

2020 Crop Vulnerability Status Report – Watermelon

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Summary

Watermelon (*Citrullus lanatus*) is an important crop globally and in the United States. Like most domesticated crops, the domesticated watermelon lacks genetic diversity. Recent insights into the center of domestication of watermelon has underscored the importance of related species (crop wild relatives) as a source of variation for watermelon breeders. There is currently 1,878 *Citrullus* accessions in the NPGC, with about 25% not available for distribution. There is an urgent need for acquiring additional accessions, especially material from northeast Africa and China, as well as continued regeneration of existing material. Future considerations include the addition of genetic/genomic stocks and functional panels to the collection and integrating the abundance of genomic information that is being generated for the accessions and stocks with GrinGlobal.

1. Introduction to the crop

Watermelon grown in the United States belongs to the genus *Citrullus*. In addition to *C. lanatus*, the sweet watermelon consumed around the world, the genus also contains *C. mucosospermus*, *C. amarus*, *C. colocynthis*, *C. rehmii*, *C. ecirrhosus* and *C. naudinianus* (Chomicki and Renner 2015). *C. amarus*, the citron or tsamma from Southern Africa is an important source of disease resistance for watermelon breeders (McGregor 2011). Watermelon is a monoecious, annual plant with a vining growth habit. *C. ecirrhosus*, *C. colocynthis* and *C. naudinianus* are perennial species, and the latter is the only dioecious member of the genus. Recent research points to northeast Africa, specifically the Darfur region of Sudan, as a likely region of domestication for the crop (Guo et al. 2019; Paris 2015; Renner et al. 2017).

Watermelon cultivar development in the United States started in earnest around 1880, although some heirloom varieties like ‘Bradford’ and ‘Georgia Rattlesnake’ predate that (Wehner 2008). Numerous significant open pollinated cultivars were developed in the latter part of the previous century by a variety of public breeding programs. These include ‘Charleston Gray’ (1954) by the USDA in Charleston, ‘Crimson Sweet’ (1963) by Kansas State University, ‘Calhoun Gray’ (1965) by Louisiana State University, and ‘Dixielee’ (1979), ‘Jubilee’ (1963), ‘Smokeylee’ (1971), ‘Sugarlee’ (1981) and ‘Mickylee’ (1986) by the very prolific University of Florida program at Leesburg (Crall 1981; Wehner 2008). F₁ Hybrid cultivars developed by commercial seed companies started becoming more popular and by the year 2000 nearly all the popular cultivars were F₁ hybrids. ‘Sangria’ (1985) was one of the most popular diploid cultivars, while Tri-X-313 was one of the most popular seedless cultivars (Wehner 2008). Seedless production continued to increase over the past 20 years and currently make up about 90% of watermelon production in the United States. With the increased use of seedless cultivars, a new type of cultivars, non-harvestable pollinizers were developed. These cultivars, like the SP-series from Syngenta, serve as pollen sources for the triploid plants, and the fruit are not edible.

With the increased popularity of F₁ hybrid cultivars since the 1980s, private seed companies have started dominating watermelon breeding. To a large degree this is due to consumer demand for seedless fruit. Seedless watermelons are produced on F₁ triploid plants developed by crossing tetraploid and diploid inbred lines. This is a difficult breeding system for public breeders to successfully execute. There is a small seeded market, especially aimed at market/organic growers, which might provide a niche for the public sector breeding. The decline in public cultivar releases led to most of the public programs focusing on molecular and genomics research and pre-breeding. Public institutions often release improved germplasm (Kousik et al. 2018; Wechter et al. 2012b) for use in cultivar development by the private sector.

Consumers value watermelon for its sweet, juicy flesh which makes it a favourite summer snack. Consumers are becoming more aware of watermelon as a source of nutritional compounds like lycopene, citrulline, arginine and Vitamin C which are associated with health benefits, including decreased risk of certain kinds of cancer, age related degenerative pathologies and heart disease (Choudhary et al. 2015; Maoto et al. 2019). Watermelon is mainly sold as fresh fruit or fresh-cut fruit. Recently several watermelon “juice” products, like WTRMLNWTR™ and TSAMMA™ have entered the market. These products are marketed as sources of antioxidants and other health promoting compounds.

