Introduction

"Cucurbit" is a general term to denote all species within the Cucurbitaceae family, which includes approximately 800 species in 130 genera. Cucurbit crops are mostly annual, herbaceous, tendril-bearing and frost sensitive vines and are among the economically most important vegetable crops worldwide. Cucurbits are growing primarily in the temperate and tropical regions. Major cucurbit crops include cucumber (Cucumis sativus L.), melon (Cucumis melo L.), watermelon [Citrulus lanatus (Thunb.) Matsum. & Nakai], and squash or pumpkin (Cucurbita pepo L., Cucurbita maxima Duch. and Cucurbita moschata Duch.).

An introduction to cucurbit crops has been provided in two full-length books (Whitaker & Davis 1962; Robinson and Decker-Walters 1997). A number of book chapters have periodical updates of our knowledge on research in cucumber (Tatlioglu 1993; Staub et al. 2008), melon (McCreight et al. 1993; Pitrat 2008), watermelon (Feher 1993; Wehner 2008), and squash/pumpkin (Ferriol and Pico 2008; Paris 2008). This chapter will give a brief review of research progress in the past several years in four major cucurbit crops with focus on the economic and biological importance of major cucurbits, new findings in cucurbit taxonomy, domestication and evolution, as well as germplasm conservation and utilization.

Economic importance of cucurbit crops

Among cucurbits, cucumber, melon, watermelon, and pumpkin are the four most commonly cultivated crops. Minor cucurbit crops include west Indian gherkin (Cucumis anguria L.) and African horned cucumber (Cucumis metuliferus E. Mey) as well as ornamentals (hedgehog gourd, gooseberry gourd), which are the topic of the second chapter of this book. Cultivars developed by breeders from cucumber, melon, watermelon and pumpkin/squash are the basis for multi-billion dollar industries. Next to tomatoes and onions, cucumbers and melons are the third most widely cultivated vegetable crops in the world (Pitrat et al. 1999). According to the United Nations’ Food and Agriculture Organization (FAO), the world total areas of harvest for cucumber/gherkins and melon in 2008 were over 2.6M ha and 1.3M ha, respectively, and China is the world’s leading producer of these two crops (Table 1). Together, these two crops represent 7% of the world’s total cultivated vegetable surface in 2001, ranking third after tomato and watermelon (http://www.fao.org). Watermelon has the largest cultivated areas among major
cucurbit crops with over 3.7M ha harvest acreage in 2008 worldwide. China, Turkey and Iran are the top three countries in watermelon production in 2008 (Table 1).

Squash and pumpkins are unique in that they represent several species for the same crop (Robinson and Decker-Walters 1997). Summer squash is *Cucurbita pepo*, but winter squash may be *C. pepo*, *C. moschata*, *C. mixta*, or *C. maxima*. The Jack O’Lantern type of pumpkin is *C. pepo*, but commercially canned pumpkin pie mix is also made from *C. moschata* or *C. maxima*. *C. mixta* and *C. ficifolia* are used for food in Mexico and in Central and South American countries. Squash and pumpkin are usually grown for their fruit, harvested immature for summer squash or mature for winter squash and pumpkin. The world total area harvested of pumpkin was approximately 1.5M ha in 2008 (Table 1).

