *Lycopersicon* accessions. J. Amer. Soc. Hort. Sci. 118(4):525-530.

Table 1. Counts of Colorado potato beetles on "Allure" and normal tomatoes. Values indicate mean number per 100 plants  $\pm$  se over four replications in 1993.

| Row | Cultivar            | # plants | June 21/22          |                     | July 22               |                       |
|-----|---------------------|----------|---------------------|---------------------|-----------------------|-----------------------|
|     |                     |          | adults <sup>Z</sup> | adults <sup>Z</sup> | immature <sup>Z</sup> | egg mass <sup>Y</sup> |
| 1   | "allure"            | 449      | 12.9 $\pm$ 2.59     | 147.1 $\pm$ 48.42   | 122.5 $\pm$ 35.88     | 4.8 $\pm$ 2.41        |
| 2   | normal <sup>X</sup> | 684      | 1.3 $\pm$ 0.73      | 0.7 $\pm$ 0.53      | 0.7 $\pm$ 0.44        | 0.0 $\pm$ 0.00        |
| 3   | normal <sup>X</sup> | 726      | 0.7 $\pm$ 0.69      | 1.7 $\pm$ 1.22      | 0.9 $\pm$ 0.7         | 0.1 $\pm$ 0.10        |
| 4   | normal <sup>X</sup> | 652      | 0.9 $\pm$ 0.57      | 1.3 $\pm$ 0.57      | 0.0 $\pm$ 0.00        | 0.0 $\pm$ 0.00        |

<sup>Z</sup>Significant difference between "Allure" and three normal rows using ANOVA at  $P < 0.001$

<sup>Y</sup>Difference not significant using ANOVA at  $P > 0.05$

<sup>X</sup>Difference between three normal rows not significant using ANOVA at  $P > 0.05$

#### Evaluation of *Solanum ochranthum* as a potential source of late blight resistance

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Breeding for late blight resistance in tomato has been on-going for more than 45 years. Several cultivars with monogenic resistance to *Phytophthora infestans* are available but cultivars with good horizontal (field) resistance have yet to be developed. A few wild tomato relatives, *Lycopersicon pimpinellifolium*, *L. hirsutum*, *L. esculentum* var. *cerasiforme* and *L. cheesmanii* var. *minor*, have been identified as possible sources of late blight resistance (Lukyanenko, 1991). *Solanum ochranthum*, a self incompatible woody vine-like species found in moist habitats, belongs to the group of *Solanum* species that is most closely related to and likely ancestral to *Lycopersicon* (Rick, 1988). Rick (1986) suggests that *S. ochranthum* may be a possible source of resistance to several fungal diseases. The potential of *S. ochranthum* as a possible source of late blight resistance was evaluated.

Three accessions of *S. ochranthum*, P.I. 230508, P.I. 473498 and P.I. 498268 were obtained from J. Bamberg (Potato Intro. Stn., Sturgeon Bay, WI). The accession LA 2117 was obtained from C.M. Rick (Univ. Calif., Davis, CA). Seeds were pretreated by soaking in 50% household bleach solution for 30 mins., rinsed thoroughly and germinated on moist filter paper in petri plates prior to planting. Plants were maintained in controlled environment chambers at 27C under 16 hour daylength. Late blight resistance was measured by a modified detached leaf test (Turkensteen, 1973). Zoospore inoculum was prepared from *Phytophthora infestans* isolated from infected leaves of tomato and potato (Deahl, et al., 1991). *S. ochranthum* leaves were inoculated by placing four 50  $\mu$ l droplets of inoculum on the abaxial surface. Leaves were incubated in plastic containers at 100% RH at 25C. Disease ratings were recorded 4 days after inoculation.

Moderate resistance against both the tomato and the potato isolates of *P. infestans* was detected among the four *S. ochranthum* accessions, with P.I. 230508 having the highest degree of resistance (Table 1). Interestingly, all of the *S. ochranthum* lines appeared to have a slightly greater tolerance to the *P. infestans* isolated from tomato than to the isolate from potato. Our results suggest *S. ochranthum* may be a promising source of tomato late blight resistance.

Table 1. Disease ratings of *Solanum ochroanthum* accessions in a detached leaf test measuring resistance to *Phytophthora infestans*.

| Accession                          | Mean disease rating ( $\pm$ S.E.) <sup>Z</sup> |                |
|------------------------------------|--|----------------|
|                                    | Potato isolate                                 | Tomato isolate |
| P.I. 230508 (8) <sup>Y</sup>       | 1.9 $\pm$ 0.4 <sup>X</sup>                     | 1.3 $\pm$ 0.4  |
| P.I. 473498 (4)                    | 2.5 $\pm$ 0.5                                  | 1.3 $\pm$ 0.6  |
| P.I. 498268 (2)                    | 4.5 $\pm$ 0.2                                  | 2.6 $\pm$ 0.7  |
| LA 2117 (1)                        | 3.0 $\pm$ 0.0                                  | 2.0 $\pm$ 1.0  |
| <i>L. esculentum</i> 'Rutgers' (4) | 4.0 $\pm$ 0.0                                  | 4.5 $\pm$ 0.5  |

<sup>Z</sup>Data represent combined results from two repeated experiments.

<sup>Y</sup>Numbers in parentheses indicate the number of plants tested for each accession.

<sup>X</sup>Scale of 0 to 5 where 0 = no infection, 1 = 0-20% of the leaflet surfaces infected, 2 = 20-40% of the leaflet surfaces infected, 3 = 40-60% of the leaflet surfaces infected, 4 = 60-80% of the leaflet surfaces infected, 5 = 80-100% of the leaflet surfaces infected.

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#### Screening of resistant materials of *Lycopersicon spp* to TSWV by means of thrips transmission.<sup>1</sup>

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Tomato Spotted Wilt Virus appeared in Spain as a disease in 1988 (Cuadrado et al., 1989; Jorda and Osca, 1989). Its appearance was followed by its spread to crops in many mild areas due to exchange and trade of plant material (Lacasa et al., 1991) and to the dispersion of *Frankliniella occidentalis*, its more efficient vector (Marchoux et al., 1993; Lacasa and Contreras, 1993; Wijkamp and Peters, 1993). Economic losses of marketable tomato yield have been important, principally in areas near the Mediterranean coast and Canary Islands (Lacasa et al., 1993), in spite of efforts made to control the vector.

Mechanical transmission is the method most frequently used to evaluate the response of infected materials in order to look for genetic resistance (Paterson et al., 1989).

TSWV is naturally spread by thrips, but it is possible to obtain different results if the infection of plant material takes place through mechanical transmission. These differences have been stated by Krishna et al. (1993) in some accessions of *Lycopersicon* and by Nuez et al. (1994) in others belonging to *Capsicum* genus. Materials screened in natural conditions versus artificial infection (including mechanical and thrips transmission) have also shown different results. The phenomenon known as field resistance or tolerance has been observed in *Lycopersicon* (Costa et al., 1994; Smith and Gardner, 1993, Krishna et al., 1993 and Boiteux et al., 1993).

Taking this fact into account, we have evaluated some varieties of *L. esculentum* and different accessions of *L. pimpinellifolium* and *L. peruvianum* by means of mechanical and thrips transmission and field conditions (Costa et al., 1994). UPV-101 and UPV-200 lines are carriers of Sw1 and Sw2 genes respectively, and RDD line has been developed from Stevens.

Seedlings of accessions were exposed to viruliferous thrips maintained on susceptible tomato (cvs. Muchamiel and Marmande) and pepper (cvs. Buketar, Negral and Sonar) previously infected. Trials were carried out in a semiclimatic room at 22-24°C, 45-50% of relative humidity during the day and 85-100% of relative humidity at night, photoperiod of 14 hours and 3500 lux of luminosity. Plants were introduced at 4-6 developed leaves stage and kept there for enough time for systemic symptoms to appear. Plants that did not show any symptom, remained in the room for three months. Samples of each plant were taken and analyzed by serological technique ELISA with antiserum TSWV-L (Loewe). Plants free of symptoms were transplanted to fields under natural infection conditions. Plant samples and analysis were carried out each 15 days.

First symptoms on susceptible accessions appeared 12-15 days after its contact with viruliferous thrips. Table 1 shows results of the three methods of inoculation

We would like to point out two aspects. First, Argentinean materials (Quilquil, Nuco, Uco Plata and Pitihue) were susceptible when thrips transmission was utilized as well as with mechanical transmission (Quilquil and Nuco). Nevertheless, level of infection under field conditions were very low. This field resistance was reported previously by Boiteux et al. (1993) for this type of material. Similar results have been obtained for *L. pimpinellifolium* CIAPAN-20, which did not show any symptoms under field conditions.

On the other hand, resistance was observed in RDD and UPV-101 when inoculated mechanically with different isolates (Jorda et al., 1994), whereas many plants showed systemic symptoms when thrips transmission was used as well as in field conditions. Plants RDD that did not show symptoms by thrips transmission were transplanted to the field where they became infected at the end of the crop period. PVY was detected in infected plant by means of electronic microscopy, as was TSWV. Therefore, we can not attribute the death of the plants to TSWV alone.

Slight local lesions appeared in *L. peruvianum* PI-126944 when plants were exposed to viruliferous thrips. Systemic symptoms did not appear. We can consider this accession resistant to TSWV.

We conclude that it is convenient to test materials by using infected thrips under controlled conditions, as interactions between host and vector have to be taken into account. The same conclusion has been drawn by Krishna et al. (1993). We would also like to emphasize that materials showing susceptibility to artificial transmission can be

of agronomic value when they are cultivated under field conditions. The Argentinean materials, RDD and UPV-101 behaved in this way. We consider that these materials can be grown at present and allow for a marketable yield.

Table 1. Behavior of different genotypes.

| Genotypes                       | Type of artificial transmission |        | Field conditions | Agronomic Value |
|---------------------------------|---------------------------------|--------|------------------|-----------------|
|                                 | Mechanical                      | Thrips |                  |                 |
| Muchamiel                       | U                               | +      | U                | 1               |
| Marmande                        | U                               | +      | U                | 1               |
| Quilquil                        | +                               | +      | ±                | 4               |
| Nuco                            | +                               | +      | ±                | 4               |
| Uco Plata                       | U                               | +      | ±                | 3.5             |
| Pitihué                         | U                               | +      | ±                | 4               |
| RDD                             | -                               | ±      | ±                | 3               |
| UPV-101                         | -                               | ±      | ±                | 3.5             |
| UPV-200                         | +                               | +      | +                | 1               |
| <i>L. pimpinellifolium</i> PE-4 | +                               | +      | ±                | -               |
| <i>L. pimpinellifolium</i>      | +                               | +      | -                | -               |
| CIAPAN-20                       |                                 |        |                  |                 |
| <i>L. peruvianum</i> PI-126944  | -                               | *      | -                | -               |
| <i>L. peruvianum</i> PE-23      | +                               | +      | ±                | -               |
| Rio Grande                      | U                               | U      | +                | 1               |

+ = Symptoms

- = With no symptoms

\* = Local lesions

± = Plant with symptoms and plant with no symptoms

U = Undetermined

Agronomic value 0-5: (0= poor, 5= good)

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*Allelism of Cf-19, of Cf-23, and of the Cladosporium resistance gene of the line Bulgaria N°1.*

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A series of tomato lines are studied in relation to *Cladosporium fulvum* (= *Fulvia fulva*) isolates from France and other countries of the Old World. Among these we have observed several groups of lines having the same type of reaction in front of the large number of studied isolates.

