**Status of *Arachis* Germplasm Collection**

**Peanut Crop Germplasm Committee**

**06/10/2020**

## Summary of significant accomplishments (2019):

* + Total number of active accessions of cultivated and wild species include 9275 and 558, respectively.
  + Acquired 62 accessions of 26 wild *Arachis* species from Dr. Charles Simpson, Texas AgriLife Research, TAMU.
  + Acquired 25 accessions of 17 wild species from Dr. Tom Stalker, North Carolina State University for replenishment.
  + Provided seeds of 2600 PIs of African origin for the genotyping project by Dr. Peggy Ozias-Akins, UGA-Tifton.
  + Provided samples of wild species for genotyping to Dr. Soraya Leal-Bertioli, UGA-Athens.
  + Completed total oil, fatty acids and protein content of 200 accessions of 46 wild species.
  + Completed total oil and fatty acid profiles of about 8,700 cultivated peanut PIs.
  + 4,527 accessions were distributed for domestic and international research and education uses.
  + Completed germ testing of 521 PIs including both cultivated and wild species accessions.

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## 1 Introduction

Peanut (*Arachis hypogaea* L.) is a native New World legume crop that was widely grown in South America in pre-Colombian times. There is conclusive agreement that genus *Arachis* is indigenous to tropical South America with widespread distribution of species in Argentina, Bolivia, Brazil, Paraguay, and Uruguay. There is no evidence of pre-Columbian occurrence of *Arachis hypogaea* in the Old World. After the Spanish incursion into the new world, the peanut traveled to Europe and subsequently spread to Africa and Asia via traders and other explorers. The first successful introductions to North America were small seeded peanuts with a runner growth habit (Higgins, 1951). These introductions were probably from northern Brazil or the West Indies, loaded as food supplies onto ships carrying slaves from Africa to North America. The domesticated species had already evolved into subspecies and varietal groups before seeds were distributed to the Old World by early Spanish and Portuguese explorers due mainly to indigenous tribes selecting for different types in the native environments in South America.

Around the world, peanut is also known as groundnut or earthnut, because of its unique habit of producing flowers above ground with pods containing seeds (kernels) formed underground. It is also called by many other names such as Amendoim, Cacahuate (earth cocoa), Goober, Guba, Mani, and Mandubi. Peanut is a legume with a seed pod, although for nutritional and culinary uses, peanuts are commonly considered as nuts.

In the United States, peanuts were initially considered a regional food for the lower classes in the south (Hammons et al. 2016). However, after the civil war, industrial advancements resulted in an increased demand for peanut oil, and other edible products such as peanut butter, roasted and salted nuts, thus making peanut a popular food crop in the US. The peanut seed has from 36 to 54% oil (Knauft and Ozias-Akins, 1995) with more than half of the global crop grown as an oilseed. Because prices on the international commodity market favor the sale of peanuts as edible seeds, most of the crop in the U.S. and South America is sold for direct consumption as food. In most other countries, the primary use of peanut is for the oil market. However, as major producers are becoming self-sufficient for oil production, a larger percentage of the peanut seed crop is consumed directly by people. In addition to seeds, the foliage is an important fodder in regions where animals are used extensively on the farm, and the meal remaining after oil extraction is also an important source of animal feed.

## 1.1 Biological features

## Peanut, *A. hypogaea* L. belongs to the tribe Dalbergieae, subfamily Papilionoideae in the family Fabaceae. It is a dicotyledonous, herbaceous legume. The seed (kernel) consists of two cotyledons which enclose the leaf primordia (shoot) and the root initials (radicle). The cotyledons are covered by a thin outer seed coat which protects the seed from soil microbes. It varies in color from white to tan to black with different shades/streaks of red or pink. The cotyledons contain stored food reserves for the growth of the emerging seedling post germination. The process of germination could take about 5-7 days before the young seedling fully emerges from the soil. The cotyledons split open to expose the leaf primordia which extends to form the primary shoot and the lower hypocotyl elongates to form the tap root. Mature plants are usually about 30-45 cm tall with lateral branches of about 30 cm wide. However, lateral branches of many *Arachis* wild species can be very long of up to several feet. The leaves are pinnately compound, each with four leaflets (tetrafoliate) and occur alternately on the main stem and lateral branches. The exceptions are the trifoliate species *A. guaranitica*, *A. tuberosa*, and *A. sesquijuga* from section *Trierectoides.* Several naturally occurring or induced mutants with different leaf shapes are also present in germplasm collections. The stems are angular, can be pubescent or glabrous, and are usually green but can be pigmented as in subspecies *fastigiata* var. *aequatoriana* or Valencia-types which are reddish purple.

Peanut is self-pollinating and displays indeterminate flowering pattern with new blooms observed even at harvesting of the crop. Flowers are formed in leaf axils on branches and on mainstems in subspecies *fastigiata* types. Peanut pod development is unique in that fertilization occurs in the flowers above ground, but the pods develop below ground. Following fertilization, an intercalary meristem at the base of the ovary undergoes active division leading to a pointed stalk-like structure called the “peg” (Smith, 1950) with fertilized ovules located at the tip of the peg. The peg elongates and penetrates the soil surface where the tip expands to form the pod. Descriptions of peanut embryo growth and development have been published by Smith (1950), Periasamy and Smapoornam (1984), Pattee and Mohapatra (1987) and Xi (1991). Normally, a mature peanut pod is developed within 60 to 80 days after fertilization. However, because plants are indeterminate and flowering occurs over an extended period, a plant will contain pods at multiple maturity stages even at the time of harvesting.

## **1.2**World production

Peanut is cultivated around the world in tropical, subtropical, and warm temperate climates. Peanut production is found in six continents, although four of them (Africa, Asia, North America, and South America) account for majority of production (99 percent). Fletcher and Shi (2016) reported that peanut production worldwide increased about 136% since the 1970s with significant increases in Asia and Africa whereas the production in the Americas decreased from 16% in 1970s to about 9% for the 2010-2013 time period. These gains are mainly due to a combination of increased area harvested with improved genetics and technological advances in production practices. Peanut is one of the principal oilseed crops in the world. According to USDA estimates for the crop year 2018 (FAS, 2018), from a world total oilseeds production of 593 million metric tons, peanuts' share was 42 million metric tons which is approximately 7%, behind soybeans (61%), rapeseed (12%), sunflower (8%) and cottonseed (7.4%). Worldwide, China, India, Nigeria, and the US produce about 70% of peanuts. China is the world's leading producer accounting for nearly 38 % of the total production. Recent production trends indicate that about 90% of world production occurred in developing countries, mainly in Asia and Africa.

## 1.3 U. S. Production regions and market types:

The U. S. contains about 3% of the world’s acreage of peanuts but produces about 10% of the world’s crop because of higher per acre yields. The estimated farmgate value of peanuts produced in 2018 was about $1 billion. The allied farm machinery and manufacturing industries add at least another $2 billion to the US economy. In the U.S., peanut production is mostly contained in the southern states stretching from Virginia through New Mexico. These states have been grouped into three main production regions. The V-C region includes Virginia, North Carolina, and part of South Carolina. The southeast region consists of South Carolina, Georgia, Florida, Alabama, Mississippi Arkansas, and Missouri, whereas, southwest region comprises of Texas, Oklahoma, and New Mexico. Four different market types are grown in of each of these three regions with each type exhibiting a unique seed size and flavor. These market types generally correspond to subspecies and varietal groups as follows: Runner (subsp. *hypogaea* var. *hypogaea*), Virginia (subsp. *hypogaea* var. *hypogaea*), Spanish (subsp. *fastigiata* var. *vulgaris*), and Valencia (subsp. *fastigiata* var. *fastigiata*).

The Virginia market type consists of large pods and seeds, is mainly grown in the V-C area with some production also in west Texas. They are primarily used as roasted in-shell or as salted peanuts. Because of their large seeds, the Virginia types also are popular as green/boiling peanuts when dug early in the fall. A premium is paid for large seeded peanuts in the U.S., which makes this market type very desirable for the growers. The Virginia types contribute about 10-12% to the U. S. peanut production. Runner market types have medium sized pods and seeds and are the dominant peanut type grown in the US. Runners have rapidly gained wide acceptance because of their attractive kernel size range; a high proportion of runners are used for peanut butter. Runners, grown mainly in Georgia, Alabama, Florida, and Mississippi account for 80% of total U. S. production. Spanish types are widely grown around the world, especially where mechanization is not available. The primary advantages of Spanish types are their short growing season and bunch-type growth habit. Spanish type peanuts have smaller kernels covered with a reddish-brown skin. They are used predominantly in candy, with significant quantities used for salted nuts and peanut butter. They have higher oil content than the other types of peanuts which is advantageous when crushed for oil. They are primarily grown in Oklahoma and Texas. Spanish-type peanuts account for 8-10% of production. The Valencia market type grown in west Texas and eastern New Mexico accounts for less than 1% of the total domestic production. Valencia types usually have long thin pods with three to five small, red seeds. They are very sweet peanuts and are usually roasted and sold in-shell; are also excellent for fresh use as boiled peanuts.

## **1.4**Domestic production, demand, and consumption

During the 2018 crop season, U. S. peanut growers planted 1.43 million acres, which was down by 24% from 2017. Of the 1.43 million acres planted, the southeast region accounted for almost 1.1 million acres, the southwest region contributing about 203,000 acres followed by the V-C region of 126,000 acres (Table 1). Georgia planted about 665,000 acres followed by Alabama (165,000 acres), Florida and Texas, each with 155,000 acres and North Carolina with 102,000 acres. Harvested area totaled at 1.37 million acres, down by 23 percent from 2017.

The U. S. peanut production increased by 39 percent over the past 7 years (2012-2018). U. S. peanut production in 2018 totaled 5.46 billion pounds, (2,730,800 tons) down 23 percent from 2017. Of this total production, the southeast region contributed about 79%, the southwest 12% and the V-C region had about 9%. Georgia alone produced about 53% of the total production in 2018, followed by Alabama (10%), Florida (9%), Texas (9%) and North Carolina (7%) with the remaining 12% coming from SC, OK, NM and VA. The average yield was 3,991 lb/acre, down 16 pounds from 2017.  In 2018, the two states with the highest average yield/acre were Georgia (4,450 lb/acre) followed by VA with 4,200 lb/acre. The lowest per acre yield was from New Mexico with 3,000 lb/acre.

Peanut stocks reported in commercial storage on January 31, 2019 totaled 4.79 billion pounds of farmer stock, compared with 5.03 billion pounds a year ago. This total includes 3.98 billion pounds of actual farmer stock (NASS, 2019) with the rest from 2017 surplus crop.

Peanuts are low carbohydrate, high protein and nutrient rich with vitamins, minerals, and antioxidants. As consumer’s preference for nutritional, health foods are growing, peanuts are becoming a part of the diet of many in the US and worldwide. The peanut manufacturing industry along with research institutions and innovative marketing strategies has been in the forefront of promoting peanuts as a health food. Due to the consumer awareness of the health benefits of eating peanut products, there is great domestic demand for peanuts. It is estimated that about 80% of the peanut supply was used for domestic food consumption. Americans consume more than two billion pounds of peanut products yearly. Archer (2016) suggested that peanut butter ranks at the top with 57% of domestic consumption followed by snack peanuts, in-shell (23%), candy (19%) and other uses of 1%.

## 1.5 Impact of U.S. Legislation on peanut production

To ensure adequate commodity supply, abate price fluctuations and safeguard availability of high-quality food products to consumers, the U. S. Congressauthorizes legislation through Farm Bills (Archer, 2016). The older Farm Bill programs set quotas for acreage or poundage based on domestic demand and supported by the government loan program or selling directly to shellers at the government loan rate. Excess quota peanuts were sold at or below the world market price (lower than the government loan rate) for export or oil crushing. Further, the Farm Security and Rural Investment Act of 2002, warranted that all domestic peanuts were sold at the world market price and quota holders were compensated with a direct cash payment. Additionally, the Food Conservation and Energy Act of 2008 provided peanut growers with a marketing loan option of with direct and counter cyclical payments. The Agricultural Act of 2014 (Farm Bill), however, ended direct payments with an option to purchase crop insurance as an economic safety net (Archer, 2016). This bill provided loans to peanut growers for the 2014-18 crop seasons at a national loan rate of $355/ton (ERS, 2014).

## 1.6 Origin and biogeographical distribution of *Arachis*

*Arachis* is a native South American genus with natural populations growing in the highlands in Argentina, Bolivia, Brazil, Paraguay, and Uruguay (Valls et al. 1985). *Arachis* likely originated in the highlands of southwestern Mato Grosso do Sul state in Brazil (Hammons 1973; Gregory et al.1980; Simpson et al. 2001) where the most ancient, trifoliate species, *A. guaranitica* Chodat. and Hassl., and *A. tuberosa* Bong. Ex Benth. and *A. sesquijuga* were collected. *Arachis guaranitica* is the most primitive and genetically isolated species and looks more like a grass plant. Subsequently, with water movement, *Arachis* species spread to drier lowlands in all directions, evolved and adapted into various river valleys and drainage systems (Gregory and Gregory 1979; Stalker and Simpson 1995; Simpson et al. 2001) with *Arachis* species growing in sandy to heavy clay/loamy soils and on schist rocks with no soil (Simpson et al. 2001). One of the species, *A. burkartii* Handro, was collected in southern Brazil in black gummy clay mixed with small stones with a soil pH of 3.2 (Stalker and Simpson, 1995), indicating the wide adaptation of *Arachis* species to extremely diverse geographical environments (Stalker and Simpson, 1995; Simpson et al. 2001; Tallury, 2017). Currently, the genus contains about 82 described species and several new species are likely described in the very near future (Simpson, personal communication; Seijo, personal communication).

The genus evolved into species that fit into nine taxonomic sections (Krapovickas and Gregory, 1994; 2007). Of the nine taxonomic sections, the most primitive section is *Trierectoides* with the trifoliate species, *A. tuberosa, A. guaranitica* and *A. sesquijuga.* From these ancient progenitors, developed the sections, *Erectoides*, *Extranervosae*, *Triseminatae*, and *Heteranthae*. The species of these four sections have varying affinities to the primitive section, *Trierectoides*, as reported by Gregory and Gregory (1979) and Krapovickas and Gregory (1994). The more advanced sections include *Caulorrhizae*, *Procumbentes*, and *Rhizomatosae*. The affinities of these latter species groups are varied as well, but with very limited successes reported in crossing with species of the most advanced section, *Arachis* (Gregory and Gregory, 1979; Krapovickas and Gregory, 1994). The geographic distribution of section *Arachis* has overlapped with that of the other sections in many areas of South America. It is not unexpected that the species in the most advanced section would be more adaptable to many environments and able to rapidly move to areas where ancient species have existed for many millennia. The cultivated species, *A. hypogaea*, was assigned to section *Arachis*, which also contains several wild species. *Arachis hypogaea* hybridizes readily with the species in section *Arachis* whereas the species in the remaining eight sections are incompatible with it. As in many other crops, the wild species are at risk of loss due to human encroachments and rapidly changing climatic patterns in their native habitats.