Table 1. Five leading countries in production of four major cucurbits in 2008

<table>
<thead>
<tr>
<th>Crops</th>
<th>Country</th>
<th>Area harvested (ha)*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cucumber</td>
<td>China</td>
<td>1,702,777</td>
</tr>
<tr>
<td></td>
<td>Cameroon</td>
<td>120,000</td>
</tr>
<tr>
<td></td>
<td>Iran</td>
<td>82,000</td>
</tr>
<tr>
<td></td>
<td>Russia</td>
<td>73,000</td>
</tr>
<tr>
<td></td>
<td>Egypt</td>
<td>67,810</td>
</tr>
<tr>
<td></td>
<td>World total</td>
<td>2,635,058</td>
</tr>
<tr>
<td>Watermelon</td>
<td>China</td>
<td>2,162,456</td>
</tr>
<tr>
<td></td>
<td>Iran</td>
<td>135,000</td>
</tr>
<tr>
<td></td>
<td>Turkey</td>
<td>139,000</td>
</tr>
<tr>
<td></td>
<td>Russia</td>
<td>133,000</td>
</tr>
<tr>
<td></td>
<td>Brazil</td>
<td>93,600</td>
</tr>
<tr>
<td></td>
<td>World total</td>
<td>3,752,568</td>
</tr>
<tr>
<td>Melon</td>
<td>China</td>
<td>570,874</td>
</tr>
<tr>
<td></td>
<td>Turkey</td>
<td>103,000</td>
</tr>
<tr>
<td></td>
<td>Iran</td>
<td>80,000</td>
</tr>
<tr>
<td></td>
<td>Egypt</td>
<td>74,417</td>
</tr>
<tr>
<td></td>
<td>Spain</td>
<td>38,600</td>
</tr>
<tr>
<td></td>
<td>World total</td>
<td>1,346,962</td>
</tr>
<tr>
<td>Pumpkin</td>
<td>India</td>
<td>360,000</td>
</tr>
<tr>
<td></td>
<td>China</td>
<td>330,212</td>
</tr>
<tr>
<td></td>
<td>Cameroon</td>
<td>110,000</td>
</tr>
<tr>
<td></td>
<td>Cuba</td>
<td>73,038</td>
</tr>
<tr>
<td></td>
<td>Russia</td>
<td>53,000</td>
</tr>
<tr>
<td></td>
<td>World total</td>
<td>1,529,935</td>
</tr>
</tbody>
</table>

* FAO Statistics 2010 (http://faostat.fao.org/)

Cucurbits are an important part of the human daily diet. Cucurbit fruits are high in moisture and low in fat, which makes them popular with consumers interested in healthy diets. Those with orange flesh like muskmelon and winter squash are excellent sources of vitamin A.
Orange-fleshed pickling cucumber germplasm have also been developed (Simon and Navazio 1997).

Cucurbit seeds can be classified as oil seeds because decorticated seeds contain by weight 50% oil and 35% protein. The oil is unsaturated and generally edible; however, the contents of conjugated trienoic fatty acids in the oil of a few species preclude edibility but increase industrial values as drying oils. Proteins of cucurbit seeds appear edible and supplementation with certain amino acids increases the nutritional value of the protein (Jacks et al. 1972; Mansour et al. 1993). For example, watermelon seeds, which are used for food in various parts of the world, are low in moisture and high in carbohydrates, fats, and protein. Varieties with very large seeds have been developed especially for use as food in China, where more than 200,000 tons are produced annually on 140,000 ha land (Zhang 1996).

**Biological importance of cucurbit crops**

All members of the Cucurbitaceae family have a lianous structure of the plant body, the development of fleshy fruits, and a similar mode of sex determination. These traits place cucurbits in a unique position for understanding some important biological processes in plants.

The monoecious cucumber has long been served as a model system for sex determination studies driven by breeding programs for hybrid seed production. Cucumber plants are mostly monoecious but can be dioecious or hermaphroditic. Sex expression is controlled primarily by the $F$ (femaleness) and $M$ (andromonoecy) loci in cucumber; and by the $a$ (andromonoecious) and $g$ (gynoecious) loci in melon, although environmental factors also play important roles in this process. Genes involved in ethylene (ET) biosynthesis/perception have been implicated in cucumber floral development. $CsACS1G$ encoding 1-amino- cyclopropane-1-carboxylate synthase (ACS) in the ET-biosynthesis pathway was mapped to the $F$ locus in cucumber (Kamachi et al. 1997; Trebitsh et al. 1997). Recently the other three genes, $M$ in cucumber, $a$ and $g$ in melon have all been cloned (Boualem et al. 2008, 2009; Li et al. 2009; Martin et al. 2009), which will give us better understanding of the important processes of sex determination in cucurbit crops and potentially contribute to better efficiency of hybrid seed production.