Until now we have demonstrated allelism or independence of various sources of partial resistance (to see TGC Report 41 and 43). Now we have to present the results of three allelism tests between the three following lines controlling a absolute and dominant *Cladosporium* resistance. This resistance is sometimes accompanied by some little necrotic spots.

- Ontario 7519 (*Cf-19*), received from E.A. Kerr (1980)
- Ontario 7523 (*Cf-23*), received from E.A. Kerr (1980)
- Bulgaria N°1, received from I.W. Boukema (1980).

For the three independent tests three plants of each line served as the basis of the crosses. Here we present the total of plants for every group. The tests were carried out using a French *Cladosporium* isolate belonging to pathotype 0.

The results (Table 1) show that not one susceptible plant was found among the tested populations. Thus the allelism of Cf-19, Cf-23 and the allele controlling the resistance of *Bulgaria N°1* can be concluded.

Table 1 : Response of plant populations and lines after inoculation with a pathotype 0 *Cladosporium* isolate.

| Populations or lines                             | Number of plants |             |
|--|------------------|-------------|
|  | resistant        | susceptible |
| F1 (ONT 7519 X ONT 7523) 1,2 and 3               | 60               | -           |
| F2 (ONT 7519 X ONT 7523) 1,2 and 3               | 160              | -           |
| F1 (ONT 7519 X ONT 7523) 1,2 and 3 X Monalbo     | 180              | -           |
| F1 (ONT 7519 X Bulgaria n°1) 1,2 and 3           | 60               | -           |
| F2 (ONT 7519 X Bulgaria n°1) 1,2 and 3           | 150              | -           |
| F1 (ONT 7519 X Bulgaria n°1) 1,2 and 3 X Monalbo | 180              | -           |
| F1 (ONT 7523 X Bulgaria n°1) 1,2 and 3           | 48               | -           |
| F2 (ONT 7523 X Bulgaria n°1) 1,2 and 3           | 180              | -           |
| F1 (ONT 7523 X Bulgaria n°1) 1,2 and 3 X Monalbo | 177              | -           |
| ONT 7519   | 13               | -           |
| ONT 7523   | 35               | -           |
| Bulgaria n°1                                     | 35               | -           |
| Monalbo (susceptible line)                       | -                | 54          |

NILs of Tomato except for Ph-2 gene

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During the 1960's we have received from M.E. Gallegly various resistant lines to *Phytophthora infestans*. All the french isolates studied attacked W Va 106 having the gene *Ph* controlling a hypersensitivity to the pathotype 0. The resistance of W Va'63 having *Ph* plus a multigenic resistance to the pathotype 1 (Gallegly 1960) given a partial control of the disease against all our isolates (Laterrot 1975). The resistance of W Va'63 was introduced from *Lycopersicon pimpinellifolium* W Va 700. The resistance of W Va 700 was attributed to a single gene : *Ph-2* (Turkenstein 1973). All our observations agree with a monogenic control with incomplete dominance of a partial resistance.

We have used the more agronomically interesting lines received from M.E. Gallegly. These lines were W Va'63 and X 384. We present here 6 NILs obtained in 6 very different genetic backgrounds. They are by chronological obtention:

| <i>Ph-2</i> lines | Year | <i>Ph-2</i> <sup>+</sup> lines | Pedigree   |
|-------------------|------|--------------------------------|--|
| Piéraline         | 1969 | Piéralbo                       | (W Va' 63 x Piéralbo) <sup>4</sup>                                     |
| Héline            | 1975 | Heinz 1706                     | (Rossol x Heinz 1706) <sup>4</sup> x (X 384 x Heinz 1706) <sup>3</sup> |
| Caline            | 1981 | Campbell 28                    | (Héline x Campbell 28) <sup>4</sup>                                    |
| Fline             | 1982 | Flora Dade                     | (Héline x Flora Dade) <sup>4</sup>                                     |
| Mécline           | 1982 | Earlymech                      | (Héline x Earlymech) <sup>4</sup>                                      |
| Piline            | 1982 | Europeel                       | (Héline x Europeel) <sup>4</sup>                                       |

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*RFLP polymorphism between two tomato lines*

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In order to map quantitative traits as soluble solids contents, it would be advantageous to work on intraspecific cross (*Lycopersicon esculentum*). The progeny has acceptable agronomic characteristics, good fertility and the segregations are not skewed compared to progeny of interspecific crosses. The two following lines were studied

- Plovdiv 43/10, origin Maritsa Institute (Bulgaria), with high soluble solids contents (7 to 7.5 °Brix) and determinate growth, derived from *L. pimpinellifolium* (Yordanov et al., 1977),
- Castone, origin INRA/CTCPA Montfavet (France), cultivated in France for paste production with mechanical harvest (Laterrot and Damidaux, 1994).

A total of 33 tomato low-copy nuclear probes (provided by S. Tanksley of the Cornell University, Ithaca, N.Y., USA), regularly distributed across the different chromosomes of the interspecific tomato map (Tanksley et al., 1992) were used to examine the restriction fragment length polymorphism between the DNA of the 2 tomato lines cut with 8 restriction enzymes (*BamHI*, *DraI*, *EcoRI*, *EcoRV*, *HaeIII*, *HindIII*, *TaqI*, *XbaI*). DNA extraction, digestion, electrophoresis, southern blotting and hybridization were performed as Lefebvre et al. (in press) described. Each probe was not systematically tested with all the digested DNA, leading to an average of 6.6 different restriction enzymes tested per probe.

Differences between enzymes were detected with respect to polymorphism. No polymorphism was found with *Oral* (22 probes), *TaqI* (24 probes) and *HindIII* (31 probes). *EcoRI*, *XbaI*, *EcoRV* were the enzymes detecting the largest amount of polymorphism (4 polymorphic on 29 probes for *EcoRI*, 4 polymorphic on 31 probes for *XbaI*, 2 polymorphic on 31 probes for *EcoRV*). This observation corroborated with the conclusions of Miller and Tanksley (1990 a) who showed that the enzymes generating the largest genomic fragments as *XbaI* and *EcoRV* detected the largest amount of polymorphism.

Among 219 enzyme-probe combinations tested, 12 (5.5 %) revealed polymorphism between Castone and Plovdiv 43/10. The polymorphism level with at least one restriction enzyme corresponded to 15.2 % (5 probes among 33). In fact, the same degree of polymorphism would have been detected if only *EcoRI* and *XbaI* had been used. Indeed when a probe is polymorphic, the polymorphism is often detected with several enzymes. If it corresponds to a chromosomal rearrangement (insertion/deletion for instance), its segregation in the progeny would be the same whatever the enzyme used. The 5 polymorphic probes were randomly distributed on the tomato map.

This preliminary study revealed a weakly higher degree of polymorphism than reported by Miller and Tanksley (1990 b) who found on average 6% of polymorphic probes with a single restriction enzyme between modern tomato cultivars. It confirmed the very low level of RFLP within *L. esculentum* and encourage us to develop other types of DNA markers.

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*Molecular cloning of a second S-allele from Lycopersicon peruvianum and assessment of allele frequencies in populations based on DNA hybridization.*

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A cDNA encoding an S-related stylar protein was cloned from *L. peruvianum* (LA2163). The corresponding gene was mapped to the S-locus, sequenced, and used to probe DNA from representatives of 10 populations of *L. peruvianum* (Rivers *et al.*, 1993). The cDNA library was further screened using the cloned, mapped S-allele ( $S_7^*$ ). The second S-allele ( $S_6$ ) was cloned and mapped to the S-locus using a backcross population (LA2157 x LA2163) x LA2163. All seed was provided by C.M. Rick.

The  $S_6$  allele was also hybridized to the DNA from the 10 populations of *L. peruvianum* used in the original survey (Table 1). In addition, the number of plants from 3 accessions was increased (25 additional plants of LA2163, 29 additional plants of LA2326, and 7 additional plants of LA1952). Southern hybridization was conducted under moderate conditions of stringency (68°C, 5X SSC during hybridization, final wash at 68°C, 0.5 X SSC).

It has been reported that the conditions under which the S-probe hybridization was conducted are capable of detecting alleles sharing between 60% and 70% sequence similarity (Bernatzky *et al.*, 1988). Based on previous findings (Ioerger *et al.*, 1990; Rivers *et al.*, 1993), the paucity of homologous DNA fragments among these populations is not surprising. It is interesting to note the lack of homologous fragments even within the accession from which these two functional S-alleles were cloned, underscoring the extraordinary sequence diversity characteristic of this locus. Since sequence divergence at this locus is extreme, absence of hybridization signals can not be taken as evidence for lack of functional S-alleles.

From this data, it would appear that  $S_6$  may be more common than  $S_7$ , or at least more homologous to a larger number of alleles. True identity of alleles can only be determined through controlled pollinations and progeny tests.

Both of these clones are available to interested researchers.

\* $S_7$  was formerly reported as  $S_5$  (Rivers *et al.*, 1993) but the designation  $S_5$  had already been used (Tsai *et al.*, 1992).

Table 1. Results of filter hybridization of *L. peruvianum* genomic DNA to the  $S_7$  and  $S_6$  probes conducted under moderate (68°C) stringency. Accessions are listed in approximately ascending south latitude.

| Accession number | Number of plants from which seed was collected | Number of plants sampled from collected seed | Number of plants that hybridize to $S_7$ | Number of plants that hybridize to $S_6$ |
|------------------|--|--|--|--|
| LA2163           | 12   | 35   | 1  | 2  |
| LA2326           | 13   | 37   | 1  | 1  |
| LA1981           | 11   | 9  | 0  | 0  |
| LA1365           | 7  | 10   | 1  | 0  |
| LA1274           | 6  | 10   | 1  | 1  |
| LA1283           | 13   | 10   | 0  | 3  |
| LA1952           | 20   | 16   | 1  | 0  |
| LA1955           | 20   | 10   | 1  | 0  |
| LA2774           | 12   | 10   | 0  | 2  |
| LA2770           | 13   | 8  | 0  | 4  |

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*Mapping of tomato genes induced in a compatible root-knot nematode interaction*

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In case of a compatible interaction, root-knot nematodes prompt the development of complex feeding sites (galls containing giant cells) in the root system by altering the expression of plant genes. Tomato (*Lycopersicon esculentum* cv. Marmande) genes that are either induced or repressed upon nematode infection (referred to as *Lemmi* genes) have been isolated from a cDNA library made from root galls induced by *Meloidogyne incognita* race 1 (Van der Eycken et al. 1992a, 1992b). Three *Lemmi* genes (*Lemmi 2*, *Lemmi 9* and *Lemmi 10*) that are highly expressed in galls, particularly in the giant cells, have been chosen for further studies (van der Eycken et al., in prep.). When looking for possible functions in giant cells, one may compare the map position of *Lemmi* genes with the position of genes already mapped (Tanksley et al., 1992). Mapping nematode induced-genes would also provide information as to their distribution among the tomato chromosomes and, thus, supplement the genetic linkage map of tomato.

We have mapped *Lemmi* genes 2, 9 and 10 by RFLP linkage analysis using an F<sub>2</sub> mapping population (84 plants) derived from a cross *L. esculentum* cv. Allround x *L. pennellii* LA716 (Odinot et al. 1992) that has been characterized with 38 RFLP markers

(TG clones) common to the map constructed by Tanksley et al. (1992). To position the *Lemmi* genes on the genetic map, we have hybridized each to Southern blots containing DNA, digested with Dra I, from the 84 plants of our mapping population and added the segregation data to the linkage data for this population, using the JoinMap computer program (Stam, 1993).

