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## **CUCUMBER VULNERABILITY STATEMENT**

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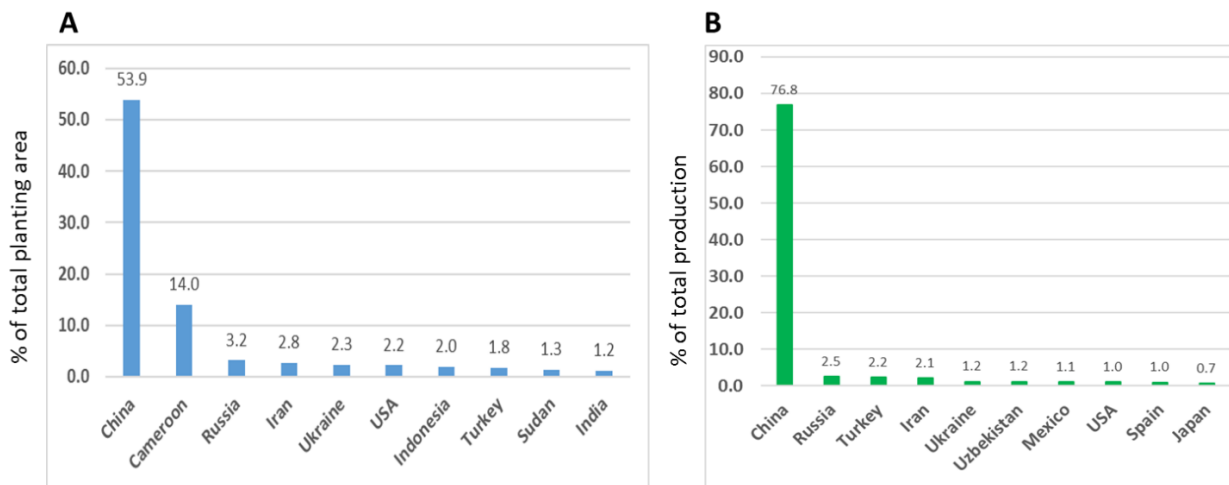
North Central Regional Plant Introduction, 1305 State Avenue, Ames, Iowa 50014

## **SUMMARY**

In the U.S., cucumber, *Cucumis sativus*, is an important vegetable crop for both fresh market and processing industries. The USDA National Plant Germplasm System's (NPGS) *C. sativus* collection currently includes 1401 accessions. This germplasm collection has played an important role in cucumber breeding both home and abroad to provide protection from damages by several important diseases. The collection will likely continue to be critical for sustainable cucumber production in the years to come. In this 'Cucumber Vulnerability Statement,' we first highlighted the economic importance, main constraints in cucumber production, and public research priorities. We reviewed contributions of the USDA germplasm collection to cucumber breeding, and the genetic resources available for reducing genetic vulnerabilities. We summarized recent efforts on cucumber germplasm collection including acquisition, maintenance, distribution, and regeneration. We described curatorial, managerial and research capacities and available tools, and discussed current limitations and issues with the cucumber germplasm collection and its utilization.

## I. Introduction

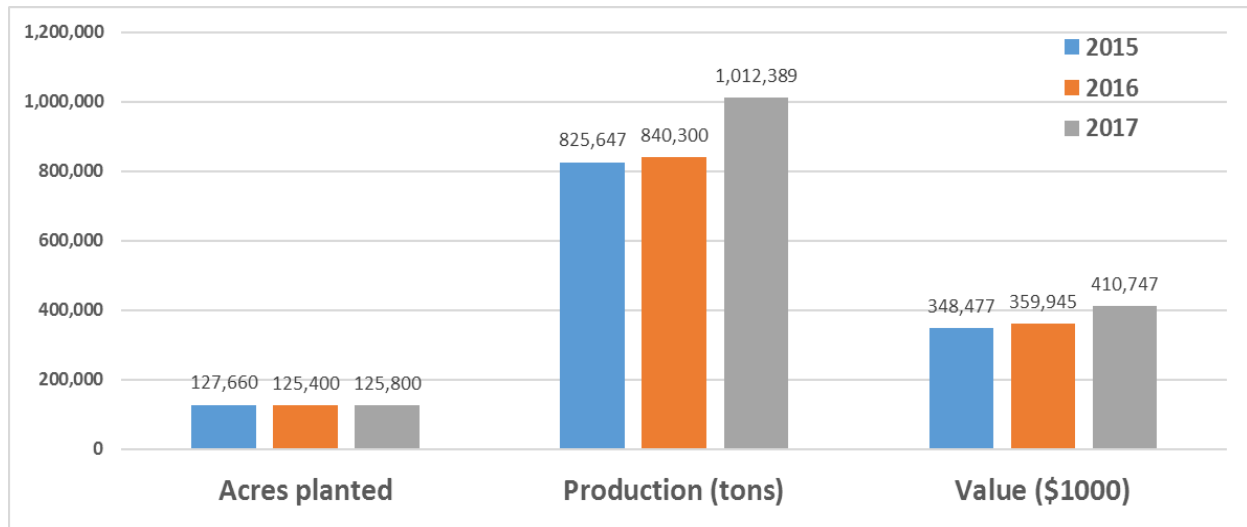
Cucumbers, *Cucumis sativus*, is an important vegetable in the human daily diet which is grown in many countries of the world. Based on FAO statistics, in 2016, cucumber was planted in more than 130 countries on nearly 2 million acres of land with a total production of 80,616,695 tons. China is by far the number one country for cucumber production in both acreage and total yield, which take approximately 53.9% and 76.8% of the world total, respectively (Figure 1). Among the top 10 cucumber producers, the U.S.A. ranks 5<sup>th</sup> and 8<sup>th</sup> on planting areas and total production, respectively (Figure 1) (<http://www.fao.org/STAT>).