Although the genus *Arachis* originated in the highlands of Brazil, the center of origin of the cultivated species, *A. hypogaea*, is believed to be southern Bolivia to northwestern Argentina. This observation was based on the presence of the parental diploid wild species donors of *A. hypogaea* in this region, the wide range of variation observed in pod and seed morphologies and that the germplasm collected in this area exhibited primitive characters associated with wild species, thus supporting the likely origin of *A. hypogaea* in this region (Hammons 1982; Stalker and Simpson 1995; Ferguson et al. 2004). Additional regions for the origin of *A. hypogaea* on the west coast of Peru and/or the eastern slopes of Cordillera in the Andes, were suggested based on archeological evidence and prevalence of ecologically distinct types, and favorable environmental conditions for survival of plants for long periods of time with abundant evidence of natural hybridization and establishment of recombinant types (Simpson et al. 2001; Hammons et al, 2016). The most convincing data to date, indicating that *A. hypogaea* originated in the gardens of primitive 'hunter gatherer/cultivator, come from archeological digs on the coast of Peru in two sites near Casma and another near Bermejo. In these locations, peanut shells resembling the shells of *A. magna* Krapov., W.C. Gregory and C.E. Simpson, *A. ipaensis* Krapov. and W.C. Gregory, and/or *A. monticola* Krapov. and Rigoni were excavated from a layer where there was no indication of the presence of corn. These shells were dated at 1800 to 1500 B.C. In another site nearby, shells were found that closely resembled *A. duranensis* Krapov. and W.C. Gregory dated at about the same time period. Archeological evidence similar to that found in Peru was also discovered in northwest Argentina, indicating that the hunter gatherers possessed, and possibly grew, wild peanuts in the high Andes of Argentina as well, although the sample sizes of excavated shells was much smaller.

The natural distribution of the wild *Arachis* appears to have occurred well before human arrival in South America, but humans have obviously played an important role in distributing some of these species, including *A. villosulicarpa*, *A. stenosperma*, and the only domesticated species, *A. hypogaea*. Following the Spanish and Portuguese explorations to South America, the cultivated peanut spread from the centers of origin and diversity in South America to Europe and then to Africa and Asia via trade voyages. There is no substantiated evidence for the occurrence of cultivated peanut in North America during this time. It was suggested that peanut was introduced into U.S. on slave trade ships from Africa via the coast of northeastern Brazil/Caribbean islands, where peanut was gathered as food source to complete the journey, strongly suggesting that the first peanut introductions into the U.S. were from Brazil rather than from Africa (Stalker and Simpson 1995).

## 1.7 Botanical classification of *A. hypogaea*

Krapovickas and Gregory (1994, 2007) indicated that genus *Arachis* is defined by its morphological features of the underground structures, including the pods, rhizomatous stems, root systems, and hypocotyls. They demonstrated that these defining characters grouped the *Arachis* collections into different geographic areas and ecological features. This, along with crossabilities of species, allowed them to group the collections into nine different sections (Gregory and Gregory 1979; Krapovickas and Gregory 1994, 2007) as described above. *Arachis hypogaea* belongs to section *Arachis*, which also contains 30 other wild species. Further, *A. hypogaea* was divided into two subspecies, subsp. *hypogaea* and subsp. *fastigiata* by Krapovickas and Rigoni (1960) based on the absence versus presence of flowers on the main stem. They also proposed two botanical varieties of subsp. *fastigiata*, vars. *fastigiata* and *vulgaris* based on pod traits. Later, Krapovickas (1968) proposed that subsp. *hypogaea* should also be divided into vars. *hypogaea* and *hirsuta*. With additional collections of *A. hypogaea*, Krapovickas and Gregory (1994, 2007) not only confirmed the two subspecies of *A. hypogaea* (subsp*. hypogaea* and subsp. *fastigiata*) but also expanded botanical varietal groups to six (vars. *hypogaea, hirsuta, fastigiata, peruviana, aequatoriana* and *vulgaris*) based on plant growth habit, leaf color and branching patterns.

## 1.8 Peanut breeding activities in the U. S.

In the U. S., peanut breeding and cultivar development are predominantly in the public sector with state land-grant universities in the lead in each of the three production regions of V-C, southeast and southwest, respectively. Additionally, the USDA-ARS peanut breeding units in Tifton, GA, and Stillwater, OK are also actively engaged in cultivar releases. A couple of private seed companies located in GA (ACI seeds) and TX (Alagrano/IPC) are also developing cultivars for the growers. Many of these breeding programs obtain plant introductions from the USDA-ARS national peanut collection in Griffin, GA. Since peanut is self-pollinated, traditional pedigree selection method combined with off-season winter nursery generation advancement is used to develop improved cultivars (Knauft & Ozias-Akins, 1995; Holbrook & Stalker, 2003; Holbrook et al., 2016). In the US., it was estimated that the average yield gain is 29.9 kg ha-1 yr-1 (Holbrook et al., 2014), which is attributed mainly to high yielding cultivars coupled with advances in crop management including cultural practices and more effective chemicals for control of weeds and diseases. Additionally, the recent advances in peanut genomic research for identification of molecular markers for important traits offers an exciting future for quicker development of high-yielding, multiple disease resistant cultivars. In the U. S., marker assisted selection (MAS) schemes are routinely used for development of high-oleic, nematode resistant cultivars (Holbrook et al., 2016). It is anticipated that the genomic advances would also provide effective selection tools for difficult to breed traits such as drought tolerance and aflatoxin contamination.

## 1.9 Development and use of genetic markers for marker assisted selection

It is paradoxical that despite the extensive morphological variation among the subspecies and botanical varieties of *A. hypogaea*, little genetic/molecular (DNA) variation was observed in the cultivated species (Kochert et al. 1991; Halward et al. 1991, 1992; Moretzsohn et al. 2004, 2013; Pandey et al. 2012), whereas the *Arachis* wild species have exhibited extensive molecular variation among and within the different sectional groups (Halward et al. 1991, 1992; Tallury et al. 2005; Friend et al. 2010; Moretzsohn et al. 2013). A commonly suggested reason for the deficiency of molecular variability in *A. hypogaea* was, that a onetime natural hybridization event followed by tetraploidization coupled with the self-reproduction (augamous) probably led to the genetic isolation of the raw tetraploid from the surrounding species diversity with no apparent gene flow between them (Kochert et al. 1996a; Seijo et al. 2007). It is likely that following domestication, the early humans selected desirable types from the original population possibly for compact habit, increased pod and seed sizes producing the different subspecies and botanical varieties, as we have today. Consequently, the vast amount of morphological variability observed in the cultivated taxon is likely to have resulted from natural and/or artificial selection rather than from the introgression of genes from different species (Seijo et al. 2007).

The earliest genetic markers identified were natural morphological mutants including chlorophyll mutants, branching habit, leaflet morphology, pod, and seed morphologies. The idea is to correlate these phenotypic variants with desirable traits as selection tools. However, the paucity of these markers led to the discovery of other marker systems based on genomic technologies such as Isozymes, Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP). Yet these marker systems detected very low levels of molecular polymorphisms among the *A. hypogaea* germplasm. Contrarily, they detected high levels of molecular variation in diploid wild species (Halward et al., 1991; 1992). Also, the tetraploid nature of peanut genome complicated the development of genomic technologies such as molecular markers and genetic maps (Guo et al., 2013; Holbrook et al., 2016).

Since the publication of the peanut genome sequence (Bertioli et al., 2016; 2019) and other advances in genomic tools such as whole genome sequencing and sequencing by genotype led to the development of Single Nucleotide Polymorphisms (SNPs) array, which enabled the identification of many hundreds of molecular markers associated with QTLs for economically important traits. An initial application of these technologies, particularly, of molecular markers for quantitative trait loci (QTL) analysis was demonstrated by Pandey et al. (2012) for use in marker assisted breeding in cultivated peanut. Holbrook et al. (2016) demonstrated the use of molecular markers for developing high-oleic, root-knot nematode and TSWV resistant TifN/V high-Ol runner cultivar.

Although several thousands of molecular markers (SNPs) are now available for cultivated peanut, reliable phenotyping of populations in multi-year, multi-location replicated testing is necessary for association of these markers with traits of value, particularly those traits with low heritability, complex inheritance and difficult to evaluate (Tanksley, 1983). It is encouraging that the recent advances in peanut genome sequencing and new genomic tools should help clarify the origin, evolution, variability, and distribution of the genus and that of the cultivated species, *A. hypogaea*. A comprehensive review of use of current genomic technologies for peanut improvement was summarized by Holbrook et al. (2016).

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

Although yield/acre is the most important economic factor for a grower, the demand to meet the industry grade standards led to the cultivation of a limited number of popular cultivars in each peanut production region/state (Table 1). The continuous monoculture or cultivation of genetically similar cultivars make the crop vulnerable to unknown threats which will affect food security. Consequently, genetically diverse cultivars are necessary for sustainable production, to thwart new pathogens and pests and adjust to rapidly changing climatic conditions. Peanut genetic resources provide a shield against these unforeseen biotic and/or abiotic stresses. They serve as experimental genetic materials for peanut breeding programs to develop improved cultivars and germplasm lines to counter these stresses.

Because peanut is not a native North American species, all cultivars necessarily trace their ancestry to plant introductions (PIs). Over the past 15 years, there have been concerted efforts to incorporate diverse germplasm sources including wild *Arachis* species into domestic breeding populations, usually with the purpose of improving resistance to diseases or pests, but also with the objective of broadening the genetic base.

## 2.1. Genetic vulnerability of the standing US peanut crop in 2019

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Although many cultivars are grown in the different production regions in the USA (Table 1 from AOSCA, 2019), within a region or state, a single cultivar predominated in near monoculture. For example, the share of Georgia 06G to the total certified seed acres in 2019 was about 70% and is about 94% of production in GA (Table 1). Table 1 shows the array of cultivars being grown in 2019/2020. It varies across the three main peanut production regions within the USA. The southeast region (Georgia, Florida, Alabama, and South Carolina) where the runner market-type predominates; the southwest region, (Texas, Oklahoma, and New Mexico) where runner, Virginia, Spanish, and Valencia market types are all grown; and the V- C region where only the Virginia market type is grown. The southeast has a history of monoculture with one dominant cultivar changing periodically. The current dominant cultivar is Georgia 06G (Table 1) which rose to prominence because of its high yield and excellent grade characteristics of attractive and uniform seed size in addition to field tolerance to *tomato spotted wilt virus* (TSWV). Because the runner market type occupies approximately about 80% of the total peanut acreage in the USA and the southeast is the largest production region, Georgia 06G is currently the most widely grown peanut cultivar in the country, occupying approximately half the peanut acreage in the USA and 80% of the acreage in the southeast (Table 1). The VC region is more diverse with 3-5 cultivars occupying 10 to 15% of the acreage.

## As of September 2019, 140 peanut cultivars have been released in the U.S.( Table 2) through the Journal of Crop Science, 53 released prior to 1961 when the Crop Science Society of America (CSSA) began to register crop cultivars and 236 germplasm line releases (Table 3) and nine genetic stocks (Table 4). Seeds of the above materials, when not under PVP, can be obtained from the National Plant Germplasm System (www.ars-grin.gov/npgs). Additionally, 137 cultivars have been registered for protection under Plant Variety Protection (Table 5). Several of them have expired, abandoned, or withdrawn from the process.

Despite the large number of cultivars available to growers, the peanut crop has been characterized as being genetically vulnerable to biotic threats. Genetic vulnerability of the crop is a function of its degree of genetic uniformity. Uniformity or diversity can be viewed simplistically as the array of cultivars being grown. The array of cultivars in a region does not wholly describe the level of genetic diversity as the cultivars may be related to a greater or lesser degree. Cultivars from different market types are much less related to each other than they are to other cultivars within the market type, particularly when the comparison is between a market type derived primarily from ancestry of subsp. *hypogaea* var. *hypogaea* and a market type derived from ancestry of subsp. *fastigiata* Waldron var. *fastigiata* (the Valencia market type) or subsp. *fastigiata* var. *vulgaris* Harz (the Spanish market type. Although there has been substantial introgression of subsp. *fastigiata* genes, particularly from Spanish ancestors, into the runner and Virginia market types (Isleib et al., 2001), the specific ancestors are different from those that figure in the ancestry of current Spanish and Valencia type cultivars.

## 2.2. Use of genetic resources in cultivar development

Because peanuts as a crop were introduced to what is now the USA, all peanut cultivars necessarily trace back to plant introductions from other parts of the world. However, much of the genetic base of current cultivars traces back to ancestors that were developed by mass selection from farmer stock peanuts in the various production areas (Isleib and Wynne, 1992). The first peanut introduction of the modern era was PI 4253, collected by B. Lathrop and D.G. Fairchild in 1899 and identified as the prize winning peanut from the 1898 exposition of the Khedival Agricultural Society of Cairo, Egypt (USDA, 1900, 1901). There have been thousands of accessions introduced and numbered by the USDA since that time. Many were donated by diplomats, missionaries, and travelers in foreign countries. Others were provided by foreign governments and agricultural research institutions as part of germplasm exchanges with U.S. institutions. Still others were collected as part of a coordinated effort by the USDA and international agencies to collect and preserve natural genetic diversity (Knauft and Gorbet, 1989) before it erodes through the displacement of farmer held seed stocks by improved cultivars.

Much of the base of improved runner and Virginia cultivars rests on four ancestors used as parents in the early years of peanut improvement, including var. *hypogaea* lines Dixie Giant and Basse and var. *vulgaris* Harz lines Small White Spanish and Spanish 18-38. Of these, only Basse is known to have been introduced in the modern era of plant collection. Most current runner and Virginia type cultivars trace their ancestry back to these two crosses through Florispan and its close siblings, derived from a cross between GA 207-1 and F230-118-2-2, and their immediate descendants, Florunner and Florigiant.

In addition to the four primary ancestors of runner-type cultivars, the early Virginia market type cultivars had additional infusion of ancestry from farmer stock selection, Jenkins Jumbo, a large seeded selection from farmer stock used as a parent in the Florida program, a group of five lines (NC 4, NC Bunch, White's Runner, Improved Spanish 2B, and PI 121067) among seven used by W.C. Gregory to initiate the breeding program at N.C. State Univ., and Atkins Runner, an ancestor used by the USDA breeding program in Virginia. Of these additional early ancestors of the Virginia market type, only PI 121067 is a modern plant introduction. A different set of introductions including PI 121070, PI 161317, PI 268661, and *A. monticola* Krapov. & Rigoni were used as parents in the Texas and Oklahoma breeding programs. The remaining five introductions that appear in the pedigrees of runner-type cultivars (PI 121067, PI 121070, PI 616317, PI 259785, and PI 221057) do so through crosses of runner type parents with Virginia type and Spanish type parents. Only three plant introductions appear in the pedigrees of improved Virginia type cultivars: Basse, PI 121067, and PI 337396.

Most runner and Virginia type cultivars are characterized as having had some introgression of genes from subsp. *fastigiata* Waldron, mostly from var. *vulgaris* but to some extent from var. *fastigiata*. Spanish type cultivars are varietally purer than other market types for the most part.