The linkage analysis showed that *Lemmi 9* is located on chromosome 1 between the markers TG71 and TG209 and that *Lemmi 2* and *Lemmi 10* map to the same position at the end on chromosome 10 below the marker TG420 (fig.1). In fact, *Lemmi 2* and *Lemmi 10* both hybridized to a 1.2kb DraI fragment. To refine the map positions of *Lemmi* genes on chromosomes 1 and 10, we have scored in our mapping population the segregation of two additional RFLP markers, TG 295 and TG 229, that are known from the published map (Tanksley et al., 1992) to be at close distance to *Lemmi 9* and *Lemmi 2* (*Lemmi 10*, respectively).

As shown in fig.1 the nematode-induced *Lemmi 9* gene maps between TG71 and TG295. Comparison with the Tanksley map shows that *Lemmi 9* is located near the previously mapped *ACC2* gene, which is induced in tomato during floral and fruit senescence (Rottmann et al., 1991). *Lemmi 2* and *Lemmi 10* genes, which cross-hybridize but show different expression patterns, probably represent two members of a gene family that are physically linked on a Dra I fragment of 1.2 kb.

To be able to draw a more general picture of how functionally related genes, like the nematode-induced ones, are distributed over the chromosomes, more genes need to be identified and mapped.

#### Acknowledgments

This research was supported in part by a grant (no.CI 1-CT91-0932) from the Commission of the European Communities.

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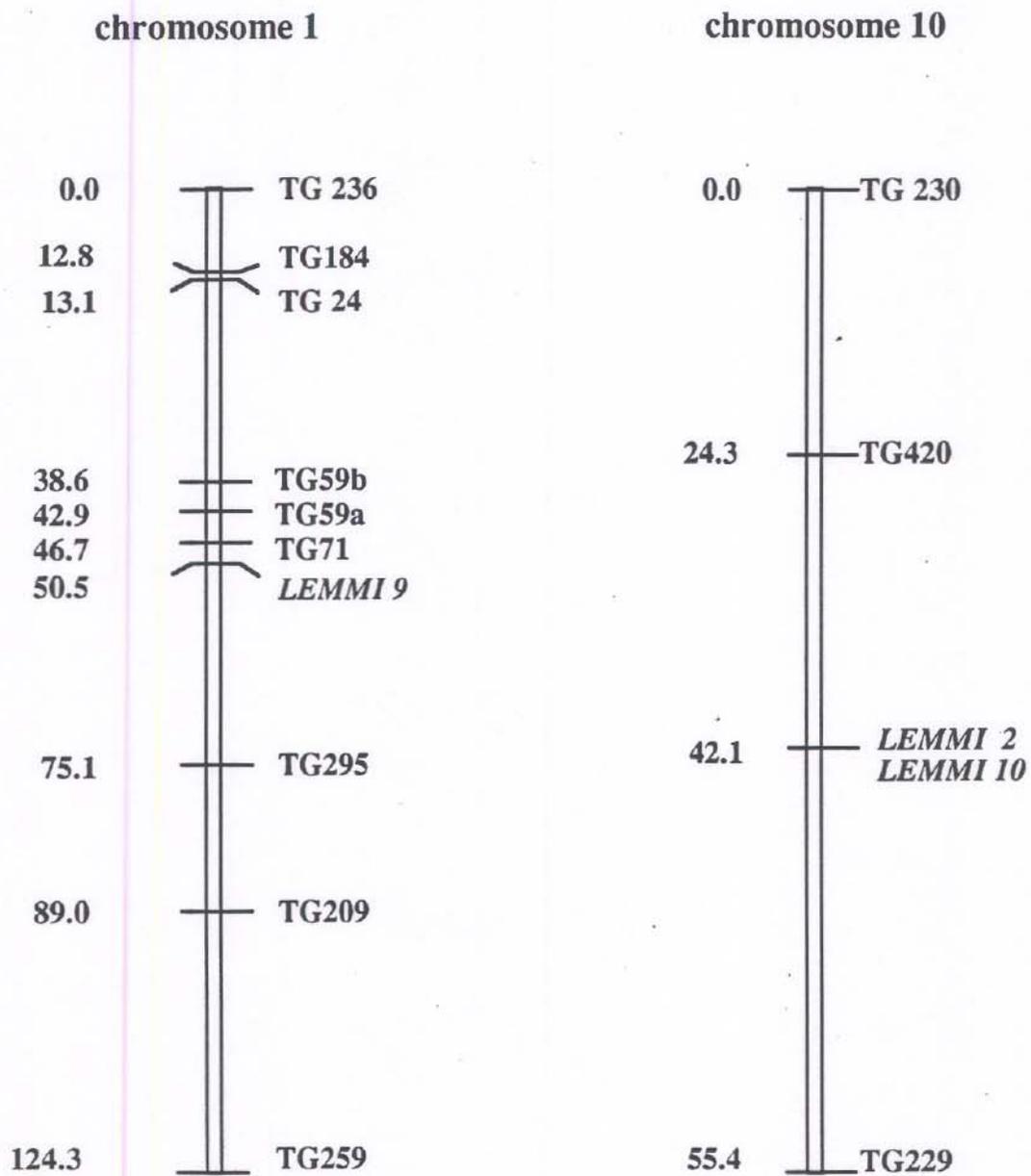


Figure 1. Position of the nematode-induced genes Lemmi 2, 9, and 10 on the molecular linkage map of tomato chromosomes 1 and 10.

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Based on a multivariate Canonic Discriminant Procedure, with 12 quantitative characteristics, it was found that a model, including the variables: petal number by flower, fruit size, locule number by fruit, pericarp width, flower number by inflorescence and soluble solids fruit content, explained, for the first and second canonic components 66% of the total variability. With the above variables, a cluster procedure was carried out and 10 clusters were produced, based on genetic distances, for 57 Latin American tomato cultivars assembled at the university of California Tomato Genetics Stock Center, which are included on Table 1.

**Table 1. Clusters of Latin American tomato Cultivars**

| Cluster Number | Genotypes | Cluster Number | Genotypes |
|----------------|-----------|----------------|-----------|
| 1              | LA 1457   | 5              | LA 117    |
|                | LA 1565   |                | LA 473    |
|                | LA 1702   |                | LA 394    |
|                | LA 408    |                | LA 468    |
|                | LA 1703   |                | LA 1241   |
| 2              | LA 1566   |                | LA 404    |
|                | LA 1567   |                | LA 403    |
|                | LA 1460   |                | LA 477    |
|                | LA 1568   |                | LA 1238   |
|                | LA 125D   |                | LA 457    |
|                | LA 2384   | LA 409         |           |
|                | LA 134A   | LA 2381        |           |
|                | LA 1564   | 6              | LA 1544   |
|                | LA 423    |                | LA 402    |
| 3              | LA 1218   |                | LA 126    |
|                | LA 1224   |                | LA 147    |
|                | LA 358    | LA 1213        |           |
|                | LA 395    | LA 478         |           |
|                | LA 459    | LA 1462        |           |
|                | LA 172    | 7              | LA 357    |
|                | LA 1215   |                | LA 466    |
|                | LA 113    | 8              | LA 416    |
|                | LA 1244   |                | 9         |
|                | LA 1162   | 10             |           |
| LA 396         |           |                |           |
| LA 405         |           |                |           |
| LA 356         |           |                |           |
| LA 1240        |           |                |           |
| 4              | LA 401    |                |           |
|                | LA 415    |                |           |
|                | LA 1216   |                |           |
|                | LA 467    |                |           |
|                | LA 393    |                |           |

Screening tomatoes (*Lycopersicon* spp) for powdery mildew (*Leveillula taurica* (Lev. Arnand) resistance in the Sudan.

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Tomato is one of the most important vegetable produced in the Sudan. Its production faces many disease problems, along which is the powdery mildew which in the recent years had resulted in significant crop losses, particularly during the relatively cool winter season. In many surveys, the disease was found to be very serious in eastern and central parts of Sudan (Mohamed Y.F., unpublished). The disease was reported to be caused by *Leveillula taurica* and *Oidium lycopersici* (Kozik, 1993).

In this study, commonly grown tomato varieties, hybrids and some lines obtained from INRA; France and from different seed companies were tested for powdery mildew resistance. The plants were subjected to natural infection in the field. Four samples of diseased leaves from each entry were examined using the microscope. Evaluation for powdery mildew resistance, was done twice, the first was at flowering stage and the *other* one month later. A rating scale of 9 (resistance), 7 (high intermediate resistance), 5 (intermediate resistance), 3 (low intermediate resistance) and 1 (susceptible) was used, and the average of the two evaluations was taken as shown in table (1):

Table 1 Reaction of *Lycopersicon* spp., varieties hybrids and lines to powdery mildew (*Leveillula taurica*).

| Rating            | Varieties Hybrid or Lines  |
|-------------------|--|
| Resistant         | LA 1478 ( <i>Lycopersicon pimpinellifolium</i> )   |
| High intermediate | FA30 F1, Calev, Belev, Hawai 7998, Hirol   |
| Low intermediate  | Rondellow F1, Top 21 F1, Mottle, Marpurum  |
| Susceptible       | Rawpack, Caston, Menang, Columbia, Marmande, Red Fantasy, Sunex calte, Alta, Sinalda, Indian IPS, Summer set, AllaKarim**, Big strike F1, F1 93 T38 (Clause), Peto 86* (Global), Peto 86* (California), Peto 86* (Sluis and Groot), Strain B* (Royal Sluis), Strain B* (sluis and Groot), Strain B* (Popvrient), Strain C* (sun seed), Super Strain B* (Keystone), UC 9703* (Pioneer), Montcarlo (Peto seed) |

\* Commercially grown.

\*\* Local variety grown on the western Sudan.

Microscopic examination proved that the causal agent of the disease was *L. taurica* and none of the samples showed the presence of *Oidium lycopersici*. Field results showed that none of the lines, varieties and hybrids was immune. The only line that showed resistance was a *Lycopersicon pimpinellifolium* (Acc. LA1478). The tomato varieties Calev and Belev which were developed at INRA as resistant to the disease showed only high intermediate level of resistance. This could be attributed to either a different race of the pathogen or more conducive environmental conditions for infection and disease development, thus they could not be utilized as a good source of resistance to be transferred in the susceptible commercial varieties grown in Sudan. The rest of *Lycopersicon esculentum* collection tested which contain F<sub>1</sub> hybrids, varieties and lines was mostly in the susceptible group. This made it necessary to go for interspecific crosses to transfer resistance into commercial varieties of tomatoes.