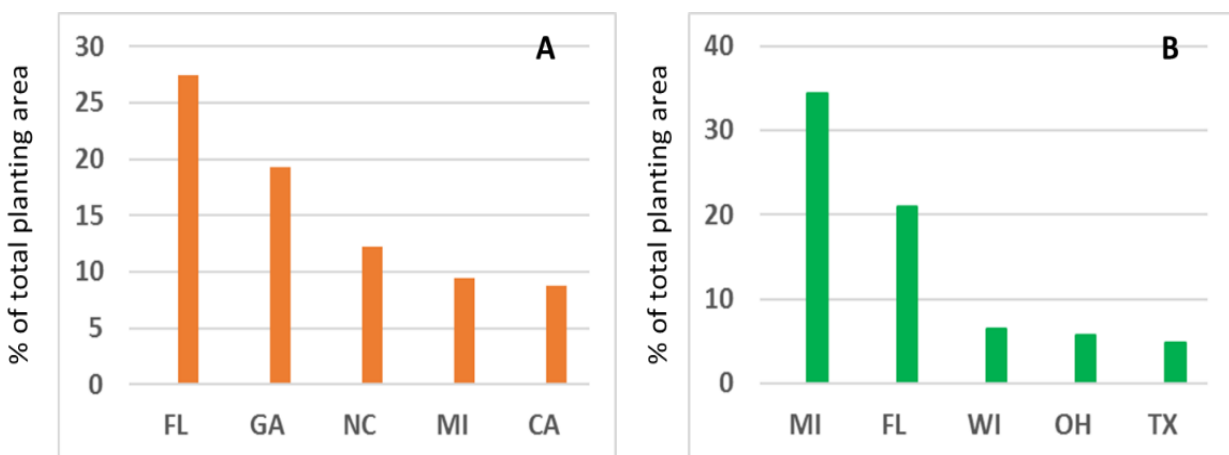
**Figure 1.** Cucumber production of top 10 countries of the world by planting areas and total production (in % of world total) (FAO STAT 2018)

In the U.S., in 2017, cucumber was planted on 125,800 acres with a farm gate value of \$410,747,000, which was ranked at 8<sup>th</sup> and 10<sup>th</sup>, respectively, among the 15 most important vegetables (Figure 2, <http://www.nass.usda.gov/>). Traditionally, two distinct types of cucumbers are grown in the US: pickling cucumber (50 to 150 mm long with thin, mottled, warty skin) and slicing cucumber (200 to 230 mm long with smooth, uniform green, thick skin). The majority of cucumbers is produced in open fields adapting to the once-over machine harvest system. However, the English cucumber or greenhouse slicer (long fruited, parthenocarpic) also has some share of the fresh market. More recently, the mini cucumber (Beit alpha or Mediterranean cucumber with very short fruit, parthenocarpic) is gaining popularity with American consumers and greenhouse growers. Production of fresh market cucumbers in protected environments is also increasing in this country.

The leading states in production of slicing cucumbers are Florida, Georgia, North Carolina, Michigan, California, New York, Texas and South Carolina (Figure 3A), whereas the leading states in production of pickling cucumbers are Michigan, Florida, Wisconsin, Ohio, and Texas (Figure 5B). The top five fresh and processing cucumber-producing states make up approximately 75% of total U.S. production, respectively (based on USDA NASS 2018 data).



**Figure 2.** US cucumber (fresh market and processing) production in 2015-2017 in planting area, total production and farm-gate values (2018 USDA NASS Statistics).



**Figure 3.** Top five cucumber producing states in the US in 2016 by planting area for fresh market (A) and processing (B) cucumbers in percentages of total acreage of the country.