Global watermelon production in 2018 was 103,931,337 tonnes produced on 3,241,239 hectares (FAOSTAT 2020). China is the largest producer and produced ~60% of all watermelon worldwide in 2018 (Figure 1). Other important watermelon producing countries include Iran,

Turkey, India and Brazil. However, all these countries produce between 1-3% of global production each. The U.S. produces approximately 2% of global watermelon.

In 2018 a total of 3.9 billion lbs of watermelon was harvested in the U.S. from approximately 112,000 acres, with an estimated value of \$668 million (Fig 2a-c) (USDA-NASS 2020). Approximately 70% of total watermelon produced in the U.S. are cultivated in Florida, California, Texas and Georgia (Fig. 1d) and approximately 90% of the watermelon produced was seedless watermelon.

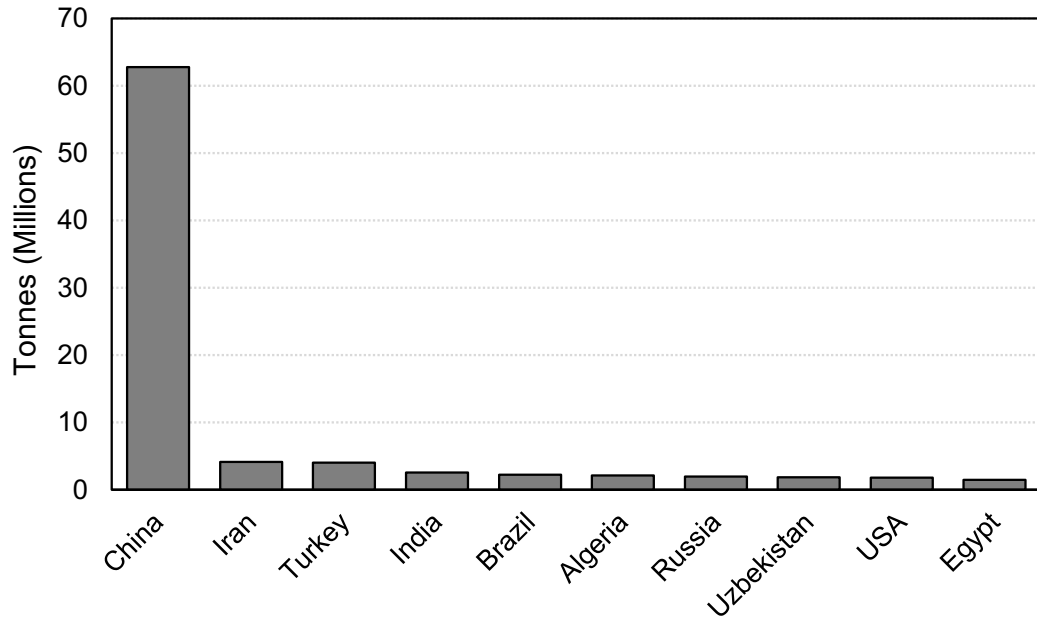


Fig. 1 Watermelon production (2018) in the top ten producing countries globally.