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*Cactiflora (ccf)*, a novel proliferated flower mutant

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This mutant (3-805) was encountered in our program of EMS mutagenesis. It bears close resemblance to a variant described in Genetics 30:374-362 (1945) and other in the intervening years, discovered as spontaneous unfruitful mutants in experimental and commercial fields and maintained clonally for several years. Since they did not appear in pedigreed families and were totally sterile, it was impossible to either maintain them via sexual reproduction or ascertain their inheritance. Patience again paid off, as this similar or identical cactiflora mutant was found in an M<sub>2</sub> of EMS-treated cv. Castelemart. The mutant plants are normal in all respects except for an extreme modification of flower morphology, also reflected in the form of its (parthenocarpic) fruits. The flower is grossly fasciated with consequent increase in corolla and calyx segments. The center of the flower is transmogrified by a distorted fusing of androecium, gynoecium, and green tissue that tends to project beyond the normal position of reproductive parts as the flower ages. This jumble of parts often continues to develop into a fruit-like structure of considerable size, up to 8 cm diam., which results in a irregular distorted mass of fruit-like tissue, in which are imbedded anthers and other flower part, lacking seeds in every dissected example. The floral structures are large and persistent, rendering them more showy at a distance than + flowers.

Since in every examination of cactiflora, male and female sterility was complete, the only mode of sexual transmission possible is via selfed heterozygous, yielding F<sub>2</sub> segregations. Of four F<sub>3</sub> families grown in 1993, two were completely normal, the other two segregated, yielding a total of 21 normal (+) plants and 5 *ccf*. Since this segregation does not deviate significantly from 3:1, it is assumed that cactiflora is determined by a single recessive gene, which we symbolize *ccf*.

Abg-- a gene on chromosome 10 for purple fruit derived from S. lycopersicoides

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Fruits of *S. lycopersicoides* in its native habitat develop strong anthocyanin, often becoming totally jet-black, in the outer cell layers of the fruit in late stages through maturity. This intensity is seldom reached in fruits of plants grown outside the native habitat, generally in greenhouses. Light intensity is implicated as a cause of the difference because areas beneath the calyx or artificially shaded portions of the fruit lack such pigmentation. Furthermore, the high intensity of solar radiation in the native area (2,000-3,600 m elevation in the Andes of S. Peru and N. Chile), which has to be experienced to be appreciated, is probably never matched in experimental plantings elsewhere.

This trait is weakly expressed in the F<sub>1</sub> intergeneric hybrids and moderately so in the alien addition line for chromosome 10, thereby ascertaining its dominance and chromosome location. Segregation was first observed in BC<sub>2</sub> and BC<sub>3</sub> progenies from a single derivative of a diploid hybrid. Pigmented BC<sub>3</sub> individuals were selfed and subsequent generations were grown and classified for presence and intensity of pigmentation. Progenies were grown in the winter greenhouse and summer field, the strongest expression being observed in the latter, particularly toward the end of the season. Expression in the derivatives did not match that of the nightshade fruits in the wild but approximated that of the more extreme expression of the latter grown under our greenhouse conditions. Variegations, as in a spotty or blotchy pattern or sharply defined radial sectors of different intensity, are other characteristic, yet erratic, features of this phenotype. Exposed areas of developing fruits in the last half of their development can be totally flushed with anthocyanin, resembling medium-pigmented eggplant fruits, hence the name Aubergine and symbol *Abg*. Anthocyanin accumulation is also enhanced by superficial wounding (punctures, scrapes) of the fruit epidermis. This type of enhancement might account for certain types of the aforementioned variegation.

Five pooled BC<sub>3</sub> families yielded 35 pigmented: 22 normal, the proportion of normals being below monogenic expectation in each family. The early progenies from selfing proved difficult to score, probably because classification was attempted under unfavorable conditions. Five BC<sub>3</sub>S<sub>3,4</sub> families segregated 18 *Abg*: 31 *+/Abg*: 16 *+*, the separation between the two pigmented classes proving difficult. Progeny tests were made from one such family with the following results:

| Parent       | Progeny                                      |
|--------------|--|
| <i>Abg</i>   | 3 families = <i>Abg/Abg</i> ; one segregated |
| <i>+/Abg</i> | 2 segregated; two = <i>Abg/Abg</i>           |
| <i>+</i>     | 5 bred true for <i>+</i> phenotype           |

It is thereby evident that we did not succeed in distinguishing *Abg/Abg* from *+/Abg* fruit phenotypes; consequently, only 2-category classifications are reliable. The total F<sub>2</sub> segregation thereby becomes 49 *Abg* ; 16 *+* - a reasonable monogenic segregation.

The assumption of monogenic control was verified by a linkage search. In screening segregation of *Abg* against a series of RAPD markers, we encountered the following cosegregation with the chromosome 10 marker D03-1200. Two small families: of BC3S3 parentage were pooled with the following totals:

| D03-1200 | + | <i>Abg</i> |
|----------|---|------------|
| +        | 6 | 1          |
| S        | 0 | 13         |

Deviation from random distribution in this contingency table is highly significant, the associated  $\chi^2$  (1 d.f.) = 13.00\*\*\*.

Thus, despite the small population size, cosegregation of *Abg* with D03-1200 is clearly proved. Such results could scarcely be obtained if the fruit pigmentation were controlled by more than one gene.

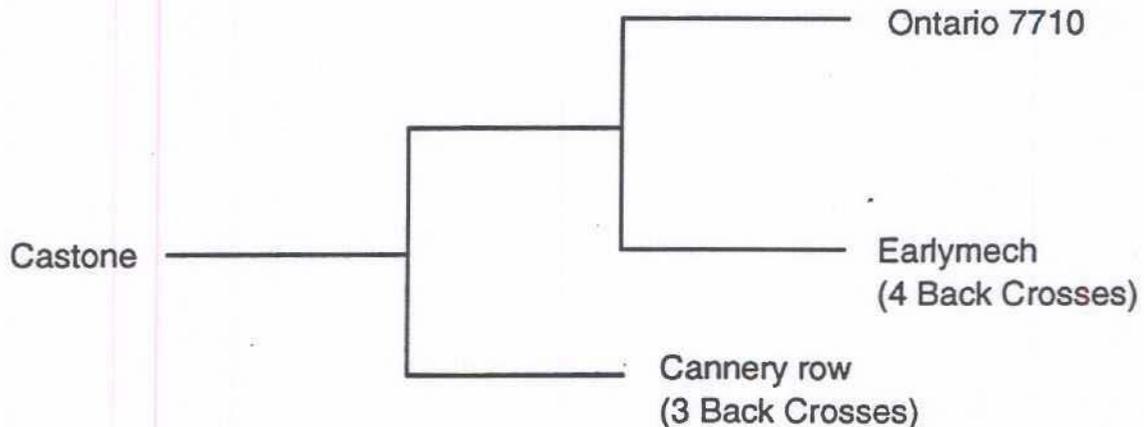
Relationships of *Abg* with other purple-fruited mutants *Af* and *atv* have not been explored except that the loci of *Abg* and *atv* reside on different chromosomes, the latter on 7. Their phenotypes differ in the respects that *Af* does not exhibit the aforementioned variegation and tends to intensify in ripe fruits, and that, in contrast to expression in *Abg* and *Af*, *atv* foliage is also pigmented.

## VARIETAL PEDIGREES

Laterrot, H and Damidaux, R. 1994. CASTONE. Station d'Amélioration des Plantes Maraichères - INRA/CTCPA - Avignon, FRANCE. Release October 1, 1990.

CASTONE  
Plant Variety Protection Certificate applied for.

### Pedigree:



### Characteristics:

**Fruit:** Red, cylindrical, 70 g, uniform ripening (*u*), jointed, excellent firmness and vine storage. Good soluble solids content and processing quality.

**Plant:** Determinate (*sp*), resistant to bacterial speck (*Pto*), *Verticillium* wilt (*Ve*), *Fusarium* wilt (*I*) and *Stemphylium* (*Sm*).

### Utility and maturity:

Similar to CANNERY ROW, early and grouped maturity, for paste production with mechanical harvest.

## TGRC STOCK LISTS

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Wild species stocks (1,008 accessions total) are listed in TGC 42 (1992). Monogenic stocks (877 accessions total) are listed in TGC 43 (1993). All stocks are also listed in SolGenes, an online database pertaining to the genomes of tomato, potato and pepper. For information, contact Edie Paul at: Dept. of Plant Breeding and Biometry, 252 Emerson Hall, Cornell University, Ithaca, NY 14853, USA. (e-mail: epaul@nightshade.cit.cornell.edu).

### MISCELLANEOUS STOCKS

This list of ca. 935 miscellaneous items represents a revision of the previous one issued in TGC41, 1991. Extinct, obsolete, and faulty accessions have been dropped and new accessions have been added. The composition of this group has changed to only a small extent during the three-year period. The new lines were contributed by many workers, to whom we are most grateful.

This list is subdivided into accession categories for the convenience of the user. Within each category, stocks are listed by accession number. Some of the multigenic combinations are weak and require special cultural care; consequently, seed supplies may be low, in some cases too reduced to permit distribution.

Names and phenotypic classes of most of the mutants are given in TGC 43:53-78; other pertinent data are presented in previous TGC Reports. Additional information concerning the origin and other aspects of these stocks will be gladly furnished on request.

### Allozymic Variants

This list assembles available stocks that carry deviants from the normal banding pattern for several enzyme systems. Phenotypes for many of the respective allozymes are illustrated in TGC 26:7-9, 15-17. We also have stocks with various combinations of these genes but they are not listed at this time. *L. pennellii* accession LA716 is homozygous for variant alleles at several isozyme loci (and 3 visual markers), which are easily scored in crosses to tomato. Together, these markers cover 11 out of 12 chromosomes, making it highly useful for linkage tests. The markers present in LA716 and their respective chromosomes (indicated in parentheses) are the following: *Idh-1*, *Prx-1*, *Skdh-1*, *Dia-2*, *Bnag-1* (1); *Est-1*, *Prx-2*, *Fdh-1* (2); *Prx-7* (3); *Tpi-2*, *Pgm-2*, *Adh-1* (4); *Aps-1*, *sp*, *B* (6); *Got-2* (7); *Aps-2*, *Pn* (8), *Est-2* (9); *Prx-4* (10); *Sod-1* (11); *Est-4*, *6Pgdh-2*, *Pgi-1*, *Aco-1* (12).

