Simpson, C. E. 1984. Plant exploration: Planning, organization, and implementation with species emphasis on *Arachis*, pp. 1-20. *In* Conservation of Crop Germplasm--An International Perspective. CSSA, Madison, WI.

Simpson, C. E., D. L. Higgins, G. D. Thomas, and E. R. Howard. 1992. Catalog of passport data and minimum descriptors of *Arachis hypogaea* L. germplasm collected in South America 1977-1986. Texas Agric. Exp. Sta. MP-1737.

Singh, A. K., and C. E. Simpson. 1994. Biosystematics and genetic resources, pp. 96-137. *In* J. Smartt (ed.) The Groundnut Crop: A Scientific Basis for Improvement. Chapman & Hall, London.

Stalker, H. T., and C. E. Simpson. 1995. Genetic resources in *Arachis*, pp. 14-53. *In* H. E. Pattee and H. T. Stalker (eds.) Advances in Peanut Science. Amer. Peanut Res. Educ. Soc., Stillwater, OK.

USDA. 1992. pcGRIN. Germplasm resource information network. Data query system for the PC. ARS-108. U.S. Govt. Print. Office, Washington, DC.

Williams, D. E. 2001. New directions for collecting and conserving peanut genetic diversity. Peanut Sci. 28:135-140.

Williams, K. A., and D. E. Williams. 2001. Evolving political issues affecting international exchange of *Arachis* genetic resources. Peanut Sci. 28:132-135.

Wynne, J. C., M. K. Buete, and S. N. Nigam. 1991. Breeding for disease resistance in peanut (*Arachis hypogaea* L.). Ann. Rev. Phytopath. 29:279-303.Wynne, J. C., and W. C. Gregory. 1981. Peanut breeding, pp. 39-72. *In* N. C. Brady (ed.) Advances in Agronomy. Vol. 34. Academic Press, New York.

Status of the *Arachis* Germplasm Collection at ICRISAT

H. D. Upadhyaya[1], M. E. Ferguson[1]* and P. J. Bramel[2]

ABSTRACT

ICRISAT maintains a substantial *Arachis* germplasm collection of 14,723 accessions, comprising 14,310 accessions of cultivated peanut (*Arachis hypogaea* L.) from 92 countries and 413 accessions of wild species representing 43 taxa. All germplasm is freely available for distribution. Forty-five percent of the cultivated peanut collection is of var. *hypogaea*, followed by 35.7% var. *vulgaris* and 16.1% var. *fastigiata*. Varieties *hirsuta* and *aequatoriana* are represented by 20 and 15 accessions, respectively. All passport and characterization data are accessible through the internet. To enhance the utilization of the collection and understand the diversity it contains, efforts have focused on characterization and documentation of the collection and the formation of a core of 1704 *A. hypogaea* accessions. These are representative of the genetic diversity in the entire collection. The core provides an entry point into the collection and is currently being evaluated for maturity, biotic, and abiotic stress resistance and quality parameters, including aflatoxin contamination. A subset of the core is used in prescreening for polymorphic molecular markers. Evaluation of the wild *Arachis* collection to major abiotic stresses is a continuing process. Future efforts in both the wild and cultivated collections will focus on germplasm exchange and acquisition, and specific regions for future collections are identified. The development of molecular markers for diversity assessments in all *Arachis* taxa and alternative strategies for utilization of the wild species are also important areas of research.

Key Words: Genebank, germplasm evaluation, groundnut, peanut.

The Int. Crops Research Inst. for the Semi-Arid Tropics (ICRISAT), is a Future Harvest center supported by the Consultative Group on Int. Agric. Res. (CGIAR). The centers, located around the world, conduct research in partnership with farmers, scientists, and policy makers to help alleviate poverty and increase food security while protecting the natural resource base. They are funded principally through the 58 countries, private foundations, and regional and international organizations that make up the CGIAR. Within this system, ICRISAT has the global responsibility for the collection, characterization, conservation, distribution, and utilization of peanut (*Arachis hypogaea* L.) germplasm and other *Arachis* species. The ICRISAT genebank was established in 1979 and now serves as one of the world's major repositories of peanut.