## 2.2.1 Geographical distribution of disease resistances in *Arachis*

## *hypogaea*

Countries of origin that are valuable sources of resistance to important diseases of peanut are presented in the Table 6. Peanut breeders or pathologists who are interested in sources of resistance to the peanut root-knot nematode should focus their efforts on accessions from China or Japan. Bolivia is an important region for sources of resistance to both leaf spot pathogens. India, Nigeria, and Sudan were also important countries for resistance to early leaf spot, whereas Ecuador was the only other country where resistance to late leaf spot was more prevalent than expected. Peru appears to be the most valuable country for resistance to CBR. Resistance to TSWV was more prevalent than expected in accessions from India, Israel, and Sudan. Researchers who are interested in parents with multiple disease resistance should consider accessions from India, Mozambique, and Senegal. These observations should enable peanut breeders to utilize genetic resources more efficiently for disease resistance that are available in accessions present in the U.S. national peanut germplasm collection.

## 2.2.2 Economic impact of genetic resources

Reducing input costs associated with pest/pathogen management is becoming increasingly important for growers in the U. S. Peanut cultivars with disease resistance will allow producers to decrease costs of production and become more competitive with world market prices. Wynne et al. (1991) summarized progress in breeding peanut for disease resistance. They concluded that, although several breeding programs initiated efforts of developing resistance to diseases during the 1980s, few cultivars had been released by the early 1990s due to the short duration of the programs. However, these efforts had resulted in the identification of many sources of disease resistance in peanut germplasm collections, and it was predicted that resistant cultivars would be forthcoming. This prediction came true during late 1990s with the release of TSWV resistant peanut cultivar, Georgia Green. Isleib et al. (2001) summarized the use of germplasm resources in peanut cultivar development and concluded that there have been significant economic impacts for the peanut farmer. The largest impact has been through the development of cultivars with resistance to Sclerotinia blight, root-knot nematodes, and tomato spotted wilt virus. Use of cultivars with these resistances have had an economic impact of more than $200 million annually for peanut producers.

## 2.2.3 Use of wild *Arachis* species for disease resistances

The desire to transfer genes from wild *Arachis* species into cultivated peanut has burned brightly since the 1940s when both W.C. Gregory and A. Krapovickas first attempted to cross wild peanuts. The first peanut cultivars released from interspecific hybridization were by Hammons (1970) and Simpson and Smith (1975). Hammons released cv. Spancross in 1970 from the cross *A. hypogaea* x *A. monticola* Krapov. & Rigoni, which was also the same source of cv. Tamnut 74 released by Simpson and Smith. Neither of these cultivars had phenotypic characters that could be identified as derived from the wild species. In 1999, Simpson and Starr (2001) released the first root-knot nematode (RKN) resistant peanut cultivar, COAN. This new cultivar contained a gene for RKN resistance from the wild species, *A. cardenasii* Krapov. & W.C. Gregory. The large-seeded Virginia cultivar, Bailey was released by Isleib et al., 2010, with superior levels of resistance to early leaf spot with resistance incorporated via *A. cardenasii* derived germplasm line. Several other germplasm lines derived from interspecific hybridization were also released (Simpson et al. 1993; Stalker and Beute, 1993; Stalker and Lynch, 2002; Stalker et al. 2002a, b; Isleib et al. 2006; and Tallury et al. 2014b).

## 2.3 Current and emerging biotic and abiotic threats

The peanut plants are attacked by many pathogens and insect pests. The pathogens causing diseases and economic losses on peanut are endemic to the peanut growing areas of the United States. Significant crop losses occur in most production areas due to soil-borne and foliar fungal pathogens. However, insect populations vary greatly among production regions and even from year to year within the same area. Also, viruses, bacteria, nematodes, and phytoplasmas attack peanut in the USA, causing economic damage.

## 2.3.1 Biotic threats

Biotic threats include biological pathogens and pests that adversely affect yield and quality of the harvested crop, thereby causing economic loss to the growers. Further, chemical control of these pathogens and pests is expensive leading to additional economic burden. Although chemical control may reduce vector populations, virus diseases such as the TSWV, have no chemical control options to protect the crop. Developing genetic resistance is the most viable option to protect the crop from virus infestations (Anderson et al. 1996).

## 2.3.1.1 Peanut diseases

Pathogens attack all parts of peanut plant and restrict plant development throughout the growing season as well as reducing seed quality in post-harvest storage (Porter et al., 1982). Cultural practices, such as the elimination of alternate host plant species from field edges, crop rotation, chemical control and use of resistant cultivars have lessened or eliminated several disease problems, but neither cultural control nor genetic resistance has been found for several others. On a global scale, the leaf spots [early leaf spot (ELS), caused by *Passalora arachidicola* (syn. *Cercospora arachidicola* Hori), and late leaf spot (LLS), caused by *Nothopassalora personata* (syn. *Cercosporidium personatum* (Berk. & Curt.) Deighton] and rust (caused by *Puccinia arachidis* Speg.) are the most destructive pathogens of peanut. Together they can cause up to 70% yield losses (Subrahmanyam et al., 1984), and even when fungicides are applied significant yield reductions can occur. Rust currently is not a serious problem in the U.S.A. but almost all U.S. producers expend significant effort on control of leaf spots. Further, shifts have occurred from one leaf spot to the other as cultivars are released with different tolerance levels. Also, regionally, several other soilborne fungal diseases such as Sclerotinia blight, CBR, white mold and *Rhizoctonia* root rot cause significant economic loss to the growers not only by the damage caused to the crop but the cost of chemical control is expensive. As a result, multiple disease resistance cultivars are needed to solve the most important disease problems of peanut. Table 7 has a list of the possible high impact pathogens on peanut.

## 2.3.1.2 Peanut insects

The peanut plant is also subject to attack by many insects. Insects causing damage and economic losses on peanut are endemic to the peanut growing areas. See table 8 for possible high impact insects on peanuts. In addition to directly lowering yields, insects serve as vectors for viruses and damage pods and seeds, making them undesirable for commerce. Both pre- and post-harvest insect pests cause significant economic losses in peanut. On a global scale, the most important insects include aphids, thrips, jassids, and *Spodoptera* (Isleib et al., 1994). In the U.S., the lesser cornstalk borer and southern corn rootworm cause the greatest damage to pods. Thrips are the most damaging insect pests because they vector the *Tomato Spotted Wilt Virus* (TSWV).

## 2.3.1.3 Weeds

Because the peanut plant produces pegs that grow into the soil from branches, weed control through tillage is more difficult in peanut than for many other crop species. Post planting, two or more months are necessary for peanut plants to completely cover the soil surface, and weeds can easily become established during this time. Further, canopy depth for runner types is relatively shallow, which does not help to suppress competitive weed species. Weeds generally cause greater yield reductions when at high population levels early in the growing season (Wilcut et al., 1995). Thus, cultivars which initially grow quickly and cover the soil surface are highly desirable. Weed control costs are estimated at $132/ha in Texas to $391 /ha in Florida (Wilcut et al., 1995).

## 2.3.1.4 Aflatoxin contamination

Aflatoxin contamination is a serious food and feed safety issue and is considered as a major challenge by the peanut industry. Breeding for resistance to *Aspergillus flavus* (causal organism for aflatoxin production) infection has been limited due to the lack of/low levels of resistance in *A. hypogaea*, high G x E interaction, lack of reliable screening techniques, and limited understanding of genetics of resistance (Nigam et al. 2009). The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) developed several breeding lines with resistance to aflatoxin contamination (Nigam et al. 2009). Additionally, Thakur et al. (2000) found significant variation in aflatoxin contamination among wild species accessions and suggested them as potential sources as parents in breeding for elimination of aflatoxin contamination. An initial screening of the peanut core collection (Holbrook et al.1993) identified 19 *A. hypogaea* accessions with reduced preharvest aflatoxin contamination and high yield. Surrogate traits to select for reduced aflatoxin contamination used by several researchers (Timper et al., 2004, 2013) demonstrated that peanut root-knot nematode can increase aflatoxin contamination of peanut kernels when the plants are subjected to drought stress during pod maturation. Peanut cultivars resistant to *Meloidogyne arenaria* may reduce the risk of aflatoxin contamination in fields infested with the nematode.

## 2.3.1.5 Emerging biotic threats:

Peanut smut caused by the soil fungus, *Thecaphora frezii*, is one of the most serious, emerging diseases with huge economic impact for the US peanut growers and the industry. Currently, the disease is contained within Argentina where it is endemic to 100% of the production areas. The disease was first reported in Brazil by Carranza and Lindquist (1962) on *A. kuhlmannii* Krapov. & W. C. Gregory, accession GKP 9824. They described the fungus based on disease symptoms and morphology of teliospores but could not complete Koch’s postulates since artificial inoculations were not possible/successful. Since the first report in Argentina by [Marinelli et al. (1995)](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-09-16-1248-FE#b40) in commercial production farms, peanut smut incidence has gradually spread to all production areas by 2012 ([Bonessi et al. 2011](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-09-16-1248-FE" \l "b9); [Cazzola et al. 2012](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-09-16-1248-FE#b19)). Disease severity varies with location but yield reductions as high as 51% have been reported. Currently, Argentina is the only country that has reported peanut smut in commercial crops. Both Bolivia and Brazil, however, have only reported cases of smut in wild peanuts ([Carranza and Lindquist 1962](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-09-16-1248-FE#b13); [Fávero 2004](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-09-16-1248-FE#b26); [Soave et al. 2014](https://apsjournals.apsnet.org/doi/full/10.1094/PDIS-09-16-1248-FE#b58)). Research on the causal agent and the disease is in its infancy as little is known about *T. frezii* biology, systematics, host-plant relations, or epidemiology. Although peanut smut is not currently found in the U.S., immediate proactive measures must be taken so that the growers and the industry are not threatened, should this disease reach the U.S. The first step in breeding efforts for peanut smut is to identify sources of resistance. The USDA-ARS in partnership with peanut industry and INTA collaborators in Argentina, has initiated an evaluation of the mini core accessions, cultivars and promising breeding lines from the U. S. Materials were evaluated in field plots at INTA in 2017 and 2018. For screening purposes, entries were retained for further testing if they scored 10% or less disease incidence. Of the 106 test entries, 35 potential sources of peanut smut resistance were identified. Thirteen entries had 0% disease incidence, 9 entries had between 0 and 5% disease incidence, and 13 entries had between 5% and 10% disease incidence. Seventy-one of the entries tested had greater than 10% disease incidence and have been eliminated from future testing (Chamberlin et al. 2018). Entries demonstrating strong resistance over multiple years can be used to incorporate peanut smut resistance into cultivars suitable for U.S. production areas.

## 2.3.2 Abiotic threats

Abiotic threats consist of natural or environmental stresses that impact yield and quality of the harvested crop. Among them, drought stress is the most prevalent around the world. Water deficit affects blooming, peg/pod formation leading to reduced yield and occasional severe drought conditions may lead to total failure of the crop. Climate change and its effect on other natural resources also impact yield and quality of the crop.

## 2.3.2.1 Drought stress

Occurrences of extended periods of drought have become more frequent across the U. S. peanut production states resulting in severe yield or crop losses. However, the extent of yield loss varies widely among the production regions and on the availability of irrigation. It is estimated that only about 30-35% of the US peanut crop is irrigated with rest grown as rainfed. In most years, the V-C and the southeast production regions receive enough rainfall on average to raise the crop under rainfed conditions; however, sandy soils, periodic droughts, and the possibility of aflatoxin contamination make water deficit a significant problem. Contrastingly, most of peanut crop in the southwest production region is irrigated by necessity due to lower average rainfall than the amount needed for growing the crop. However, as subsurface water for irrigation is depleted, the acreage is decreasing, due to reduced dryland production (Terrell et al. 2002; Steward et al. 2013).

Identifying drought tolerant germplasm sources is the first step in breeding for this trait. Several recent studies (Upadhyaya, 2005; Hamidou et al. 2012; Kottapalli et al. 2009; Selvaraj et al. 2010 and Belamkar et al. 2010) summarized lists of potential germplasm sources that can be used as parents in breeding programs for drought tolerance. Further, Leal-Bertioli et al. (2012), identified accessions of diploid wild species, *A. magna* and *A. duranensis* with superior ability to regulate transpiration under water deficit stress. Holbrook et al. (2016) summarized several germplasm sources from earlier reported research where drought tolerant mechanisms or symptoms were used to understand the genetic basis of drought tolerance (Gautreau, 1978; Harris et al. 1988; Rucker et al. 1995; Wright et al. 1996; Holbrook et al. 2000a; Rachaputi et al. 2000; Clavel et al. 2006; Devi et al. 2009; Ratnakumar et al. 2009). The list included ‘Tifton-8’ (high root mass and T ); ‘Chico’ (very early maturity); ‘CSMG 84-1’ (continued flowering under drought stress and T); ‘55-437’ and ‘Fleur 11’ (early maturity); ‘ICGS-76’ [high SPAD chlorophyll content, HI (harvest index), and heat tolerance]; ‘ICGV 86031’ (high TE); ‘ICG 476’ (high HI); ‘TAG 24’ (high HI); TMV 2 (high TE); and ‘JL 24’ (high TE).

## 2.3.2.2 Climate and natural resource challenges

The U.S. Government Global Food Security Strategy (2016) highlighted the drastic effects of climate change on agriculture and other natural resources. It concluded that extreme weather events such as droughts, floods, and extended periods of extreme temperatures pose major challenges to global food security, necessitating new food production practices along with enhanced monitoring and response to the growing threat of agricultural pests and diseases. Consequently, new tools and approaches are necessary to combat these challenges for increased agricultural productivity by developing more productive and resilient cultivars. Peanut germplasm collections offer such resource for combating the challenges posed by climate change.

## 2.3.3 Accessibility and CBD

In addition to the scarcity of money, trained personnel, and institutional support that have long been limiting factors for peanut genetic resources exploration and conservation, researchers must now also comply with an entirely new set of legal regulations before further international collaborations involving access and exchange can be implemented. To promote the conservation, sustainable use, and equitable sharing of benefits derived from genetic resources, the Convention on Biological Diversity (CBD), adopted internationally in 1994, recognized national sovereignty over genetic resources and prescribed national regulation of access to those resources. As a result, all South American countries which have rich *Arachis* diversity placed a significant constraint on international exchange. One of the immediate tangible effects of this regulation was an abrupt end to internationally supported peanut explorations and germplasm exchange. Ironically, many of these countries possess peanut's greatest diversity, yet where, in many cases, the national capacity to conserve and use these genetic resources is significantly lacking or non-existent.

While a considerable amount of *Arachis* germplasm has been conserved in international collections, additional wild and cultivated materials are needed to cover the full spectrum of genetic diversity in the genus (Simpson, 1991; Stalker and Simpson, 1995; Williams, 2001). The additional materials can be obtained only through exchange with foreign gene banks and research institutions or by conducting new plant explorations. Most of the existing accessions in the National Plant Germplasm System (NPGS) and other *Arachis* germplasm collections were obtained when genetic resources were considered the common heritage of humankind and available without restrictions. Since the Convention on Biological Diversity (CBD) entered into force, the free and open access to genetic resources from other countries largely became a thing of the past. Consequently, cumbersome regulations governing access and exchange of genetic resources recently have been put into effect in many countries.

