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T G R C

Tomato Genetics Resource Center



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ANNUAL PROGRESS REPORT

2012



Figure 1. Inflorescence of *S. habrochaites* LA1986. The TGRC regenerated this year a number of wild species accessions which had been stored in our seed vault but had never been grown for seed increase. Several new and interesting items were discovered. The image above is of an accession of *S. habrochaites* collected by Charley Rick and Jon Fobes in 1979 near Casmiche, Rio Moche, Peru. [photo by S. Peacock]

SUMMARY

Acquisitions. Six new accessions of cultivated tomato were acquired from Muriel Quinet at the Univ. Catholique de Louvain, in Belgium. These new stocks are double or triple mutant combinations of *uniflora* (*uf*), *blind* (*bl*), *compound inflorescence* (*s*), *jointless* (*j*), and *self-pruning* (*sp*). These stocks should be useful for genetic studies of meristem, flower and inflorescence development. In addition, we regenerated 34 previously inactive accessions of wild species, most of which had never been grown before, representing a significant expansion of our wild species collection at a time when opportunities for new germplasm collections are limited and many wild tomatoes have disappeared *in situ*. The current total of number of active accessions is 3,652.

Maintenance and Evaluation. A total of 971 cultures were grown for various purposes, of which 270 were for seed increase (136 of which were of wild species) and 204 for germination tests. 63 stocks were grown for progeny tests of selected mutants that are maintained via heterozygotes, such as recessive lethals, nutritional disorders, and male-sterilities. 13 stocks were grown to test for the presence of transgenes (none were found). Other stocks were genotyped to confirm wild species introgressions. Newly regenerated seed lots were split, with one portion stored at 5° C (our working collection, used for filling seed requests), the other at -18° C for extended longevity. Backup seed samples were also submitted to the USDA Natl. Center for Genetic Resources Preservation in Colorado, and to the Svalbard Global Seed Vault.

Distribution and Utilization. The TGRC distributed 4,966 seed samples of 1,931 different accessions in response to 273 requests from 200 colleagues in 23 countries. At least 25 purely informational requests were also answered. The overall utilization rate (i.e. number of samples distributed relative to the number of active accessions) exceeded 135%. These statistics show that our collection continues to be intensively used and that demand for our stocks remains high. Information provided by requestors indicates our stocks are used for a wide variety of research and breeding projects. Our annual literature search uncovered 105 publications mentioning use of TGRC stocks.

Documentation. Our website was updated in various ways to improve usability. Queries of wild species accessions can now be viewed in a datasheet format, in addition to a form view. The underlying data records can be downloaded to a spreadsheet, and groups of related accessions can be plotted on GoogleMaps. In addition, our web-based query pages were rewritten to meet enhanced security standards in our web server environment. We finished digitizing Charley Rick's field notebooks from his collecting trips to South America. Containing the records of 15 trips to Peru, Ecuador and Chile made between 1948 and 1995, these notebooks are a trove of information about the wild species accessions, including directions to collection sites, general habitat, likely stress tolerances, disease symptoms, morphological traits, genetic variability, degree of cross pollination, and other details.

Research. Our research focuses on understanding the mechanisms of prezygotic reproductive barriers that prevent crosses between cultivated tomato and its wild relatives. We are studying the role of two pollen factors, *ui1.1* and *ui6.1*, in self- and interspecific incompatibility. Another project is to develop a set of introgression lines representing the genome of *S. sitiens* in cultivated tomato. Molecular marker analysis of early backcross generations (BC2-BC3) indicated that roughly 80% of the *S. sitiens* genome has been captured.

ACQUISITIONS

The TGRC acquired six new accessions, all of cultivated tomato, during 2012. The new stocks were various double and triple mutant stocks of genes affecting shoot growth and inflorescence or flower development. The genes involved and their phenotypes are as follows: *uniflora* (*uf*) produces inflorescences with reduced numbers of flowers (usually a single flower); *blind* (*bl*) causes shoot growth to terminate after a very limited number of leaves and flower clusters (usually just one) are produced; *compound inflorescence* (*s*) produces highly subdivided inflorescences with a greatly increased number of flowers; *jointless* (*j*) eliminates the normal pedicel abscission zone (joint) in the flower; and *self-pruning* (*sp*) causes determinate growth habit. The two- or three-gene combination stocks were synthesized by Prof. Muriel Quinet at the Univ. Catholique de Louvain, in Belgium. We expect these stocks will be useful for genetic studies of meristem, flower and inflorescence development. More detailed information on these new accessions can be found on our website at <http://tgrc.ucdavis.edu/acq.aspx>.

We made a major effort this year to regenerate a large number of previously inactive wild species accessions. These stocks had not been grown since they were acquired by the TGRC, either because they were judged to be redundant with other accessions from similar geographic regions, or because space and resources at the time were limiting. Many of these had been stored in our seed vault since the 1980's or earlier. Thus germination rates for some seed lots were low and viable populations were obtained from only 34 accessions. The main motivation for rescuing these old collections from our vault is that obtaining permission to conduct new collections in the native region has become impractical or impossible. Since the 1992 Convention on Biological Diversity, plant collecting activities have been curtailed in many countries. Another consideration is that wild tomato populations are not being protected *in situ*, and many previous collections have disappeared. For example, during a trip to Peru in 2009 we observed very few wild tomatoes growing in the agricultural valleys. This genetic erosion was especially severe in the northern half of Peru, and at elevations below 1000 m elevation, a zone where *S. pimpinellifolium* once flourished and exhibited its highest genetic diversity. In light of these trends, there is an urgent need to regenerate the available *ex situ* collections while they still have adequate seed viability.

Among the 34 inactive accessions we grew this year, there were a number of interesting items. *S. habrochaites* LA1986 produced extremely vigorous plants with unusually large, showy flowers and fruit up to 2.5 cm in diameter (Figures 1, 2). LA1986 represents only our second collection of this species from the upper Rio Moche (the other accessions are from lower elevations). Another *S. habrochaites* collection, LA2868, represents our first accession from El Oro province in Ecuador. We also revived a collection of *S. pennellii* (LA1773) from the Rio



Figure 2. Fruit of *S. habrochaites* LA1986.

Casma, one of only a handful from that region of Peru. Flowers of LA1773 have their pedicel joint in the 'mid' position, unlike nearly all other accessions of *S. pennellii* which show a basal articulation. *S. chilense* LA1931 is a noteworthy new accession from the Rio Acari drainage, an area where relatively few wild tomato populations are known. The Acari drainage

is the northernmost boundary of the natural geographic range of *S. chilense*, and populations there are morphologically and genetically distinguishable from populations in the center of the

distribution. A newly regenerated accession of *S. huaylasense*, LA1979, provides additional representation *ex situ* for a species that has a limited geographic distribution with relatively few known populations. Finally, we regenerated a large number of inactive *S. pimpinellifolium* accessions from northern Peru. Many of these were from previously uncollected locations, and most were the large-flowered, facultatively outcrossing type, and thus likely to be genetically diverse.

