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T G R C

Tomato Genetics Resource Center

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ANNUAL PROGRESS REPORT

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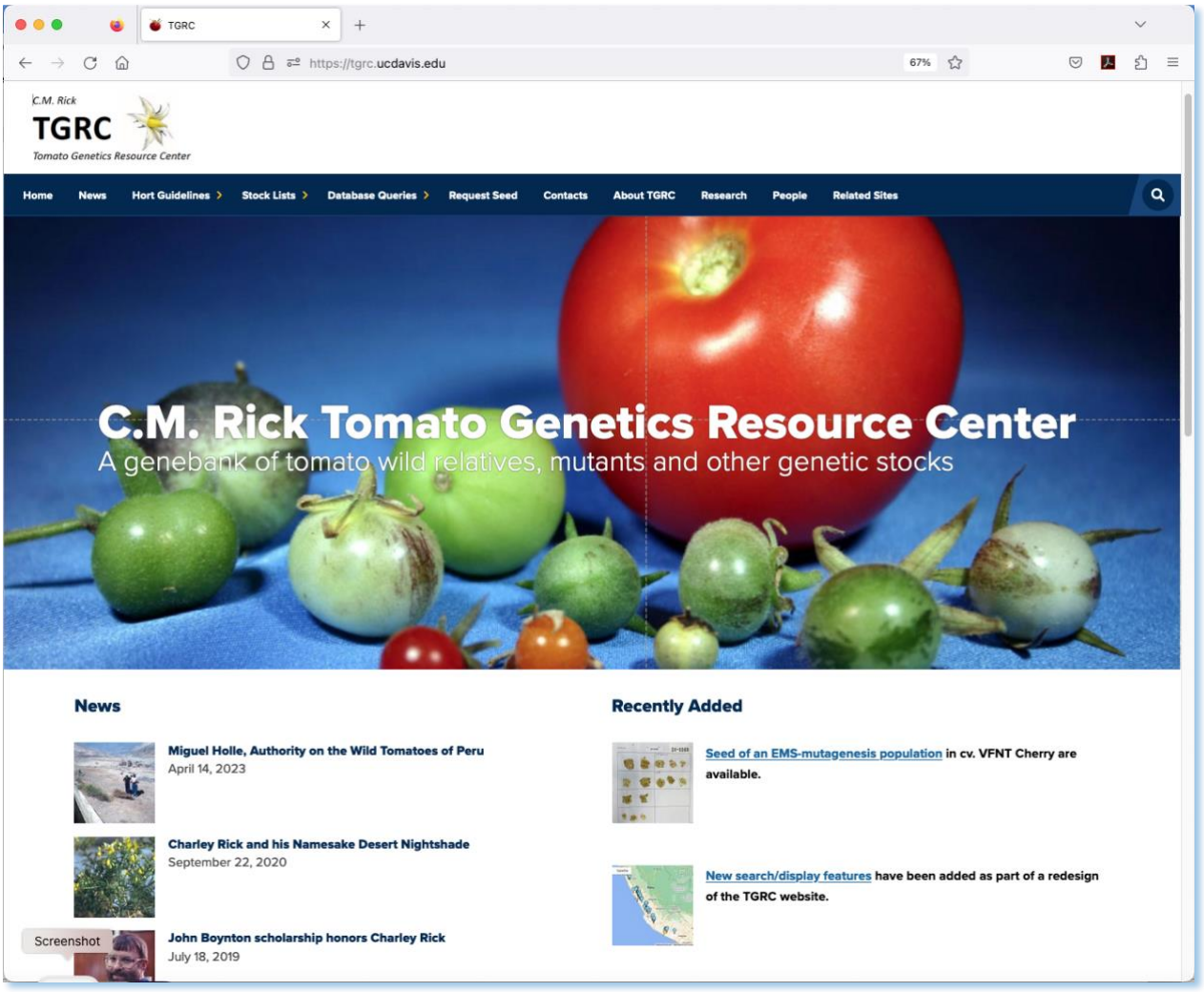

The TGRC website was redesigned and rewritten. The new site is more stable, faster, and provides additional search features and fresh content across the site.