Many germplasm donor countries believe that there has been an inequitable distribution of benefits derived from plant genetic resources obtained from their countries. Monetary benefits, such as payment of royalties, are often at the center of discussions on benefit sharing, while important non-monetary in-kind benefits go unrecognized or underappreciated (Secretariat of the Convention on Biological Diversity, 1998). Past USDA plant explorations have included non-monetary benefits to the host country such as paying the travel and equipment costs of the exploration, sharing half of the collected germplasm, preparation of herbarium specimens, and joint publication of research results. Today, additional non-monetary benefits may be necessary to obtain access to germplasm. The approach taken by USDA and IPGRI to benefit sharing is that the additional support contributes to conservation of plant genetic resources in the host country, preferably by strengthening the capacity of the national plant genetic resources program.

## 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

The USDA-ARS maintains an extensive collection of *Arachis* germplasm. The working collection is maintained by the Plant Genetic Resource Conservation Unit (PGRCU) in Griffin, GA. Much of this collection is maintained also under long-term seed storage condition at the National Laboratory for Genetic Resources Preservation (formerly the National Seed Storage Laboratory) in Ft. Collins, CO. The working collection consists of 9,275 accessions of *A. hypogaea* L. (Table 9) and 558 accessions of *Arachis* species (Table 10). In the U. S., large *Arachis* species collections are also maintained at Texas A&M Univ. and North Carolina State Univ. (Stalker and Simpson, 1995). For cultivated peanut, 8685 accessions (94%) are available for distribution. A total of 9092 accessions (98%) are backed up at Ft. Collins with an additional 881 accessions backed up at the Svalbard Global Seed Vault. For wild peanut germplasm, 488 accessions (87%) are available for distribution. A total of 409 accessions (73%) are backed up a Ft. Collins and an additional 116 accessions backed up at Svalbard seed vault in the arctic. Distribution inventories are maintained at 4C with 25% humidity, and an additional inventory intended for long term preservation is maintained at -18C. A majority of cultivated peanut germplasm has both inventories. However, the wild species germplasm has ~1% in the long-term storage. There are two reasons for the lack of split inventories of the wild species. A part of the wild species germplasm is maintained vegetatively in the greenhouses as they reproduce via rhizomes and produce little seed, if any. Many of the wild species have reduced seed numbers making splitting the accessions difficult. However, with the recent regenerations of wild species accessions from the original seed lots or the very first seed inventory, in the greenhouse in Griffin during 2016-18, efforts are underway to split them into two inventories, one for long-term storage at -18C and the other for routine distributions at 4C. Viability testing has been performed on 8719 cultivated accessions (94%) and 347 wild accessions (62%). Viability tests are conducted on all newly regenerated samples to determine a baseline for seed viability before they are put in the -18C. In 2018, a total of 521 accessions were tested for seed viability. Further, 58 accessions were re-tested for germination. They were tested earlier and were at least 10 years older and stored at -18C to see if there is any deviation so they can be replenished sooner.

In the PGRCU collection, about half of the accessions are unimproved landraces collected from expeditions made to South America, which contains the centers of origin and diversity for peanut. These expeditions were sponsored by the USDA and the International Board of Plant Genetic Resources (IBRGR) in cooperation with state experiment stations in the U.S., and by several other countries as described by Isleib et al. (1994) and Stalker and Simpson (1995) (Table 11). About one-third of the accessions in the collection originated from Africa. Much of this germplasm was introduced into the U.S. by J. Smartt during the 1960s (Wynne and Gregory, 1981).

In many cases, collected *Arachis* germplasm has been deposited in both the US National Plant Germplasm System and in the Genetic Resource Unit of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India. The extent of duplication between the USDA and ICRISAT collections has been estimated to be about one-half of the ICRISAT collection (Knauft and Ozias-Akins, 1995).

Additionally, important germplasm collections exist in the peanut breeding programs of Texas A&M Univ., North Carolina State Univ., Univ. of Georgia, Univ. of Florida, Auburn University, USDA-ARS at Oklahoma State Univ., Virginia Tech, and New Mexico State Univ, and a few private seed companies. Many unique breeding lines developed to have tolerance to various biotic and abiotic stresses are maintained and preserved in these programs.

## 3.1.2Genetic coverage and gaps

The accessions of cultivated peanut in the genebank reasonably provide a coverage of the all existing/known genetic diversity of the cultigen, with a few gaps. However, the botanical varieties, *aequatoriana* and *peruviana* types are limited in number compared to the other botanical varieties. There continue to be lines of cultivated peanut in the ICRISAT genebank which might be of value to US breeders, and the expanse of germplasm in China is a real unknown but is perceived to be of significant quantity. Contrastingly, significant gaps occur in the genetic coverage of the wild species. There are at least 20 wild species that are not in the NPGS collection. Twelve of these mentioned are recently collected in Brazil and Bolivia and are thus, by law, not available to the USA. Efforts to correct this are ongoing since the 1997 enactment of these international laws (Convention on Biological Diversity (CBD, 1993) and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA, 2004) with little success.

## Acquisitions

For historical accessions (those listed in GRIN but no longer available in the NPGS system) of *A. hypogaea*, acquisitions are usually made from the germplasm collections at US universities, other USDA researchers or private seed companies. A list of historic and unavailable wild species accessions was shared with Dr. Charles Simpson (Texas AgriLife Research and TAMU) for assistance with replenishing of those that are available in his collection. From 2017-19, Dr. Simpson sent about 62 accessions of 26 wild *Arachis* species. Some of these have been regenerated to add to the wild species collection. Also, in 2018, we acquired 25 accessions of 17 wild species from Dr. Tom Stalker (NCSU) for replenishment.

No efforts in acquiring new germplasm from foreign countries have been carried out in recent years. Since the Convention on Biological Diversity (CBD) in 1993, many countries containing high levels of diversity of *Arachis* have implemented laws regulating access to their genetic resources. Currently, all countries in South America have regulations restricting access to their germplasm. Although US became a signee on the International Treaty of Plant Genetic Resources for Food and Agriculture (ITPGRFA) in 2016, peanut was not on the list of crops in the treaty and as a result, no peanut species can be acquired from countries in South America. Dr. Charles Simpson (Texas AgriLife Research and TAMU) continued to participate in the Brazilian efforts to identify and collect new germplasm of wild *Arachis* but to date he has not been successful in getting approval to bring new materials out of Brazil.

Additionally, in 2017, APHIS imposed a quarantine restriction for Peanut Clump Virus (PCV) and Indian Peanut Clump Virus (IPCV) for acquisition/importation of peanuts from ALL countries. Since these viruses are absent in the domestic peanut production regions, no diagnostic tools are available to detect them. The peanut curator is actively collaborating with University of Georgia-Tifton campus virologist, Dr. Sudeep Bag, to develop, standardize and validate molecular diagnostic tools for detection of these two viruses. In addition, with USA commodity groups insisting that US peanut breeders not be allowed to license varieties outside the USA that were developed in part, no matter how small the part, by commodity group funding, the door for germplasm “exchange” with most countries will be closed even tighter. Further, with the current restrictions and the unwillingness of the USDA and the US universities to sign revenue-sharing agreements with the host countries, there is little hope to acquire any new germplasm in the foreseeable future.

## 3.1.4 Maintenance

The USDA-ARS managed PGRCU in Griffin maintains the US national peanut collection. The seed storage unit is well equipped with dedicated staff to care for the maintenance and distribution of germplasm. Maintenance of accessions is generally straightforward. Seed regeneration is based on the total number of seed available for distribution, length of interval between the regenerations and germination percentage. Peanut curator and peanut breeders from universities, USDA and private industry have cooperated in the regeneration of materials to assure adequate seed supply. All cultivated peanut germplasm is stored at -18C for long-term storage as well as a sample stored at 4C with 25% humidity as the working collection for routine and regular distributions. The seed storage unit is connected to an emergency alert system in case of an interruption of electrical power and to back-up generators. The facility remains locked and is only accessed by the unit staff.

Preservation of wild *Arachis* species is much more difficult than for *A. hypogaea*, particularly for accessions that produce few, if any, seed. Approximately 30% of the species accessions produce very few seed, especially the section *Rhizomatosae*, which are maintained as vegetative materials in the greenhouse. An international cooperative effort is needed to ensure that these vegetatively propagated species are maintained in multiple environments so that they can be suitably conserved while minimizing the danger of loss (Singh and Simpson, 1994). Such an effort should involve the cooperation of the USDA, North Carolina State Univ., Texas A&M Univ., ICRISAT, the Brazilian Corporation for Agricultural Research Botanical Institute (EMBRAPA), the Brazilian National Center for Genetic Resources and Biotechnology (CENARGEN), the Argentina National Institute of Agricultural Technology (INTA), and the Argentina Botanical Institute of the Northeast (IBONE).

## 3.1.5 Regeneration

**Cultivated species:**

All cultivated peanut regenerations are being conducted in field plots (2x10 ft. rows) at the USDA-ARS Southeastern Fruit and Tree Nut Research Station, Byron, GA. Occasionally, a few of the collaborators from the CGC help in regenerations of some materials. For annual regenerations of both cultivated and wild species, the curator uses information on the quantity of seed available, germination percentage and length of interval between regenerations as the main criteria for replenishing fresh seed into the collection. The goal is to regenerate the entire collection every 20 years so viable collections are maintained, but some materials need to be increased much more often. This latter group would include the peanut core and the mini-core PIs and other popularly requested PIs.

## Wild Species

The wild species present additional problems for regeneration as many do not produce enough seed or rarely produce seed. All *Arachis* wild species are regenerated in the greenhouses in Griffin. The curator has access to about 3400 sq. ft of greenhouse bench space to regenerate *Arachis* wild species. In addition, the curator also has access to a large screenhouse to grow additional *Arachis* regenerations. For regeneration of the wild peanut species, each accession should be grown no less than every 6-8 years or sooner if resources are available. However, some *Arachis* species such as those from section *Erectoides*, tend to lose viability faster than other species groups, so they must be regenerated more often and/or maintained as live plants in the greenhouses. As far as the non-seed producing accessions which include section *Rhizomatosae,* live plants need to be grown continuously. A significant issue with doing this include the great difficulty to maintain the plants through the winter months as many of them enter a dormant state during the short days of the dry winter in their native habitats. Duplicating this scenario in the greenhouse is very difficult, if not impossible. Thus, an effort is made to simply keep the plants in a “growing” state year-round. Some species adapt to this effort well and continue their growth (i.e., Section *Rhizomatosae*), while other groups do not do well (e.g., Section *Caulorrhizae*, and *Extranervosae*). Overall, regeneration and maintenance of wild species is more challenging, labor intensive and time consuming. It needs skill and experience to care for plants to maintain the purity of species during the regeneration process.

## 3.1.6 Distributions and outreach

Peanut germplasm is mostly distributed as seeds for cultivated types and as pods for the wild species. The default distribution seed amount is 25 for the cultivated accessions. However, for wild species accessions, the distribution amount is 10 pods or less depending on the quantity of pods available. A total of 29,229 accessions of both cultivated and wild species were distributed between 2003 and 2018. When required, all international distributions were examined and issued a phytosanitary certificate by APHIS inspectors before they were shipped. Throughout the year, many students and teachers from nearby schools, colleges, and universities, researchers from US and foreign countries and stakeholder groups visit the peanut collection. Throughout the year, the peanut curator provides short talks to commodity groups and other organizations on the maintenance and use of the national peanut collection.

## 3.2 Associated information

## 3.2.1 Genebank and/or crop-specific website(s)

For the US peanut collection, the GRIN-Global database system (<https://www.ars-grin.gov/npgs/index.html>) is the only comprehensive source of information. Additionally, the peanutbase (<https://peanutbase.org/>), specifically provides genomic information of peanut in addition to other related information. Similarly, <https://legumeinfo.org/> also has genomic information and some *Arachis* species descriptions for interested researchers. Further, the ICRISAT genebank has information similar to the GRIN-Global system and their groundnut collection can be accessed at [https://www.genesys-pgr.org](https://www.genesys-pgr.org/). Lastly, the below web link, <https://www.ars.usda.gov/southeast-area/griffin-ga/pgrcu/> provides information about the peanut curator and contact details for assistance with US peanut collection.

## 3.2.2 Passport information

The GRIN-Global system provides passport information of all *Arachis* (cultivated as well as wild) germplasm in the US collection for public access. The GRIN-Global passport data consists of general description of collection site information including its GPS coordinates, donor name, accession/PI and collector numbers and other identifiers, backup status, other narrative descriptions of plant, pod and seed traits and related digital images. It also has a link to the Plant Introduction books detailing when the materials were introduced into the US collection and other pertinent information. Further, the peanut curator regularly consults with Drs. Simpson (Texas A&M University), Stalker (NC State University) and Valls (EMBRAPA, Brazil) to clarify and update any errors noticed, particularly with *Arachis* species names with corresponding accessions and collector numbers. Based on the passport data, Holbrook et al. (1993) developed a working core collection of 821 lines for the cultivated peanut. Later, Holbrook and Dong (2005) developed a mini core of 112 lines. The efficiency gained by screening the peanut core collection has greatly increased the use of the peanut germplasm collection. Data generated from research with the core collection have been used to identify the geographical distribution of resistance to five important diseases of peanut (Holbrook and Isleib, 2001; Table 6). By screening germplasm more intensely from these countries, peanut breeders can utilize more efficiently the genes for disease resistance that are available in the germplasm collection.

## 3.2.3 Genotypic characterization data

The peanutbase (<https://peanutbase.org/>) contains genomic information including the genome sequences of the tetraploid cultivar, Tifrunner along with the sequence information of the two diploid progenitor species, *A. duranensis* and *A. ipaensis*. Further, the site has information on genetic maps and molecular markers available for peanut breeding research. Varshney et al. (2009) using simple sequence repeat (SSR) markers with a diverse set of 189 *A. hypogaea* accessions observed significant polymorphisms and grouped the accessions into four different clusters. Molecular profiling of a composite collection consisting of 1000 diverse peanut accessions which included both cultivated and wild species demonstrated rich allelic diversity within the wild species with more than 100 unique alleles (Upadhyaya et al. 2008a, b) whereas the number of unique alleles in the two *A. hypogaea* subspecies, *hypogaea* and *fastigiata* were only 11 and 50, respectively. Further, the highest number of unique alleles were found in *A. hypogaea* accessions from the Americas with few unique alleles among the accessions from Asia and Africa. This study also demonstrated that the two subspecies, *hypogaea* and *fastigiata* accessions shared 70 alleles among them. Although the wild species shared only 15 alleles with subspecies *hypogaea* and 32 alleles with subspecies *fastigiata*, the wild species accessions grouped with subspecies *hypogaea* accessions (Upadhyaya et al. 2008a, b).