Composition of the ICRISAT Peanut Collection

Acquisition and collection of peanut germplasm resources commenced at ICRISAT in 1976 with the establishment of the Groundnut Improvement Program. Since then the genebank has acquired 12,675 accessions of wild or cultivated *Arachis* by donation and/or request from 83 organizations in 39 countries (Table 1). In addition, 2667 accessions have been collected through 66 expeditions in 27 countries (Table 2).

The collection currently contains 14,310 cultivated peanut accessions with adequate seed supply, representing all six botanical varieties. This is comprised of 45% var. *hypogaea* (6766 accessions), 35.7% var. *vulgaris* (5102 accessions), 16.1% var. *fastigiata* (2302 accessions), 0.1% var. *aequitoriana* (15 accessions), 0.14% var. *hirsuta* (20 accessions), and 1.72% var. *peruviana* (249 accessions). Approximately 43% of the collection consists of landrace germplasm, 7% is made up of cultivars, 31% is breeding lines, and 19% other genetic stocks (mutants and experimental germplasm).

Of those accessions with adequate passport information, the greatest representation is from Asian countries

[1]Scientist and Special Project Scientist (Genetic Resources), respectively, at Genetic Resources and Enhancement Program, Int. Crops Research Inst. for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, Andhra Pradesh, India.

[2]Prin. Scientist and Genetic Resources Coordinator, ICRISAT, Matopos Res. Sta., P.O. Box 776, Bulawayo, Zimbabwe.

*Corresponding author (email: m.ferguson@cgiar.org).

Table 1. List of the countries, institutions, and *Arachis* germplasm accessions donated to ICRISAT between 1976 and 1999.

Country	Institutions	Accessions
	no.	no.
Australia	1	4
Brazil[a]	1	312
Burundi	1	39
Chad	1	75
China	4	46
CIS	1	3
Costa Rica	1	21
Cuba	1	1
Cyprus	1	4
Egypt	1	38
France	1	4
Gambia	1	17
Ghana	1	6
Great Britain[a]	2	56
ICRISAT	4	315
India[a]	22	5282
Indonesia	2	66
Italy	2	83
Japan	2	77
Korea	1	90
Malawi	2	305
Malaysia	1	1
Mali	2	68
Nepal	1	21
The Netherlands	1	4
Niger	1	222
Nigeria	1	105
Pakistan	1	2
Philippines	1	14
Senegal	2	674
South Africa	1	118
Sudan	1	1
Surinam	1	3
Tanzania	1	41
Trinidad & Tobago	1	1
Uganda	1	2
Unknown[a]	0	23
USA[a]	9	4276
Vietnam	1	24
Zambia	1	1
Zimbabwe	2	230
Total	83	12,675

[a]Includes accessions of wild *Arachis* species.

Table 2. Germplasm collection expeditions and *Arachis* accessions collected by ICRISAT staff since 1979.

Country	Expeditions	Accessions
	no.	no.
Brazil[a]	5	31
Cameroon	2	100
Central Africa	1	112
Gambia	1	8
Ghana	1	35
India	26	1040
Indonesia	1	73
Malawi	1	15
Mali	1	175
Malyasia	1	35
Mozambique	1	126
Myanmar	3	89
Namibia	2	24
Nepal	1	29
Nigeria	2	136
Philippines	1	9
Rwanda	1	1
Sierra Leon	1	4
Somalia	1	7
South Africa	1	3
Sudan	1	7
Tanzania	3	129
Togo	1	35
Uganda	1	81
Vietnam	1	27
Zambia	2	132
Zimbabwe	3	204
Total	66	2667

[a]Wild *Arachis* accessions.

(35.7%), followed closely by accessions from Africa (32.7%), representing 15 countries. Seventeen percent of accessions are from South America, 13.6% from North America, 0.6% from Europe, and only 0.5% from Oceania (see Table 3). Of these, 67.1% of the South American germplasm is designated as landrace material, 53.9% of the African germplasm and 42.1% of the Asian germplasm are landraces (see Table 3). The largest number of accessions from any one country is from India, providing 5282 accessions as donation by 22 institutions and 1040 accessions through 22 collection missions.