## II. Urgency and extent of crop vulnerabilities and threats to food security

### *Vulnerabilities*

The level of diversity of available cultivars has been surveyed with both phenotypic observations and molecular markers (Wang et al. 2018). Data indicate that many cucumber cultivars grown in the U.S. are similar in parentage. Many of the pickling cucumber hybrids have Gy14 as a

significant source of germplasm in the seed parent. There is also much usage of 'Sumter' and M21 in the germplasm of the pollen parent. The same is true of fresh-market cucumbers, where much use is made of 'Marketmore' and 'Poinsett', either directly or as a component of a hybrid.

Growers, buyers and processors all demand uniformity in plant type, fruit type, and maturity, so it is necessary that cultivars developed for sale in the U.S. meet commercial standards. It is also necessary to have resistance to the major disease problems in each production area. If those resistances are from a single source, the resulting cultivars are more vulnerable to threats of possible virulence change of pathogens in the field. A most recent example is the downy mildew (DM) resistance. Almost all cucumber varieties in this country carry the *dm1* locus originated from PI 197087, which has been very effective in protection cucumbers from DM infection for nearly four decades. In 2004, a new DM strain emerged in the cucumber field which rendered *dm1* less effective. The breakdown devastated the cucumber industry. The heavy toll taken by the loss of resistance emphasizes the importance of diversifying sources of disease resistances. This, however, may likely become more an issue due to disappearance of many small seed companies in the last decade.

The changing production systems may also pose new challenges. For example, there is a growing trend in greenhouse production of cucumbers. While breeding cucumbers for open field remains a priority, breeding cultivars for production of protected cultivation need to be considered. At this time, the cucumber green mottle mosaic virus (CGMMV) is becoming a major problem in greenhouse cucumber production.

Solutions to the problem of uniformity involve using different sources of genes for the simply inherited traits or use of quantitative genes for those traits. New molecular marker technologies should facilitate use of quantitative genes more efficiently in breeding cucumbers for disease resistance.

### *Research priorities*

In 2014, a survey of the global cucumber community was conducted to align public research priorities with community needs (See **Appendix I** for design of questionnaire) (Weng 2017). Data from 38 respondents were analyzed. Several critical issues common to major market classes of cucumbers were identified including resistances for downy mildew (DM), cucurbit yellow stunting disorder virus (CYSDV) or cucumber green mottle mosaic virus (CGMMV), higher fruit yield and better pre-harvest fruit quality, increase of genetic diversity in cultivated cucumber, as well as development of molecular tools to expedite cucumber breeding. Priority issues for specific market classes or geographic regions of cucumber production were also identified. For North American pickling and slicing cucumbers, top research priorities included resistances to the post-2004 downy mildew strains, Phytophthora fruit rot (PFR) and angular leaf spot (ALS) pathogens. Additional important topics include improvement of post-harvest fruit quality, and development of parthenocarpic pickling varieties. The survey results were reflected by the goals in the USDA NIFA-SCRI-fund CucCAP projects (2015-2019, and 2020-2024) being carried out by the US public cucumber research community, which aims to characterize

and transfer of high-level DM and PFR resistances from resistant PI lines into elite cucumber lines.

### **III Status of cucumber genetic resources in the NPGS**

#### **3.1 Germplasm collections and *in situ* reserves**

##### Holding:

The USDA *Cucumis sativus* collection is maintained at the North Central Regional Plant Introduction Station NCRPIS at Ames, Iowa. As of September 2020, there are 1,401 *C. sativus* accessions in this collection which are from 64 countries. This is considered a mature collection with 95% of the accessions (1,330) available for distribution and backed up at National Laboratory for Germplasm Resources Preservation (NLGRP) in Ft. Collins, CO. Also, the NLGRP has 180 accessions which are cultivars or breeding lines primarily developed in the US. In addition to the NLGRP backups, 1098 accessions were sent for backup in the Svalbard Global Seed Vault in Norway.

##### Acquisition:

New acquisitions for all cucurbits have been extremely limited due to difficulties in securing permission for plant exploration and collecting in the regions of interest, and acceptance of the Standard Material Transfer Agreement (SMTA) stipulating the NPGS policy of freely distributing germplasm in its collections. Most new acquisitions have been from discontinued breeding programs, expired PVPs, or old cultivars no longer being conserved by seed companies. Since 2014, only seven *C. sativus* accessions (landraces) from the Republic of Georgia, and 12 cultivars from NLGRP (Fort Collins) were added to the NCRPIS inventory.

##### Maintenance:

Seed storage facilities at Ames, Iowa are adequate to excellent. *Cucumis* distribution lots are stored at 4° C, RH 28% and the original/parent seed lots are stored at -20° C. However, the Ames location is rapidly running out of space in both the 4° C and -20° C storage rooms.