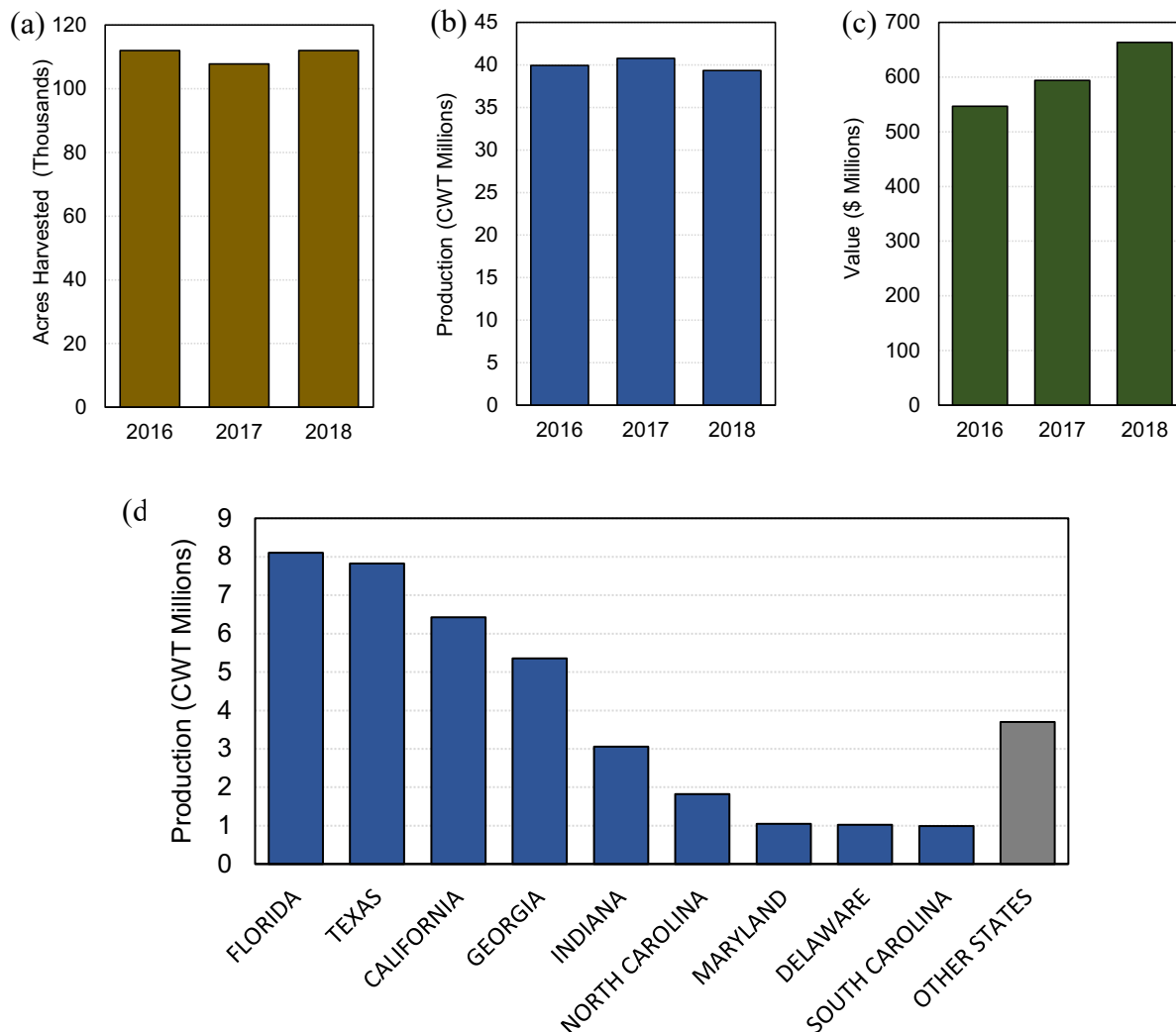


Fig. 2 Annual U.S. watermelon (a) area harvested, (b) production and (c) value from 2016 to 2018. (d) Average annual production in 2018 by state.

2. Urgency and extent of crop vulnerabilities

Based on resequencing data, the amount of genetic diversity in watermelon is lower than maize, soybean and rice (Guo et al. 2013). Watermelon cultivars in the U.S. have a very narrow genetic base that makes them especially vulnerable to pest and disease pressure. However, diversity in *C. colocynthis* and *C. amarus* is much higher than in *C. lanatus* (Guo et al. 2019) so these crop wild relatives can serve as important sources of diversity for watermelon breeders. The outlook for conservation of these species *in situ* are uncertain and therefore acquiring additional germplasm should be an important goal for germplasm collections.