Major cucurbits have several-fold size differences in their mitochondrial genomes (Ward et al. 1981). Watermelon possesses a relatively small mitochondrial genome of 380 kb; squash has a larger one of 980 kb (Alverson et al. 2010), while cucumber and melon mitochondrial genomes are huge, which is 1,500 kb and 2,400 kb, respectively. The chloroplast genomes of melon, squash, and watermelon are maternally transmitted. While the mitochondrial genomes of squash and watermelon are maternally transmitted, those of melon and cucumber exhibit paternal transmission (Havey 1997). Because the chloroplast, mitochondrial, and nuclear genomes of *Cucumis* are differentially transmitted, this genus is an excellent system to study the role of intergenomic transfer in the evolution of extremely large mitochondrial genomes (Havey et al. 1998).

Phloem transport systems have been extensively researched because they perform vital functions in plants, including distribution of photoassimilates, nutrients, and signaling molecules to spatially separated organs. Cucurbits, especially cucumber and pumpkin/squash are preferred models for phloem physiology because of both the ease of sampling phloem sap and the facile visualization of their large phloem sieve elements (Eschrich et al. 1971; Clark et al. 1997; Zhang et al. 2010). Cucurbit phloem transport is unique in that sucrose diffuses symplastically into
intermediary cells (a form of companion cell), where it is converted into raffinose-family oligosaccharide sugars (Turgeon 1996).

Most cucurbit are consumed as either immature (for example cucumber, summer squash) or mature (for example, melon, watermelon or winter squash) fruits. A number of fruit development and ripening studies in melon and cucumber have been conducted. Considering its morphological, physiological, and biochemical diversity in flavor development and textural changes during fruit ripening, melon was proposed to be a model plant for the elucidation of key traits in fruit development (Ézura & Owino 2008).

Most species in the Cucurbitaceae family has basic chromosome numbers of 7, 11, 12, 13, or 20, and relatively small genome sizes. The chromosome numbers and genome size of the major cucurbit crops are listed in Table 2. This fact also provides us a good opportunity to study chromosome evolution in cucurbits.

Table 2. Chromosome number and genome size of major cucurbit crops

<table>
<thead>
<tr>
<th>Name</th>
<th>Scientific name</th>
<th>Chromosome #</th>
<th>Genome size (Mbp)*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cucumber</td>
<td><em>Cucumis sativus</em> L.</td>
<td>2n = 2x = 14</td>
<td>367</td>
</tr>
<tr>
<td>Melon</td>
<td><em>Cucumis melo</em> L.</td>
<td>2n = 2x = 24</td>
<td>450</td>
</tr>
<tr>
<td>Watermelon</td>
<td><em>Citrullus lanatus</em> Mats. &amp; Nakai</td>
<td>2n = 2x = 22</td>
<td>430</td>
</tr>
<tr>
<td>Squash/pumpkin</td>
<td><em>Cucurbita maxima</em> Duch.</td>
<td>2n = 2x = 40</td>
<td>440</td>
</tr>
<tr>
<td></td>
<td><em>Cucurbita moschata</em> Duch.</td>
<td>2n = 2x = 40</td>
<td>417</td>
</tr>
<tr>
<td></td>
<td><em>Cucurbita pepo</em> L.</td>
<td>2n = 2x = 40</td>
<td>460-520</td>
</tr>
</tbody>
</table>

* Based on Arumuganathan and Earle (1991), and Tatum et al. (2006).

In the past two years, due to the use of next-generation sequencing technologies, the whole genomes of many plants have been sequenced. Among the four major cucurbits, the whole genomes of three, namely, cucumber (Huang et al. 2009; Woycicki & Przybecki 2010; Weng et al. unpublished data), melon (Benjak et al. 2010) and watermelon (Xu et al. 2009) have been sequenced or is near completion. It is reasonable to say that cucumber (and other cucurbits) genomics has come of age. Thus, we can expect more by exploring cucumber and other cucurbit genomics resources. Particularly, cucumber may offer some advantages for genomic research due to its economic importance, small genome size with relatively low percentage of repetitive DNA, short life cycle (50-70 days) and its unique position in the phylogenetic tree of the Cucurbitaceae family.