##### Regeneration:

Regenerations are accomplished through the use of isolation field or greenhouse cages and insect pollinators (honey bees, alfalfa leaf cutting bees, bumble bees) or hand pollination. Basic characterization data and images are taken as part of the regeneration and maintenance process to document the accession and verify taxonomy. NCRPIS pathology personnel survey plots to monitor plant/seed health during the regeneration process. This disease monitoring is critical to meeting import requirements for distribution of international germplasm requests.

Regeneration efforts have focused on new acquisitions, accessions having limited inventory, accessions with older distribution seed lots, and accessions having uncertain taxonomy. In the last five years (2015-2019), 296 *C. sativus* accessions were regenerated.

The accession taxonomy is verified as part of the regeneration process. Progress is being made in correcting the taxonomy of accessions currently identified as *Cucumis spp.* through regenerations in the greenhouse. The accessions with taxonomic reassignment since 2014 are listed in **Appendix II**.

Distribution:

*Cucumis* seeds are distributed freely worldwide for breeding, scientific research, and educational uses. Germplasm requests are submitted via the Public GRIN-Global website (<https://npgsweb.ars-grin.gov/gringlobal/search.aspx>) or directly to the collection curator.

In the last five years (2015-2019), the NCRPIS received 195 requests of orders, and 8,909 packets were distributed, which covered all *C. sativus* accessions with seed availability (see Table 1 for details). In 2019, 996 packets from 631 accession were distributed from 40 order requests. Orders distributed for scientific purposes were for breeding of novel traits, disease and insect resistance, and evaluating wild crop relatives as potential sources for heat and drought tolerance; molecular characterization; evaluation for potential use as root stocks; and educational activities. In accordance with the NPGS distribution policy (<https://npgsweb.ars-grin.gov/gringlobal/distribution>), the NCRPIS does not generally distribute germplasm for non-research request (e.g., home gardener) orders for which genetic diversity is not needed. Requestors may be asked to provide additional information regarding their need for the germplasm, and it is at the curator’s discretion whether an order will be filled. Whenever possible, commercial sources and seed-saving organizations are suggested as alternative sources for cultivated varieties or to replace accessions that did not suit the intended use stated by the requestor. The NPGS provides germplasm to support research and education objectives, and due to the intensive effort and resources required to ensure availability of germplasm for this purpose, we are unable to distribute it for home gardening or other purposes that can utilize readily available commercial cultivars.

**Table 1. NCRPIS 5-Year Order Summary**

| Sitecrop         | Year | Number of Orders | Number of Recipients | Number of Items Distributed | Number of Accessions Distributed |
|------------------|------|------------------|----------------------|-----------------------------|----------------------------------|
| NC7-cucumis.cucs | 2015 | 38               | 37                   | 637                         | 448                              |
|                  | 2016 | 43               | 38                   | 2753                        | 1291                             |
|                  | 2017 | 41               | 38                   | 1938                        | 1024                             |
|                  | 2018 | 33               | 26                   | 2585                        | 1275                             |
|                  | 2019 | 40               | 37                   | 996                         | 631                              |
| Subtotal         |      | 195              |                      | 8909                        |                                  |

### 3.2 Associated information

Passport, phenotypic and evaluation data, and images of *Cucumis* germplasm can be obtained from the GRIN-Global website (<https://npgsweb.ars-grin.gov/gringlobal/search.aspx>). Passport data includes information on collection date, location, collector, donor, donor date, taxonomic classifications, etc. GRIN also allows for bibliographic citations of research papers

Characterization data for fruit characteristics, flowering dates, and plant habit are recorded during regenerations. There is a significant backlog of these data, which are being loaded into GRIN and time and resources allow. Plant and fruit images taken during regeneration are also loaded into GRIN. Thus far, over 2000 images have been loaded for cucurbits maintained at the NCRPIS.

Several field studies were conducted in the 1980's and 1990's to evaluate this USDA cucumber collection on horticulturally important traits such as resistance to the downy mildew, target leaf spot (TLS), angular leaf spot (ALS), gummy stem blight (GSB), anthracnose, belly rot, scab, and powdery mildew. Tolerance to drought, heat stresses and low temperature germination was also tested for a subset of the PI collection. All the phenotypic data sets have been uploaded to the GRIN website except for GSB screening data. Since 2000, the PI collection has been systematically screened for responses to powdery mildew (Block and Reitsma 2005), the post-2004 new downy mildew strain(s) (Call et al. 2012), and the *Phytophthora* fruit rot (*Phytophthora capsici*) (Colle et al. 2014). Many PI lines have also been evaluated for other traits by individual investigators. These phenotypic data are scattered in the literature and have not been input into the GRIN-Global database. The Cucurbit CGC encourage investigators to send the evaluation data published in peer-reviewed publications to be deposited into the GRIN database without further CGC review.