|         |                            |      |                            |
|---------|----------------------------|------|----------------------------|
| LA 2901 | <i>Aco</i> -1 <sup>1</sup> | 2417 | -1 <sup>2</sup>            |
| 2902    | -1 <sup>2</sup>            | 2985 | -2 <sup>1</sup>            |
| 2903    | -1 <sup>3</sup>            | 1810 | <i>Aps</i> -1 <sup>n</sup> |
| 2904    | -2 <sup>1</sup>            | 1811 | -1 <sup>1</sup>            |
| 2905    | -2 <sup>2</sup>            | 1812 | -1 <sup>2</sup>            |
| 2416    | <i>Adh</i> -1 <sup>1</sup> | 1813 | -2 <sup>n</sup>            |

|      |                         |      |                      |
|------|-------------------------|------|----------------------|
| 1814 | -2 <sup>1</sup>         | 2435 | Pgi -1 <sup>1</sup>  |
| 1816 | -2 <sup>3</sup>         | 2436 | -1 <sup>2</sup>      |
| 2986 | Bnag -1 <sup>1</sup>    | 2437 | Pgm -1 <sup>1</sup>  |
| 2987 | Dia -2 <sup>1</sup>     | 2438 | -2 <sup>1</sup>      |
| 3345 | -3 <sup>1</sup>         | 1836 | Prx -1 <sup>n</sup>  |
| 1817 | Est -1 <sup>n</sup> (?) | 1837 | -1 <sup>1</sup>      |
| 1818 | -1 <sup>1</sup>         | 1838 | -1 <sup>2</sup>      |
| 1819 | -1 <sup>2</sup>         | 1839 | -1 <sup>3</sup>      |
| 1820 | -1 <sup>3</sup>         | 1840 | -1 <sup>4</sup>      |
| 1821 | -1 <sup>4</sup>         | 1841 | -1 <sup>5</sup>      |
| 2419 | -1 <sup>5</sup>         | 1842 | -2 <sup>n</sup>      |
| 2420 | -2 <sup>1</sup>         | 1843 | -2 <sup>1</sup>      |
| 2421 | -3 <sup>1</sup>         | 1845 | -2 <sup>3</sup>      |
| 2422 | -4 <sup>1</sup>         | 1846 | -3 <sup>n</sup>      |
| 2423 | -4 <sup>2</sup>         | 1847 | -3 <sup>1</sup>      |
| 2424 | -4 <sup>3</sup>         | 1848 | -3 <sup>2</sup>      |
| 2425 | -4 <sup>4</sup>         | 1849 | -3a <sup>1</sup>     |
| 2426 | -4 <sup>5</sup>         | 1850 | -4 <sup>1</sup>      |
| 2427 | -4 <sup>6</sup>         | 1851 | -4 <sup>2</sup>      |
| 2428 | -4 <sup>7</sup>         | 1852 | Prx -4 <sup>3</sup>  |
| 2429 | -4 <sup>8</sup>         | 1853 | -4 <sup>4</sup>      |
| 2430 | -5 <sup>1</sup>         | 1854 | -4 <sup>5</sup>      |
| 2431 | -6 <sup>1</sup>         | 1855 | -4 <sup>6</sup>      |
| 2432 | -7 <sup>1</sup>         | 1856 | -4 <sup>7</sup>      |
| 2433 | -7 <sup>2</sup>         | 1857 | -4 <sup>8</sup>      |
| 2988 | -8 <sup>1</sup>         | 1858 | -4 <sup>9</sup>      |
| 2989 | Fdh -1 <sup>1</sup>     | 1859 | -4 <sup>10</sup>     |
| 1822 | Got -1 <sup>1</sup>     | 1860 | -4 <sup>11</sup>     |
| 1823 | -1 <sup>2</sup>         | 1861 | -4 <sup>12</sup>     |
| 1824 | -2 <sup>n</sup>         | 1862 | -4 <sup>13</sup>     |
| 1825 | -2 <sup>1</sup>         | 1863 | -4 <sup>14</sup>     |
| 1826 | -2 <sup>2</sup>         | 1864 | -4 <sup>15</sup>     |
| 1827 | -2 <sup>3</sup>         | 1866 | -4 <sup>17</sup>     |
| 1828 | -2 <sup>4</sup>         | 1867 | -4 <sup>18</sup>     |
| 1829 | -3 <sup>n</sup>         | 1868 | -4 <sup>19</sup>     |
| 1831 | -3 <sup>2</sup>         | 1869 | -4 <sup>20</sup>     |
| 1832 | -3 <sup>3</sup>         | 1870 | -4 <sup>21</sup>     |
| 1833 | -4 <sup>n</sup>         | 1871 | -4 <sup>22</sup>     |
| 1834 | -4 <sup>1</sup>         | 1872 | -4 <sup>23</sup>     |
| 1835 | -4 <sup>2</sup>         | 1873 | -7 <sup>1</sup>      |
| 2906 | ldh -1 <sup>1</sup>     | 1874 | -7 <sup>2</sup>      |
| 3344 | Mdh -1 <sup>2</sup>     | 1875 | -7a <sup>n</sup>     |
| 2990 | -4 <sup>1</sup>         | 2439 | Skdh -1 <sup>1</sup> |
| 2908 | Nir -1 <sup>1</sup>     | 2909 | Sod -1 <sup>1</sup>  |
| 2991 | 6Pgdh -2 <sup>1</sup>   | 2910 | -2 <sup>1</sup>      |
| 2434 | -3 <sup>1</sup>         | 2440 | Tpi -2 <sup>1</sup>  |

### Cytoplasmic Variants

The following three lines are cytoplasmically-inherited chlorotic variants maintained in the TGRC collections 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 is 100% variant.

- LA1092 Uniform yellow induced by fast neutrons, found by G.S. Khush in hybrid background  
 1438 Light green induced by X-rays, found by K. Verkerk in cv. Moneymaker  
 2979 Cyto-variegated in cv. Glamour (contributed by R.W. Robinson)

### Chromosome Marker Stocks

This series consists of stocks in each of which has been assembled a series of marker genes for a single chromosome. In a few cases markers of other chromosomes are also present. Commas are used to separate genes on the same chromosome, semicolons to separate those on different chromosomes. We have combined some of the more useful groups with male steriles in order to make them useful for large scale testcrossing. These stocks are listed below according to chromosome, and within each chromosome group by accession number.

|        |   |        |          |   |
|--------|---|--------|----------|---|
|        | <u>Chromosome 1</u>                       |        | 3352     | <i>imb, au, Lpg/+</i>                   |
| LA 910 | <i>per, inv</i>                           |        |          |   |
| 984    | <i>scf, inv</i>                           |        |          |   |
| 985    | <i>Jau, inv, per</i>                      |        |          |   |
| 995    | <i>um, deb</i>                            |        |          |   |
| 1003   | <i>scf, inv, per</i>                      |        |          |   |
| 1082   | <i>era, um</i>                            |        |          |   |
| 1169   | <i>scf, dgt</i>                           |        |          |   |
| 1173   | <i>gas, co</i>                            |        |          |   |
| 1184   | <i>aut<sup>l</sup>, dgt</i>               |        |          |   |
| 1185   | <i>aut<sup>l</sup>, scf, inv</i>          |        |          |   |
| 1186   | <i>aut<sup>l</sup>, scf, inv, dgt</i>     |        |          |   |
| 1431   | <i>aut<sup>l</sup>, scf, dgt</i>          |        |          |   |
| 1490   | <i>aut<sup>l</sup>, co, inv, dgt</i>      |        |          |   |
| 1529   | <i>aut<sup>l</sup>, co, scf, inv, dgt</i> |        |          |   |
| 2354   | <i>br,y; p; 1</i>                         |        |          |   |
| 3301   | <i>fla, in</i>                            |        |          |   |
| 3302   | <i>imb, in</i>                            |        |          |   |
| 3303   | <i>imb, inv</i>                           |        |          |   |
| 3304   | <i>au, Lpg</i>                            |        |          |   |
| 3305   | <i>imb, Lpg</i>                           |        |          |   |
| 3306   | <i>in, inv</i>                            |        |          |   |
| 3307   | <i>in, Lpg</i>                            |        |          |   |
| 3346   | <i>au, bs</i>                             |        |          |   |
| 3347   | <i>au, ms-32</i>                          |        |          |   |
| 3348   | <i>au, com; Tm-2<sup>2</sup></i>          |        |          |   |
| 3349   | <i>au, imb; Tm-2<sup>2</sup></i>          |        |          |   |
| 3350   | <i>au, br</i>                             |        |          |   |
| 3351   | <i>imb, Lpg/+</i>                         |        |          |   |
|        |   |        |          | <u>Chromosome 2</u>                     |
|        |   | LA 157 |          | <i>p, d, m</i>                          |
|        |   | 271    |          | <i>aw, O</i>                            |
|        |   | 286    |          | <i>d, m</i>                             |
|        |   | 330    |          | <i>bk, o, p, d, s, r, y</i>             |
|        |   | 342    |          | <i>Wo<sup>m</sup>, d; ms-17</i>         |
|        |   | 514    |          | <i>aw, Wo<sup>m</sup>, d</i>            |
|        |   | 639    |          | <i>Me, aw, d</i>                        |
|        |   | 650    |          | <i>aw, d</i>                            |
|        |   | 715    |          | <i>Wo<sup>m</sup>, Me, aw, d</i>        |
|        |   | 732    |          | <i>suf, d</i>                           |
|        |   | 754    |          | <i>aw, p, d, m, o</i>                   |
|        |   | 777    |          | <i>dil, d</i>                           |
|        |   | 789    |          | <i>Me, aw, d, m</i>                     |
|        |   | 790    |          | <i>wv, Me, aw, d</i>                    |
|        |   | 986    |          | <i>s, bk, Wo<sup>m</sup>, o, aw, p,</i> |
|        |   |        | <i>d</i> |   |
|        |   | 1525   |          | <i>aa, d</i>                            |
|        |   | 1526   |          | <i>are, wv, d</i>                       |
|        |   | 1699   |          | <i>Wo<sup>m</sup>, bip</i>              |
|        |   | 1700   |          | <i>wv, aa, d</i>                        |
|        |   | 2366   |          | <i>bk, d; ds, j; nc; pox</i>            |
|        |   | 3132   |          | <i>Prx-2<sup>1</sup>, ms-10, aa</i>     |
|        |   |        |          | <u>Chromosome 3</u>                     |
|        |   | LA 644 |          | <i>r, wf</i>                            |

782 sy, sf  
 877 pau, r  
 987 pli, con  
 988 ru, sf  
 1070 cur, ru, sf  
 1071 sy, bls, sf  
 1101 cn, sy, sf  
 1175 bls, aut  
 1180 sy, bls, sf; ms-31  
 1430 sy, Ln, bls, sf  
 2379 wf, r

Chromosome 4

LA 774 ful, e  
 885 ful, e, di  
 886 ful, ra, e  
 888 ful, ven, e  
 889 ra, di  
 890 ra, ven  
 902 ful, ra<sup>2</sup>, e; ms-31  
 911 clau, afl, ful  
 915 clau, ful  
 916 clau, ra, di  
 917 clau, ful, ra, e, di  
 920 ful, ra, e, di  
 989 afl, ful  
 990 cm, ful, e, di  
 993 ra, si  
 994 cm, ver  
 1073 clau, afl  
 1074 clau, ver  
 1075 ver, e, di

Chromosome 5

LA 512 mc, tf, wt  
 1188 frg, tf

Chromosome 6

LA 336 c, sp; a; y  
 640 yv, c  
 651 m-2, c  
 773 yv, m-2, c  
 802 yv, m-2, c; ms-2  
 1078 ves-2, ria  
 1178 yv, coa, c  
 1189 pds, c  
 1190 pds, yv  
 1489 yv, vf, c  
 1527 d-2, c

Chromosome 7

LA 882 La, deb  
 923 ig, La  
 924 not, La  
 1083 ig, flc  
 1103 var, not  
 1104 deb, not

Chromosome 8

LA 513 l, bu, dl  
 712 l, bu, dl; ms-2  
 776 l, va<sup>virg</sup>  
 897 l, bu, dl, al  
 998 l, bu, dl, Pn  
 999 tp, dl  
 1179 l, bu, dl, al; ms-31  
 1191 spa, ae  
 1442 l, dl, glg  
 1666 l, bu, dl, ae

Chromosome 9

LA 884 wd, marm  
 1000 nv, ah  
 1001 pum, ah, marm  
 1100 ah, pla, marm  
 1112 marm, lut  
 1176 Crk, ah, marm  
 3353 pct, ah, marm