Taxonomy, origin and domestication and evolution of cucurbit crops

The Cucurbitaceae family is well defined which includes 118 genera and over 800 species (Jeffrey 1980). Cucurbitaceae can be divided into two subfamilies: Zanonioidae and Cucurbitoideae. The food plants all fall within the subfamily Cucurbitoideae. Further definition finds cucumber, melon and watermelon belonging to the tribe Benincaseae and squash/pumpkin was assigned to the tribe Cucurbiteae (Fig. 1). However, molecular phylogenetic studies in recent
years have significantly changed our classical view of many species in this family, which is particularly true for *Cucumis* that contains the two very important cucurbit crops, cucumber and melon. Our current view of *Cucumis* is illustrated in Fig. 1.

**Fig. 1.** Cucurbit phylogenetic tree. Chromosome numbers and common names follow each species name (when available). Molecular clock in million years ago, if available, was shown on branching points. The tribe to which the species belongs was shown to the right of vertical bars. Geographical occurrence of species: Green - America; Black - mainland African; Red - Asia; Blue – Australia. The tree was redrawn after Schaefer et al. (2009).

*Cucumber and melon*

The genus *Cucumis* traditionally contained 32 species that were further divided into two subgenera, *Melo* and *Cucumis* (Kirkbride 1993). Subgenus *melo* is centered in Africa with 30 species (2n = 24); subgenus *Cucumis* includes the cultivated cucumber *C. sativus* (2n = 14) and its wild relative *C. hystrix* (2n = 24), both of which have an Asian origin. However, in recent molecular data-based phylogenetic trees, a number of other genera like *Cucumella*, *Mukia*, *Dicaelospermum*, *Myrmecosicyos* and *Oreosyce* were nested within *Cucumis*, thus, an expansion of *Cucumis* was proposed to include these nested genera (Ghebretinsae et al. 2007a, b; Renner et al. 2007). The revised genus *Cucumis* now has 52 species, which were grouped into two subgenera: *Humifructus* (2 species, *C. humifructus* and *C. hirsutus*) and *Cucumis* (the remaining 50 species) (Schaefer 2008). In the new phylogenetic tree, *C. hystrix* remains the closest relative of cucumber, followed by a clad containing *D. ritchiei*, *Mukia javanica* and *Mukia*
maderaspatana (Ghebretinsae et al. 2007a; Renner et al. 2007; Renner & Schaefer 2008; Schaefer et al. 2009). Given the geographic distribution of these extant closest relatives, melon (C. melo), which was traditionally assumed to have Africa origin, was proposed to have originated somewhere in Asia and then reached Africa from there (Renner et al. 2007; Schaefer et al. 2009). More recently (Sebastian et al. 2010), from molecular data for nearly 100 Cucumis accessions from Africa, Australia, and Asia, it was shown that both melon and cucumber are of Asian origin and have numerous previously overlooked species-level relatives in Australia and around the Indian Ocean. Wild progenitors of C. melo occur in India, but the Southeast Asian C. hystrix is the closest relative of cucumber. Most surprisingly, the closest relative of melon is Cucumis picrocarpus from Australia. Melon diverged from this Australian sister species approximately 3 million years ago. Further revision of Cucumis is likely. These new insights about the closest relatives of melon and cucumber may have implications for ongoing genomics and breeding efforts in cucurbits.

**Watermelon**

The genus Citrullus is taxonomically complex and its composition is not unanimously accepted by all taxonomists yet. Currently, Citrullus consists of four diploid (2n = 2x = 22) species. C. lanatus var. lanatus is the domesticated watermelon. Wild watermelon also known as citron is C. lanatus var. citroides (L. H. Bailey) Mansf (but citron is known to be cultivated; Laghetti and Hammer 2007). Three other wild species are Citrullus colocynthis (L.) Schrad., C. eccirrhosus Cogn and C. rehmi De Winter. The perennial C. colocynthis grows in Northern Africa, southwestern Asia and the Mediterranean, whereas the perennial C. eccirrhosus and annual C. rehmi are endemic to the Namib Desert (Levi et al. 2005; Dane and Liu 2006). Watermelon is thought to have originated in southern Africa because it is found growing wild throughout the area, and reaches maximum diversity there. Watermelon may have been cultivated in Africa for over 4,000 years. C. colocynthis is considered to be a wild ancestor of watermelon with small fruits and seeds, and bitter flesh. Interspecific crosses of C. lanatus with C. colocynthis can produce viable F₁ hybrids. Although Citrullus species grow wild in southern and central Africa, C. colocynthis also grows wild in India. Thus, India and China may be considered secondary centers of diversity for the genus.