Attempts are in progress to genotype the African collection (PIs tracing back to countries in Africa) contained in the national peanut collection (Peggy Ozias-Akins, unpublished). Also, the peanut core collection is being genotyped (Ethy Cannon, unpublished). Another future goal is to genotype rest of the collection, if funding and other resources become available. Recently, efforts are ongoing to SNP genotype the *Arachis* wild species collection (Leal-Bertioli, unpublished).

## 3.2.4 Phenotypic characterization data

Without adequate characterization data, it would be difficult to know which accessions to choose as desirable parents for cultivar development. Standards for characterizing *A. hypogaea* accessions have been published by IBPGR and ICRISAT (1992) and the USDA (Pittman, 1995). This involves using a range of attributes called descriptors to characterize the germplasm collection.. Simpson et al. (1992) applied 53 of the IBPGR and ICRISAT descriptors to 2000 accessions collected from 1977 to 1986 in South America and observed a large amount of variation in pod and seed characteristics. Holbrook and Anderson (1993) applied the USDA descriptors to accessions in the core collection. Currently, descriptor data is accumulated from annual regenerations for plant, pod and seed traits in addition to capturing digital images of pods and seeds. Additional information such as resistance to diseases/pests and other quality parameters are also included in the database, where available.

Development of the Germplasm Resource Information Network-Global (GRIN Global) [“http://www.ars-](http://www.ars-grin.gov/)g[rin.gov”,](http://www.ars-grin.gov/) a database of descriptor information for each plant introduction in the USDA system, has made it much more efficient to access information regarding the collection. This information can be easily accessed, and plant introductions containing desired characteristics can be ordered for use in research or cultivar development.

## 3.3 Plant genetic resource research associated with the NPGS

## 3.3.1 Goals and emphases

PGRCU actively supports research collaborations with public and private entities by freely providing necessary germplasm to understand and develop knowledge of the collection for effective and efficient use by breeders and other researchers. One of the inhouse research projects has helped determine total oil and fatty acid profiles of nearly 8,700 cultivated peanut accessions (Wang, unpublished). Additionally, 200 accessions of 46 wild species were also characterized for 100-seed weight, total oil, and fatty acid profiles (Tallury, unpublished). Currently, research collaborations using SNP array for genotypic characterizations of selected cultivated as well as wild species germplasm are in progress.

## 3.3.2 Significant accomplishments

The NPGS peanut collection is one of the most comprehensive and genetically diverse collections in the world. The wild species accessions display extremely high levels of resistance to many of the common peanut diseases including leaf spots, TSWV, sclerotinia blight and a host of insect pests (Stalker and Moss, 1987; Stalker and Beute, 1993; Stalker and Lynch, 2002; Tallury, et al. 2014b). The peanut core and mini-collections were also evaluated for drought, nutritional quality and aflatoxin production (Belamkar et al. 2010; Holbrook et al. 1997. 1998; 2000 a, b,c; Selvaraj et al., 2010). Several studies also highlighted the genetic diversity, patterns and distribution of genetic variation within the cultivated as well as the wild species to provide knowledge about the genetic structure of the genus and species compatibilities (Kochert et al. 1996b; Seijo et al. 2007; Simpson et al. 2001; Stalker and Holbrook, 2003 ; Tallury et al. 2005; Friend et al. 2010; Bertioli et al. 2011). Production of interspecific hybrids and derived germplasm lines led to novel sources of materials to broaden the genetic basis of the cultivated peanut (Simpson and Starr, 2001; Stalker and Beute, 1993; Stalker and Lynch, 2002; Stalker et al. 2002a and 2002b; Tallury et al. 2014a). The distribution and use of peanut germplasm from the national collection resulted in many improved cultivars for the growers and the peanut germplasm collection is truly a national treasure.

## 3.4 Curatorial, managerial and research capacities and tools

## 3.4.1 Staffing

There is one full-time technician supported with S-009 funds to assist the curator with peanut germplasm curation activities. The curator and the technician work together to maintain plants in the greenhouses with daily watering, periodical fertilization and chemical sprays. They also coordinate field planting, harvesting and post-harvest activities involving shelling, cleaning seeds, recording descriptor data, and filling vegetative requests for peanut germplasm. In addition, a part time worker (October thru’ May) assists with postharvest activities and other general greenhouse tasks such as weeding, trimming and cleaning.

## 3.4.2 Facilities and equipment

Adequate greenhouse space which includes 3400 square feet of greenhouse bench space, is available for the maintenance of perennial peanut germplasm and regeneration of other wild species. Additionally, a large screenhouse is also available for peanut regenerations. A locally fabricated mechanical shaker is available to harvest wild species pods. A 27 ft x 3 ft mist bed is available for propagating materials from vegetative cuttings. For field operations, Kincaid cone planter and threshers are available for planting and harvesting pure seed from field plots. Also available are three stationary shellers, two shaker tables for cleaning and preparing seeds to process into the gene bank collection.

A full-fledged analytical laboratory is available for measuring total oil, fatty acid profiles and protein content of the peanut germplasm. The laboratory is also equipped with facilities to conduct basic PCR work such as for detection of the FAD genes for high-oleic acid content.

Adequate field space and manual support is available in the unit for planting, managing the crop, and harvesting operations.

## 3.5 Fiscal and operational resources

Sufficient fiscal and operational resources via project fund allocation are available to curate between 550 and 650 PIs annually in field plots and another 200 wild species accessions in the greenhouses. Also, the curator has been receiving an annual grant from the National Peanut Board for $7000 which is used to hire a part-time temporary worker to help with postharvest processing of PIs and assist with other operations.

## 4. Other genetic resource capacities

An up-to-date information of the national peanut collection along with all released cultivars, germplasm lines and genetic stocks is in the appendix in table 2-5. All of this information is available at the GRIN Global website <https://www.ars-grin.gov/npgs>. The website also provides a link to the Crop Germplasm Committee (CGC). Additionally, the below organizations are actively involved with peanut research and industry.

American Peanut Research and Education Society (APRES) <https://apresinc.com>

The Peanut Foundation [www.peanutfoundation.org](http://www.peanutfoundation.org)

Peanut Bioscience <https://peanutbase.org>

The National Peanut Board <https://www.nationalpeanutboard.org>

American Peanut Council <https://www.peanutsusa.com>

Several state universities and USDA-ARS research centers also maintain germplasm, release cultivars, and conduct research in all areas of peanut improvement. Additionally, many international research centers also maintain germplasm and conduct research such as the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India, EMBRAPA in Brazil, INTA and IBONE in Argentina and many regional research institutes in China in the provinces of Henan, Shandong and Wuhan.

## 5. Prospects and future developments

Disease resistance has been a key component of all peanut breeding programs in the US. Many of the popular cultivars in each market type in the respective production areas were developed to possess higher levels of resistance to one or more of the common diseases in that area. Breeders routinely use Plant Introductions (PIs) from the National Peanut Collection as sources of parents in hybridization programs to develop desirable populations for cultivar releases. The national collection likely contains significant amount of genetic diversity to not only develop high yielding cultivars but also to combat any new challenges due to climate change or biotic threats. However, breeders should not be complacent as the evolution of a new race/virulent strain of a pathogen or occurrence of a new pathogen would potentially disrupt the production causing severe economic losses to growers and the industry. For example, peanut smut caused by the soilborne fungus, *Thecaphora frezii*, is a new disease currently limited to Argentina. The present estimates indicate that all peanut production areas in Argentina are infected with this fungus. If this pathogen would ever enter the US, it would potentially shutdown the entire peanut industry. We could only presume that all current cultivars are highly susceptible to this pathogen and there is an urgent need to identify resistant sources to peanut smut. Cooperative research effort to combat peanut smut is underway between the USDA-ARS, US peanut industry and the Argentinian researchers to identify potential resistant sources and initiate crossing programs to develop resistant populations. Additionally, vigilant methods should be pursued to prevent any accidental introduction of this pathogen into the US through proper quarantine guidelines.

Further, genetic uniformity also poses a risk for genetic vulnerability of the crop as shown by the southern corn leaf blight in the 1970s. The recent promotion and adoption of all high-oleic cultivars in peanut may have unintended/unknown consequences and needs further consideration. The recent advances in the genomics are already providing new tools to develop improved peanut cultivars efficiently and quicker. The genomics tools will also aid in understanding the amount of unique diversity in the germplasm collection and clarify duplicate samples.

Despite the popularity of current high yielding cultivars, there is a consensus among the breeders that the genetic base of the crop needs expansion. *Arachis* wild species offer novel sources of alleles that are not present in the cultivated germplasm. Research programs to mine wild species resources should be encouraged and supported to not only expand the genetic base of the crop but also for long-term, sustainable peanut production in the US. Overall, it is reasonable and realistic to suggest that there is adequate genetic diversity present in the US National Peanut Collection to combat immediate or future challenges for sustainable domestic production.