Table 1. Number of accessions of each species maintained by the TGRC. Totals include accessions that are temporarily unavailable during seed regeneration.

| <i>Solanum</i> name | <i>Lycopersicon</i> equivalent | No. of Accessions |
|----------------------------|--|-------------------|
| <i>S. lycopersicum</i> | <i>L. esculentum</i> , including var. <i>cerasiforme</i> | 2,652 |
| <i>S. pimpinellifolium</i> | <i>L. pimpinellifolium</i> | 311 |
| <i>S. cheesmaniae</i> | <i>L. cheesmanii</i> | 41 |
| <i>S. galapagense</i> | <i>L. cheesmanii</i> f. <i>minor</i> | 29 |
| <i>S. chmielewskii</i> | <i>L. chmielewskii</i> | 27 |
| <i>S. neorickii</i> | <i>L. parviflorum</i> | 52 |
| <i>S. arcanum</i> | <i>L. peruvianum</i> , including f. <i>humifusum</i> | 47 |
| <i>S. peruvianum</i> | <i>L. peruvianum</i> | 78 |
| <i>S. huaylasense</i> | <i>L. peruvianum</i> | 18 |
| <i>S. corneliomulleri</i> | <i>L. peruvianum</i> , including f. <i>glandulosum</i> | 53 |
| <i>S. chilense</i> | <i>L. chilense</i> | 114 |
| <i>S. habrochaites</i> | <i>L. hirsutum</i> , including f. <i>glabratum</i> | 123 |
| <i>S. pennellii</i> | <i>L. pennellii</i> , including var. <i>puberulum</i> | 52 |
| <i>S. lycopersicoides</i> | n/a | 24 |
| <i>S. sitiens</i> | n/a | 13 |
| <i>S. juglandifolium</i> | n/a | 6 |
| <i>S. ochranthum</i> | n/a | 9 |
| Interspecific hybrids | n/a | 2 |
| Total | | 3,652 |

Certain obsolete, erroneous, or redundant stocks were de-accessioned and will no longer be maintained. These included stocks that lacked the correct phenotype and could not be rescued from older seed lots. As in previous years, we continue to prune our collection of multiple marker stocks to a more reasonable number, discarding in some cases those genotypes for which each mutation is available in other, more useful or more easily maintained lines. This year we dropped a fairly large group of multiple marker stocks which had been donated by Dr. Aleksandr Kuzemskiy, but which lacked sufficient documentation. The total number of accessions maintained by the TGRC is now 3,652 (Table 1).

MAINTENANCE

Under the guidance of Peter March and Scott Peacock, our crew of undergraduate student assistants again managed large field and greenhouse plantings this year. A total of 971 families were grown for various purposes; 270 of these were for seed increase, including 136 of wild species accessions, most of which required greenhouse culture. The rest were grown for germination tests, evaluation, introgression of the *S. sitiens* genome, research, or other purposes. 13 stocks were tested for the presence of transgenes, and all tests were negative.

Identifying accessions in need of regeneration begins with seed germination testing. Seed lots with a germination rate that fails to meet our threshold of 80% are normally

regenerated in the same year. Other factors, such as available space, age of seed and supply on hand, are also taken into account. Newly acquired accessions are typically regenerated in the first year or so after acquisition because seed supplies are limited and of uncertain viability. This year, 204 seed lots were tested for germination responses. Average germination rates continued to be relatively high (Table 2), indicating conditions in our seed vault are satisfactory.

For accessions grown in the field, the usual sequential plantings were made to spread out the work load. Seedlings were transplanted in the field on four separate dates, the first on April 25th, for a total of 34 field rows. Early growth and establishment were favorable, except for a worse than usual incidence of curly top virus (CTV). Conditions in the field were relatively mild and nearly ideal for fruit set, with only a few periods of excessive temperatures, during which manual pollinations were suspended. The male-steriles and other lines with low fruit set were intensively pollinated by the crew, resulting in adequate seed yields in most cases. We grew 3 male-sterile groups this year to produce adequate seed of F2 (ms/+ x self) or BC (ms/ms x ms/+) generations. Many others were grown for progeny testing of male-sterile seed lots produced in previous years. Stocks that failed to produce sufficient seed under field conditions will be repeated in the greenhouse.

Table 2. Results of seed germination tests of wild species accessions. Values are based on samples of 50-100 seeds per accession, and represent the % germination after 14 days at 25°C. Seed lots with a low germination rate are defined as those with less than 80% germination.

| <i>Solanum</i> Species | Date of Tested Lots | Avg % Germ. | # Tested | # Low Germ | # Grown ^a |
|---|---------------------|-------------|----------|------------|----------------------|
| <i>S. cheesmaniae</i> , <i>S. galapagense</i> | 2001 | 76 | 5 | 2 | 4 |
| <i>S. chilense</i> | 1997-2001 | 90 | 6 | 1 | 5 |
| <i>S. chmielewskii</i> , <i>S. neorickii</i> | 1991-1999 | 99 | 11 | 0 | 6 |
| <i>S. habrochaites</i> | 1982-2002 | 97 | 50 | 1 | 6 |
| <i>S. lycopersicoides</i> | - | - | - | - | 1 |
| <i>S. pennellii</i> | 1997-1999 | 93 | 4 | 0 | 6 |
| <i>S. peruvianum</i> clade | 1981-2002 | 87 | 78 | 11 | 13 |
| <i>S. pimpinellifolium</i> | 1997-2002 | 95 | 19 | 1 | 9 |
| <i>S. sitiens</i> | 1989 | 98 | 1 | 0 | 0 |
| <i>S. juglandifolium</i> | | | 1 | 1 | 1 |
| <i>S. ochranthum</i> | 1996-2000 | 80 | 3 | 0 | 1 |

^a Includes all accessions grown for seed increase in the 2012 pedigree year, whether for low germ or for other reasons.

For various reasons, many of the wild species, mutants and certain other genetic stocks require greenhouse culture. For the mutant stocks, we start the weakest lines first, and finish with lines of normal vigor. We now grow most of the introgression lines in the greenhouse, both to assure adequate seed set (some are partially sterile in the field) and to reduce the risk of outcrossing. For the wild species, plantings in the greenhouse are based on daylength response: those with the least sensitivity are planted first; next, those with intermediate reaction; last, the most sensitive (i.e. flower best under short days). Optimal planting dates for each species are listed on our website, at <http://tgrc.ucdavis.edu/spprecomm.html>.

This year we grew a number of *S. habrochaites* accessions in the field for experimental crosses. These are normally grown for seed multiplication in the greenhouse because they are self-incompatible (obligate outcrossers), and therefore vulnerable to insect cross pollination outdoors.