Chromosome 10

LA 158 Xa/+, u, t  
 328 Xa, t, h  
 341 h, ag; ms-2  
 642 u, 1-2; al, d, h, j, wt  
 643 u, 1-2  
 649 t<sup>v</sup>, ag  
 711 t<sup>v</sup>, ag; ms-2  
 1002 h, u, 1-2, t, ag; pe, lg  
 1085 h, res  
 1086 h, ten  
 1110 icn, ag  
 1192 hy, ag  
 1487 icn, t<sup>v</sup>  
 2493 Xa-2, hy, h, ag  
 2494 Xa-2, u, h, l-2, t  
 2495 Xa-2, h, ten, ag, al  
 2496 Xa-2, h, l-2, t  
 2497 hy, u, icn, h, ag  
 2498 u, Xa-3, h  
 2499 u, nor, t

|      |  |      |                                |
|------|--|------|--------------------------------|
| 2500 | <i>u, icn, h</i>                       | 803  | <i>hl, a, pro; ms-2</i>        |
| 2501 | <i>u, icn, h, ag</i>                   | 881  | <i>neg, hl, a</i>              |
| 2502 | <i>u, h, auv, 1-2, t<sup>v</sup></i>   | 925  | <i>j, hl, a, f</i>             |
| 2503 | <i>u, h, l-2, t<sup>v</sup>, ag</i>    | 1109 | <i>mnt, hl, j</i>              |
| 2504 | <i>u, h, t, nd, ag</i>                 | 1113 | <i>j, hl, a, f; ms-31</i>      |
| 2505 | <i>u, l-2, t, ag, Xa-1</i>             | 1488 | <i>neg, ini</i>                |
| 2507 | <i>h, t, nd, ag</i>                    | 1786 | <i>j, f, a; bi; c</i>          |
| 2508 | <i>h, t, ag, Xa-1</i>                  | 2352 | <i>j, f; p; c</i>              |
| 2509 | <i>oli, l-2, t<sup>v</sup>, ag; wf</i> | 2364 | <i>j, a, f; y; wt; c; l; u</i> |
| 2592 | <i>u, h, t, ag</i>                     | 2489 | <i>ne-2, a</i>                 |
| 2593 | <i>u, auv, ag</i>                      |      |                                |

#### Chromosome 12

|                      |                    |         |                 |
|----------------------|--------------------|---------|-----------------|
| <u>Chromosome 11</u> |                    | LA 1111 | <i>fd, alb</i>  |
| LA 291               | <i>hl, a; ms-1</i> | 1171    | <i>aud, fd</i>  |
| 729                  | <i>neg, a</i>      | 1177    | <i>alb, mua</i> |
| 730                  | <i>a, pro</i>      |         |                 |

#### Miscellaneous Marker Combinations

We have acquired and synthesized, in addition to the above categories, a group of stocks in which various mutant genes have been combined for various purposes. A few of these items include linked genes (comma separation); they are classified here because other linkage testers include the same combinations and because they are more useful as markers of several chromosomes.

|       |                               |      |                                  |
|-------|-------------------------------|------|----------------------------------|
| LA 13 | <i>a; c; d; l; r; y</i>       | 775  | <i>tf; h; au; +/-d</i>           |
| 14    | <i>al; d; dm; f; j; wt; h</i> | 779  | <i>clau; rv</i>                  |
| 52    | <i>j; wt; br</i>              | 783  | <i>Wo<sup>m</sup>; d; au; tf</i> |
| 85    | <i>Wo, d; h</i>               | 788  | <i>dil; La</i>                   |
| 137   | <i>dl; wd; gq</i>             | 796  | <i>vms; Hrt; lg-5</i>            |
| 154   | <i>u; d; sp; h</i>            | 875  | <i>hp; u; sp</i>                 |
| 159   | <i>a; e; mc; t, u; y; wf</i>  | 876  | <i>hp; sp</i>                    |
| 169   | <i>ps; wf; wt</i>             | 895  | <i>tp; sp; u; Hr</i>             |
| 189   | <i>bl; cl-2</i>               | 907  | <i>Lut; pr</i>                   |
| 190   | <i>wf; br; bk</i>             | 908  | <i>per; var</i>                  |
| 215   | <i>at; y</i>                  | 909  | <i>con; sf</i>                   |
| 281   | <i>e; t, u</i>                | 912  | <i>ht; di</i>                    |
| 296   | <i>br; bk; gs; wf</i>         | 913  | <i>ful; di; ht</i>               |
| 297   | <i>tf; ug; Nr</i>             | 914  | <i>com; ful</i>                  |
| 298   | <i>Xa; Wo, dv; tf</i>         | 996  | <i>um; ig</i>                    |
| 299   | <i>ag; rv</i>                 | 997  | <i>um; not</i>                   |
| 302   | <i>ag; dv; h; sp</i>          | 1072 | <i>sy, sf; um; +/-not</i>        |
| 312   | <i>cm; vms; u; f</i>          | 1105 | <i>con; cur</i>                  |
| 497   | <i>ch; j-2; sf</i>            | 1159 | <i>ep; obl</i>                   |
| 499   | <i>Od; sn; at; cm/+</i>       | 1163 | <i>wv, d; tf</i>                 |
| 508   | <i>gf; d; c; a; r; y</i>      | 1170 | <i>cn; con</i>                   |
| 511   | <i>ps (exserted); a; c; y</i> | 1219 | <i>d; u</i>                      |
| 638   | <i>ht; d; r</i>               | 1663 | <i>Ln; Wo<sup>m</sup></i>        |
| 646   | <i>gh; r; d</i>               | 1664 | <i>hp; lp</i>                    |
| 648   | <i>rv; e; Wo; wf; j; h</i>    | 1784 | <i>afr; h; gs; sp</i>            |
| 719   | <i>Jau; clau</i>              | 1785 | <i>afr; gs; u</i>                |
| 727   | <i>wv; d; c; r</i>            | 1786 | <i>bi; f, a, j; c</i>            |
| 740   | <i>yg-4; al</i>               | 1787 | <i>Bk-2; en</i>                  |
| 741   | <i>sy; d; u</i>               | 1789 | <i>s<sup>lCS</sup>; a</i>        |
| 759   | <i>lg; vi; pe; t</i>          | 1791 | <i>Gp; Tm-2<sup>a</sup></i>      |
| 760   | <i>lg; vi</i>                 |      |                                  |

- 1796 *Rs; d; h*  
1797 *Rs; d; wf; gf; h*  
1798 *Rs; wf; h; a*  
1804 *sr; sp; u*  
1805 *sr; y*  
1806 *ti; y; wf; al; j*  
1807 *ti; a; e; u, h; mc; wf*  
1808 *ti; c; mc*  
2349 *p, d; r; wt; j, f*  
2350 *y; ne; p; c, sp; a*  
2351 *c; l; u, h*  
2352 *p; c; j, f*  
2353 *y; wt; n*  
2354 *br, y; p; l*  
2355 *sp; ug*  
2359 *y; Wo; r; c*  
2360 *e; wt; l; u*  
2363 *y; Wo; wt; c; t; j*  
2364 *y; wt; c; l; u; j, a, f*  
2365 *wf, r; sp; wd*  
2366 *bk, d, ds; j; nc; pox*  
2367 *y; m; t; f*  
2368 *r; wt; mc; c; l; j*  
2369 *p; Tm-1*  
2370 *wf; n; gs*  
2371 *d; wf; wt; c; f*  
2372 *sp; fl*  
2475 *ug; inc; tf; gs; al; Nr; h; hp*  
2477 *vo; cjf; wf; sp; l; u, h*  
2478 *afr; r; gs; h*  
2479 *ck; s, p, d*  
2480 *ck; o, aw, p, m, d*  
2481 *fn; in; bls; mc; gs*  
2482 *fu; r, wf; mc; c; gs; u, h; hp*  
2483 *fu; wf; mc; pdw; gs; u; hp*  
2485 *inc; y; d; r, wf; mc; c; gs; l, gf; h; a*  
2486 *inc; pds, sp; u, t*  
2487 *int; sp; u, t*  
2488 *mon; y; r; h; a; alb*  
2490 *pdw; mc; pst; dl*  
2491 *stu; mc; c; gs; dl; u, h; j*  
2492 *ti; wf; e; mc; u; a*  
2510 *inc; d; r, wf; mc; gs; gf; h; a*  
2512 *y; lg, pe; r, wf; m-2, c; gs; gf; marm; h; hp*  
2513 *y; d; at, mc; m-2, c, sp; gs; u; yg-2; wf*  
2514 *y; d; at, mc; m-2, c, sp; gs; u; yg-2 wf*  
2515 *y; r, wf; m-2, c, sp; gs; gf; u; a; yg-2*  
2516 *r, wf; c; u, h; j; rvt, lg, pe, tmf; cjf, vo*  
2517 *rvt; r, wf; m-2, c; gs; gf; marm; h; hp*  
2518 *dp; m-2, c; gs; gf; h*  
2520 *r, wf; mc; m-2, c; gs; l; marm; h; hp*  
2521 *r; clau; m-2, c; gs; gf; marm; u, h*  
2522 *r; mc; m-2, c; gf; marm; u, h; f; hp*  
2523 *r; mc; c; pdw; u, h; f*  
2524 *af, sd*  
2526 *dp; sp; u*  
2527 *allele of 1; sp; u*  
2528 *ti; y; wf, sf; f*  
2595 *br; d; dm; wt; al; h; j, f*  
2596 *y; d; wf; at; m-2, c, sp; u; a; yg-2*  
2597 *y; r, wf; mc; m-2, c; gs; gf; marm; h*  
2598 *y; wf; at; m-2, c, sp; u; a; yg-2; gs*  
2599 *y; wf; at; m-2, c; gf; h; a; yg-2*  
2600 *y; wf; at; m-2, c, sp; u; a; yg-2*  
2601 *y; e; mc; gs; gf; u, t (dk purple)*  
2602 *scf, dp; r, wf; m-2, c; gs; marm; u; hp*  
2603 *scf, dp; r, wf; c; gs; marm; u; hp*  
2605 *scf, dp; r, wf; c; gs; marm; a; hp*  
2606 *lg, pe, Nr-2, tmf, cjf; jl, j-2*  
2607 *lg, pe, tnf, cjf; wf; c; gs; marm; h; j*  
2608 *lg, pe, tnf; d; r; c; gf; marm; h; greenstem*  
2609 *lg, pe, tnf; d; r; c; gf; marm; h; (al?)*  
2611 *lg, pe; wf; m-2, c; gs; gf; marm; h; hp*  
2612 *d; at; m-2, c, sp; gs; u; a; yg-2*  
3208 *y, rot; d; c; l*  
3209 *y, irr, imb*  
3210 *y, lg, pe; r; l, gf; h; a; segs; c*  
3211 *lg, pe, tmf, cjf; y; d; r; c; h*  
3212 *tmf; d; sp; u*  
3217 *glg; Pts*
- In the following group (LA3248-3311) accessions with *u* are NIL with cv. Craigella; the others with cv. Ailsa Craig.
- 3248 *bls; u*  
3249 *a; c; longstyle*