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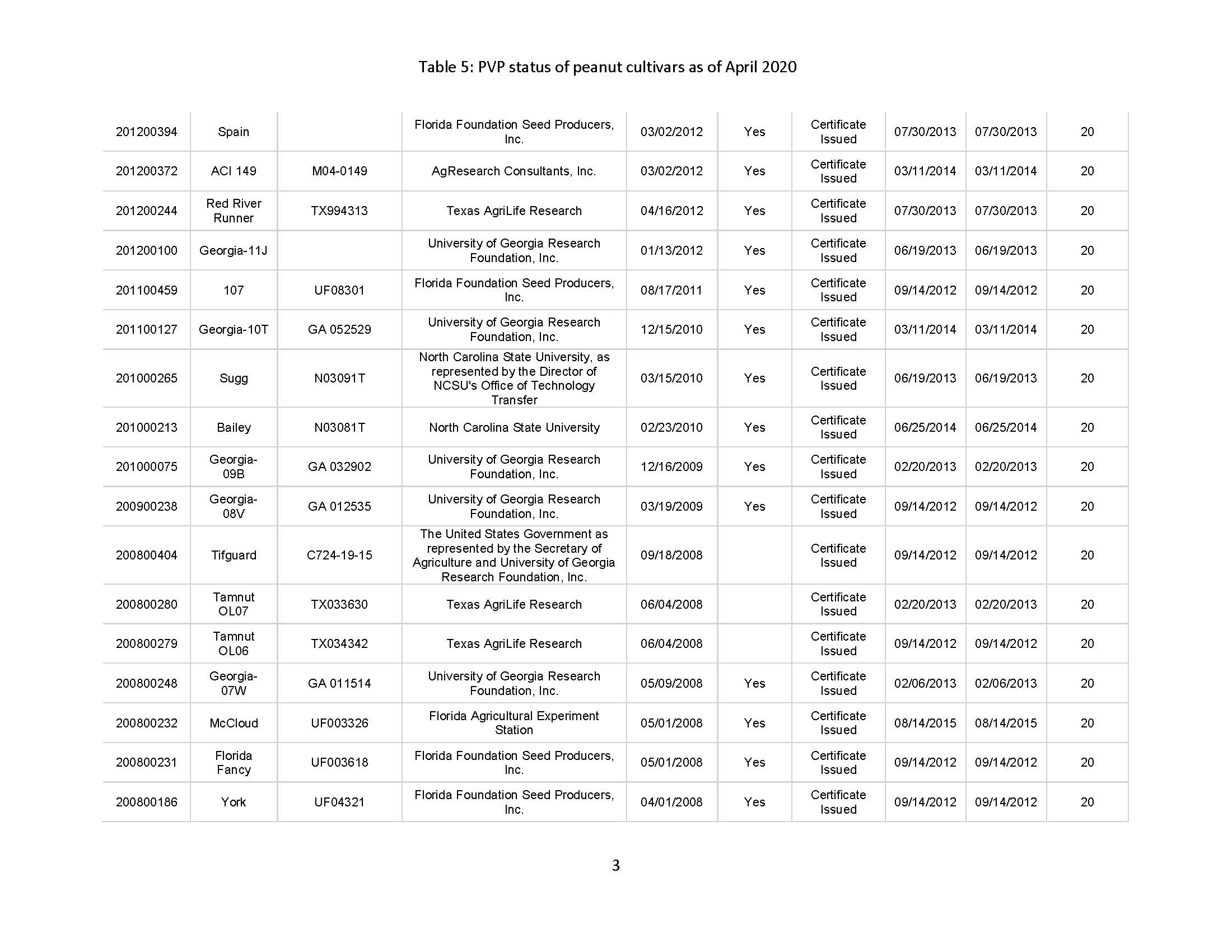
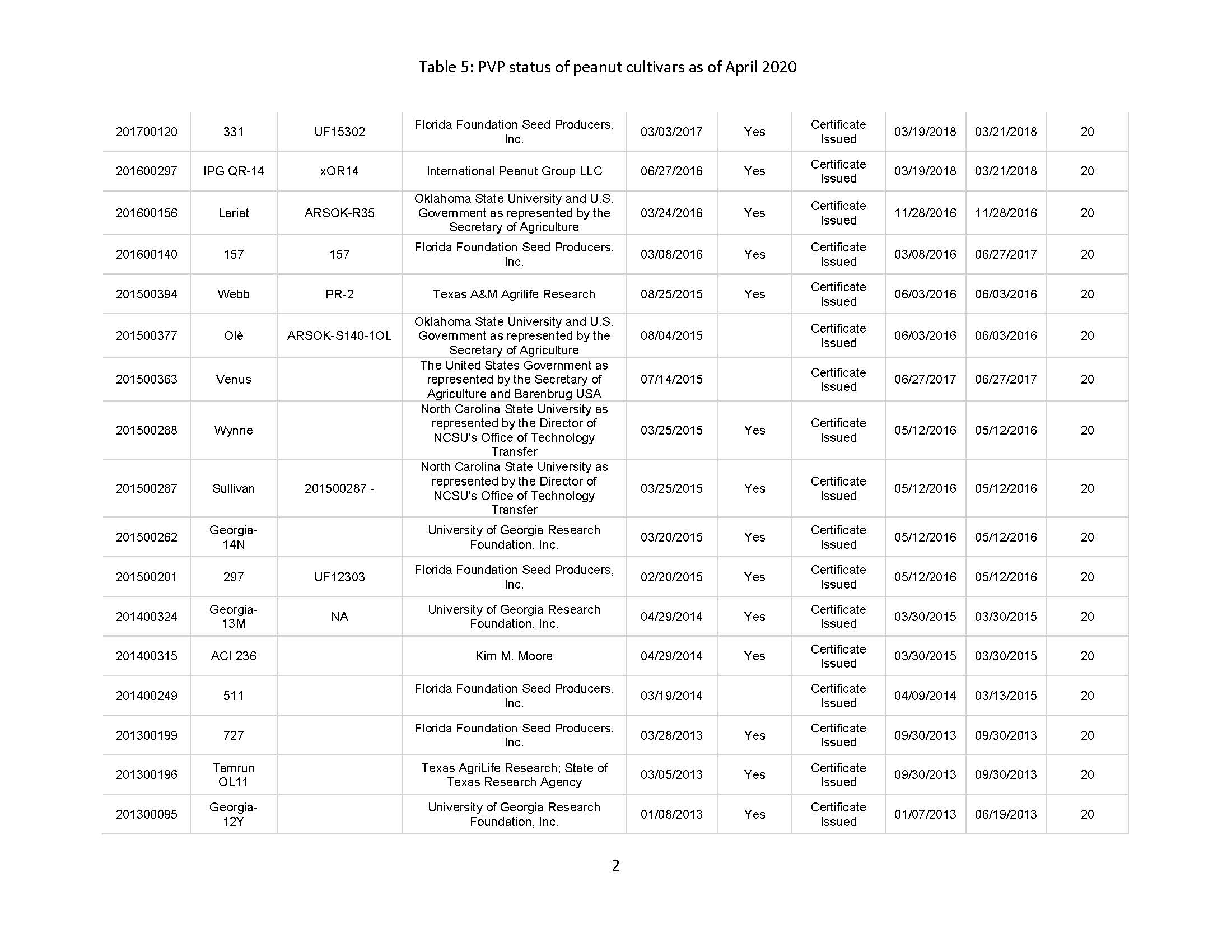
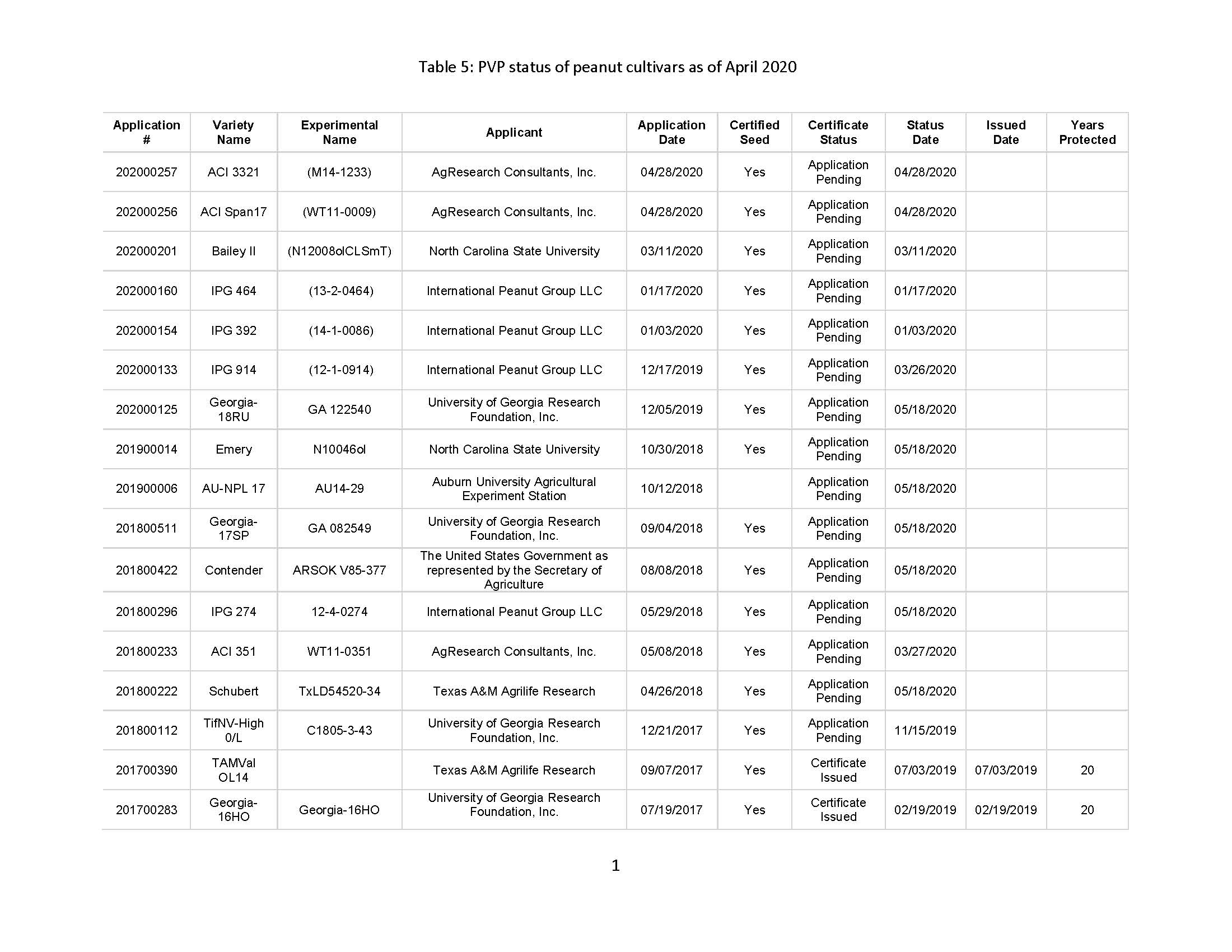
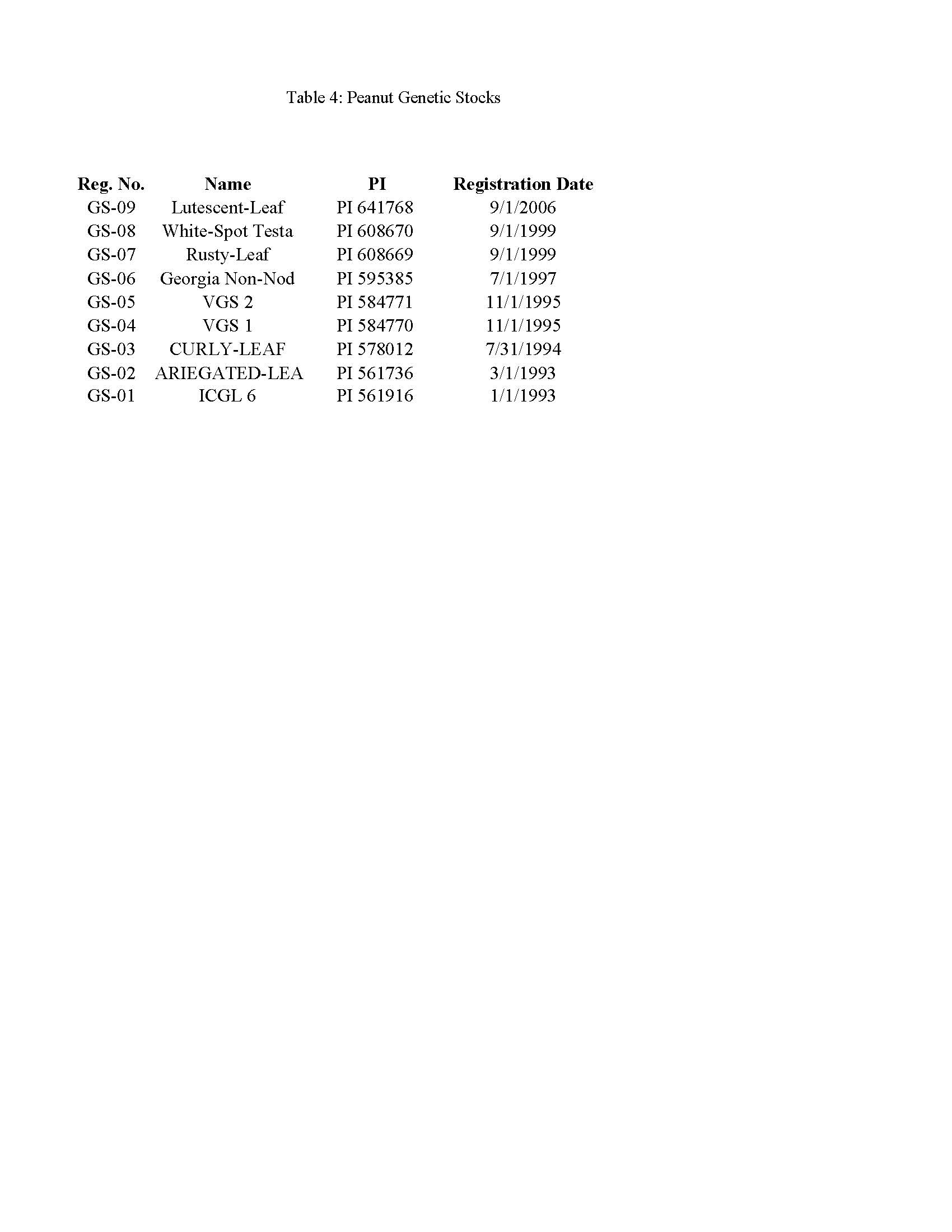