**Squash/pumpkin**

The genus Cucurbita (squashes and pumpkins) is composed of 12–14 species including five cultivated ones: Cucurbita pepo, Cucurbita maxima, Cucurbita moschata, Cucurbita ficifolia and Cucurbita mixta. The later two have less economic importance and a narrower distribution (Robinson and Decker-Walters 1997).

While Cucurbita has an America origin in general, current genetic, bio-geographic, and archaeological data suggest that the five cultivated species were domesticated in different places, ranging from North America to southern South America (Sanjur et al. 2002; Piperno & Stothert 2003). Each species probably represents an independent domestication event from different ancestor populations. Based on analysis of mitochondrial genes, Sanjur et al. (2002) found that at least six independent domestication events from distinct wild ancestors. Cucurbita mixta likely was domesticated from a wild Mexican gourd, Cucurbita sororia. The wild ancestor of Cucurbita moschata is still unknown, but will probably be found in lowland northern South
America. *Cucurbita andreana* may be the wild progenitor of *Cucurbita maxima*, but humid lowland regions of Bolivia in addition to warmer temperate zones in South America from where *C. andreana* was originally described should possibly be considered as an area of origin for *C. maxima*.

Archaeological evidence of domestication of *Cucurbita pepo* in southern Mexico dates back 10,000 years. Sanjur et al. (2002) suggested two separate domesticaions in the *Cucurbita pepo* complex. The potential zone of domestication for one of the domesticated subspecies, *C. pepo* subsp. *ovifera*, includes eastern North America and should be extended to northeastern Mexico. The wild ancestor of the other domesticated subspecies, *C. pepo* subsp. *pepo*, is undiscovered but is closely related to *C. pepo* subsp. *fratema* and possibly will be found in southern Mexico.

**Evolutionary relationships among cucurbit crops**

Knowing the geographical origin of economically important plants is important for genetic improvement and conservation. In a comprehensive, multi-gene phylogenetic study including over 100 species in 114 genera, Schaefer et al. (2009) revealed an Asian origin of Cucurbitaceae in the Late Cretaceous, followed by the repeated spread of lineages into the African, American and Australian continents via transoceanic long-distance dispersal. North American cucurbits stem from at least seven range expansions of Central and South American lineages; Madagascar was colonized 13 times, always from Africa; Australia was reached 12 times, apparently always from Southeast Asia. Overall, Cucurbitaceae underwent at least 43 successful long-distance dispersal events over the past 60 million years (Fig. 1).

The four major cucurbit crops have distinct chromosome numbers (Table 2). How the seven cucumber chromosomes of cucumber evolved from its ancestor has long been an interesting and hot topic. Cross species transferability of molecular markers among cucurbit crops has been well documented. The availability of large numbers of molecular markers (Ren et al. 2009) makes it possible to do comparative mapping to reveal syntenic relationships among cucurbit genomes. By comparing the melon and watermelon genetic maps to the cucumber genome, Huang et al. (2009) were able to assign 348 (66.7%) of the 522 melon markers and 136 (58.6%) of the 232 watermelon markers onto cucumber chromosomes. The comparison revealed that, except chromosomes 4 and 7, which are largely collinear to melon chromosomes 7 and 1, respectively, each of the remaining five cucumber chromosomes may result from a fusion of two ancestral chromosomes (Huang et al. 2009). Fluorescence in situ hybridization of 45S rDNA and CsCent1 repetitive DNA probes to cucumber pachytene chromosomes also suggested that cucumber chromosomes 1 and 2 may have evolved from fusions of an ancestral karyotype with 2n = 24 (Koo et al. 2010). Meanwhile, during this process, many inter-chromosomal rearrangements including centromere repositioning may likely have occurred (Han et al. 2009). The seven meiotic chromosomes of *C. sativus* are larger than the 12 of its wild sister species or progenitor *C. hystrix* (Chen et al. 2004) and consist of six metacentrics and one submetacentric chromosome (Koo et al. 2005). It should be enlightening to examine *Cucumis hystrix* to look for its roles in the evolution of modern cucumber. In addition, it is also necessary to investigate some *Dicaelospermum* and species of *Mukia* species (Fig. 1) which were moved into *Cucumis*.