SUMMARY

Acquisitions. We acquired 57 new accessions in 2023, most of which were a set of backcross inbred lines, donated by Dani Zamir, representing the genome of *S. pennellii* LA5240 in the background of the processing variety 'LEA'. These BILs are part of a larger set of 1400 lines that can be used study the interactions between genes controlling complex traits (epistasis). We also acquired two new stocks of cv. Rutgers: one from the USDA to replace our previous source of this variety because it had the wrong phenotype, and the other a Rutgers line with the *Ve* gene, which we obtained from Dina St. Clair at UC Davis. Several previously inactive wild species accessions that had not been multiplied before were 'rescued' from our long-term seed storage and are now available. The total of number of accessions maintained by the TGRC is now 4,535.

Maintenance and Evaluation. Over 1760 cultures were grown for various purposes, of which 433 were for seed increase, including 78 wild species accessions. Germination tests were run on 648 seed lots. Progeny tests were performed on 43 stocks of male-steriles and other segregating genes, or to check accessions with unexpected phenotypes. GMO tests were performed on 61 recently acquired stocks, all of which were negative. *S. sitiens* introgression lines were grown for marker assisted selection or for heat tolerance testing. All plants were monitored throughout development for evidence of disease. An outbreak of ToMV was detected in our fall greenhouse plantings but was eradicated. Newly regenerated seed lots were split, with one sample stored at 4° C for filling seed requests, the other stored in foil pouches at -20° C for long term preservation. 171 samples were sent up to the USDA's seed storage facility in Ft. Collins for off-site security backup.

Distribution and Utilization. A total of 4,763 seed samples representing 1,786 different accessions were distributed in response to 210 requests from 161 researchers and breeders in 21 countries. The overall utilization rate (# samples distributed / # active accessions) was 105%. Over 20 purely informational requests were also answered. Information provided by requestors indicates our stocks continue to be used to support a wide variety of research and breeding projects. Our annual literature search uncovered 110 publications that mention use of TGRC stocks.

Documentation. Our website was completely revised to improve stability and to provide a user interface consistent with other campus websites. The new website has many advantages: it is faster and more stable, and data tables are reloaded automatically from our production database on a daily basis; edits/additions to the site are easy to implement using the SmartSite web design system; webpages are scaled automatically for display on mobile devices; new query functions and new content were added. As in the past, seed request records and passport information on seed samples submitted for off-site back up were provided to the USDA for uploading to the GRIN-Global database.

Research. We continue to work towards identifying QTLs/genes contributing to seed vigor/dormancy, and seed/fruit set under heat stress conditions. We are mapping QTLs for these traits using our *S. sitiens* introgression lines, each of which contains a defined chromosomal segment from the wild nightshade in the genetic background of a modern fresh market variety. This work is funded by a grant from the Foundation for Food and Agriculture Research. We also continue to study the molecular mechanisms of pollen rejection in tomato interspecific crosses.

ACQUISITIONS

The TGRC acquired 57 new stocks this year. Dani Zamir at the Hebrew University of Jerusalem donated 54 backcross inbred lines representing the genome of *S. pennellii* LA5240 in cultivated tomato. Also known as the "LOST" accession, LA5240 was discovered as an apparent seed contaminant in a seed sample from the IPK, Gatersleben genebank in Germany. However, we are confident LA5240 is really a derivative of *S. pennellii* LA2963, with which it shares several morphological features, including self-compatibility and various seed and whole plant traits that together make this accession relatively easy to recognize among other populations of the species. The 54 BILs – with the background genotype control variety "LEA" – were chosen by Shai Torgeman, Dani Zamir and colleagues (*PNAS* 120(14) e2205787119 and *The Plant Journal* in press) to capture nearly an entire *S. pennellii* genome in as few lines as possible. They are only a fraction of the entire BIL collection of ca. 1400 lines. The BILs were generated by backcrossing the F1 LEA x LOST hybrid to LEA for two generations, then selfing via single seed descent for several generations to allow the wild species introgressions to recombine and to become homozygous (or be eliminated). The background genotype LEA is an inbred extracted from a Heinz processing tomato hybrid cultivar. The full BIL set is expected to be useful for studying epistasis for quantitative traits such as yield. They offer the advantage of providing relatively high resolution for trait mapping due to their high level of recombination, which should make it possible to identify the specific gene(s) underlying traits of interest in most cases. Also, each line contains multiple introgressions, which makes it possible to study the effects of multiple loci interacting. The TGRC does not have the resources to maintain the full set of lines, however they can be obtained from Zamir's group.