There are numerous emerging, evolving pathogens, insects and pests that threaten watermelon production (Kousik et al., 2016) in changing environmental conditions. Fusarium wilt has emerged as a very serious disease in the southeast and most breeding programs are actively trying to improve resistance by introgressing alleles from wild relatives obtained from the germplasm collection (Branham et al. 2019; Branham et al. 2020; Fall et al. 2018; Meru and McGregor 2016a, b; Wechter et al. 2012a; Wechter et al. 2012b). The *Citrullus* collection is a source of many important traits, including firm flesh, host-plant resistance to diseases (fusarium wilt, potyvirus, powdery mildew and downy mildew) and pests (nematodes) (Boyhan et al. 1994a; Boyhan et al. 1992; Boyhan et al. 2003; Boyhan et al. 1994b; Branham et al. 2020; Dane et al. 1998; Gusmini et al. 2005; Martyn 1987; Martyn and Netzer 1991; Sowell and Pointer 1962).

A constraint for researchers in the United States is the limited availability of genetic resources from major production areas like China as well as and the major centers of diversity in Africa. International movement of germplasm are becoming increasingly difficult. An additional limitation to the use of the collection is the presence of seedborne diseases in some accessions.

3. Status of plant genetic resources in the NPGS available for reducing genetic vulnerabilities

3.1 Germplasm collections and in situ reserves

3.1.1 Holdings

Currently there are 1,878 *Citrullus* accessions in the NPGS (Table 1), with approximately 75% available for distribution and 1,856 accessions have a backup. For several years now about 25% of the accessions have not been available for distribution.

Table 1. Active *Citrullus* accession in the NPGC.

Species	Number of Accessions
<i>C. amarus</i>	151
<i>C. colocynthis</i>	24
<i>C. ecirrhosus</i>	3
<i>C. lanatus</i>	1,613
<i>C. mucospermus</i>	75
<i>C. naudinianus</i>	7
<i>C. rehmii</i>	4
<i>Citrullus spp.</i>	1

3.1.2 Genetic coverage and gaps

The collection includes at least one accession of each of the seven species of *Citrullus*. Considering recent insights into the origin and diversity of watermelon (Paris 2015; Renner et al. 2017; Wu et al. 2019), additional accessions should be acquired, especially for northeast Africa.

3.1.3 Acquisitions

In this past five years, two new *Citrullus* accessions have been added to the collection. There are significant *Citrullus* germplasm collections in China and India, and it would be very valuable for the U.S. collection to add some accessions from those collections. Collecting new material are becoming very challenging, but a concerted effort needs to be launched to collect more material from Africa, including northeast Africa.

3.1.4 Maintenance

The watermelon collection is stored in the Freezer (-18°C/0°F) and Cold room (4°C/40°F with 25% Relative Humidity).

3.1.5 Regeneration

Current regeneration is done by agreement with Vilmorin (France/Thailand) and locally (Griffin) using available greenhouse space for pre-increase.

Additional budgetary support is crucial for expanded NPGS *Citrullus* PGR management capacity, especially regeneration. Keeping the collection viable is very critical for the breeders and the watermelon industry. High quality seed increase of the collection is urgently needed. Since *Citrullus* is an outcrosser, regeneration requires considerable effort and resources (cages, etc), but it is essential that this germplasm is preserved and regenerated. The *Citrullus* collection is one of the most valuable Cucurbit collections, and it is essential that accessions are available for crop improvement. It is important that proper sanitation and rigorous screening protocols are maintained so that seedborne diseases are not spread when germplasm is being distributed.

3.1.6 Distributions and outreach

Two hundred and nine (209) distribution orders containing 7,928 items were shipped in 2019 and 2020. Of these 60% (4,771) were foreign distributions and 40% (3,557) domestic.

3.2 Associated information

3.2.1 Genebank and/or crop-specific web site(s)

GrinGlobal

3.2.2 Passport information

Available in GrinGlobal. The classification of all *Citrullus* accessions has been updated on GRIN in accordance with the taxonomy as defined by Chomicki and Renner (2015).

3.2.3 Genotypic characterization data:

No new information received in the past 5 years.