Figure 3. *S. habrochaites* growing in the field (L) and *S. juglandifolium* in the greenhouse (R). [photos J. Petersen, S. Peacock]

Furthermore, they are daylength sensitive, and do not flower well in the greenhouse during the summer. The material we grew in the field, on the other hand, flowered strongly throughout summer and most set abundant fruit (Figure 3). The accessions from Ecuador did better than ones from southern Peru. Therefore, *S. habrochaites* could be grown in the field for seed multiplication, provided that isolation cages are used.

Our greenhouse plantings were relatively trouble-free this year, except for recurring infestations of thrips. We continue to search for a good method for inducing *S. juglandifolium* and *S. ochranthum* to flower and set seed (Figure 3). This year we had some success growing *S. juglandifolium* plants in very small pots; they quickly became pot bound and growth was limited, but the flowering response was stronger.

As in the past, we continue to store samples of all newly regenerated seed lots in our seed vault at 5-7°C; this is our ‘working’ collection, used for filling seed requests. In addition, we package seed samples of each accession in sealed foil pouches for storage at -18°C in order to extend seed longevity and reduce the number of regeneration cycles. As in the past, large samples of newly regenerated seed lots were sent to the USDA-NCGRP in Ft. Collins, Colorado, for long-term backup storage. This year, 70 accessions were sent to NCGRP, and 165 to the Svalbard Global Seed Vault in Norway.

EVALUATION

All stocks grown for seed increase or other purposes are systematically examined and observations recorded. Older accessions are checked to ensure that they have the correct phenotypes. New accessions are evaluated in greater detail, with the descriptors depending upon type of accession (wild species, cultivar, mutant, chromosomal stocks, etc.). In the case of new wild species accessions, plantings are reviewed at different growth stages to observe foliage, habit, flower morphology, mating system, and fruit morphology. We also record the extent of variation for morphological traits, and in some cases assay genetic variation with markers. Such observations may reveal traits that were not seen at the time of collection, either because plants

were not flowering or were in such poor condition that not all traits were evident, or because certain traits were overlooked by the collector.

Many genetic stocks, including various sterilities, nutritional, and weak mutants, cannot be maintained in true-breeding condition, hence have to be transmitted from heterozygotes. Progeny tests must therefore be made to verify that individual seed lots segregate for the gene in question. This year we performed progeny tests on 63 seed lots to confirm the segregation of specific markers or to resolve segregation problems. The tested stocks included several male-steriles mutants, *thiamineless* (*tl*), and *mortalis* (*mts*). We also initiated allele tests of a provisional mutant that exhibits purplish leaves and dark anthers by crossing to two anthocyanin enhancer mutants, *Anthocyanin fruit* (*Aft*) and *atroviolacium* (*atv*). Stocks grown for observation included the accessions of *S. lycopersicum* that form part of the SolCAP core collection.

DISTRIBUTION AND UTILIZATION

The TGRC again filled a very large number of seed requests this year. A total of 4,966 seed samples representing 1,931 different accessions were sent in response to 273 seed requests from 200 investigators in 23 countries. In addition, at least 25 purely informational requests were answered. Relative to the size of the TGRC collection, the number of seed samples distributed was equivalent to a utilization rate of approx. 136% -- a high level of use for any genebank, and proof that demand for our stocks remains high.

The various steps involved in filling seed requests – selecting accessions, packaging seeds, entering the information into our database, providing cultural recommendations, obtaining phytosanitary certificates and import permits, etc – involve a large time commitment. Led by Alison Gerken and Jennifer Petersen, the TGRC crew did a splendid job filling requests promptly and accurately. The online payment system we implemented last year to recover the costs of phytosanitary certificates continues to function well, allowing us to keep up with the rising cost of phytos (USDA-APHIS raised their prices again this year). Many countries are increasing the stringency of their import regulations, and obtaining the necessary phytosanitary certificates and/or import permits is becoming more onerous and time consuming. For instance, Japan now requires an import permit for some tomato species but not for others, so shipments need to be split, with different sets of documents accompanying each group of seed samples. We can no longer ship seed to countries in the E.U. zone unless the requestor provides a letter of authorization with the appropriate phytosanitary exemptions.

Information provided by recipients regarding intended uses of our stocks is summarized below (Table 3). Breeding for resistance to various diseases and/or investigations of the molecular biology of host-pathogen interactions were major areas of research interest, as in previous years. In particular, many requests mentioned research or breeding related to begomoviruses, bacterial speck or late blight. Research on responses to abiotic stresses emphasized salinity and low temperature stresses this year. In the area of fruit quality, there seems to be less interest in carotenoids and greater focus on fruit flavor than in the past. There continues to be high demand for studies of rootstocks and grafting. Many requests for genetic research now mention gene expression and/or evolutionary studies. Other research topics accounting for many requests were: interspecific reproductive barriers, flower and inflorescence development, the soil microbial community, wounding responses, and metabolites. We also received a large number of requests for educational / instructional uses, and one request for an archeological study. As in the past, we received a large number of requests for unspecified breeding or research purposes, particularly from users in the private sector.

There continues to be high demand for introgression lines (ILs) -- stocks containing a defined wild species chromosome segment in the background of cultivated tomato -- as they offer many advantages for breeding and research. A total of 23 requests and 255 seed samples were processed for the *S. pennellii* ILs, 21 requests and 446 samples for the *S. habrochaites* ILs, and 13 requests and 149 samples for the *S. lycopersicoides* ILs. The relatively high demand for the *S. habrochaites* ILs this year was noteworthy.

Table 3. Intended uses of TGRC stocks as reported by requestors. Values represent the total number of requests in each category. Requests addressing multiple topics may be counted more than once.

| Category | # Requests | Category | # Requests |
|-------------------------------|------------|-------------------------------|------------|
| Biotic Stresses | | Abiotic Stresses | |
| Viruses: | | Drought | 6 |
| PepMV | 1 | High temperatures | 3 |
| TBSV | 1 | Low temperatures | 7 |
| ToMV | 3 | P-efficiency | 1 |
| TSWV and other tospoviruses | 2 | Salinity | 10 |
| TYLCV and other begomoviruses | 6 | Shade | 1 |
| Viroids | 1 | Unspecified abiotic stresses | 5 |
| Bacteria: | | Fruit Traits | |
| Bacterial canker | 1 | Anthocyanins and antioxidants | 2 |
| Bacterial speck | 6 | Cuticle/wax properties | 2 |
| Bacterial spot | 1 | Development and ripening | 3 |
| Bacterial wilt | 2 | Flavor, volatiles | 4 |
| Septoria | 1 | Food safety | 1 |
| Zebra complex | 1 | Nutritional quality | 1 |
| Unspecified bacteria | 2 | Postharvest and shelf life | 3 |
| Fungi: | | Quality | 1 |
| <i>Cladosporium</i> | 2 | Size and shape | 2 |
| Early blight | 2 | Sugars | 1 |
| <i>Fusarium</i> wilt | 1 | Tomatine | 1 |
| Late blight | 5 | Miscellaneous Breeding | |
| Powdery mildew | 1 | Heterosis, yield | 1 |
| Southern blight | 1 | Grafting, rootstocks | 7 |
| <i>Verticillium</i> wilt | 1 | Haploids | 1 |
| Unspecified fungi | 1 | Home garden cultivars | 2 |
| Nematodes: | | Marker assisted selection | 1 |
| Pale cyst nematode | 3 | Marker development | 2 |
| Root knot nematode | 3 | Ornamentals | 1 |
| Unspecified nematodes | 1 | Prebreeding | 2 |
| Unspecified diseases | 11 | Wild species introgressions | 1 |
| Insects: | | Yield | 1 |
| Aphids | 3 | Unspecified breeding uses | 26 |
| <i>Bemisia</i> | 2 | Genetic Studies | |
| Bollworms | 1 | Association mapping | 3 |
| Mites | 1 | Biosystematics | 2 |
| Thrips | 1 | Centromeres | 1 |
| Unspecified insects | 1 | | |
| Unspecified biotic stresses | 7 | | |