***S. habrochaites* LA2322 growing in the greenhouse.** Originally collected in 1980, this accession had never been multiplied at Davis. [photo Matt Valle]

We also added two new stocks of cv. Rutgers after we determined that our existing accession (LA1090) is phenotypically incorrect, possibly due to an outcross in an earlier generation. Our new stock of Rutgers, LA5412, was obtained from the USDA's Plant Genetic Resources Unit at Geneva, NY as PI 647196. We also acquired a stock of cv. Rutgers *Ve* with the Verticillium resistance gene from Dina St. Clair's tomato breeding germplasm collection at UC Davis. This provides another nearly isogenic line for *Ve* (we also have it in the Ailsa Craig and Moneymaker backgrounds) and adds to our collection of Rutgers NILs (the others are mostly fruit ripening or fruit color genes).

We generated F_1 interspecific hybrids of *S. lycopersicum* cv. NC 84173 x *S. habrochaites* LA0407 and plan to maintain it in the future for use as a rootstock hybrid in grafting experiments.

We rescued a previously inactive accession of *S. habrochaites* – LA2322 from Chancleta, Amazonas, Peru – that had never been grown at Davis before. This adds one more accession from the Amazonas area, a relatively underrepresented region for tomato germplasm in general, and for *S. habrochaites* in

particular. A few obsolete or redundant accessions were dropped. The current total of number of accessions maintained by the TGRC is 4,535.

Table 1. Number of accessions of each species maintained by the TGRC. The figures include accessions that are temporarily unavailable for distribution.

***Solanum* spp.**	**# Accessions**	***Solanum* spp.**	**# Accessions**
S. lycopersicum	3,117	*S. corneliomulleri*	58
S. lycopersicum var. *ceras.*	421	*S. chilense*	115
S. pimpinellifolium	331	*S. habrochaites*	122
S. cheesmaniae	42	*S. pennellii*	47
S. galapagense	28	*S. lycopersicoides*	23
S. chmielewskii	16	*S. sitiens*	13
S. neorickii	47	*S. juglandifolium*	7
S. arcanum	45	*S. ochranthum*	7
S. peruvianum	71	Other	4
S. huaylasense	16	**Total**	**4,535**

MAINTENANCE AND EVALUATION

The TGRC grew over 1761 families for various purposes: 433 were for seed increases, of which 78 were wild species accessions, and 43 were for progeny tests to verify the presence of segregating genes (e.g. male-sterility loci) or to confirm phenotypes. 156 cultures were grown for introgression and analysis of the *S. sitiens* genome or to study interspecific reproductive barriers. Testing for the presence of GMOs was performed on 61 recently acquired accessions – all were negative.

Identifying accessions in need of regeneration begins with seed germination testing. We start testing seed lots after 10 years of storage. Seed samples that do not meet our minimum of 80% germination after two weeks are normally regenerated in the same year. Seed lots that exceed this threshold are retested again every two to three years. Other factors, such as available greenhouse space, age of seed and supply on hand, are also considered. 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, 648 germ tests were run on seed lots from 2013 or earlier. Average germination rates were satisfactory overall, except for *S. corneliomulleri* and *S. galapagense* for which a large share of seed lots did not meet our 80% minimum viability (Table 2).

Table 2. Results of seed germination tests. Values are based on samples of 25-100 seeds per accession, and represent the % germination after 10-14 days at 25°C. Seed lots with a low germination rate are defined as those with less than 80% germination. Germination tests were performed by sowing 25-50 seed on ½ MS media, except for *S. lycopersicum*, *S. galapagense*, and *S. cheesmaniae*, which were sown on blotter paper.