Understanding the genetic diversity and population structure of the USDA cucumber collection is important for conservation and use in cucumber breeding. Several studies in 1990's evaluated geography-based accessions in the USDA collection using RAPD markers. Later, Lu et al. (2009) assessed genetic diversity of 887 PI lines using 23 highly polymorphic SSR markers. More recently, the US CucCAP project conducted genotyping-by-sequencing (GBS) of 1,234 PI accessions. The genetic diversity and population structure of the USDA cucumber collection were characterized with more than 23,000 SNPs (Wang et al. 2018). Based on GBS data and phenotypic data, 394 lines were selected to formulate a GWAS (genome-wide association study) panel for further marker-trait association studies, which will be one objective in the new USDA-SCRI CAP project (CucCAP II, 2021-2014). Inbreds for the 394 PI lines will be obtained through self-pollination, and re-sequenced. By the end of this project, seeds of these inbred lines are expected to be deposited in a place accessible for the public.

### 3.3 Plant genetic resource research associated with the NPGS



From the review of the breeding history of US cucumber breeding (e.g., Peterson 1975; Wehner and Robinson 1991; Staub et al., 2008), it is clear that the production of cucumbers for both processing and fresh market in the U. S. depends almost entirely on cultivars with important characteristics derived from plant introduction lines. For example, the cucumber variety Wis SMR 18 and other cultivars with CMV resistance derived from ‘Chinese Long’ cucumber virtually saved the processing industry in Wisconsin and Michigan in the 1950’s. The use of gynoecious sex expression gene from PI 260860 from Korea made it possible for large-scale use of commercial F<sub>1</sub> hybrids in cucumber production and once-over machine harvest system (Peterson 1975). The deployment of anthracnose resistance gene from PI 197087 from India allowed fall cucumber crop season in the Southwest in 1950’s. The *dm1* gene for DM resistance also from PI 197087 provided effective control of this pathogen since 1960’s. Several PI line such as PI 197085, PI 197086, PI 197088, PI 330628, and PI 605996 were identified with high resistance to the post-2004 DM strain (Call et al. 2014; Wang et al. 2016, 2017, 2019). Commercial hybrids carrying DM resistance from PI 190788 have been released, but with mixed results with regard to performance of disease resistance in the field. However, no resistance to the southern root knot nematode (SRKN, *Meloidogyne incognita*) is available in the USDA *Cucumis sativus* collection.

In recent years, significant progress has been made in molecular mapping, and identification of genes and QTL responsible for key phenotypic traits in cucumber. Two recent reviews systematically documented simply inherited trait genes or major-effect QTL that have been cloned or fine mapped in cucumber (Pan et al. 2020; Wang et al. 2020). Also, through collaborative efforts among public and private cucumber researchers, 130 quantitative traits were identified and a set of recommendations for QTL nomenclature were developed, which should be a useful resource for the cucurbit research community (Wang et al. 2020).

The following is a list of PI lines as donors of traits that are critical for US cucumber production (ALS: angular leaf spot; AR: anthracnose; BW: bacterial wilt; CMV: cucumber mosaic virus; DM: downy mildew; PFR: Phytophthora fruit rot; PM: powdery mildew, TLS: target leaf spot). Many genes underlying these traits have been molecularly mapped or cloned; the detail could be found in Weng and Wehner (2017), and Wang et al. (2020).

|               |   |
|---------------|---|
| Chinese Long: | CMV resistance (Wehner & Robinson 1991)           |
| PI 109483     | PFR (Colle et al. 2014; Grumet and Colle 2017)    |
| PI 197087     | AR, ALS, DM, PM (Peterson 1975; Wang et al. 2019) |
| PI 197088     | DM, PM (Call et al. 2014; Wang et al. 2017)       |
| PI 200815     | BW (Peterson 1975; Peterson et al. 1982)          |
| PI 200818     | BW (Peterson 1975)                                |
| PI 212233     | PM (Peterson 1975; Block and Reitsma 2005)        |
| PI 220860     | Gynoecious sex expression (Peterson 1975)         |
| PI 234517     | PM (Peterson 1975; Block and Reitsma 2005)        |
| PI 265887     | non-bitterness (Peterson 1975)                    |

PI 330628                      DM, TLS (Wang et al. 2016)  
PI 605996                      DM (Call et al. 2014)

### **3.4 Curatorial, managerial and research capacities and tools**

#### **3.4.1 Staffing**

The NSRPIS Vegetable Project is comprised of one full-time Iowa State University Research Scientist III (Curator), one part-time Iowa State University Agricultural Assistant III, and one half-time Iowa State University Agricultural Specialist I (position shared with NCRPIS Farm Management team) which is responsible for not only the NCRPIS cucurbit collections (*Cucumis melo*, *C. sativus*, wild species of *Cucumis*, and *Cucurbita*), but also the NPGS *Cichorium*, *Daucus*, *Ocimum*, and *Pastinaca* collections (almost 8,000 accessions). They are assisted by three to four full-time-equivalent Iowa State University student employees as well as supported by the station's administrative, farm management, plant pathology, information technology, seed storage, order processing, and seed germination personnel. Germplasm management includes germplasm preservation and regeneration, viability testing, plant and seed health assays, characterization and evaluation, taxonomic verification, distribution, and record keeping. Collection sizes and workloads continue to increase, but resources to accomplish the work do not.