The wild *Arachis* collection consists of 413 accessions representing 43 taxa. Of these, 292 are FAO-designated. Several of these accessions are derived, however, from splitting an original accession on the basis of a morphological character difference such as flower color, main stem length, or leaf shape. Sixty-nine accessions are either duplicates or selections of another accession. These have been identified and documented. The total number of accessions excluding lost samples, accessions with no passport data, and duplicates and selections is 307. Emphasis is placed on seed increase, characterization, and multiplication of this germplasm. All passport information is available through SINGER at http://singer.cgiar.org.

Future Collection Priorities

The primary objective of the ICRISAT genebank is to conserve the maximum amount of genetic variation with the least amount of duplication. At present, collection priorities are mainly determined on the number of accessions already available from a particular region, the importance of that region in terms of diversity (from agro-morphological studies and increasingly molecular diver-

Table 3. Current status of *Arachis hypogaea* germplasm collection from different countries with 100 or more accessions at ICRISAT.

Continent/country	Total	Landraces
	no.	no.
North America	1807	73
USA	1807	73
South America	2261	1517
Argentina	359	140
Bolivia	427	353
Brazil	720	457
Paraguay	148	117
Peru	344	316
Asia	4759	2003
China	213	67
India	3605	1491
Myanmar	105	70
Africa	4362	2349
Cameroon	104	88
Central African Republic	108	108
Malawi	149	29
Mali	207	193
Mozambique	148	142
Niger	241	21
Nigeria	417	165
Senegal	286	99
South Africa	141	40
Sudan	216	54
Tanzania	417	286
Uganda	243	139
Zaire	110	46
Zambia	272	256
Zimbabwe	653	312
Europe	75	15
Oceania	60	15

sity), and the threat to that diversity. Northern Argentina and southern Bolivia are the primary centers of diversity of peanut (Krapovickas, 1969; Gregory and Gregory, 1976), yet are only represented by 368 and 444 accessions, respectively, in the ICRISAT collection, together constituting only 5.7% of the total. There is an urgent need to collect germplasm from these areas. Similarly, the representation from the secondary centers of diversity—namely Brazil, Paraguay, Peru, Uruguay, and Ecuador—is only 9.54% (Table 3). There is a need to fully explore these areas. Regions of early peanut introduction and those areas that still maintain traditional varieties, such as Laos and China in Asia, and Angola, Madagascar, Namibia and South Africa in Africa, also have been identified as priorities collection areas. There is a need to enhance the diversity of both variety *aequitoriana* and *hirsuta*, which are represented in the ICRISAT collection by just 15 and 20 accessions, respectively.

Conservation Conditions and Collection Management

In the past, peanut germplasm has been conserved under medium-term storage conditions [4 C and 30% relative humidity (RH)] in the form of pods. Under these conditions viability is maintained for 20 to 25 yr. Recently however, due to FAO standards and space restrictions, a decision was made to conserve the collection in the form of seeds, under long-term conditions. These seeds are dried to a moisture content of 4-5% in dryers maintained at 15 C and 15% RH. The seeds are then hermetically sealed in aluminum packets before being transferred to long-term chambers (-18 C, no RH control). Under these conditions, it is predicted that viability will be maintained for 35-50 yr. To date, seeds of 5331 accessions of *A. hypogaea* have been transferred to long-term storage. To enhance the use of groundnut genetic resources, particularly in Africa, a regional working collection is being established in Chitedze, Malawi.

Wild *Arachis* from section *Rhizomatosae* are maintained as vegetative material in concrete ring containers under screen-house conditions. Regeneration and multiplication of wild *Arachis* stored as seed is undertaken in pots in sandy soils under glasshouse conditions. Low seed set of wild *Arachis* is a problem, and seed supply for evaluation and distribution is a limiting factor for many accessions. Optimum regeneration conditions are being investigated for problem species.

Germplasm Distribution

On 26 Oct. 1994, all germplasm collected or acquired by ICRISAT prior to the Convention of Biological Diversity (CBD) was placed under the auspices of the FAO Int. Network of *ex-situ* collections, providing for the free distribution of germplasm provided that no Intellectual Property Rights are taken out on the germplasm by the receiving party or any subsequent party. Germplasm is thus distributed with a Material Transfer Agreement to this effect. Any germplasm collected or acquired post-CBD is obtained from donor countries with a Material Acquisition Agreement. ICRISAT has supplied a total of 86,068 seed samples worldwide over the past 20 yr, together with relevant passport information (Table 4).