**Cucurbit germplasm conservation and utilization**
Cucurbit germplasm conservation

Globalization, demands for greater dietary diversity, climate change will have a big effect on the crop diversity in farmers’ fields. The development of new varieties and cropping systems adapted to the socio-economic and new environmental conditions will be crucial in order to take advantage of new opportunities in some regions and limit yield losses in others. Attention has been paid in some countries to increase genetic diversity within production systems as a way to reduce risk, particularly in light of changes in climate, pests and diseases. Plant breeders and farmers will need to be able to access an even wider range of germplasm than today (FAO 2009).

Cucurbit genetic resources include cucurbit crops and their relatives. Cucurbit gene banks are located on all continents, but there are relatively fewer in Africa compared to the rest of the world. Around the globe, cucurbit genetic resources are maintained in specified facilities known as gene banks at the local and national level by governments, universities, companies, farmers and others in the private and public sectors either acting alone or networked with other institutions. In contrast to the gene banks of the Consultative Group on International Agricultural Research (CGIAR) Centers hold the major field crops, national gene banks are the major repositories for cucurbit germplasm.

Fewer countries account for a larger percentage of the total world ex situ cucurbit germplasm. Major holders of cucurbit crop genetic resources are listed in Table 3. Many biotic and abiotic stresses are the most limiting factors affecting cucurbit production around the world. There will undoubtedly be an increase in demand for varieties that are adapted to the new environmental conditions and pest and disease spectra. The ability to access a wide range of genetic diversity is central to meeting this demand, implying that in future there will be even greater interdependence between countries and regions than is the case today. The concentration of ex situ germplasm in fewer countries and research centers highlights the importance of mechanisms to ensure facilitated access. The ability of a potential recipient to access a particular accession is often limited by the size of a stored sample and its phytosanitary status, characterization, adequate information systems, and international treaty. The most easily accessible gene bank in the world is the USDA National Plant Germplasm System (NPGS). A significant amount of information is publicly available. Passport information is freely accessible through the web-based Germplasm Resources Information Network (GRIN) (Table 3). And germplasm is distributed free of charge and restriction. The establishment of the European Central Cucurbits Database (ECCUDB) (http://www.comav.upv.es/eccudb.html) also facilitates germplasm use. The database contains the passport information on 22,815 accessions of 21 cucurbit genera and more than 75 species from 33 institutions belonging to 19 European countries (Díez et. al. 2007). In contrast, the documentation and characterization of many collections at national gene banks of developing countries is still inadequate and much of the existing data is not accessible electronically. To encourage an increased use of the germplasm, documentation, characterization and evaluation all need to be strengthened and harmonized and the data need to be made more accessible. Access to and exchange of plant genetic resources have become increasingly formal and more restricted in the last 20 years. International treaty on Plant Genetic Resources for Food and Agriculture established a Multilateral System for facilitated access to germplasm of a number of crops. Unfortunately, cucurbit crops are not included in this treat.
## Table 3 Major gene banks for cucurbit crops

<table>
<thead>
<tr>
<th>Genera</th>
<th>Gene Bank*</th>
<th>Accessions</th>
<th>Reference</th>
</tr>
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<tr>
<td><strong>Cucumis</strong></td>
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<td>628</td>
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<td></td>
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<tr>
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<td>NIAS, Japan</td>
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<td>840</td>
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<tr>
<td></td>
<td>UzRIPI, Uzbekistan</td>
<td>805</td>
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* AVRDC = AVRDC – The World Vegetable Center, Taiwan
  CAAS = Chinese Academy of Agricultural Sciences, P. R. of China
  CATIE = Centro Agronomico Tropical de Investigacion y Ensenanza, Costa Rica
  CNPH = Embrapa Hortaticulturas, Brazil
  CENARGEN = Embrapa Recursos Geneticos e Biotecnologia, Brazil
  ECCUDB = European Central Cucurbit Database
  IGB = Israel Gene Bank for Agricultural Crops, ARO, Volcani Center, Israël
  INIFAP = Instituto Nacional de Investigaciones Forestales, Agricolas y Pecuarias, Mexico
  NIAS = National Institute of Agrobiological Sciences, Japan
  NPGS = National Plant Germplasm System, USDA
  UzRIPI = Uzbek Research Institute of Plant Industry, Uzbekistan