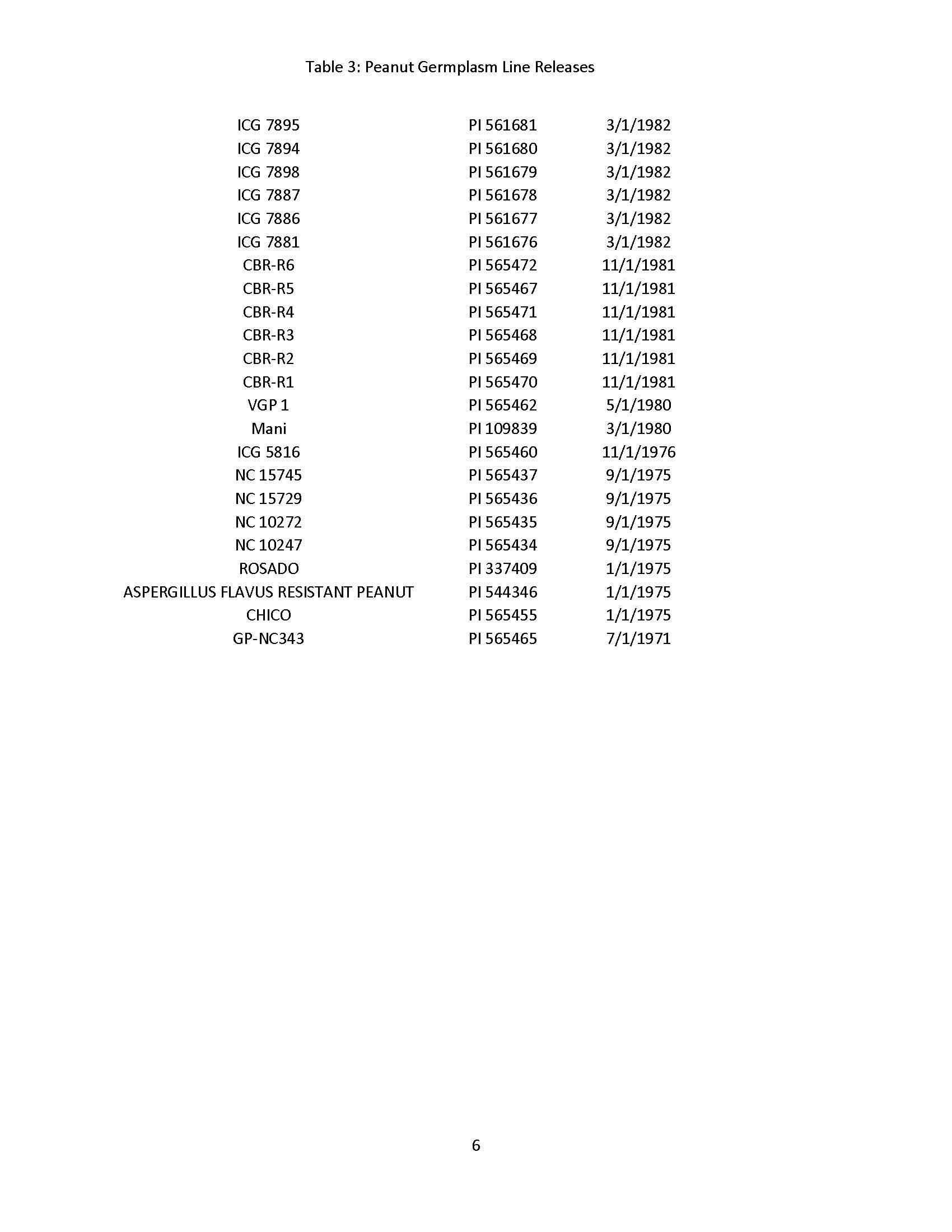
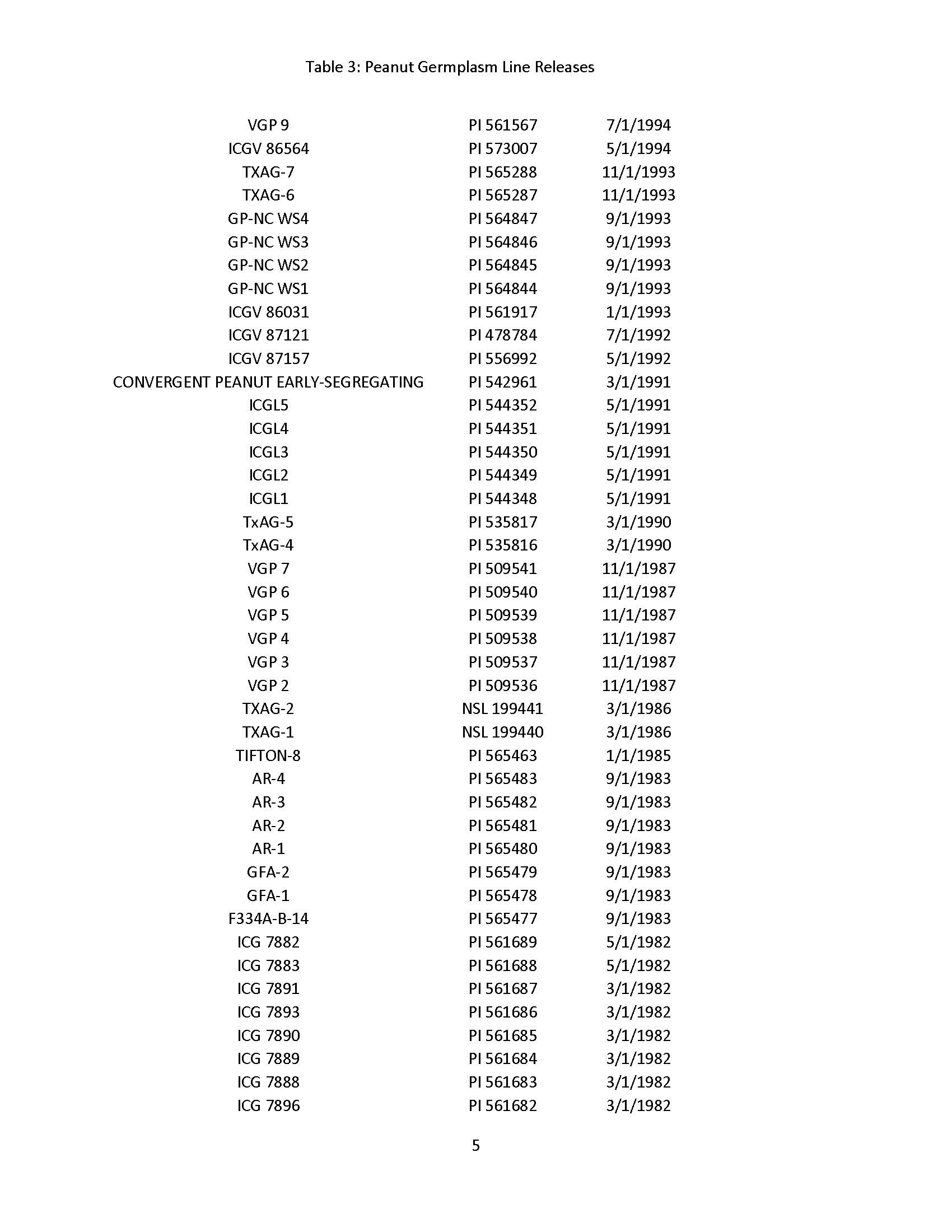
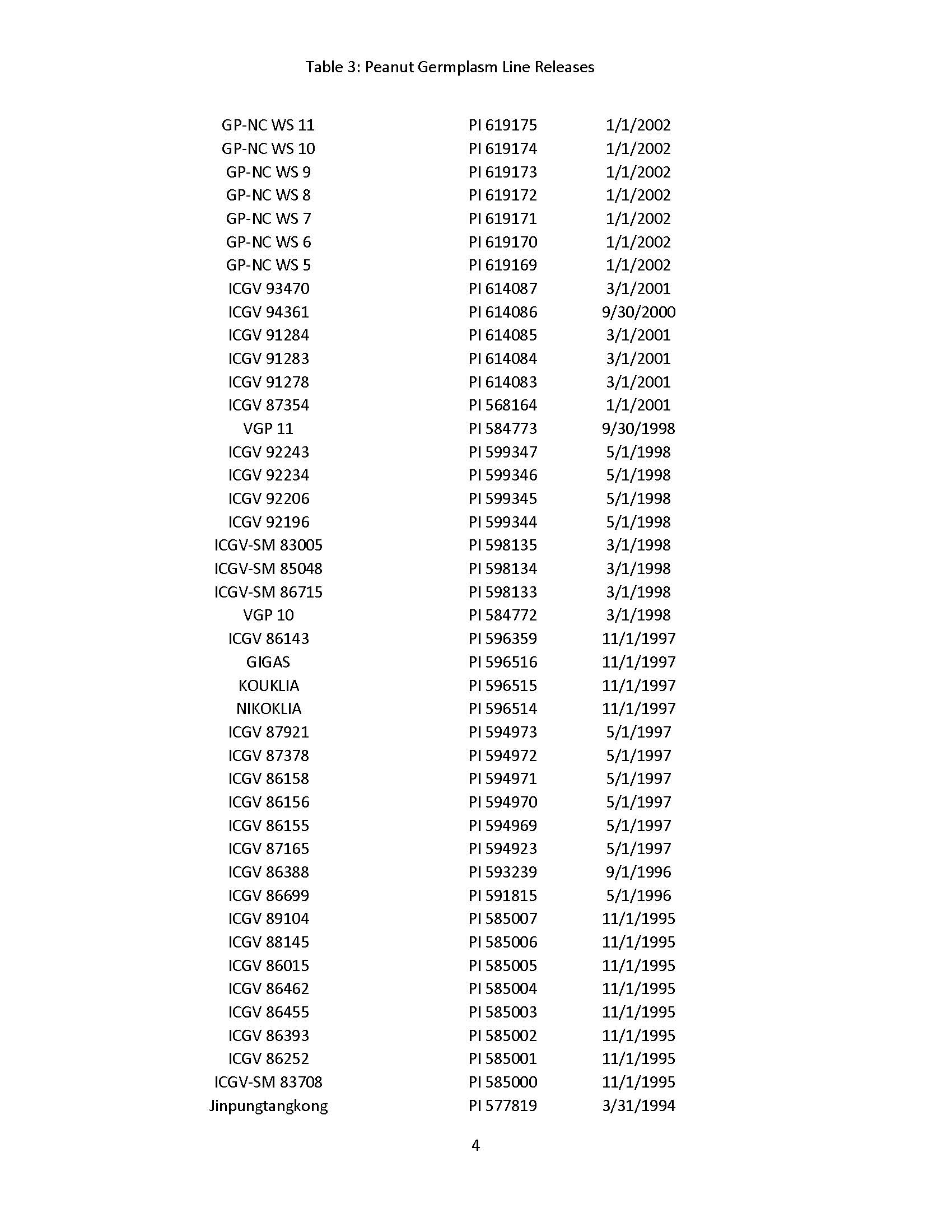
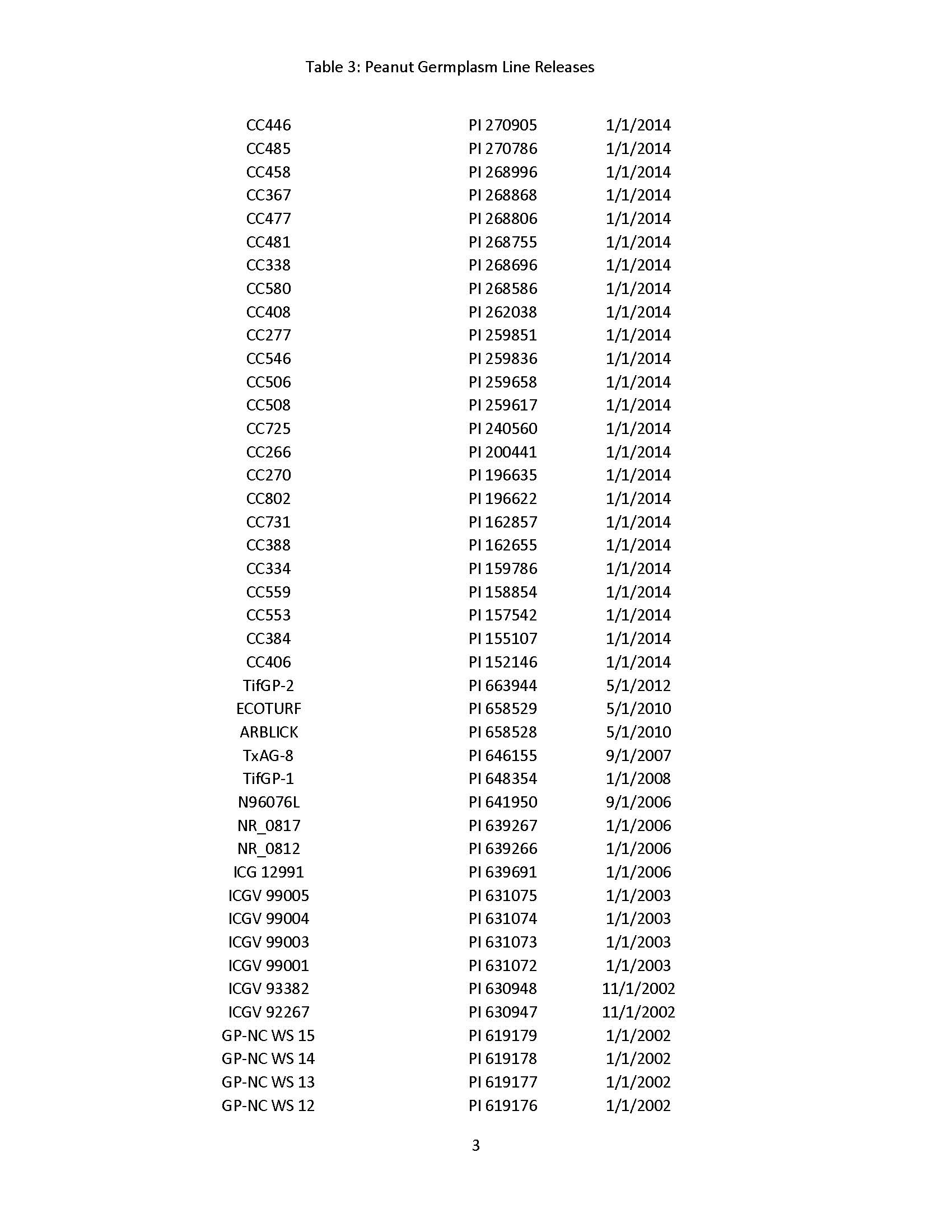
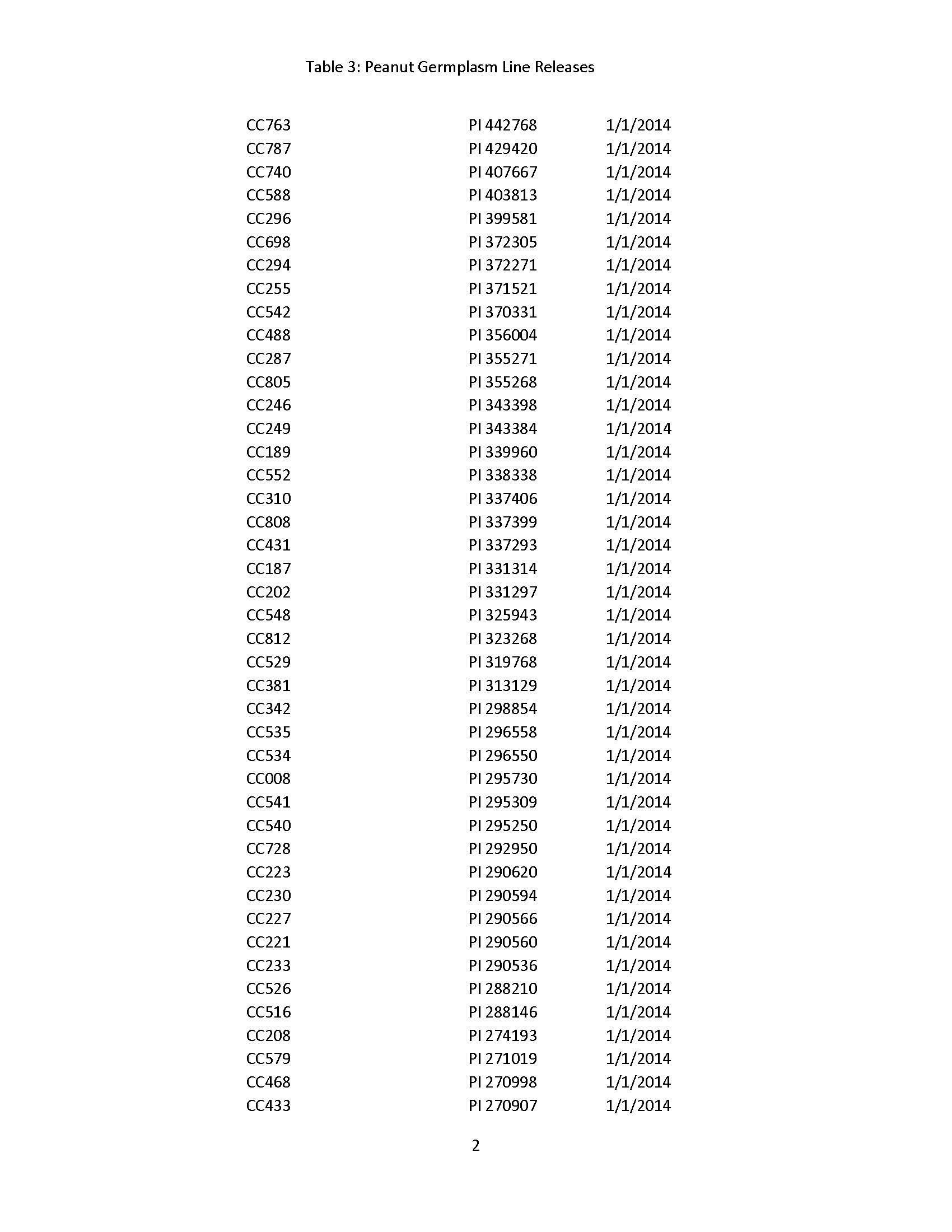
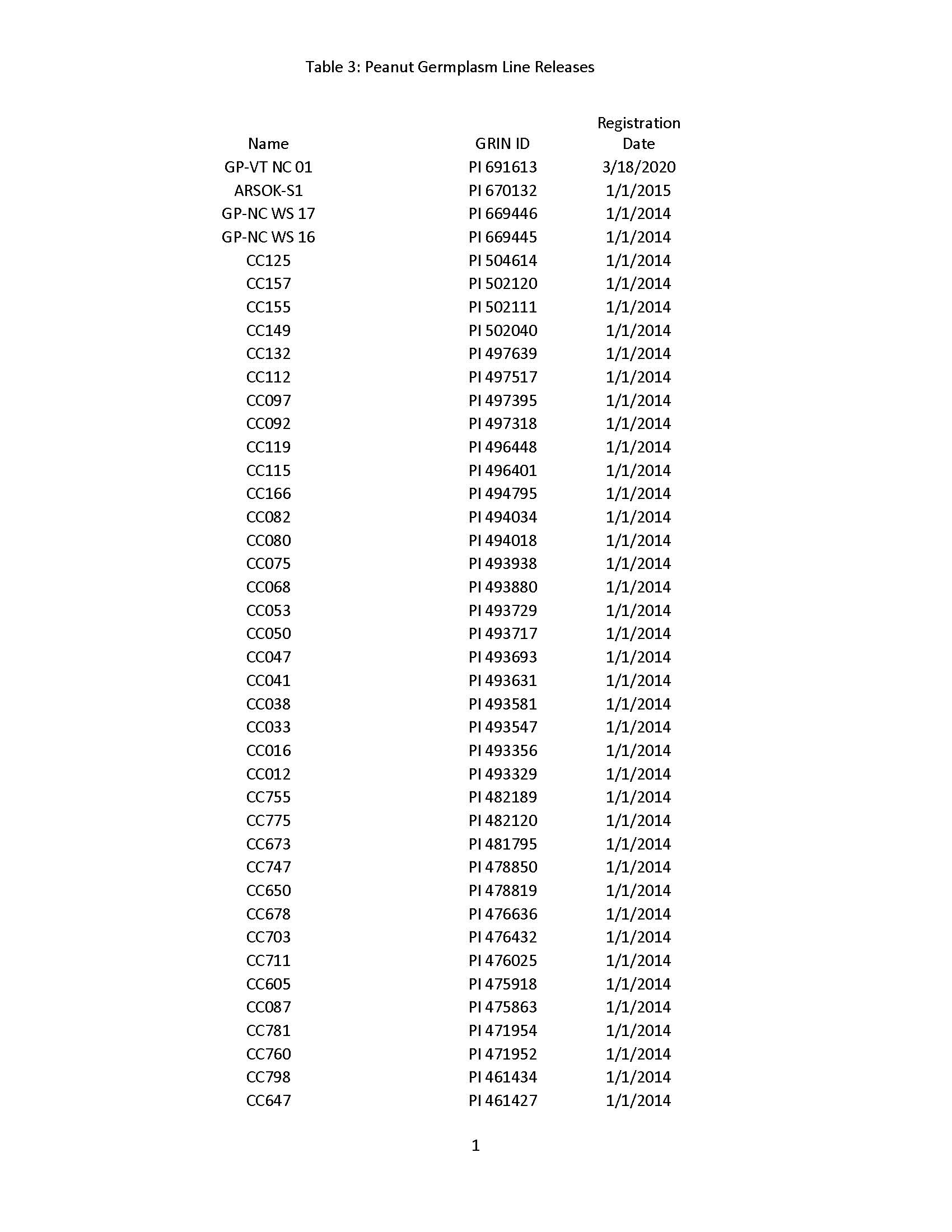