Characterization

The vast majority of the peanut germplasm collection has been characterized at ICRISAT Headquarters, Patancheru, Andhra Pradesh, India. Accessions are characterized during both the rainy (June to October) and post-rainy (November to April) seasons for 12 quantitative

Table 4. Status of *Arachis* germplasm distributed to various regions by ICRISAT, 2000.

Region	*A. hypogaea*	*Arachis* species
	no.	no.
Africa	27,281	147
Asia	55,806	1442
Central America	44	5
Europe	1116	45
North America	546	70
Oceania	529	67
South America	516	0
Total	86,068	1776

traits and in either of these seasons for 14 qualitative traits. The range in variation for these traits is shown in Table 5.

Phenotypic Diversity Assessment

Phenotypic diversity in the peanut germplasm collection has been estimated using Shannon Weaver's diversity index (H`) (Shannon and Weaver, 1949) for each of the 14 morphological descriptors in the six botanical varieties (Table 6). A low H` indicates extremely unbalanced frequency of classes for an individual trait and lack of genetic diversity. Among the morphological descriptors, leaf shape had lowest average H` (0.009 ± 0.0038) and the pod beak had the highest average H` (0.431 ± 0.0247). Among the botanical varieties, *vulgaris* has the lowest average H` (0.157 ± 0.0375) and *aequitoriana* had the highest average H` (0.294 ± 0.0480).

Evaluation

A large portion of the peanut collection has been screened for resistance to major biotic and abiotic stresses. Late leaf spot (LLS) caused by *Cercosporidium personatum* (Berk. et Curt.) Deighton [syn.: *Phaeosariopsis personata* (Berk. & Curt.) V. Arx.], rust caused by *Puccinia arachidis* Speg., and early leaf spot (ELS) caused by *Cercospora arachidicola* Hori are the most widely distributed and economically important fungal diseases of peanut. Field screening of approximately 12,000 accessions from 87 countries has revealed 143 rust-resistant lines (Mehan *et al.*, 1994; Subrahamanyam *et al.*, 1995). Fifty-four lines have been identified with resistance to LLS, of which 29 (from nine countries) also show rust resistance (Subrahamanyam *et al.*, 1995). Previous evaluations of wild *Arachis* for LLS have revealed high levels of resistance in seven species. Recently, an additional 58 accessions were evaluated using the detached leaf technique in growth chambers. Fifteen accessions were free from LLS symptoms and 12 accessions were highly resistant.

Evaluation of 11,955 accessions of cultivated peanut in Chitedze, Malawi for reaction to ELS revealed few resistant accessions. In contrast, a recent unreplicated screening trial of 43 accessions of wild *Arachis* species in the same location revealed four entries—*A. triseminata* Krapov. & W.C. Gregory (ICG 8131, PI 338449, GK 12922), *A. sylvestris* (A. Chev.) A. Chev. (ICG 13211, PI 497567, VSW 6676), *A. pintoi* Krapov. & W.C. Gregory (ICG 13222, PI 497575, VSWSa 6791 wh. fl.), and *A. dardani* Krapov. & W.C. Gregory (ICG 14924, VKVeSv 7215)—which were highly resistant (score 2, on a 1-9 scale) to the disease. In a replicated advanced screening trial, seven entries [ICG 14855 (WWs 108), ICG 14856 (PI 221070, WPn 123), ICG 14888 (VpzBmVaDb 13363), ICG 14875 (VfaPzSv 13080), ICG 14907 (WPn 189), ICG 14939 (VPmSv 12893), and ICG 14946 (VSgSv 13371)] were scored as highly resistant (scores 2.0 to 2.3).

Aflatoxin contamination of peanut is a serious problem in most peanut-producing countries. Invasion of peanut seeds by the fungus Aspergillus flavus Link:Fr. and subsequent contamination with aflatoxins may occur pre- or post-harvest. At ICRISAT, screening of 850 germplasm accessions for seed invasion and colonization resulted in

Table 5. Range of variation in cultivated peanut germplasm at ICRISAT.