Solanum Species	**Tested Seed Years**	**# Tested**	**Avg %Germ**	**# Low Germ**
S. arcanum	1994 - 2011	9	85.1	2
S. cheesmaniae	2003 - 2013	23	80.61	7
S. chilense	1990 - 2013	43	81.9	13
S. chmielewskii	2004 - 2010	5	89.4	1

Solanum Species	Tested Seed Years	# Tested	Avg %Germ	# Low Germ
S. corneliomulleri	1997 - 2013	15	76.9	6
S. galapagense	2003 - 2013	6	61.6	1
S. habrochaites	1992 - 2013	20	87.3	3
S. huaylasense	2005 - 2011	4	83.0	1
S. lycopersicum	2003 - 2013	410	84.7	98
S. neorickii	2005 - 2013	26	93.5	2
S. pennellii	2003 - 2013	17	92.7	1
S. peruvianum	1994 - 2013	19	84.2	4
S. pimpinellifolium	2000 - 2013	51	92.1	4
Total		**648**		**143**

Most stocks of *S. lycopersicum* and the predominantly selfing accessions of *S. pimpinellifolium* are grown for seed multiplication in the field unless they require greenhouse culture. Each family is typically represented by 8 or 9 plants, except for segregating families (e.g. male-steriles), which are grown from larger plantings. Our field plot this year occupied approx. 2 acres. As usual, sequential plantings were made to spread the workload, with the first transplanting on April 24. Conditions were generally favorable throughout the growing season, despite the usual summer hot spells, and plants were mostly healthy, although as usual we lost some plants to TSWV. Growth under drip irrigation – initially surface, then subsurface – was again quite good and we shut off the water early to keep plants to manageable size. As in the last two year, our plants went into ground that had not seen tomatoes in many years. As a result, there were virtually no volunteer tomatoes sprouting within the beds, which avoided the need to pull out the young plants to prevent seed admixture.

Wilty phenotype of the *fri* (*far red light insensitive*) mutant, LA4356, which lacks phytochrome A.

Most of the wild species, many mutants and certain other genetic stocks require greenhouse culture, either for isolation purposes or because they do not grow or flower well under field conditions. For the mutant stocks, we sow the weakest lines first, and finish with lines of normal vigor. Our schedule of greenhouse plantings of the wild species is based on photoperiod responses: those with the least sensitivity are planted first, in the early spring; those with intermediate reaction are planted in early summer; the most sensitive (i.e. flower best under short days) are planted in mid-summer for fall blooming. Optimal planting dates and other growing recommendations for each species are listed on our website. Wild accessions are grown from large population sizes (50-75 plants) to maintain diversity, maximize heterozygosity, and avoid inbreeding across successive rounds of seed increase.

We completed seed multiplications started in 2022 of a previously inactive *S. habrochaites* accession that had never been grown at Davis. This accession was 'rescued' from the original, and very old seed collections, which fortunately had not lost all seed viability, by using various tricks to coax a few seeds to germinate. The newly active accession, LA2322, was collected from

Chancleta, Amazonas, Peru, and is one of only a handful of collections of that species from the Amazonas region. Given the near impossibility of getting permission to make new collections in the native region, mining the existing collections for these sorts of inactive wild accessions is one way to increase diversity of the available germplasm.

Preventing the spread of seed borne pathogens is an important aspect of any seed regeneration program. We inspect all our plantings throughout the growing cycle for disease symptoms. Plants displaying signs of disease are tested with Agdia ImmunoStrips. Our most persistent disease challenge is TSWV, vectored by the difficult to control Western flower thrips. In the greenhouse we had an outbreak of ToMV in several groups. In response, we discarded all infected plants as well as plants in close proximity that might have been exposed in order to eliminate the virus from our greenhouse plantings. We don't know where the ToMV originated, however we think seed transmission is unlikely because all seed lots were treated with 2.75% hypochlorite for 30 mins prior to sowing to inactivate any virus in the seed coat. Seed lots received from external sources are also heat treated (3 days at 65°C) to inactivate any virus particles inside the seed. Mechanical transmission during plant growth seems the most likely source, and we have taken steps to prevent or reduce spread in the future. All our harvested seed are treated with acid and bleach as part of the seed extraction process, which should greatly reduce the likelihood of transmission via seed that we distribute.