3.2.4 Phenotypic evaluation data

Currently pictures of fruit and seed are available for most of the accessions in GRIN and new images were added in 2017-2018. Depending on the accession, data might also be available for a variety of other traits. Data are typically acquired during seed regenerations in Griffin or other regeneration sites. A summary of current trait descriptors is provided in Appendix 1. No new phenotypic data was received in the past 5 years.

3.3 Plant genetic resource research associated with the NPGS

3.3.1 Goals and emphases

Pre-increase of critically low inventory accessions.

3.3.2 Significant accomplishments

3.4 Curatorial, managerial and research capacities and tools

3.4.1 Staffing

0.2 SY (RLJ), 0.2 FTE Technical support (CT) – but varies year – to -year due to changes in priorities.

3.4.2 Facilities and equipment

As allocated by the RL

3.5 Fiscal and operational resources

As allocated by the RL.

4. Other genetic resource capacities

Most public sector researchers have in-house germplasm collections, including selections of accessions from NPGC and other breeding efforts and research activities. These materials are usually available to other researchers through MTAs. Many public programs also have populations specifically developed for genetic and genomic studies, like recombinant inbred line populations.

Genotyping-by-sequencing was carried out on 1,365 accessions from the germplasm collection (Wu et al. 2019) through the USDA SCRI [CucCap](#) project (Grant Number: 2015-51181-24285). About 400 accessions was also selected for a functional panel through this project. These accessions are being selfed and a single plant will be re-sequenced as part of the same project. Progeny from these single plants will be available for public distribution.

5. Prospects and future developments

In addition to acquiring additional germplasm from other parts of the world for use in plant breeding as mentioned above, and increasing current germplasm for distribution, there are two other additional points to consider.

Firstly, significant genomic resources are being developed for watermelon, including sequence information for accessions held at the NPGC (Guo et al. 2013; Guo et al. 2019; Wu et al. 2019). This data is currently available through various different databases, for example [CuGenDB](#). However, the data is not directly linked to the accessions in GrinGlobal.

Consideration should be given to how to efficiently integrate this data and future genomic data to GrinGlobal to ensure that the data can be exploited to its full potential.

Secondly, researchers and large projects are creating useful populations and functional panels, for example the mapping populations and functional panel being created through the CucCap project. These resources will be extremely useful to the entire watermelon breeding and research community. Ideally NPGC would play a role in maintaining, regenerating, and distributing these materials to users. However, it is not clear whether NPGC have the resources to fulfill this role, considering the resources needed to increase outcrossing crops like watermelon. If NPGC is unable to fulfill this role, there is a risk that these useful genetic resources will be lost when project funding runs out or researchers leave specific programs.