| Category | # Requests | Category | # Requests |
|--------------------------------------|-------------------|---------------------------------------|-------------------|
| Diversity studies | 3 | Flower, inflorescence development | 5 |
| Double mutants | 1 | Flowering time | 2 |
| Evolution and domestication | 4 | Gibberellin responses | 1 |
| Functional genomics | 4 | Hormone responses | 1 |
| Gene cloning | 1 | Metabolites, metabolomics | 6 |
| Gene expression / transcriptomics | 6 | Mycorrhizae, rhizosphere | 5 |
| Gene silencing | 2 | Photomorphogenesis, photosynthesis | 1 |
| Mapping | 2 | Pollination biology | 1 |
| Phenotyping | 1 | Reproductive barriers, mating systems | 12 |
| Population genetics | 3 | Root biology and architecture | 7 |
| Recombination, segregation | 2 | Seed development, germination | 1 |
| Sequencing | 2 | Trichomes, volatiles, exudates | 3 |
| SNP genotyping | 1 | Wounding, defense signaling | 5 |
| TILLING | 1 | Unspecified physiological studies | 2 |
| Transformation | 1 | | |
| Unspecified genetic, genomic studies | 5 | | |
| | | Miscellaneous | |
| | | Horticultural studies | 2 |
| | | Archaeological studies | 1 |
| | | Instructional uses | 7 |
| | | Unspecified research | 23 |
| | | Unspecified uses | 8 |
| Physiology & Development | | | |
| ABA responses | 1 | | |
| Abscission | 4 | | |
| Acyl-sugars | 4 | | |

Our survey of the 2012 literature (and unreviewed papers of previous years) again uncovered a large number of publications that mention use of TGRC stocks (see Bibliography below). This year's bibliography includes 105 journal articles, reports, abstracts, theses, and patents. Many references were undoubtedly missed, and cases of utilization by the private sector are generally not publicized. This publication record demonstrates the important role of the TGRC as a research resource, and its positive impact on many fields of investigation. The value of the collection for improving the tomato crop is shown by the many publications that address economic traits.

DOCUMENTATION

Various modifications and enhancements were made to our database and website by Tom Starbuck. Our website (<http://tgrc.ucdavis.edu>) was updated in various ways to improve usability. Queries related to wild species accessions can now be viewed in a datasheet (tabular) format, in addition to a form view. The underlying data records can now be downloaded to a spreadsheet file, including all the fields that make up the essential 'passport' data on each accession. Groups of related accessions can now be displayed using an imbedded GoogleMap function. For example, one can plot the locations of all accessions of a species, or view all the collections of any species from a particular country or province. Clicking on individual accessions brings up all the accession details. In addition, many of our web-based query pages were rewritten to meet enhanced security standards in our web server environment.

Our database was modified in various ways to further improve internal record keeping. We also finished our project to digitize the information contained in Charley Rick's field notebooks from his collecting trips to South America. These notebooks represent the records of 15 trips to Peru, Ecuador and Chile, made by Dr. Rick and his associates between 1948 and 1995. They contain potentially useful information about our wild species accessions, including the locations of populations, local habitat characteristics, probable abiotic stress tolerances,

disease symptoms, plant growth type, evidence of cross pollination, fruit shape and color, extent of genetic variability, indigenous plant names and medicinal uses, etc. During this process we used GoogleEarth to translate the relatively detailed collection site information (e.g. “50 Km East of Panamerican highway on the road to Cajamarca”) into more accurate and precise latitude and longitude coordinates for each accession (all were collected pre-GPS).

As usual, our annual distribution records were provided to the USDA for incorporation into the GRIN database. We also issued a revised list of miscellaneous genetic stocks, which is available on our website and will be published in the Tomato Genetics Coop. Report (TGC), volume 62.

RESEARCH

In addition to the core genebank functions described above, the TGRC conducts research synergistic with the overall mission of the Center. Our current research focuses on the genetics of interspecific reproductive barriers. Wentao Li continued his study of pollen factors involved in unilateral incompatibility (UI), i.e. interspecific crosses that are compatible in one direction but incompatible when the pollen and pistil parents are reversed. He previously isolated the *ui6.1* gene, one of two pollen factors from *S. pennellii* (the other is *ui1.1*) that are required for pollen to overcome UI on pistils of interspecific hybrids. He continues to study the role of *ui6.1* in self-incompatibility (many of the wild species are self-incompatible), and is working towards isolating the *ui1.1* gene. Jennifer Petersen is studying natural variation at *ui1.1* and *ui6.1* among the green-fruited self-compatible species, and other pollen factors that are evident in certain crosses.

Another TGRC research project is to advance breeding lines representing the *S. sitiens* genome in the background of cultivated tomato, with the goal of developing a set of introgression lines for this wild species. Visiting scientist Yosuke Moritama genotyped a sample of early backcross generation lines (BC2-BC3) using DNA markers, and found that roughly 80% of the *S. sitiens* genome has been captured in these lines. They are still at a very early stage and more backcrosses and marker aided selection will be needed to recover a uniform cultivated tomato genome and to obtain lines with a single chromosome segment from *S. sitiens*. In addition, the missing genomic regions need to be recovered, and the overlap between adjacent chromosome segments in different lines verified.

PUBLICATIONS

- Chetelat, R. T. (2012) Revised list of miscellaneous stocks. *Tomato Genetics Coop. Rep.* 62.
- Powell, A. L. T., C. V. Nguyen, et al. (2012) *Uniform ripening* encodes a *Golden2*-like transcription factor regulating tomato fruit development. *Science* 336: 1711-1715.
- S.C. Sim, A. VanDeynze et al. (2012) High-density SNP genotyping of tomato (*Solanum lycopersicum* L.) reveals patterns of genetic variation due to breeding. *PLoS ONE* 7(9): e45520. doi:10.1371/journal.pone.0045520.