#### **3.4.2 Facilities and equipment**

The Ames location is rapidly running out of space in both the 4° C and -18° C seed storage rooms. A request has been made for support for a 2500 sq. ft. -20° C storage building. A -20° C cold room could essentially double the longevity of viability of many of the taxa maintained at the NCRPIS. Greenhouse space is inadequate, and the facilities are outdated. We continue to upgrade as funding becomes available such as the purchase of LED lighting fixtures to improve plant productivity and reduce costs. A few new germplasm regeneration cage frames and screens are purchased annually to replace old and damaged equipment that cannot be repaired on-site.

### **3.5 Fiscal and operational resources**

The operations of the North Central Regional Plant Introduction Station are supported by the USDA-ARS Plant Introduction Research Unit's CRIS Project, by Hatch Multistate Project NC-007, and from in-kind support from Iowa State University, its host institution. This funding support provides for the Station's farm and facilities operations and the scientific, technical, and administrative personnel responsible for curation, maintenance and distribution of more than 1700 plant taxa, including 1401 accessions of *Cucumis sativus* and associated information. These funds also support phytosanitary and pollination efforts, and software development focused on improved genebank information workflows.

#### 4. Other genetic resource capacities

Germplasm collection/acquisition efforts since 1990's is minimal due to reasons mentioned above. The U.S. cucumber research community in this country is relatively small. The last two decades have witnessed significant reduction in research personnel in both public institutions and private seed companies. Major cucumber commodity groups include the Pickle Packer International (PPI) (<http://www.ilovepickles.com/>), and the Midwest Pickles Association (MWPA). The public and private research programs that are actively involved in germplasm activities are listed below under the groupings of public and private research.

##### Public research

- Rebeca Grumet (Michigan State University, East Lansing, MI; [grumet@msu.edu](mailto:grumet@msu.edu)) focusing on biotechnology, fruit development, and disease resistance of cucumber.
- Michael Havey (USDA-ARS, Madison, WI; [Michael.Havey@ars.usda.gov](mailto:Michael.Havey@ars.usda.gov)) with research interests in cucumber organellar genetics and cold tolerance.
- Chandrasekar S. Kousik (USDA-ARS, Charleston, SC; [Shaker.Kousik@ars.usda.gov](mailto:Shaker.Kousik@ars.usda.gov)) with research interests in cucurbit disease resistances focusing on PM and DM.
- Kai-Shu Ling (USDA-ARS, Charleston, SC; [Kai.Ling@ars.usda.gov](mailto:Kai.Ling@ars.usda.gov)) emphasizing on cucurbit virus resistances.
- Lina Quesada-Ocampo (North Carolina State University, Raleigh, North Carolina), [lina\\_quesada@ncsu.edu](mailto:lina_quesada@ncsu.edu), pathology of downy mildew pathogen
- Kathleen Reitsma (USDA-ARS, North Central Regional Plant Introduction Station, Iowa State University, Ames, IA; [Kathleen.Reitsma@ars.usda.gov](mailto:Kathleen.Reitsma@ars.usda.gov)). Major activities include maintenance of the working collection of *Cucumis*; evaluation of the PI accessions for disease resistance, yield and earliness.
- Todd C. Wehner (North Carolina State University, Raleigh, NC; [todd\\_wehner@ncsu.edu](mailto:todd_wehner@ncsu.edu)). Research activities include breeding of pickling and fresh-market cucumbers; evaluation of cucumber germplasm for disease and nematode resistance, yield, earliness, fruit quality, insect resistance, and cold tolerance; gene linkage.
- Yiqun Weng (USDA-ARS, Madison, WI; [Yiqun.Weng@ars.usda.gov](mailto:Yiqun.Weng@ars.usda.gov)) with research activities including cucumber breeding, cucumber germplasm for horticulturally important traits, mapping and cloning of genes /QTL, cucumber genome evolution, marker-assisted selection

##### Private research

- Adam Call (Harris Moran Clause Seed Company, [Adam.Call@hmclause.com](mailto:Adam.Call@hmclause.com)) focusing on cucumber breeding; germplasm evaluation.
- Nischit Shetty (Monsanto Vegetable Seeds; [Nischit.Shetty@monsanto.com](mailto:Nischit.Shetty@monsanto.com)) emphasizing on cucumber breeding; germplasm evaluation.