### Cucurbit gene pools and utilization

The primary gene pool of cucumber consists of several botanical varieties including *C. sativus* var. *sativus*, the cultivated cucumber and *C. sativus* var. *hardwickii*. *C. sativus* var. *hardwickii* is a wild relative of *C. sativus* var. *sativus* that grows in most parts of India. This botanical variety is cross-compatible with *C. sativus* var. *sativus* and possesses a multiple fruiting and branching habit that is not common in cucumber (Horst and Lower 1978). *C. sativus* var. *hardwickii*, therefore, represents the extreme in variation in *C. sativus* germplasm (Dijkhuizen et al. 1996), and, thus, has potential for increasing genetic diversity in commercial cucumber (Staub et al. 1992).
Wild *Cucumis* species are cross-incompatible with cucumber and melon, which in many cases are themselves cross-incompatible (Kroon et al. 1979). However, through embryo rescue, interspecific hybrids, amphidiploids (*Cucumis hystivus*), aneuploidy derivatives as well as introgression lines were successfully produced between cucumber and the wild, free-living *C. hystrix* (Chen et al. 1997, 2000, 2004). *C. hystrix* has resistance to a number of diseases such as resistance against gummy stem blight, *Didymella bryoniae*, downy mildew (Zhou et al. 2008), *Pseudoperonospora cubensis* and southern root-knot nematode, *Meloidogyne incognita* (Chen et al. 2001). Resistance to gummy stem blight was partially transmitted to cultivated cucumber through interspecific hybridization and backcrossing with cucumber (Chen et al. 2004). Thus, *C. hystrix* constitutes an important member of the secondary gene pool for cultivated cucumber. Despite many attempts, *C. melo* is not cross-compatible with any other *Cucumis* species. However, *C. melo* may be the most variable of the genus *Cucumis*. Melon genetic resources are not threatened (Pitrate 2008). Through recent work, *Cucumis* has been expanded to include 52 species (Ghebretinsae et al. 2007a; Renner et al. 2007). It is clear that significant work is needed to investigate those newly added *Cucumis* species to see the possibility of using these resources in cucumber improvement.

Obtaining resistance to diseases and pests is a major objective in most breeding programs of watermelon. However, because of limited resistance within US plant introductions (PIs) of *C. lanatus var. lanatus*, limited progress has been accomplished in this respect in watermelon. Although there is great phenotypic diversity among watermelon cultivars developed in the United States, they appear to have a narrow genetic background (Levi et al. 2001).

The genus *Cucurbita* has 12-14 species including five domesticated ones and their wild progenitors. These species are naturally distributed in North and South Americas with the greatest diversity in Mexico. Both domesticated and wild Cucurbita have a high potential value for breeding. The five domesticated species are partially crossable allowing transferring genes from one to another. Many wild species are also cross-compatible with the domesticated ones thus being used for germplasm improvement of cultivated species, e.g. powdery mildew and virus resistance, through interspecific crossings. The zucchini yellow mosaic virus (ZYMV) resistance gene(s) of *C. moschata* and the powdery mildew resistance gene of *C. okeechoboeensis* have been introgressed into *C. pepo* (Robinson and Decker-Walters 1997; Whitaker and Robinson 1986). Multiple virus (ZYMV, watermelon mosaic virus, and papaya ringspot virus) resistance genes, derived from *C. ecuadorensis*, have been bred into *C. maxima* (Robinson and Decker-Walters 1997; Herrington et al. 2001). The powdery mildew gene of *C. okeechoboeensis* spp. *martinezii* has been incorporated into *C. moschata* (Robinson and Decker-Walters 1997; Cho et al. 2003).

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