Trait	Minimum	Maximum	Intermediate (mean)
Stem color	Absent	Present	
Stem hair	Glabrous	Wooly	Hairy, very hairy
Branching pattern	Sequential	Alternate	Irregular
Growth habit	Erect	Procumbent	Decumbent
Leaf color	Yellowish green	Dark green	Light green, green, bottle green
Leaf shape	Cuneate	Lanceolate	Obcuneate, elliptic
Leaf hair	Subglabrous	Profuse and long	Scarce and short, scarce and long, profuse and short
Flower color	Yellow	Garnet	Lemon yellow, light orange, orange, dark orange
Streak color	Yellow	Garnet	Lemon yellow, light orange, orange, dark orange
Peg color	Absent	Present	—
Pod beak	Absent	Prominent	Slight, moderate
Pod constriction	Absent	Very deep	Slight, moderate, deep
Pod reticulation	Smooth	Prominent	Slight, moderate
Seeds per pod	1	5	2, 3, 4
Primary seed color	Off white	Dark purple	Yellow, shades of tan, rose, shades of red, grey-orange, shades of purple
Days to emergence	3 (5)*	18 (20)	8.5 (12.0)
Days to flower	15 (20)	45 (60)	25.1 (37.0)
Leaflet length	15 (15)	86 (94)	52.7 (54.3)
Leaflet width	7 (8)	45 (54)	23.5 (25.3)
Pod length	12 (14)	70 (70)	28.6 (30.4)
Pod width	6 (8)	30 (23)	12.2 (13.2)
Seed length	8 (4)	21 (23)	13.3 (14.1)
Seed width	5 (5)	15 (18)	7.8 (8.7)
100-seed weight	14 (11)	120 (140)	43.7 (51.4)

Table 6. Shannon-Weaver diversity index* for 14 morphological descriptors in the six botanical varieties of peanut in the ICRISAT collection.

Descriptor	Botanical varieties						Avg ± s.e.
	vulgaris	*aequitoriana*	*fastigiata*	*hirsuta*	*hypogaea*	*peruviana*	
Stem color	0.192	0.300	0.267	0.184	0.088	0.246	0.213 ± 0.031
Stem hair	0.207	0.371	0.295	0.538	0.223	0.459	0.349 ± 0.054
Branching pattern	0.092	0.252	0.051	0.086	0.058	0.011	0.092 ± 0.034
Leaf color	0.146	0.217	0.151	0.338	0.113	0.296	0.210 ± 0.037
Leaf shape	0.006	0.000	0.018	0.000	0.080	0.023	0.009 ± 0.004
Leaf hairs	0.087	0.171	0.132	0.141	0.102	0.354	0.164 ± 0.04
Flower color	0.083	0.349	0.233	0.225	0.044	0.253	0.198 ± 0.046
Streak color	0.019	0.349	0.076	0.184	0.044	0.440	0.184 ± 0.071
Peg color	0.020	0.106	0.079	0.000	0.014	0.301	0.087 ± 0.046
Pod beak	0.429	0.541	0.414	0.356	0.428	0.417	0.431 ± 0.025
Pod constriction	0.323	0.461	0.356	0.372	0.359	0.305	0.363 ± 0.022
Pod reticulation	0.384	0.468	0.499	0.281	0.392	0.219	0.374 ± 0.044
Seeds per pod	0.199	0.534	0.596	0.324	0.383	0.040	0.346 ± 0.085
Seed color pattern	0.012	0.000	0.184	0.000	0.077	0.249	0.087 ± 0.044
Average ± s.e.	0.157 ± 0.038	0.294 ± 0.048	0.239 ± 0.048	0.216 ± 0.048	0.167 ± 0.048	0.258 ± 0.048	

*The higher the value the greater the diversity.

the identification or confirmation of resistance in 10 sources (Ah 7223, J 11, U 4-47-7, Var 27, Faizpur, Monir 240-30, PI 337394 F, PI 337409, and UF 71513) (Mehan, 1989). All these genotypes, except Var 27, were resistant also to natural seed infection in the field (Mehan, 1989). Five hundred two accessions also were evaluated for their ability to support aflatoxin B_1 production. Two accessions, U 4-7-5 and VRR 245, only supported production of very low levels of aflatoxin (Mehan *et al.*, 1986). Some genotypes which are resistant to seed colonization by aflatoxigenic fungi support high levels of aflatoxin production, while others that are susceptible to fungal colonization do not support high levels of aflatoxin production, indicating the existence of different resistance mechanisms.