All stocks grown for seed increase or other purposes were systematically checked to verify that they expressed the expected phenotypes. New accessions were evaluated in greater detail, with the descriptors depending upon the type of accession (wild species, cultivar, mutant, chromosomal stocks, etc.). Plantings were reviewed at different growth stages to observe foliage, habit, flower morphology, fruit set, and fruit morphology. Images of selected accessions were uploaded to our website.

Plants of the *double dwarf* (*dd*) mutant in the field compared to wild type (+). This is one of several mutants we grew for progeny testing to verify the presence of the desired gene.

Many genetic stocks, including various sterilities, nutritional, and weak mutants, cannot be maintained as true-breeding lines and must be transmitted from heterozygotes. Progeny tests are therefore made after each generation of seed increase to verify that individual seed lots segregate for the gene in question. Other accessions may show unexpected segregation or off-types due to outcrossing or mix-ups and need to be progeny tested to reestablish true breeding lines with the correct traits. This year we progeny tested 43 seed lots of male-steriles, other segregating mutants, and stocks with questionable phenotypes, including the mutants *ms-31*, *ms-38*^{40}, *gh*, *dd*, *ga*, *syv*, *alc*, *Lpg*, *Tm-2*^{a}, *w-4* and *Me*. We also grew stocks of Latin American cultivars LA0762 and LA1540 for observation and checking.

Samples of newly regenerated seed lots were catalogued, with most of the seed stored at -20°C for long term storage, and smaller quantities stored at 4°C for filling seed requests. Following our standard

practice, samples of seed were treated with acid and bleach to prevent transmission of seed borne pathogens and to meet import requirements for certain countries. As in the past, up to 1000 seed of newly regenerated seed lots were sent to the USDA National Laboratory for Genetic Resources Preservation in Ft. Collins, Colorado for long-term backup storage. This year 171 seed samples were backed up to NLGRP.

DISTRIBUTION AND UTILIZATION

A total of 4,763 seed packets of 1,786 different accessions were distributed in response to 210 seed requests from 161 scientists, breeders, and educators in 21 countries. Relative to the size of the TGRC collection (4,535 accessions), the number of seed samples distributed represents a utilization rate of 105%. Approx. 40% of our accessions were requested at least once in 2023, demonstrating that a large share of the collection is utilized. We also answered at least 20 purely informational requests regarding our stocks, growing recommendations, and related questions.

We continue to receive many requests for introgression lines (ILs), recombinant inbred lines (RILs), and backcross inbred lines (BILs). A total of 297 seed samples of the *S. pennellii* ILs were distributed, 109 samples of the *S. habrochaites* ILs, 26 samples for the *S. lycopersicoides* ILs, and 24 samples of the *S. sitiens* ILs. We also sent out 177 samples of *S. lycopersicum* x *S. pimpinellifolium* RILs and BC-RILs, and 39 samples of *S. pennellii* BILs. Exotic germplasm libraries such as these require considerable time and expense to develop, but the investment is clearly justified by their continued long-term use in breeding and research.

The various steps involved in filling seed requests – selecting accessions, treating, and packaging seeds, entering the information into our database, providing cultural recommendations, obtaining phytosanitary certificates, etc. – involve a large time commitment. The TGRC crew worked diligently to fill seed requests in a timely manner. Overseas shipments involve ever changing and increasingly stringent phytosanitary requirements, which we must keep up to date with. Shipment of seed to the European Union and many other countries continues to be challenging due to requirements for Tomato Brown Rugose Fruit Virus (ToBRFV) testing, however researchers can obtain a Letter of Authority or import permits granting exception to this rule. Fortunately, the ToBRFV restrictions so far apply only to seed of cultivated tomato, and not to its wild relatives.

Information provided by recipients regarding intended uses of our stocks are summarized in Table 3. As in previous years, there was a notable emphasis on biotic stresses, especially viral, bacterial, and fungal diseases, both for breeding purposes and for research. By far the most requests were for screening against ToBRFV, a major threat to production in many areas. Research and breeding for resistance to *Tuta absoluta* leaf miner continues to be emphasized, reflecting the spread of this insect pest. There continues to be strong interest in abiotic stress responses, especially drought, high temperatures and salinity. Many other requests mentioned fruit traits (quality, carotenoids, etc), or breeding-related uses, notably grafting, marker development and increasing diversity of breeding germplasm. Our stocks continue to be used for a broad array of genetic, physiological, or developmental studies, with some emphasis this year on evolutionary studies, metabolomics/secondary metabolites, and stomatal control.