## 5. Prospects and future developments

Many PI lines are genetically heterogeneous in nature, and it is the goal to maintain the genetic diversity within each line during regeneration efforts. However, phenotypically distinct lines were identified during regeneration. New PI numbers (Ames xxxxx) were assigned for those lines. Over the years, segregants from self-pollination of cucumber PI lines were also identified from different research programs were identified. Mutant stocks and mapping populations (such as recombinant inbred lines, introgression lines) were developed. Many cucumber mutant stocks have been lost due to coming-and-going of research programs and lack of a central location to keep those stocks. Whether the NPGS GRIN should maintain these valuable materials remains an issue.

We are entering genomics, and post-genomics era. Tons of molecular data such as genome sequences, transcriptome sequences, and molecular markers are being generated for many PI lines. How to deal with such large amount of data for germplasm conservation and utilization is likely an important task to address in the coming years. One potential ‘solution’ for the USDA germplasm storage would be to use genomic information on the collection to both reduce duplicity and guide the increasing process in terms of number of plants needed to maintain the genetic diversity of the line. A comprehensive database combining collection information, phenotypic data, molecular data is ideal which will also be a daunting task.

Continuing acquisition of to the NPGS *Cucumis* collection is imperative. At this time, accessions of the wild cucumber (*C. sativus* var. *hardwickii*) are underrepresented. There is only one accession of the semi-wild Xishuangbanna (*C. sativus* var. *xishuangbannensis*) cucumber, and no accession for the closest relative of cucumber, *C. hystrix*. These taxa may harbor unique genes that are important for cucumber improvement.

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## 7. Appendices

**Appendix I. Public cucumber research priority survey (2014)**

**1. I am a (check all that apply)**

Grower                                       Processor                                       Salter, green shipper  
 Public researcher                                       Private researcher                                       State extension specialist  
 Others. Please specify \_\_\_\_\_

**2. My work focuses primarily on**

Fresh market cucumber                                       Processing cucumber                                       Both  
**Target market** of my work is (geographic region) \_\_\_\_\_

**3. Fungal/bacterial diseases (rank top 10 priorities of research, 1 = highest priority)**

3.1  Downy mildew (DM)  
3.2  Powdery mildew (PM)  
3.3  Angular leaf spot (ALS)  
3.4  Target leaf spot (TLS)  
3.5  Fusarium wilt (FW)  
3.6  Phytophthora fruit rot (FPR)  
3.7  Bacterial wilt (BW)  
3.8  Gummy stem blight (GSB)  
3.9  Anthracnose  
3.10  Belly rot  
3.11  Scab  
3.12  Other diseases. Please specify \_\_\_\_\_

**4. Virus diseases (rank top 5 priorities of research, 1 = highest priority)**

4.1  Cucumber mosaic virus (CMV)  
4.2  Cucurbit yellow stunting disorder virus (CYSDV)  
4.3  Papaya ring spot virus (PRSV)  
4.4  Watermelon mosaic virus (WMV)  
4.5  Zucchini yellow mosaic virus (ZYMV)  
4.6  Other viruses. Please specify \_\_\_\_\_

**5. Insect pests (rank top 5 priorities of research, 1 = highest priority)**

5.1  Cucumber beetles  
5.2  Whiteflies  
5.3  Spider mites  
5.4  Leaf miners  
5.5  Pickleworm  
5.6  Thrips  
5.7  Aphids  
5.8  Others. Please specify \_\_\_\_\_

**6. Abiotic stresses (rank top 5 priorities, 1 = highest priority)**

- 6.1 \_\_\_\_\_ Chilling damage
- 6.2 \_\_\_\_\_ Cold germination
- 6.3 \_\_\_\_\_ Drought stress
- 6.4 \_\_\_\_\_ Heat damage
- 6.5 \_\_\_\_\_ Salt stress
- 6.6 \_\_\_\_\_ Herbicide damage
- 6.7 \_\_\_\_\_ Others. Please specify \_\_\_\_\_

**7. Fruit yield and quality (rank top 4 priorities, 1 = highest priority)**

- 7.1 \_\_\_\_\_ High fruit yield
- 7.2 \_\_\_\_\_ Parthenocarpic pickling cucumber
- 7.3 \_\_\_\_\_ Pre-harvest fruit quality: fruit shape, color, taste/texture, internal defect etc.
- 7.4 \_\_\_\_\_ Postharvest fruit quality: brining quality, shelf-life etc.
- 7.5 \_\_\_\_\_ Others. Please specify \_\_\_\_\_

**8. Molecular/biotechnological tool development (rank top 5 priorities, 1 = highest priority)**

- 8.1 \_\_\_\_\_ Improve cucumber draft genome assembly and genome annotations
- 8.2 \_\_\_\_\_ Develop molecular markers for important traits for marker-assisted selection
- 8.3 \_\_\_\_\_ Develop more applied genomic resources (maps, genome sequencing etc.)
- 8.4 \_\_\_\_\_ Develop genetic transformation techniques for cucumber
- 8.5 \_\_\_\_\_ Broaden cucumber genetic diversity through exploring other *Cucumis* resources
- 8.6 \_\_\_\_\_ Others. Please specify \_\_\_\_\_