|      |                               |      |  |
|------|-------------------------------|------|--|
| 3250 | <i>t, u</i>                   | 3274 | <i>ah; Tm-2; nv; u; lethal</i>         |
| 3251 | <i>Del; y</i>                 | 3275 | <i>ah; Gp; Tm-2<sup>2</sup></i>        |
| 3252 | <i>Del; t</i>                 | 3276 | <i>Tm-1; u; Ve</i>                     |
| 3253 | <i>r; y</i>                   | 3278 | <i>bls; l; u; Ve</i>                   |
| 3254 | <i>a; c; l; Ve; longstyle</i> | 3279 | <i>at; Del</i>                         |
| 3256 | <i>at; t</i>                  | 3284 | <i>at; gf</i>                          |
| 3257 | <i>gf; gs; r</i>              | 3285 | <i>gf; ug; y</i>                       |
| 3258 | <i>u; Ve</i>                  | 3286 | <i>r; ug; y</i>                        |
| 3259 | <i>bls; u; Ve</i>             | 3287 | <i>hp; r; ug</i>                       |
| 3260 | <i>bls; l; u</i>              | 3288 | <i>hp; ug; y</i>                       |
| 3261 | <i>Del; gs</i>                | 3289 | <i>gf; r; y</i>                        |
| 3262 | <i>Del; ug</i>                | 3290 | <i>gf; hp; y</i>                       |
| 3264 | <i>Tm-2<sup>2</sup>; u</i>    | 3291 | <i>at; hp; t</i>                       |
| 3265 | <i>bls; Tm-1; Tm-2; nv</i>    | 3292 | <i>Tm-2; u</i>                         |
| 3266 | <i>bls; Cf-/?; u</i>          | 3294 | <i>bl; d; u</i>                        |
| 3267 | <i>Cf-?; u</i>                | 3297 | <i>Tm-1; Tm-2; nv</i>                  |
| 3268 | <i>Tm-2; nv; u</i>            | 3298 | <i>ep; sp; u</i>                       |
| 3269 | <i>Tm-1; u</i>                | 3299 | <i>ep; u</i>                           |
| 3270 | <i>bls; Tm-2; nv; u</i>       | 3311 | <i>og<sup>C</sup>; u</i>               |
| 3271 | <i>Cf-?; Tm-1; u</i>          |      |  |
| 3272 | <i>bls; Cf-?; u</i>           | 3315 | <i>sp; pst; u; j-2; up; viresc; vo</i> |
| 3273 | <i>Gp; Tm-2<sup>2</sup></i>   | 3354 | <i>sp; pst; u; j-2; up; viresc; vo</i> |

#### Linkage Screening Testers

As explained previously (TGC 22:24), we have endeavored to synthesize a set of linkage testers, each of which has two pairs of strategically situated markers on two different chromosomes. They are intended primarily for screening new, unlocated markers. The chromosomal marker stocks 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. Numbers of the respective chromosomes are indicated in parentheses. The mutant *scf* is bracketed in stocks in which it was inadvertently lost in the course of segregation and selection.

|        |                                   |      |                                    |
|--------|-----------------------------------|------|------------------------------------|
| LA 780 | <i>yv, c (6); h, ag (10)</i>      | 1183 | <i>clau, ra (4); icn, ag (10)</i>  |
| 781    | <i>ful, e (4); neg, a (11)</i>    | 1441 | <i>coa, c (6); hl, a (11)</i>      |
| 784    | <i>ful, e (4); hl, a (11)</i>     | 1443 | <i>(scf), dgt (1); 1, al (8)</i>   |
| 982    | <i>clau, e (4); hl, a (11)</i>    | 1444 | <i>wv, d (2); af, tf (5)</i>       |
| 983    | <i>1, dl (8); ah, marm (9)</i>    | 1445 | <i>clau, di (4); icn, ag (10)</i>  |
| 1164   | <i>var, not (7); ah, marm (9)</i> | 1491 | <i>(scf), dgt (1); spa, ae (8)</i> |
| 1166   | <i>clau, di (4); icn, ag (10)</i> | 1665 | <i>(scf), dgt (1); 1, al (8)</i>   |
| 1182   | <i>sy, sf (3); alb, mua (12)</i>  |      |                                    |

#### Translocations

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, and B. Snoad. As far as we know, they are all homozygous for the indicated structural changes. They are listed in the order presented by Gill *et al.* (TGC 24:10-12). This list is followed by a few items in our collections originated by G.S. Khush. Special thanks are due to Dr. Gill and his colleagues for their efforts in assembling and increasing this collection.

|        |             |      |            |        |            |
|--------|-------------|------|------------|--------|------------|
| LA1876 | T1-2*       | 1889 | T3-8*      | 1904   | T2-9d      |
| 1877   | T2-4        | 1890 | T9-12*     | 1905   | T1-3 or -8 |
| 1878   | T2-7        | 1891 | T7-9       | 1906   | T2-10      |
| 1879   | T2-9        | 1892 | 2 0 4      |        |            |
| 1880   | T2-11       |      | (T9-12)+?  | 1049   | T5-9 (af   |
| 1881   | T2-12       | 1894 | T2-9a      | stock) |            |
| 1882   | T12-3 or -8 | 1895 | T2-9b      | 1116   | T1-11      |
| 1883   | T3-7        | 1896 | T1-12      | 1121   | T4-9       |
| 1884   | 2 0 4       | 1897 | T7 or 11-? | 1124   | T3-9       |
| 1885   | T5-7*       | 1898 | T2-10*     | 1125   | T5-7       |
| 1886   | T12-3 or -8 | 1899 | T6-11*     | 1126   | T3-9       |
| 1887   | T6-12*      | 1902 | T2 or -7   | 1127   | T3-5       |
| 1888   | T7-11       | 1903 | T4-7*      |        |            |

\*Comprise the tester set

### Stress Tolerant Stocks, Chromosome Substitutions and Other Prebred Lines

This group of miscellaneous items, mostly derived from wild species, is included because we received many requests for such stocks. 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.

#### A. Stress tolerances

##### 1. Soil moisture

- a. Deficiency (drought tolerance)
  - L. pennellii* (general feature) Ex: LA716
  - L. chilense* (coastal habitats) LA1958, 1959, 1972
  - S. rickii* (general feature) LA1974, 2876, others
- b. Excess (waterlogging tolerance)
  - L. esculentum* var. *cerasiforme* (wet tropical habitats): LA1421
  - S. juglandifolium*, *S. ochranthum* (probably a general feature)

##### 2. Ambient temperature

- a. High (heat tolerance)
  - L. esculentum* (select lines) cv. Nagcarlang (LA2661), Saladette (LA2662), Malintka-101 (LA3120), Hotset (LA3320)
- b. Low (chilling tolerance)
  - L. hirsutum* (from high altitudes) LA1363, 1393, 1777
  - L. chilense* (from high altitudes) LA1969, 1971
  - S. lycopersicoides* (possibly a general feature) LA1964, 2408

##### 3. Aluminum tolerance (suspected): *L. esc.* var. *cerasiforme* LA2710

##### 4. Salinity (salt/alkali tolerance)

*L. cheesmanii* (from littoral habitat): LA1401

*L. pennellii*: LA716, 2656, 1926, 1809, 1940  
*L. peruvianum*: LA462, 1278, 2744  
*L. chilense*: LA2748, 2931, 2880, 1930, 1932, 2747, 1958  
*L. esculentum* var. *cerasiforme*: LA1310  
*L. esculentum* cv. Edkawi LA2711  
*L. pimpinellifolium* LA1579

5. Arthropods

*L. hirsutum*, esp. *f. glabratum*: LA407 and many others

B. *L. pennellii* chromosome substitution lines. In the course of our study of segregation and recombination in *L. esculentum* x *L. pennellii* hybrids, we progressively backcrossed certain chromosomes of *L. pennellii* LA716 into *L. esculentum* (see Genetics 26:753-768; Biol. Zbl. 91:209-220). Selected heterozygotes of later generations were selfed and subsequent progenies free of *esculentum* markers were selected as the substitution lines.

|               |        |               |         |
|---------------|--------|---------------|---------|
| chromosome 1: | LA2091 | chromosome 6: | LA 3142 |
| 2:            | LA1639 | 8:            | LA1642  |
| 3:            | LA1640 | 11:           | LA1643  |

C. High soluble solids derivatives from *L. chmielewskii* (see Hilgardia 42:493-510). LA1500, 1501, 1502, 1503, 1563.

D. Exserted stigma line derived from LA1585 (see TGC 33:13-14): LA2380.

Modern and Vintage Cultivars

We maintain the following limited list of cultivars for various purposes, mainly as isogenic stocks for various mutants, standards for other genetic comparison, and additional purposes. Marglobe is maintained as the standard for tomato genetics nomenclature. The stock of San Marzano originated from a haploid and is therefore a true autodiploid. Other lines have been bred by selfing for many generations.

|        |                                |      |                        |
|--------|--------------------------------|------|------------------------|
| LA 818 | A - 1                          | 1219 | Dwarf San Marzano      |
| 516    | Ace                            | 313  | Dwarf Stone            |
| 2838A  | Ailsa Craig                    | 3238 | Earliana               |
| 2463   | Allround                       | 266  | Earlipak               |
| 3143   | Anahu                          | 517  | Early Santa Clara      |
| 1995   | Angela                         | 2711 | Edkawi                 |
| 3244   | Antimold-B                     | 3245 | E.S. 1                 |
| 657    | Beaverlodge (Chanasyk's early) | 3024 | Fireball               |
| 1499   | Break O'Day                    | 3242 | Floridade              |
| 2414   | Cal Ace                        | 3030 | Gardener               |
| 1439   | Calmart                        | 3231 | Gulf State Market      |
| 3316   | Campbell 24                    | 314  | Hardin Miniature       |
| 3317   | Campbell 28                    | 806  | High Crimson           |
| 3228   | Canary Export                  | 3110 | Hires Rootstock        |
| 2374   | Caro Red                       | 3237 | Homestead              |
| 2400   | Castlemart                     | 3320 | Hotset                 |
| 3121   | Chico Grande                   | 3144 | Hunt 100               |
| 3213   | Columbian                      | 1089 | John Baer              |
| 533    | Condine Red                    | 1131 | Kallio's Alaskan Dwarf |
| 817    | CP-2                           | 3240 | Kokomo                 |
| 1162   | Cuba Plum                      | 505  | Laketa                 |
|        |                                | 3118 | Laurica                |