SERVICE AND OUTREACH

Presentations. Lectures, seminars and other presentations on the TGRC, our research projects, and related topics were given to the following groups:

- presentation to Yolo County Master Gardeners.
- seminar in the Plant and Microbial Biology Dept., UC-Berkeley
- lecture to UCD class on Plant Conservation Genetics (ENH150)

- presentation to the Seed Central group
- presentation at the Plant and Animal Genome Conference, San Diego
- presentation to the International Conference on Genetic Improvement for Crop Development, Santiago, Chile

Press Coverage. Articles or videos mentioning or featuring the TGRC appeared in the following media sources:

- Interview with NPR: <http://www.npr.org/blogs/thesalt/2012/06/28/155917345/how:-the-taste-of-tomatoes-went-bad-and-kept-on-going.html>
- Interview with KQED radio: <http://science.kqed.org/quest/audio/building-a-better-tastier-tomato/>
- Interview with Rocky Mountain Collegian: <http://archives.collegian.com/?p=31748>
- Interview with Nancy Stamp, Binghamton University, SUNY.
- Interview with *Organic Gardening* magazine: <http://www.organicgardening.com/learn-and-grow/preventing-late-blight>

Visitors. Individuals from the following institutions visited the TGRC:

- Juan Carlos Brevis, Enza Zaden Seed Company
- Steven Loewen, University of Guelph, Canada
- Suchila Techawongstien, Khon Kaen University, Thailand
- George Kotch, Seed Biotechnology Center
- William Reinert, Morning Star Co.
- Elena Albrecht, Keygene

PERSONNEL AND FACILITIES

The TGRC lost two highly qualified and experienced staff members this year when Peter March and Alison Gerken resigned to pursue their interests in dentistry and veterinary medicine, respectively. They were replaced by Scott Peacock and Jennifer Petersen, both former members of the TGRC and exceptionally well qualified. Scott worked for Arcadia Biosciences in Davis after graduating and before returning to the TGRC. Jennifer completed her Ph.D. in Dan Potter's lab and now works part time at the TGRC answering seed requests; she also works in the lab studying evolutionary aspects of interspecific reproductive barriers. Wentao Li continued his research on the molecular genetics of intra- and interspecific incompatibility. Yosuke Moritama from Sakata Seeds was a visiting scientist for 6 months and gave our *S. sitiens* introgression project a real boost by genotyping a large number of lines. Undergraduate students Samantha Melendy and Daniel Short assisted with greenhouse, field and seed lab operations at the TGRC. Christine Nguyen was a student intern. Tom Starbuck continues to maintain our database and website. Many thanks to each of these individuals for contributing to the success of our Center!

FINANCIAL SUPPORT

We gratefully acknowledge receiving financial support from the following institutions this year.

California Tomato Research Institute
National Science Foundation
Nunhems USA, Inc.
UC-Davis Department of Plant Sciences
UC-Davis College of Agricultural and Environmental Sciences
USDA-ARS National Plant Germplasm System
USDA-ARS Solanaceae Coordinated Agricultural Project

TESTIMONIALS

“I think the TGRC is doing a really great job as a resource center for tomato research.”

-- Maria Ivanchenko, Oregon State University

“Nice website.”

-- Hakan Aktas, UC Davis

“Thank you for your cooperation and support to researchers all over the world.”

-- Hisham Hussain, University Technology of Malaysia

“The germplasm you maintain is a remarkable resource, and, of course, many of us wish we could have worked alongside Dr. Rick.”

-- Lee Goodwin, J&L Gardens, Espanola, New Mexico

“I greatly appreciate that this project in scientific solidarity exists.”

-- Juan Sebastián Schneider, Argentina

“It is an opportunity to say how important is your work for the breeders community, thanks!”

-- Ari Efrati, Rootability, Israel

BIBLIOGRAPHY

(publications that mention use of TGRC accessions)

- Akhtar, K. P., M. Y. Saleem, et al. (2012). "RESISTANCE OF SOLANUM SPECIES TO PHYTOPHTHORA INFESTANS EVALUATED IN THE DETACHED-LEAF AND WHOLE-PLANT ASSAYS." Pakistan Journal of Botany **44**(3): 1141-1146.
- Arikita, F. N., M. S. Azevedo, et al. (2012). "Solanum pennellii LA716 as a source of genes improving in vitro organogenesis in cultivated tomato." Acta Hort. **961**: 327-333.
- Ashrafi, H., M. P. Kinkade, et al. (2012). "Identification of novel quantitative trait loci for increased lycopene content and other fruit quality traits in a tomato recombinant inbred line population." Molecular Breeding **30**(1): 549-567.
- Baccio, D. d., L. Ederli, et al. (2012). "Similar foliar lesions but opposite hormonal patterns in a tomato mutant impaired in ethylene perception and its near isogenic wild type challenged with ozone." Environmental and Experimental Botany **75**: 286-297.
- Balacheva, E. and e. al. (2012). "The diversity of tomato colours - potential for diversity in tomato nutritive quality." Acta Hort. **960**: 31-.
- Barry, C. S., G. M. Aldridge, et al. (2012). "Altered Chloroplast Development and Delayed Fruit Ripening Caused by Mutations in a Zinc Metalloprotease at the lutescent2 Locus of Tomato." Plant Physiology (Rockville) **159**(3): 1086-1098.
- Barry, C. S., G. M. Aldridge, et al. (2012). "Altered Chloroplast Development and Delayed Fruit Ripening Caused by Mutations in a Zinc Metalloprotease at the lutescent2 Locus of Tomato." Plant Physiology (Rockville) **159**(3): 1086-1098.
- Blanca, J. and e. al. (2012). "SolCAP and morphological tomato variability, insights regarding the domestication process." SOL 2012 Proc.s: 154.
- Blanca, J., J. Canizares, et al. (2012). "Variation Revealed by SNP Genotyping and Morphology Provides Insight into the Origin of the Tomato." PLoS One **7**(10): e48198.
- Bondel, K. and e. al. (2012). "The evolutionary history of a plant resistance gene: balancing selection and introgression between species." SOL 2012 Proc.s: 194.
- Carrera, E., O. Ruiz-Rivero, et al. (2012). "Characterization of the procera Tomato Mutant Shows Novel Functions of the SIDELLA Protein in the Control of Flower Morphology, Cell Division and Expansion, and the Auxin-Signaling Pathway during Fruit-Set and Development." Plant Physiology (Rockville) **160**(3): 1581-1596.
- Casals, J., L. Pascual, et al. (2012). "Genetic basis of long shelf life and variability into Penjar tomato." Genetic Resources and Crop Evolution **59**(2): 219-229.
- Chibon, P.-Y., H. Schoof, et al. (2012). "Marker2sequence, mine your QTL regions for candidate genes." Bioinformatics (Oxford) **28**(14): 1921-1922.