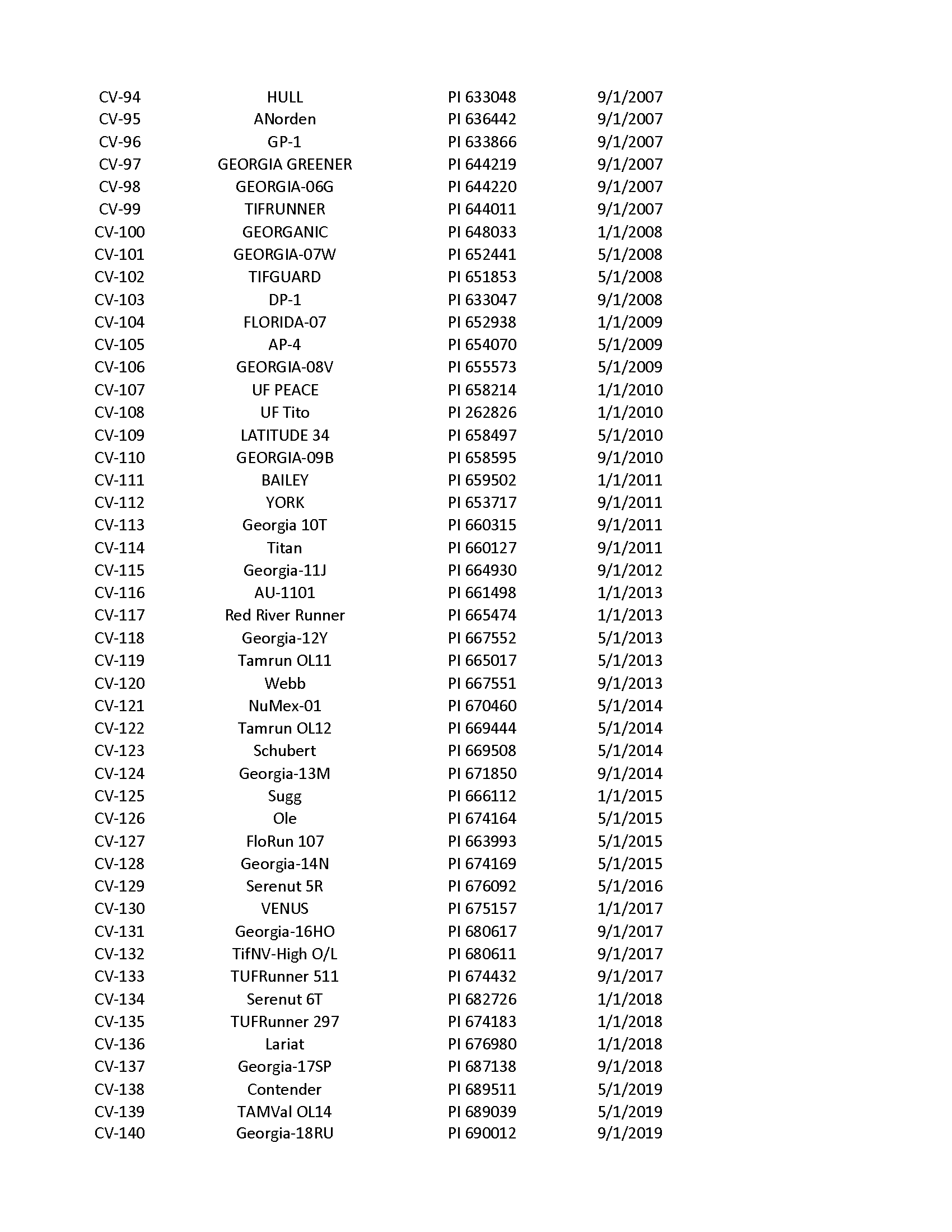
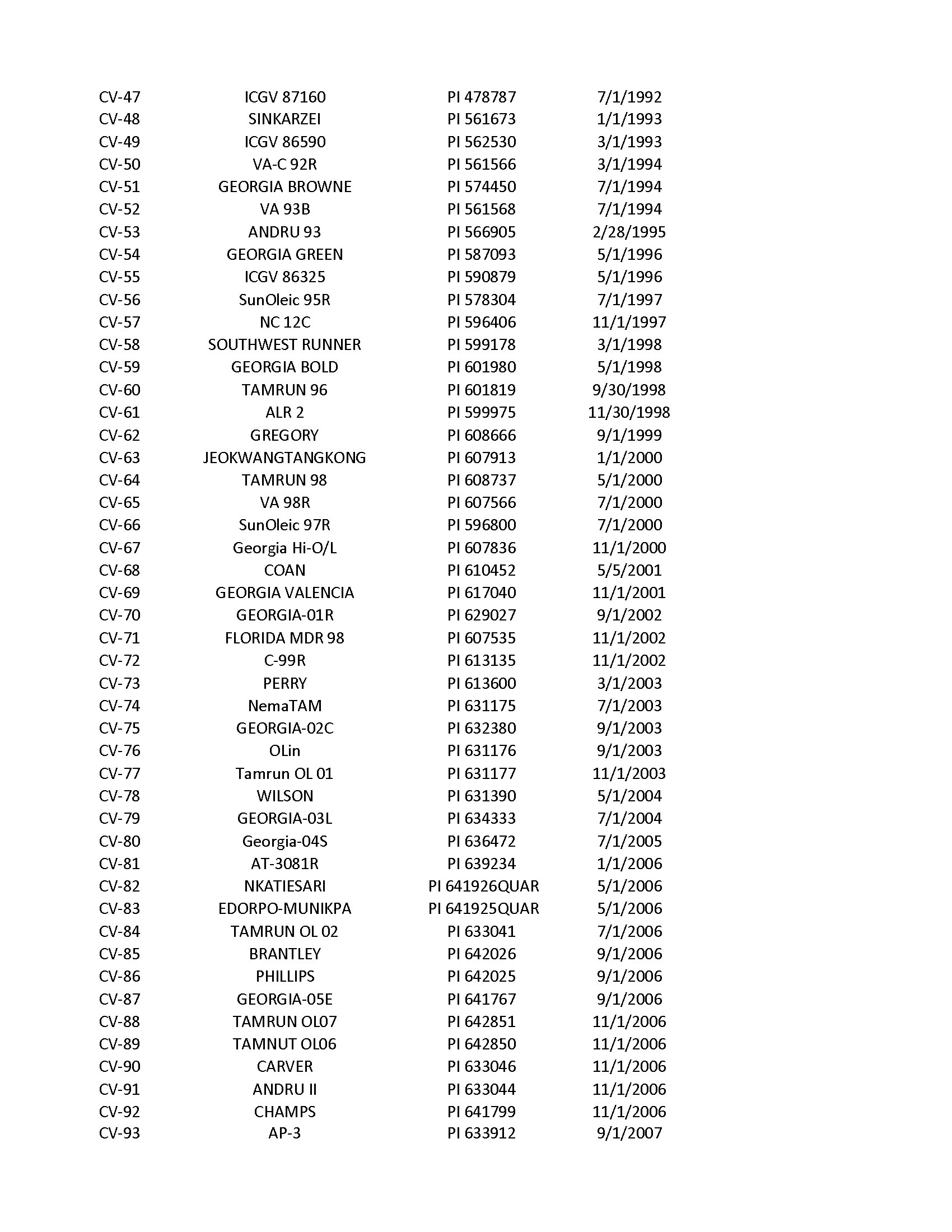
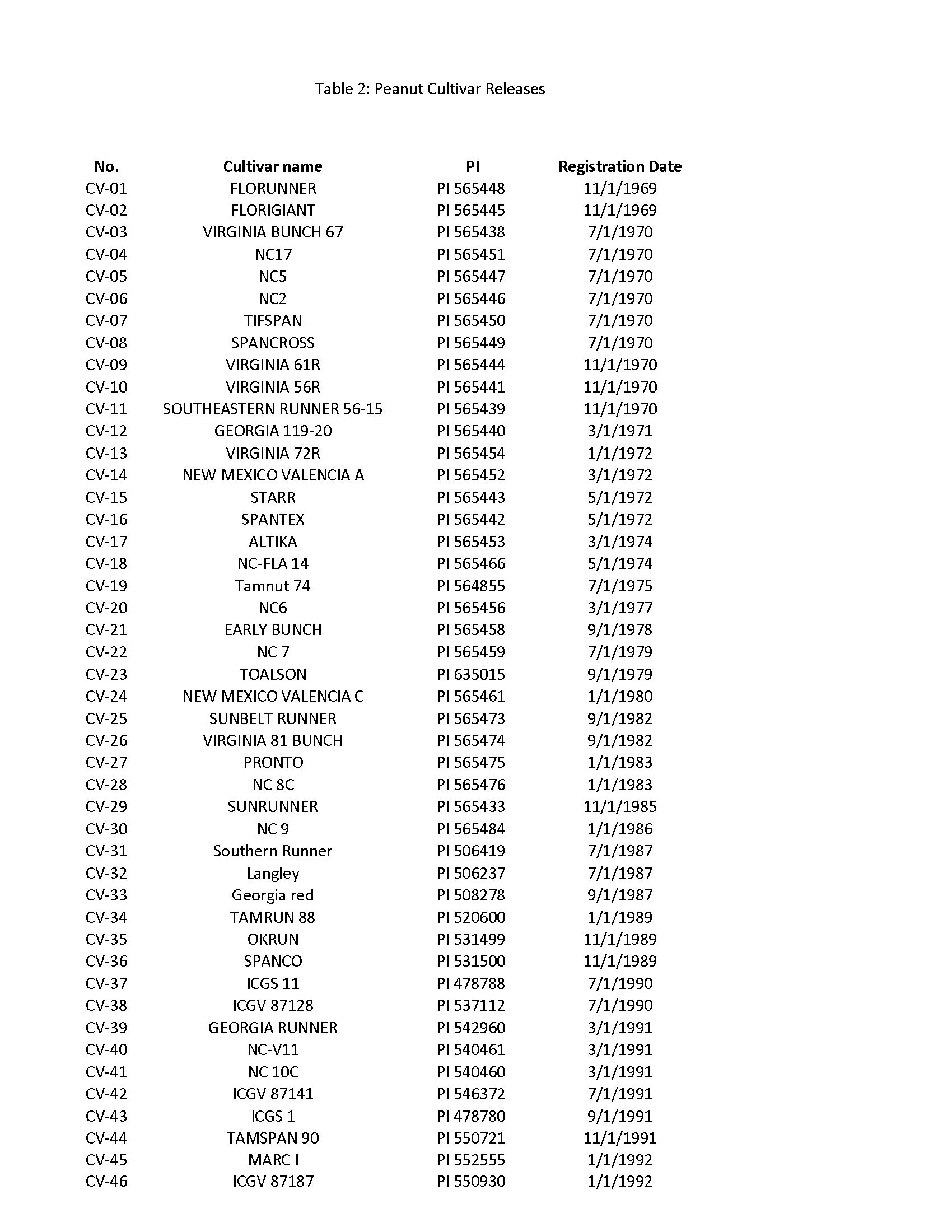
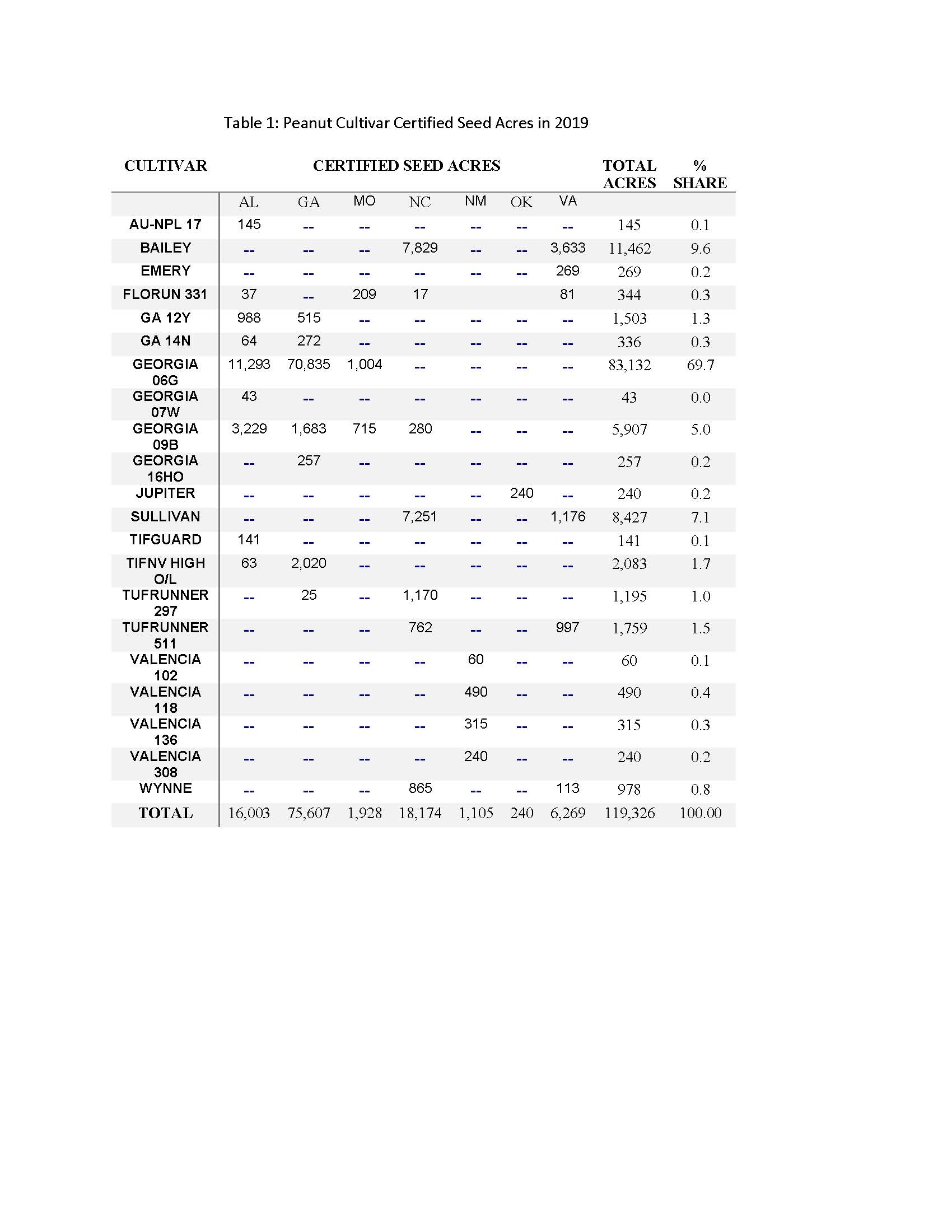
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