|         |                           |       |                      |
|---------|---------------------------|-------|----------------------|
| 3232    | Long Red                  | 1091  | Stokesdale           |
| 534     | Lukullus                  | 1506  | Stone                |
| 3120    | Malintka-101              | 164   | Sutton's Best of All |
| 2451    | Manapal                   | 2399  | T5                   |
| 502     | Marglobe                  | 2590  | T9                   |
| 1504    | Marmande                  | 3230  | Targinnie Red        |
| 278     | Marzano Grande            | 154   | Tiny Tim             |
| 3151    | Mecline                   | 2803  | Tropic               |
| 11      | Michigan State Forcing    | 1706  | UC82                 |
| 2825    | Mobaci                    | 2801  | UC82B                |
| 2824    | Moboglan                  | 1714  | UC134                |
| 3152    | Moboline                  | 3130  | UC204C               |
| 2821    | Mobox                     | 2937  | UC-MR20              |
| 2830    | Mocimor                   | 2938  | UC-N28               |
| 2828    | Momor                     | 2939  | UC-T338              |
| 2829    | Momor verte               | 2940  | UC-TR44              |
| 2818    | Monalbo                   | 2941  | UC-TR51              |
| 2706    | Moneymaker                | 3246  | Vagabond             |
| 2819    | Monita                    | 3122  | Vendor               |
| 2827    | Moperou                   | 2968  | Vendor (Tm-2)        |
| 2822    | Mossol                    | 2444  | Vetomold K10         |
| 2820    | Motabo                    | 745   | V-9 Red Top          |
| 2826    | Motaci                    | 743   | VF-6                 |
| 2823    | Motelle                   | 744   | VF-11                |
| 2661    | Nagcarlang                | 1023  | VF-13L               |
| 2009    | New Yorker                | 742   | VF-34                |
| 1088    | Ohio Globe A              | 490   | VF-36                |
| 3321    | Ohio 7663                 | 816   | VF-145 22-8          |
| 2969-73 | Oxheart variants          | 1222  | VF-145 78-79         |
| 2376    | Pan American              | 1507  | VF-145 21-4          |
| 12      | Pearson                   | 1022  | VFN-8                |
| 20      | Pennheart                 | 815   | VFN-14               |
| 3125    | Pomodorini Napolitani     | 1221  | VFNT Cherry          |
| 3236    | Prairiana                 | 2705  | VFNT Cherry (sp)     |
| 89      | Prince Borghese           | 279   | Webb Special         |
| 3233    | Pritchard                 | 2464  | White Beauty         |
| 3229    | Prospero                  | 2-473 | Yellow Cherry        |
| 2446    | Purdue 135                | 2357  | Yellow Peach         |
| 337     | Red Cherry                |       |                      |
| 276     | Red Top                   |       |                      |
| 2356    | Rey de los Tempranos Sw-1 |       |                      |
| 535     | Rheinlands Ruhm           |       |                      |
| 3343    | Rio Grande                |       |                      |
| 3145    | Rockingham                |       |                      |
| 3214    | Rowpae                    |       |                      |
| 503     | Roumanian Sweet           |       |                      |
| 2088    | Royal Red                 |       |                      |
| 3215    | Roza                      |       |                      |
| 1090    | Rutgers                   |       |                      |
| 2662    | Saladette                 |       |                      |
| 3216    | Saladmaster               |       |                      |
| 180     | San Marzano autodiploid   |       |                      |
| 1021    | Santa Cruz                |       |                      |
| 2912    | Short Red (cherry)        |       |                      |
| 3234    | Sioux                     |       |                      |
| 30      | Stemless Pennorange       |       |                      |
| 2443    | Stirling Castle           |       |                      |

### Latin American Cultivars

This collection of Latin-American cultivars has been assembled from various sources but principally from our collecting trips. 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.

#### ARGENTINA

3243 cv. Platense

#### BOLIVIA

LA 172 Santa Cruz  
2871 Chamaca (Yungas)  
2873 Lote Pablo Luna (Yungas)  
2874 Playa Ancha (Yungas)

#### BRAZIL

1021 Santa Cruz

#### CHILE

LA 466 Hda. Rosario (Azapa)  
467 Lluta  
468 Iquique

#### COLOMBIA

LA 356 Buenaventura  
357 Buenaventura  
358 Buenaventura  
359 Buenaventura

#### COSTA RICA

LA 1215 (no location)

#### CUBA

LA 1162 (no location)

#### ECUADOR

LA 126 Quito  
408 Guayaquil  
409 Guayaquil  
410 Guayaquil  
415 Daular  
416 Puna  
423 Wreck Bay (Galapagos)  
1224 Puyo (3 items)  
1238 Viche  
1239 Esmeraldas  
1240 Esmeraldas  
1241 Esmeraldas  
1244 Carmela (Guayas)  
1249 Loja  
1251 Loja  
2381-  
2384 Malacatos

#### GUATEMALA

LA 1460 Antigua

#### HONDURAS

LA 147 Tegucigalpa

#### NICARAGUA

LA 1213 (no location)

#### MEXICO

LA 146 Mexico City  
1218 Vera Cruz  
1457 Tehuacan  
1459 Huachinango  
1462 Yucatan  
1544 Laguna  
1564 Sinaloa  
1565 Oaxaca  
1566 Oaxaca  
1567 Oaxaca  
1568 Yucatan  
1702 Sinaloa  
1703 Sinaloa

#### PANAMA

LA 1216 (no location)

#### PERU

LA 113 Hda. Galera (La Libertad)  
117 Piura  
125 Trujillo  
131 Arequipa  
134 Ayacucho  
393 Chiclayo  
394 Chiclayo  
395 Chiclayo  
396 Chiclayo  
401 Piura  
402 Piura  
403 Piura  
404 Piura  
405 Piura  
457 Tacna  
473 Calana (Tacna)  
477 Chincha  
478 Chincha  
1313 Convento de Sivia  
(Cuzco)  
1315 Ayna  
1390 La Molina (Lima)  
1397 Iquitos  
1398 Iquitos  
1650 La Bogotalla-Ingenio  
1654 Tarapoto

|       |                   |       |                              |
|-------|-------------------|-------|------------------------------|
| 1655  | Tarapoto          | 2264  | La Huarpia                   |
| 1669  | Jahuay (Ica)      | 2265- |                              |
| 1698  | Chancay           | 2268  | Pacaisapa                    |
| 2207- |                   | 2269- |                              |
| 2212  | Naranjillo        | 2276  | km 57                        |
| 2213- |                   | 2278- |                              |
| 2220  | Nueva Cajamarca   | 2282  | Tabalosas                    |
| 2221- |                   | 2283- |                              |
| 2235, |                   | 2307  | Tarapoto Mercado             |
| 2259  | Moyobamba mercado | 2309- |                              |
| 2237- |                   | 2311  | Pto. St. Cruz                |
| 2244  | Habana            | 2841  | Chinuna (Amazonas)           |
| 2245- |                   | 2842  | Sta. Rita (San Martin)       |
| 2253  | Soritor           | 2843  | Moyobamba                    |
| 2254- |                   | 2844  | Shanhoa                      |
| 2256  | Pto. Moyobamba    | 2845  | Moyobamba mercado            |
| 2257  | Hotel Albricias   | 3221- |                              |
| 2258  | Yautalo           | 3226  | San Isidro mercado<br>(Lima) |
| 2260- |                   |       |                              |

#### Autotetraploids

We are currently maintaining only the following group of stocks. Whereas we formerly stocked many more lines, the rapid deterioration, low seed yields, and lack of demand required that we prune them to a smaller group of more frequently used lines. Several autotetraploids appear in the species list (TGC 36).

|        |                    |      |                |
|--------|--------------------|------|----------------|
| 2-95   | cv San Marzano     | 2339 | cv Pearson     |
| 2-483  | cv Red Cherry      | 2340 | cv Red Currant |
| LA 793 | a, c, d, l, r, y   | 2341 | Red Currant    |
| 794    | ag, t <sup>v</sup> | 2342 | cv Danmark     |
| 2335   | Red Currant        | 2343 | cv Waltham Fog |
| 2336   | r                  | 3131 | cv UC82B       |
| 2337   | cv Stokesdale      | 3255 | cv Ailsa Craig |
| 2338   | cv Break O'Day     |      |                |

#### Trisomics

The following series includes various kinds of extra chromosomes. Since the extras are transmitted irregularly, each stock necessarily consists of a majority of diploids, the remainder aneuploid. Primary trisomics yield primaries, rarely tetrasomics. 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, correspondents should keep these points in mind.

|          |             |              |
|----------|-------------|--------------|
| Primary: | 10 Triplo-1 | 1 Triplo-10  |
|          | 6 Triplo-2  | 40 Triplo-11 |
|          | 8 Triplo-3  | 9 Triplo-12  |
|          | 2 Triplo-4  |              |
|          | 4 Triplo-5  | Telo:        |
|          | 12 Triplo-6 | 14 2n + 3S   |
|          | 7 Triplo-7  | 17 2n + 3L   |
|          | 3 Triplo-8  | 21 2n + 4L   |
|          | 5 Triplo-9  | 20 2n + 7L   |
|          |             | 19 2n + 8L   |

|               |    |  |           |    |                      |
|---------------|----|--|-----------|----|----------------------|
|               | 35 | $2n + 10S$                                     |           | 29 | $2n + 12L \cdot 12L$ |
| Secondary:    | 44 | $2n + 2S \cdot 2S$                             | Tertiary: | 18 | $2n + 2L \cdot 10L$  |
|               | 43 | $2n + 5L \cdot 5L$                             |           | 16 | $2n + 4L \cdot 10L$  |
|               | 36 | $2n + 7S \cdot 7S$                             |           | 39 | $2n + 5L \cdot 7S$   |
|               | 26 | $2n + 9S \cdot 9S$                             |           | 15 | $2n + 7S \cdot 11L$  |
|               | 30 | $2n + 9L \cdot 9L$                             |           | 25 | $2n + 9L \cdot 12L$  |
|               | 28 | $2n + 10L \cdot 10L$                           |           | 23 | $2n + 1L \cdot 11L$  |
|               | 41 | $2n + 11L \cdot 11L$                           |           |    |                      |
| Compensating: | 32 | $2n - 3S \cdot 3L + 3S + 3L \cdot 3L$          |           |    |                      |
|               | 33 | $2n - 3S \cdot 3L + 3S \cdot 3S + 3L \cdot 3L$ |           |    |                      |
|               | 34 | $2n - 7S \cdot 7L + 7S \cdot 7S + 7L \cdot 7L$ |           |    |                      |

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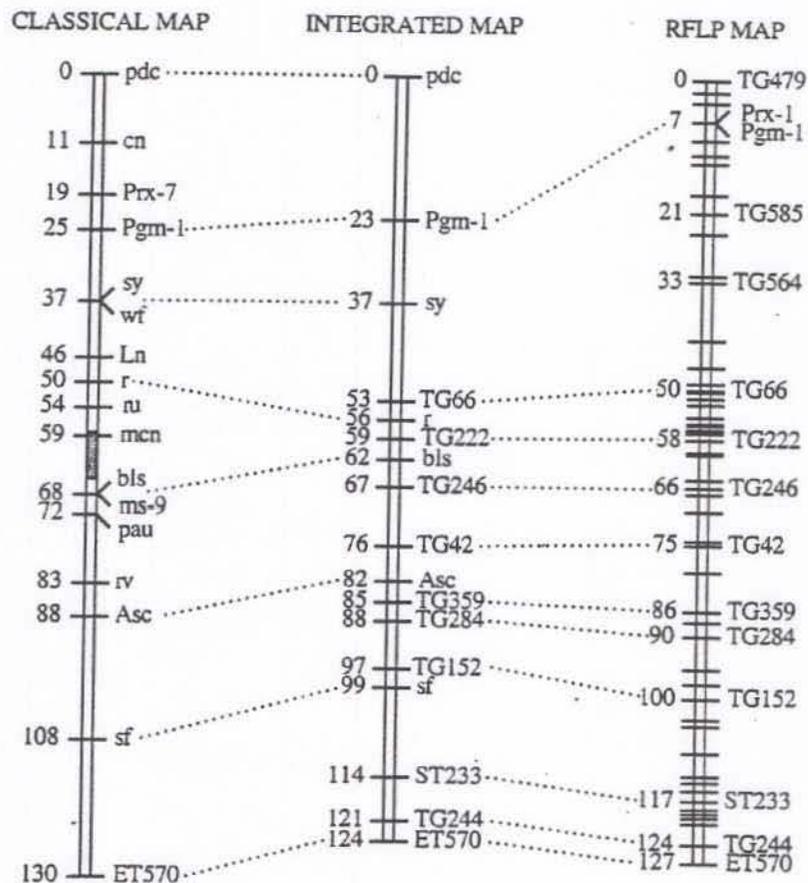
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