6. References

- Boyhan G, Norton JD, Abrahams BR (1994a) Screening for resistance to anthracnose (race 2), gummy stem blight, and root knot nematode in watermelon germplasm. *Cucurbit Genetics Cooperative Report* 17:106-110
- Boyhan G, Norton JD, Jacobsen BJ, Abrahams BR (1992) Evaluation of watermelon and related germ plasm for resistance to zucchini yellow mosaic virus. *Plant Dis* 76:251-252
- Boyhan GE, Langston DB, Granberry DM, Lewis PM, Linton DO (2003) Resistance to *Fusarium* wilt and root-knot nematode in watermelon germplasm. *Cucurbit Genetics Cooperative Report* 26:18-25
- Boyhan GE, Norton JD, Abrahams BR, Wen HH (1994b) A new source of resistance to Anthracnose (Race 2) in watermelon. *HortScience* 29:111-112
- Branham SE, Levi A, Wechter WP (2019) QTL mapping identifies novel source of resistance to *Fusarium* wilt race 1 in *Citrullus amarus*. *Plant Dis* 103:984-989
- Branham SE, Patrick Wechter W, Ling K-S, Chanda B, Massey L, Zhao G, Guner N, Bello M, Kabelka E, Fei Z, Levi A (2020) QTL mapping of resistance to *Fusarium oxysporum* f. sp. *niveum* race 2 and Papaya ringspot virus in *Citrullus amarus*. *Theor Appl Genet* 133:677-687
- Chomicki G, Renner SS (2015) Watermelon origin solved with molecular phylogenetics including Linnaean material: another example of museomics. *New Phytol* 205:526-532
- Choudhary BR, Haldhar SM, Maheshwari SK, Bhargava R, Sharma SK (2015) Phytochemicals and Antioxidants in Watermelon (*Citrullus Lanatus*) Genotypes under Hot Arid Region. *Indian J Agric Sci* 85:414–417
- Crall JM (1981) Fifty years of watermelon breeding at ARC Leesburg. *Proc Fla State Hort Soc* 94:156-158
- Dane F, Hawkins LK, Norton JD, Kwon Y-S, Om Y-H (1998) New resistance to race 2 of *Fusarium oxysporum* f.sp. *niveum* in watermelon. *Cucurbit Genetics Cooperative Report* 21:37-39
- Fall LA, Clevenger J, McGregor C (2018) Assay development and marker validation for marker assisted selection of *Fusarium oxysporum* f. sp. *niveum* race 1 in watermelon. *Mol Breed* 38:130
- FAOSTAT (2020) Crop Production.
- Guo S, Zhang J, Sun H, Salse J, Lucas WJ, Zhang H, Zheng Y, Mao L, Ren Y, Wang Z, Min J, Guo X, Murat F, Ham B-K, Zhang Z, Gao S, Huang M, Xu Y, Zhong S, Bombarely A, Mueller LA, Zhao H, He H, Zhang Y, Zhang Z, Huang S, Tan T, Pang E, Lin K, Hu Q, Kuang H, Ni P, Wang B, Liu J, Kou Q, Hou W, Zou X, Jiang J, Gong G, Klee K, Schoof H, Huang Y, Hu X, Dong S, Liang D, Wang J, Wu K, Xia Y, Zhao X, Zheng Z, Xing M, Liang X, Huang B, Lv T, Wang J, Yin Y, Yi H, Li R, Wu M, Levi A, Zhang X, Giovannoni JJ, Wang J, Li Y, Fei Z, Xu Y (2013) The draft genome of watermelon (*Citrullus lanatus*) and resequencing of 20 diverse accessions. *Nat Genet* 45:51–58
- Guo S, Zhao S, Sun H, Wang X, Wu S, Lin T, Ren Y, Gao L, Deng Y, Zhang J, Lu X, Zhang H, Shang J, Gong G, Wen C, He N, Tian S, Li M, Liu J, Wang Y, Zhu Y, Jarret R, Levi A, Zhang X, Huang S, Fei Z, Liu W, Xu Y (2019) Resequencing of 414 cultivated and wild watermelon accessions identifies selection for fruit quality traits. *Nat Genet* 51:1616-1623