- Chitwood, D. H., L. R. Headland, et al. (2012). "Native Environment Modulates Leaf Size and Response to Simulated Foliar Shade across Wild Tomato Species." PLoS One **7**(1): e29570.
- Chitwood, D. H., L. R. Headland, et al. (2012). "The Developmental Trajectory of Leaflet Morphology in Wild Tomato Species." Plant Physiology (Rockville) **158**(3): 1230-1240.
- Clergeot, P.-H., H. Schuler, et al. (2012). "The Corky Root Rot Pathogen *Pyrenochaeta lycopersici* Secretes a Proteinaceous Inducer of Cell Death Affecting Host Plants Differentially." Phytopathology **102**(9): 878-891.
- Coaker, G. and G. Miyao (2012). "Breeding for resistance to bacterial speck and monitoring California *Pseudomonas syringae* strains." Annual Project Report, California Tomato Research Institute 101-107.
- Cortada, L., S. Mantelin, et al. (2012). "Marker analysis for detection of the Mi-1.2 resistance gene in tomato hybrid rootstocks and cultivars." Nematology **14**(Part 5): 631-642.
- Dekkers, B. J. W., L. Willems, et al. (2012). "Identification of Reference Genes for RT-qPCR Expression Analysis in Arabidopsis and Tomato Seeds." Plant and Cell Physiology **53**(1, Sp. Iss. SI): 28-37.
- Di Baccio, D., L. Ederli, et al. (2012). "Similar foliar lesions but opposite hormonal patterns in a tomato mutant impaired in ethylene perception and its near isogenic wild type challenged with ozone." Environmental and Experimental Botany **75**: 286-297.
- Di Matteo, A., A. Sacco, et al. (2012). "Comparative Transcriptomic Profiling of Two Tomato Lines with Different Ascorbate Content in the Fruit." Biochemical Genetics **20**(11-12): 908-921.
- Dosmann, M. and A. Groover (2012). "The importance of living botanical collections for plant biology and the "next generation" of evo-devo research." Frontiers in Plant Science **3**: 1-5.
- Firdaus, S. (2012). "Identification of whitefly resistance in tomato and hot pepper." Ph.D. Thesis: 167.
- Firdaus, S. and e. al. (2012). "Resistance to *Bemisia tabaci* in tomato wild relatives." Euphytica **187**: 31-45.
- Fukuoka, H., K. Miyatake, et al. (2012). "Development of gene-based markers and construction of an integrated linkage map in eggplant by using *Solanum* orthologous (SOL) gene sets." Theoretical and Applied Genetics **125**(1): 47-56.
- Gallo, M., R. Zorzoli, et al. (2011). "Genetic linkage among tomato fruit quality traits and polypeptides expressed at two ripening stages." Revista de la Facultad de Ciencias Agrarias Universidad Nacional de Cuyo **43**(2): 145-156.
- Gonzales-Vigil, E., D. E. Hufnagel, et al. (2012). "Evolution of TPS20-related terpene synthases influences chemical diversity in the glandular trichomes of the wild tomato relative *Solanum habrochaites*." Plant Journal **71**(6): 921-935.
- Gonzalez-Cabezuelo, J. M., J. Capel, et al. (2012). "Genotyping selection for resistance against tomato yellow leaf curl virus (TYLCV) conferred by Ty-1 and Ty-3 genes in tomato." Molecular Breeding **30**(2): 1131-1142.
- Goulet, C., M. H. Mageroy, et al. (2012). "Role of an esterase in flavor volatile variation within the tomato clade." Proceedings of the National Academy of Sciences of the United States of America **109**(46): 19009-19014.
- Hazra, P., S. Akhtar, et al. (2012). "Effect of mutant genes on the content of the nutritive quality related compounds in tomato (*Solanum lycopersicum*) fruits." Acta Horticulturae Sinica **960**: 311-318.
- Hoerger, A. C., M. Ilyas, et al. (2012). "Balancing Selection at the Tomato RCR3 Guardee Gene Family Maintains Variation in Strength of Pathogen Defense." PLoS Genetics **8**(7): e1002813.
- Huang, S. and e. al. (2012). "A map of genome variation in the red tomato cluster." SOL 2012 Proc.s: 76.
- Hutton, S. F., J. W. Scott, et al. (2012). "Recessive Resistance to Tomato yellow leaf curl virus from the Tomato Cultivar Tyking Is Located in the Same Region as Ty-5 on Chromosome 4." Hortscience **47**(3): 324-327.
- Johnson, E. B., J. E. Haggard, et al. (2012). "Fractionation, Stability, and Isolate-Specificity of QTL for Resistance to *Phytophthora infestans* in Cultivated Tomato (*Solanum lycopersicum*)." G3-Genes Genomes Genetics **2**(10): 1145-1159.
- Kachanovsky, D., S. Filler, et al. (2012). "Epistasis in tomato color mutations involves regulation of phytoene synthase 1 expression by cis-carotenoids." Proceedings of the National Academy of Sciences of the United States of America **109**: 19021-19026.
- Kartzeva, T., E. Balacheva, et al. (2012). "Effect of three anthocyaninless genes on germination ability of the brown seed (bs) mutant in tomato." Seed Science and Technology **40**(2): 177-184.
- Kim, J., K. Kang, et al. (2012). "Striking Natural Diversity in Glandular Trichome Acylsugar Composition Is Shaped by Variation at the Acyltransferase2 Locus in the Wild Tomato *Solanum habrochaites*." Plant Physiology (Rockville) **160**(4): 1854-1870.
- Kimbara, J., M. Yoshida, et al. (2012). "A novel class of sticky peel and light green mutations causes cuticle deficiency in leaves and fruits of tomato (*Solanum lycopersicum*)." Planta (Berlin) **236**(5): 1559-1570.
- Kumar, R., M. K. Sharma, et al. (2012). "Transcriptome analysis of rin mutant fruit and in silico analysis of