**9. Now, from Categories 3 to 8 above, please list the overall TOP 10 priorities (# 1= highest priority; #10 = lowest priority). You can put the item number (for example 3.1) in the blanks.**

- |          |           |
|----------|-----------|
| #1 _____ | #6 _____  |
| #2 _____ | #7 _____  |
| #3 _____ | #8 _____  |
| #4 _____ | #9 _____  |
| #5 _____ | #10 _____ |

**10. Additional comments related to public research needs.**

**11. If you wish to receive the survey results, please provide your email/mail address or other methods of communication.**

**Appendix II.** Reassignment of taxonomical status of *Cucumis* accessions during regeneration process.

| <b>Year</b> | <b>Accession</b> | <b>Incorrect Taxon</b>       | <b>Correct Taxon</b>                             |
|-------------|------------------|------------------------------|--|
| 2014        | PI 494825        | <i>Cucumis</i> spp.          | <i>Cucumis zambianus</i> Widrlechner et al.      |
| 2014        | PI 500406        | <i>Cucumis</i> spp.          | <i>Cucumis metuliferus</i> E. May. ex Naudin     |
| 2014        | PI 669557        | <i>Cucurbita maxima</i>      | <i>Cucurbita pepo</i>                            |
| 2015        | PI 500397        | <i>Cucumis</i> spp.          | <i>Cucumis anguria</i> var. <i>longaculeatus</i> |
| 2015        | PI 500375        | <i>Cucumis</i> spp.          | <i>Cucumis melo</i> subsp. <i>agrestis</i>       |
| 2015        | PI 500392        | <i>Cucumis</i> spp.          | <i>Cucumis melo</i> subsp. <i>agrestis</i>       |
| 2015        | PI 500387        | <i>Cucumis</i> spp.          | <i>Cucumis metuliferus</i> E. May. ex Naudin     |
| 2015        | PI 500402        | <i>Cucumis</i> spp.          | <i>Cucumis metuliferus</i> E. May. ex Naudin     |
| 2015        | PI 500429        | <i>Cucumis</i> spp.          | <i>Cucumis metuliferus</i> E. May. ex Naudin     |
| 2015        | PI 500433        | <i>Cucumis</i> spp.          | <i>Cucumis metuliferus</i> E. May. ex Naudin     |
| 2016        | PI 542112        | <i>Cucumis</i> spp.          | <i>Cucumis africanus</i>                         |
| 2016        | PI 537392        | <i>Cucumis</i> spp.          | <i>Cucumis melo</i> subsp. <i>agrestis</i>       |
| 2016        | PI 618817        | <i>Citrullus naudinianus</i> | <i>Cucumis myriocarpus</i>                       |
| 2016        | PI 671961        | <i>Citrullus naudinianus</i> | <i>Cucumis myriocarpus</i>                       |
| 2016        | Ames 33373       | <i>Citrullus naudinianus</i> | <i>Cucumis</i> spp.                              |
| 2017        | PI 635740        | <i>Citrullus lanatus</i>     | <i>Cucumis melo</i> L.                           |
| 2017        | PI 635762        | <i>Citrullus lanatus</i>     | <i>Cucumis melo</i> L.                           |
| 2017        | PI 635764        | <i>Citrullus</i> spp.        | <i>Cucumis melo</i> L.                           |
| 2018        | PI 500391        | <i>Cucumis</i> spp.          | <i>Cucumis melo</i> L.                           |
| 2018        | PI 500394        | <i>Cucumis</i> spp.          | <i>Cucumis melo</i> L.                           |
| 2018        | PI 500403        | <i>Cucumis</i> spp.          | <i>Cucumis metuliferus</i> E. May. ex Naudin     |
| 2018        | PI 500407        | <i>Cucumis</i> spp.          | <i>Cucumis metuliferus</i> E. May. ex Naudin     |
| 2018        | PI 500413        | <i>Cucumis</i> spp.          | <i>Cucumis metuliferus</i> E. May. ex Naudin     |
| 2018        | PI 500415        | <i>Cucumis</i> spp.          | <i>Cucumis metuliferus</i> E. May. ex Naudin     |
| 2018        | PI 500414        | <i>Cucumis</i> spp.          | <i>Cucumis zambianus</i> Widrlechner et al.      |
| 2018        | PI 500432        | <i>Cucumis</i> spp.          | <i>Cucumis zambianus</i> Widrlechner et al.      |
| 2018        | PI 500436        | <i>Cucumis</i> spp.          | <i>Cucumis zambianus</i> Widrlechner et al.      |