- Gusmini G, Song R, Wehner T (2005) New sources of resistance to gummy stem blight in watermelon. *Crop Sci* 45:582-588
- Kousik CS, Ikerd J, Mandal M, Adkins S, Turechek WW (2018) Watermelon Germplasm Lines USVL608-PMR, USVL255-PMR, USVL313-PMR, and USVL585-PMR with Broad Resistance to Powdery Mildew. *HortScience* 53:1212-1217
- Maoto MM, Beswa D, Jideani AIO (2019) Watermelon as a potential fruit snack. *Int J Food Prop* 22:355-370
- Martyn RD (1987) *Fusarium oxysporum* f. sp. *niveum* race 2: A highly aggressive race new to the United States. *Plant Dis* 71:233-236
- Martyn RD, Netzer D (1991) Resistance to races 0, 1, and 2 of *Fusarium* wilt of watermelon in *Citrullis* sp. PI 296341-FR. *HortScience* 26:429-432
- McGregor CE (2011) *Citrullus lanatus* germplasm of Southern Africa. *Isr J Plant Sci* 60:403 – 413
- Meru G, McGregor C (2016a) A genetic locus associated with resistance to *Fusarium oxysporum* f. sp. *niveum* race 2 in *Citrullus lanatus* type watermelon. *Journal of the Amer Society for Horticultural Science* 141:617–622
- Meru G, McGregor C (2016b) Genotyping by sequencing for SNP discovery and genetic mapping of resistance to race 1 of *Fusarium oxysporum* in watermelon. *Scientia Horticulturae* 209:31-40
- Paris HS (2015) Origin and emergence of the sweet dessert watermelon, *Citrullus lanatus*. *Ann Bot* 116:133-148
- Renner SS, Sousa A, Chomicki G (2017) Chromosome numbers, Sudanese wild forms, and classification of the watermelon genus *Citrullus*, with 50 names allocated to seven biological species. *Taxon* 66:1393-1405
- Sowell G, Pointer GR (1962) Gummy stem blight resistance in introduced watermelons. *Plant Disease Reporter* 46:883-885
- USDA-NASS (2020) United States Department of Agriculture - National Agricultural Statistics Service, Agricultural Statistics, Access Date 09/26/2020
- Wechter WP, Kousik C, McMillan M, Levi A (2012a) Identification of resistance to *Fusarium oxysporum* f. sp. *niveum* race 2 in *Citrullus lanatus* var. *citroides* plant introductions. *HortScience* 47:334-338
- Wechter WP, Kousik CS, McMillan ML, Farnham MW, Levi A (2012b) Three improved *Citrullus lanatus* var. *citroides* lines USVL246-FR2, USVL252-FR2, and USVL335-FR2, with resistance to *Fusarium oxysporum* f. sp. *niveum* race 2. *Phytopathology* 102:133
- Wehner T (2008) Watermelon. In: Prohens J, Nuez F (eds) *Vegetables I: Asteraceae, Brassicaceae, Chenopodiaceae, and Cucurbitaceae*. Springer, New York, NY, pp 381-418
- Wu S, Wang X, Reddy U, Sun H, Bao K, Gao L, Mao L, Patel T, Ortiz C, Abburi VL, Nimmakayala P, Branham S, Wechter P, Massey L, Ling K-S, Kousik C, Hammar SA, Tadmor Y, Portnoy V, Gur A, Katzir N, Guner N, Davis A, Hernandez AG, Wright CL, McGregor C, Jarret R, Zhang X, Xu Y, Wehner TC, Grumet R, Levi A, Fei Z (2019) Genome of ‘Charleston Gray’, the principal American watermelon cultivar, and genetic characterization of 1,365 accessions in the U.S. National Plant Germplasm System watermelon collection. *Plant Biotechnol J* 17:2246–2258.

Appendix 1 Trait descriptors for Citrullus Germplasm.

Seed	Diseases	Pests	Growth	Fruit	Fruit Uniformity
<ul style="list-style-type: none"> • Oil content (%) • Arachidic acid (20:0) percentage • Linoleic acid (18:2) percentage • Oleic acid (18:1) percentage • Palmitic acid (16:0) percentage • Stearic acid (18:0) percentage • Seed Coat Percentage • Percent of total seed weight attributable to embryo 	<ul style="list-style-type: none"> • Resistance to unknown race of Colletotrichum lagenarium • Anthracnose race 2 • Bacterial fruit blotch • Downey Mildew • Gummy stem blight • Leaf Spot • Powdery Mildew race 2 • Powdery Mildew race 2 • Seed Blight • Resistance to Verticillium Wilt • Watermelon Mosaic Virus II 	<ul style="list-style-type: none"> • Root-knot nematode egg race • Root-knot nematode gall race 11 	<ul style="list-style-type: none"> • Plant Growth Habit • Vine type • Relative time of maturation 	<ul style="list-style-type: none"> • Fruit rind background color • Color pattern of fruit rind • Color of ripe fruit flesh • Flesh firmness • Fruit diameter • Fruit length • Fruit shape • Fruit weight • Longitudinal grooves • Brix • Rind stripe color • Rind thickness 	<ul style="list-style-type: none"> • Uniformity of the fruit color • Uniformity of the rind color • Uniformity of size • Uniformity of shape • Uniformity of fruit surface features