Thirty-five germplasm accessions of wild *Arachis* belonging to 24 species in six sections were evaluated for *in vitro* colonization by artificial inoculation with a recently identified, highly virulent and toxigenic strain of *A. flavus* (isolate *Af* 11-4) and aflatoxin production (Thakur *et al.*, 2000). Four of the 35 accessions tested, including members of *A. triseminata* [ICG 8131 (PI 338449, GK12922) and ICG 14875(VfaPzSv 13080)], *A. chiquitana* Krapov., W.C. Gregory & C.E. Simpson [ICG 11560 (PI 476004, KSSc 36025)], and *A. pusilla* Benth. [ICG 13212 (PI 497572, VSW 6773)] recorded a score of 1 on a 1-4 colonization rating (1 < 5% seed surface colonized and 4 > 50% seed surface colonized). Two of these (ICG 8131 and ICG 11560) recorded very low levels of aflatoxin B_1 (4 and 21 mg/kg, respectively) compared with very high level (> 8000 mg/kg) in susceptible cultivars. Some other promising accessions were ICG 8193 (PI 468154, GK 30011), ICG 8904 (PI 262142, GKP 10034), ICG 13212 (PI 497572, VSW6773), ICG 13261 (PI 476138, VveSv6188), and ICG 14875 (VfaPzSv13080 which showed variation for *in vitro* seed colonization and aflatoxin B_1 content between replications.

The peanut collection has been evaluated for sources of resistance to the major virus diseases of the crop. In epidemic years, groundnut rosette virus disease is devastating in Africa. Evaluation of 11,972 accessions in Malawi has revealed 154 resistant lines. Many of these are breeding lines, and may have been derived from the same source of resistance. Efforts are underway to diversify sources of groundnut rosette virus resistance. Wild *Arachis* germplasm has been screened over the past 3 yr for rosette virus resistance, in Chitedze, Malawi (Subrahmanyam *et al.*, 2001). Twelve accessions showed no incidence of the disease. Accessions of *A. pintoi*, *A. appressipila* Krapov. & W.C. Gregory, and *A. stenosperma* Krapov. & W.C. Gregory consistently showed a very high degree of resistance; in fact, all accessions tested of *A. pintoi* are resistant. In addition, several accessions showed the absence of all three components of groundnut rosette [groundnut rosette assistor virus (GRAV), groundnut rosette virus (GRV), and its satellite RNA] in ELISA and PCR tests. It is important that the mechanisms of resistance are fully understood.

Peanut bud necrosis virus is an important disease in India, and several lines with less than 20% disease incidence in the field have been reported (Dwivedi *et al.*, 1995). Among 42 wild species tested, only *A. diogoi* Hoehne (formerly *A. chacoense*) showed no infection after mechanical or vector-effected inoculation (Subrahmanyam *et al.*, 1985). No source of resistance has been found in the cultivated species against peanut stripe virus (PStV), an important disease in East and Southeast Asia, despite the fact that 9000 accessions have been screened for the disease in Indonesia. Of the 54 wild species evaluated, *A. cardenasii* Krapov. & W.C. Gre-

gory (ICG 11558, PI 475995) could not be infected by mechanical, aphid, and graft transmission tests; while *A. diogoi* (ICG 4983, PI 276235), *A. cardenasii* (ICG 11562, PI 476012 and ICG 12168, PI 476013), *A. stenophylla* Krapov. & W.C. Gregory (ICG 8215, PI 468170), *A. chiquitana* (ICG 11560, PI 476004), and *A. paraguariensis* Chod. et Hassl. (ICG 8973, PI 468176) were infected by grafting, but not by aphid and mechanical inoculations (Prasad Rao *et al.*, 1991). Certain germplasm lines have shown reduced yield loss due to peanut mottle virus (PMV). None of the 7000 accessions screened for peanut clump virus (PCV), causing economic damage in West Africa and India, have shown useful resistance. Fifty wild *Arachis* accessions from section *Arachis* were evaluated in a PCV field trial. Infection was scored visually and using two ELISA tests, each with replicates. Four accessions (ICG 14861, VpoBi9214, *A. kuhlmannii* Krapov. & W.C. Gregory; ICG13217, PI 475887, KSSc 36036, *A. duranensis* Krapov. & W.C. Gregory; ICG 11555, PI 475885, KSBScC 36005-1, *A. duranensis*; and ICG 8206, PI 468322, KGBSPSc 30076, *A. ipaensis* Krapov. & W.C. Gregory) showed no sign of infection in any of the replications in either of the tests.