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

Biotic Stresses	PepMV	1	ToMV	1
Viruses:	ToBRFV	10	TYLCV	1

Unspecified viruses	4	Salinity	7	Micro RNAs	1
Bacteria:		Unspec. abiotic stresses	13	Polyploidy	1
Bacterial spot	1	**Fruit Traits**		Recombination	1
Bacterial wilt	3	Alkaloids		Transformation	1
Candidatus Liberibacter	1	Anthocyanins	1	Transcription, RNAseq	1
Phytoplasma	1	Blossom end rot	1	Unspecified genetics	5
Fungi:		Carotenoids, color	6	**Physiology / Develop.**	
Alternaria alternata	1	Flavonoids	1	ABA responses	1
Botrytis cinerea	1	Flavor, volatiles	1	Acylsugars	1
Cladosporium leaf mold	1	Fruit develop/ripening	4	Edema	2
Fusarium wilt	1	Fruit quality	4	Leaf anatomy	1
Late blight	2	Fruit sugars	1	Leaf volatiles	1
Powdery mildew	2	**Other Breeding**		Metabolomics	5
Verticillium	1	Grafting, rootstocks	6	Microbiomes	2
Nematodes	3	Germplasm diversity	4	Plastomes	1
Unspecified diseases	16	Heterosis	1	Proteomics	1
Insect pests:		Horticultural traits	1	Pollen biology	1
Corn earworm	1	Marker development	8	Roots	3
Leaf miners	1	Male sterility	1	Secondary metabolites	3
Tuta absoluta	3	Molecular breeding	1	Stomatal responses	4
Whiteflies	2	Prebreeding, wide cross	3	Trichomes	2
Unspecified insects	1	Plant architecture	2	Wounding, herbivory	4
Unspec. biotic stresses	2	Tissue culture	1	Unspecified physiol/dev	1
Abiotic Stresses		Unspecified breeding	11		
Drought	6	**Genetic Studies**		**Miscellaneous**	
Flooding	1	Association studies	2	Backup seed storage	2
High temperatures	6	Allele mining	2	Germplasm exchange	1
Low temperatures	3	Evolution, domestication	4	Instructional uses	5
Oxygen	1	Genome sequencing	5	Unspecified research	21

Our survey of the 2023 literature and unreviewed papers of previous years uncovered 110 journal articles, abstracts, theses, patents, and other publications that mention use of TGRC stocks (see Bibliography below). Many additional papers were undoubtedly missed, and cases of utilization by the private sector are generally not publicized. These publications, including many in high impact journals, demonstrate the positive impact of TGRC germplasm on basic and applied research and tomato breeding.

DOCUMENTATION

Our website was thoroughly redesigned and rewritten this year to improve stability and to conform to campus-wide website branding standards. James Cubbage in the Plant Sciences IT group rewrote the query pages, while RTC reformatted and revised the other parts of the website and added content. Overall, the new website is not only more stable but also faster and easier for users to navigate. The display format now automatically adjusts for the device type, providing a much-improved experience on mobile devices. We added a simplified accession query with a single field that requires no knowledge of how the data are structured. It uses a "fuzzy" search algorithm to find accessions even when the accession number is not a perfect match. Besides the accession number, the query also searches other key identifiers, including gene symbols for mutants or collection sites of wild species accessions. The advanced query page offers more power to find accessions based on multiple criteria. It's similar to our previous accession query form, but

we've added the ability to search for specific gene variants (alleles) or to find accessions donated by specific individuals. Our display maps for wild species accessions now display all active accessions of the species in addition to the selected accession, which provides a quick way to find neighboring collections for stocks that are not currently available. Our geographic mapping page now has the ability to search for and plot accessions by elevation of collection. For example, one could search for collections made above 3000m, or below 500m elevation to target accessions with low temperature or high temperature tolerance respectively. We also added several biographical pages that describe the contributions of some key collaborators from Peru, Ecuador and Chile who were instrumental in finding and collecting wild tomato populations. Future website changes will be easier to implement now because most of the site is designed using the SmartSite web design environment. We expect that the programming behind the search pages will also be easier to modify in the future, with James Cubbage's help. We provided the USDA National Plant Germplasm System with basic passport data on accessions backed up to Ft. Collins for uploading into the GRIN-Global database, as well as seed distribution records and the numbers of requests from different organizational categories (i.e. domestic or foreign, public, or commercial, etc.).