- promoters of differentially regulated genes provides insight into LeMADS-RIN-regulated ethylene-dependent as well as ethylene-independent aspects of ripening in tomato." MGG Molecular Genetics and Genomics **287**(3): 189-203.
- Labate, J. A. and L. D. Robertson (2012). "Evidence of cryptic introgression in tomato (*Solanum lycopersicum* L.) based on wild tomato species alleles." BMC Plant Biology **12**: 133.
- Lahaye, M., B. Quemener, et al. (2012). "Hemicellulose fine structure is affected differently during ripening of tomato lines with contrasted texture." International Journal of Biological Macromolecules **51**(4): 462-470.
- Leckie, B. M., D. M. De Jong, et al. (2012). "Quantitative trait loci increasing acylsugars in tomato breeding lines and their impacts on silverleaf whiteflies." Molecular Breeding **30**(4): 1621-1634.
- Lee, J. M. and e. al. (2012). "Combined transcriptome, genetic diversity and metabolite profiling in tomato fruit reveals that the ethylene response factor SIERF6 plans an important role in ripening and carotenoid accumulation." Plant J. **70**: 191-204.
- Leide, J. and e. al. (2012). "Abscisic acid mediates the formation of a suberized stem scar tissue in tomato fruits." New Phytologist **194**: 402-415.
- Leiva-Brondo, M., M. Valcarcel, et al. (2012). "Exploring alternative germplasm for the development of stable high vitamin C content in tomato varieties." Scientia Horticulturae (Amsterdam) **133**: 84-88.
- Li, H. and e. al. (2012). "Ultra-performance liquid chromatographic separation of geometric isomers of carotenoids and antioxidant activities of 20 tomato cultivars and breeding lines." Food Chemistry **132**: 508-517.
- Li, H. and e. al. (2012). "Microwave-assisted extraction of phenolics with maximal antioxidant activities." Food Chemistry **130**: 928-936.
- Li, J., W. Sima, et al. (2012). "Tomato SIDREB gene restricts leaf expansion and internode elongation by downregulating key genes for gibberellin biosynthesis." Journal of Experimental Botany **63**(18): 6407-6420.
- Liu, H., B. Ouyang, et al. (2012). "Differential Modulation of Photosynthesis, Signaling, and Transcriptional Regulation between Tolerant and Sensitive Tomato Genotypes under Cold Stress." PLoS One **7**(11): e50785.
- Liu, L., Y. Song, et al. (2011). "Mapping of QTLs for drought tolerance during seedling stage using introgression line populations in tomato." acta Hort. Sinica **38**: 1921-1928.
- Lombardi-Crestana, S., M. d. S. Azevedo, et al. (2012). "The Tomato (*Solanum Lycopersicum* cv. Micro-Tom) Natural Genetic Variation Rgl1 and the DELLA Mutant Procera Control the Competence Necessary to Form Adventitious Roots and Shoots." Journal of Experimental Botany **63**(15): 5689-5703.
- Lopez-Casado, G., P. A. Covey, et al. (2012). "Enabling proteomic studies with RNA-Seq: The proteome of tomato pollen as a test case." Proteomics **12**(6): 761-774.
- Loukehaich, R., T. Wang, et al. (2012). "SpUSP, an annexin-interacting universal stress protein, enhances drought tolerance in tomato." Journal of Experimental Botany **63**(15): 5593-5606.
- MacAlister, C. A., S. J. Park, et al. (2012). "Synchronization of the flowering transition by the tomato TERMINATING FLOWER gene." Nature Genetics **44**(12): 1393-1398.
- Mageroy, M. H., D. M. Tieman, et al. (2012). "A *Solanum lycopersicum* catechol-O-methyltransferase involved in synthesis of the flavor molecule guaiacol." Plant Journal **69**(6): 1043-1051.
- Maloof, J. N. and e. al. (2012). "Natural variation in tomato shade avoidance." SOL 2012 Proc.s: 78.
- Martinez, J.-P., A. Antunez, et al. (2012). "EFFECTS OF SALINE WATER ON WATER STATUS, YIELD AND FRUIT QUALITY OF WILD (*SOLANUM CHILENSE*) AND DOMESTICATED (*SOLANUM LYCOPERSICUM* VAR. *CERASIFORME*) TOMATOES." Experimental Agriculture **48**(4): 573-586.
- Mboup, M., I. Fischer, et al. (2012). "Trans-Species Polymorphism and Allele-Specific Expression in the CBF Gene Family of Wild Tomatoes." Molecular Biology and Evolution **29**(12): 3641-3652.
- Merk, H. L., S. C. Yarnes, et al. (2012). "Trait Diversity and Potential for Selection Indices Based on Variation Among Regionally Adapted Processing Tomato Germplasm." Journal of the American Society for Horticultural Science **137**(6): 427-437.
- Mignolli, F., L. Mariotti, et al. (2012). "Tomato fruit development in the auxin-resistant dgt mutant is induced by pollination but not by auxin treatment." Journal of Plant Physiology **169**(12): 1165-1172.
- Mohan, V. and e. al. (2012). "A study on natural genetic variations in chromoplast specific lycopene beta cyclase gene in tomato." SOL 2012 Proc.s: 127.
- Moreno, A., E. Claveria, et al. (2012). "Development of a methodology for the production of doubled haploid lines in *Solanum lycopersicum* L." Acta Hort. **935**: 95-100.
- Moy, M. and e. al. (2012). "Tandem duplications in the promoter of the soluble invertase gene TIV are causal to the evolution of hexose accumulation in *Solanum* fruit." SOL 2012 Proc.s: 49.

- Nadakuduti, S. S., M. Pollard, et al. (2012). "Pleiotropic Phenotypes of the sticky peel Mutant Provide New Insight into the Role of CUTIN DEFICIENT2 in Epidermal Cell Function in Tomato." Plant Physiology (Rockville) **159**(3): 945-960.
- Nakazato, T., R. A. Franklin, et al. (2012). "POPULATION STRUCTURE, DEMOGRAPHIC HISTORY, AND EVOLUTIONARY PATTERNS OF A GREEN-FRUITED TOMATO, SOLANUM PERUVIANUM (SOLANACEAE), REVEALED BY SPATIAL GENETICS ANALYSES." American Journal of Botany **99**(7): 1207-1216.
- Netting, A. G., J. C. Theobald, et al. (2012). "Xylem sap collection and extraction methodologies to determine in vivo concentrations of ABA and its bound forms by gas chromatography-mass spectrometry (GC-MS)." Plant Methods **8**: 11.
- Nitsch, L., W. Kohen, et al. (2012). "ABA-deficiency results in reduced plant and fruit size in tomato." Journal of Plant Physiology **169**(9): 878-883.
- Oh, K. and e. al. (2002). "Fine mapping in tomato using microsynteny with the Arabidopsis genome: the Diageotropica (Dgt) locus." Genome Biology **3**: research0049.0041-0049.0011.
- Pablo Lara-Avila, J., M. Isabel Isordia-Jasso, et al. (2012). "Gene Expression Analysis during Interaction of Tomato and Related Wild Species with *Clavibacter michiganensis* subsp. *michiganensis*." Plant Molecular Biology Reporter **30**(2): 498-511.
- Park, S. J., K. Jiang, et al. (2012). "Rate of meristem maturation determines inflorescence architecture in tomato." Proceedings of the National Academy of Sciences of the United States of America **109**(2): 639-644.
- Piterkova, J., J. Hofman, et al. (2011). "Dual role of nitric oxide in *Solanum* spp.-*Oidium neolycopersici* interactions." Environmental and Experimental Botany **74**: 37-44.
- Powell, A. L. T., C. Nguyen, V., et al. (2012). "Uniform ripening encodes a Golden 2-like transcription factor regulating tomato fruit chloroplast development." Science **336**: 1711-1715.
- Qi, H., Y. Jiang, et al. (2012). "Responses to short-term low night temperature of sucrose-metabolizing in domesticated tomato and wild relative." Acta Hort. Sinica **39**: 281-288.
- Qiao, H., H. H. Offenberg, et al. (2012). "Altered distribution of MLH1 foci is associated with changes in cohesins and chromosome axis compaction in an asynaptic mutant of tomato." Chromosoma (Berlin) **121**(3): 291-305.
- Qin, P., D. Ting, et al. (2012). "Callose plug deposition patterns vary in pollen tubes of *Arabidopsis thaliana* ecotypes and tomato species." BMC Plant Biology **12**: 178.
- Ranc, N., S. Munos, et al. (2012). "Genome-Wide Association Mapping in Tomato (*Solanum lycopersicum*) Is Possible Using Genome Admixture of *Solanum lycopersicum* var. *cerasiforme*." G3-Genes Genomes Genetics **2**(8): 853-864.
- Rao, E. S., P. Kadirvel, et al. (2012). "Using SSR markers to map genetic diversity and population structure of *Solanum pimpinellifolium* for development of a core collection." Plant Genetic Resources Characterization and Utilization **10**(1): 38-48.
- Ruiu, F. and e. al. (2012). "Novel insights and perspectives for the breeding of high-anthocyanin tomatoes." SOL 2012 Proc.s: 32.
- Sahu, P. P., N. K. Rai, et al. (2012). "Dynamics of Defense-Related Components in Two Contrasting Genotypes of Tomato Upon Infection with Tomato Leaf Curl New Delhi Virus." Molecular Biotechnology **52**(2): 140-150.
- Schillmiller, A. L., A. L. Charbonneau, et al. (2012). "Identification of a BAHD acetyltransferase that produces protective acyl sugars in tomato trichomes." Proceedings of the National Academy of Sciences of the United States of America **109**(40): 16377-16382.
- Schmidt, A., C. Li, et al. (2012). "Characterization of a flavonol 3-O-methyltransferase in the trichomes of the wild tomato species *Solanum habrochaites*." Planta (Berlin) **236**(3, Sp. Iss. SI): 839-849.
- Shivaprasad, P. V., R. M. Dunn, et al. (2012). "Extraordinary transgressive phenotypes of hybrid tomato are influenced by epigenetics and small silencing RNAs." EMBO (European Molecular Biology Organization) Journal **31**(2): 257-266.
- Sim, S.-C., G. Durstewitz, et al. (2012). "Development of a Large SNP Genotyping Array and Generation of High-Density Genetic Maps in Tomato." PLoS One **7**(7): e40563.
- Sim, S. C., A. Van Deynze, et al. (2012). "High-density SNP genotyping of tomato (*Solanum lycopersicum* L.) reveals patterns of genetic variation due to breeding." PLoS One **7**: e45520. doi:45510.41371/journal.pone.0045520.
- Sinha, N. R. and e. al. (2012). "Genome assisted developmental analyses in wild and domesticated tomato." SOL 2012 Proc.s: 47.

- Snyder, J. and C. Min (2012). "Insect resistance in *Lycopersicon hirsutum* LA2329 - current status." Acta Hort. **944**: 15-21.
- Staniaszek, M. and e. al. (2012). "The novel ps and ps-2 specific markers for selection of functional male sterile tomato lines in breeding programs and hybrids seeds production." J. Agrc. Sci. **4**: 61-.
- Strickler, S. and e. al. (2012). "Comparative genomics of *Solanum galapagense*, a wild relative of tomato, endemic to the Galapagos Islands." SOL 2012 Proc.s: 139.
- Szczepaniak, M. and D. Kulpa (2012). "Response of *Lycopersicum peruvianum* L. line to salinity in vitro culture." Folia Pomeranae Universitatis Technologiae Stetinensis, Agricultura, Alimentaria, Piscaria et Zootechnica **295**: 53-58.
- Szinay, D., E. Wijnker, et al. (2012). "Chromosome evolution in *Solanum* traced by cross-species BAC-FISH." New Phytologist.
- Thouet, J., M. Quinet, et al. (2012). "Repression of Floral Meristem Fate Is Crucial in Shaping Tomato Inflorescence." PLoS One **7**(2): e31096.
- Tian, D., J. Tooker, et al. (2012). "Role of trichomes in defense against herbivores: comparison of herbivore response to woolly and hairless trichome mutants in tomato (*Solanum lycopersicum*)." Planta (Berlin) **236**(4): 1053-1066.
- Uozumi, A., H. Ikeda, et al. (2012). "Tolerance to salt stress and blossom-end rot in an introgression line, IL8-3, of tomato." Scientia Horticulturae (Amsterdam) **138**: 1-6.
- van der Knaap, E. and e. al. (2012). "Identification of QTNs controlling a domestication trait in tomato." SOL 2012 Proc.s: 80.
- Van Schalkwyk, A., P. Wenzl, et al. (2012). "Bin mapping of tomato diversity array (DARt) markers to genomic regions of *Solanum lycopersicum* x *Solanum pennellii* introgression lines." Theoretical and Applied Genetics **124**(5): 947-956.
- Verlaan, M. G., D. Szinay, et al. (2011). "Chromosomal rearrangements between tomato and *Solanum chilense* hamper mapping and breeding of the TYLCV resistance gene Ty-1." Plant Journal **68**(6): 1093-1103.
- Wang, H. e. a. (2005). "The tomato Aux/IAA transcription factor IAA9 is involved in fruit development and leaf morphogenesis." Plant Cell **17**: 2676-2692.
- Xu, P., H. Wang, et al. (2012). "Genetic Loci Controlling Lethal Cell Death in Tomato Caused by Viral Satellite RNA Infection." Molecular Plant-Microbe Interactions **25**(8): 1034-1044.
- Yeats, T. H., G. J. Buda, et al. (2012). "The fruit cuticles of wild tomato species exhibit architectural and chemical diversity, providing a new model for studying the evolution of cuticle function." Plant Journal **69**(4): 655-666.
- Yiftar, T. and e. al. (2012). "Failure of the tomato trans-acting short interfering RNA program to regulate AUXIN RESPONSE FACTOR3 and ARF4 underlies the wiry leaf syndrome." Plant Cell **24**: 3575-3589.
- Yoshida, M. and e. al. (2012). "Evaluation of tomato introgression lines under Japanese climatic conditions and identification of carotenoid-associated loci." SOL 2012 Proc.s: 153.
- Zhang, C., L. Liu, et al. (2012). "Identification of QTLs conferring resistance to late blight in *Solanum lycopersicoides* LA2951 introgression line population." Scientia Agric. Sinica **45**: 1093-1105.
- Zhang, N., M. T. Brewer, et al. (2012). "Fine mapping of fw3.2 controlling fruit weight in tomato." Theoretical and Applied Genetics **125**(2): 273-284.
- Zhou, J. and e. al. (2012). "Hydrogen peroxide is involved in the cold acclimation-induced chilling tolerance of tomato plants." Plant Physiology Biochemistry **60**: 141-149.
- Zong, Y., L. Liu, et al. (2012). "Mapping of QTLs conferring the resistance to Tomato yellow leaf curl virus (TYLCV) in *Solanum lycopersicoides*." Acta Hort. Sinica **39**: 915-922.