RESEARCH

One of our research projects is to map genetic factors (QTLs) controlling seed vigor/dormancy, seed size, and seed and fruit set under heat stress. We are using a set of *S. sitiens* introgression lines (ILs) in cultivated tomato, developed at the TGRC, to map QTLs for these traits. We carried out greenhouse experiments to validate potential fruit set and seed set QTLs under heat stress. For seed trait QTLs, increased dormancy (i.e. reduced germination vigor) was mapped to several chromosomal regions, several of which harbor ABA-related genes that could affect seed germination. We generated CRISPR mutants in these ABA genes in the corresponding IL background (e.g. *abi4* mutants were generated in the background of the IL containing the *ABI4* locus). We plan to evaluate their germination traits once seeds become available next year. This project is funded by a grant from the Foundation for Food and Agriculture Research.

A plant of *S. sitiens* growing in the Atacama Desert at Cerro Quimal, Chile. The TGRC developed a set of prebred lines that capture the *S. sitiens* genome in the background of cultivated tomato.

Our other research focus is the study of the mechanisms of pollen rejection in tomato wide crosses. Previously we showed that pollen rejection in crosses onto *S. pennellii* pistils result in part from high level expression of an ornithine decarboxylase (*ODC2*) gene in the pistils. This acts as a barrier to pollen tube growth when pollen lack sufficient expression of a farnesyl pyrophosphate synthase (*FPS2*) gene which is required for compatibility on *S. pennellii*. We continue to explore how this pollen rejection mechanism has evolved in related wild species, particularly *S. habrochaites*, and how the ODC2-based barrier interacts with other pollen rejection mechanisms.

PUBLICATIONS

Chetelat, R.T. and X. Qin (2023) Ornithine decarboxylase gene expression mediates pollen rejection in *Solanum*. Plant Polyamine Research Workshop, Oct. 12-13, Budapest, Hungary.

Chetelat, R.T., X. Qin, and M. Valle (2023) Genetic control of unilateral incompatibility: overlapping pollen rejection mechanisms and opportunities for wide hybridization. Tomato Breeders Roundtable, Oct. 9-10, Monterey.

Chetelat, R.T., X. Qin, and M. Valle (2023) Update from the TGRC: new germplasm resources, website changes, and future prospects. Tomato Breeders Roundtable, Oct. 9-10, Monterey.

SERVICE AND OUTREACH

RTC gave presentations on the TGRC, research projects, and related topics to PLS 222 (a UCD graduate course in plant breeding), HRT 200B (graduate class in horticulture), the Tomato Breeders Roundtable, the UCD Plant Breeding Retreat, the Seed Central networking event, the Foundation for Food and Agriculture Research, and the Plant Polyamine Workshop. RTC, MV and/or XQ gave tours to and/or consulted with scientists from East West Seeds, Kagome, Takii Seeds, Syngenta, Meiogenix, and the UCD Plant Biology and Plant Pathology Departments.

PERSONNEL

Matthew Valle, Assistant Curator, supervised undergraduate students Naomi Lavin, Sabrina Colación and Jessica Carver in the greenhouse, field and seed lab. Sabrina and Naomi both graduated and were replaced by Mercury Komjak and Kallan Arimura. Jessica took over as our seed request specialist from Jay Francisco who graduated last year. Dr. Xiaoqiong Qin continues to lead our research on pollen thermotolerance and seed vigor using *S. sitiens* introgression lines, and the mechanisms of pollen-pistil incompatibility. She was assisted in the lab by undergraduate students Sarah Ng (now a graduate student at UCD) and Elizabeth Paul. Qin and her students also provided DNA marker services to the TGRC.

TESTIMONIALS

"On behalf of KeyGene Inc, I wanted to express our gratitude for the service you provide to the tomato research community. The stocks you maintain and provide are invaluable to our research as we strive to support clients that feed the world. Your support enables us to shorten our research timelines and dig deeper into tomato biology, diversity, and genetic potential. Beyond these sentiments, our recent donation to TGRC is a small token of our appreciation for service provided to date and we hope it will support your work going forward." -- Alan Chambers

"On behalf of East West Seed breeders and researchers, I wish to thank you and the TGRC personnel who took effort in processing our seed orders and its shipment to the Philippines. Thank you so much. We look forward to your generosity in sharing TGRC's germplasm collection this year." -- Marilyn Belarmino

"Thanks for your wonderful services to the tomato scientific community." -- Jianhua Zhu

"Thanks for all the TGRC does!" -- Christopher Muir

"Thanks so much! I really appreciate your help and efforts. I am so excited to receive these seeds." -- Changtian Pan

"I am writing this email to thank all the Davis team for their patient cooperation!" -- Susanna Cialli

"I appreciate the help and organization of TGRC. The contribution of TGRC will be appreciated in the future publication." -- Zhaojun Liu

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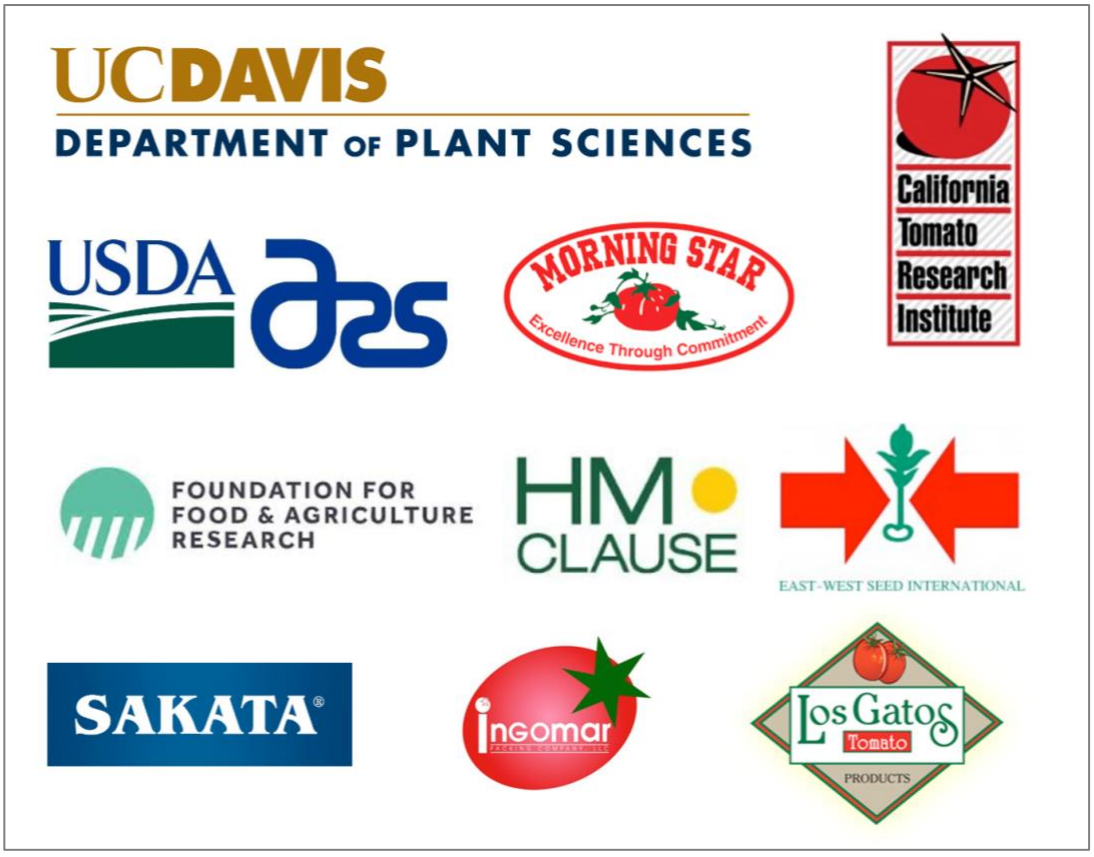

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