Over 6500 accessions of cultivated peanut have been evaluated for resistance to jassids (*Empoasca kerri* Pruthi), 5000 accessions for resistance to thrips (*Thrips palmi* Karny), 500 accessions for resistance to aphids (*Aphis craccivora* Koch), 900 accessions for resistance to leaf miner (*Aproaerema modicella* Deventer), and 500 accessions for termites (*Odontotermes* spp.). Several sources of resistance to jassids (31 accessions) and thrips (14 accessions) and tolerance to leaf miner (14 accessions), termites, and aphids have been identified. A number of genotypes have shown multiple resistance. Wightman and Ranga Rao (1994) have listed several wild *Arachis* species that show high levels of resistance to pests. In a recent study, ICG 11555 and ICG 8195 *A. duranensis*. ICG 8216 *A. cardenasii*, ICG 8963 *A. paraguariensis*. and ICG 13212 *A. pusilla* showed high levels of resistance to leaf miner (*A. modicella*), cotton bollworm, (*Helicoverpa armigera* Huv.), and jassid (*E. kerri*).

Oil and protein contents are important quality attributes of peanut. Nearly 8000 accessions have been screened for oil content and 5501 accessions for protein content. Sixty-six lines with > 50% oil and 125 lines with > 30% protein have been identified. Peanut germplasm has been evaluated also for crop growth rate, water use efficiency, and assimilate partitioning (Nageswara Rao *et al.*, 1994). A present priority within the genebank is to compile all evaluation data into a relational database that will be made available through the world-wide web.

Utilization of the Germplasm Collection: Core Collection Development

Utilization of the genetic variability available within the genebank has been limited, with the result that most peanut cultivars are derived from a narrow genetic base. Improvement programs often aim at rapid cultivar development and have relied mostly on use of established cultivars and elite breeding lines (Halward and Wynne, 1991). Novel genetic variation has been used mainly to exploit sources of resistance to pests and diseases (Knauft and Gorbet, 1989). Little effort has been targeted towards identifying germplasm lines for increasing yield potential other than for pest resistance and for nutritional quality (Halward and Wynne, 1991). To enhance the utilization of the collection and provide an entry point for the further exploration of the collection, Frankel (1984) proposed pruning of the collection to a manageable sample or core collection. A core collection contains a subset of accessions from the entire collection that captures most of available genetic diversity of the species (Brown, 1989a). Frankel and Brown (1984) and Brown (1989a,b) described methods to select a core collection using information on the origin and characteristics of the accessions. Based on sampling theory of selectively neutral alleles, it has been argued that a core subset should consist of approximately 10% of the total number of accessions in the collection, with a ceiling of 3000 accessions per species (Brown, 1989a). This level of sampling should retain approximately 70% of the alleles in the entire collection.

The formation of a core collection of 831 accessions by Holbrook *et al.* (1993) from the U.S. germplasm collection of 7432 peanut accessions has provided the basis for a two-stage process for identifying valuable genes in the collection (Holbrook and Anderson, 1995; Holbrook *et al.*, 2000). The first stage involves examining all accessions in the core collection. These data are then used to determine additional accessions in the entire germplasm collection for a second stage of screening. The core collection thus provides an entry point into the entire core collection. Seventy percent of this core was selected by stratification by country of origin, followed by multivariate analyses on morphological data to cluster accessions into groups and then randomly sample 10% from each group. The remaining entries in the core were selected either randomly or randomly after stratification by country of origin, depending on the availability of data.

At ICRISAT the core was selected from a total of 14,310 accessions from 92 countries (Upadhyaya *et al.*, 2001) using a slightly different approach to that of Holbrook *et al.* (1993). Data were recorded for 14 qualitative morphological descriptors—stem color, stem hair, branching pattern, leaf color, leaf shape, leaf hair, flower color, streak color, peg color, pod beak, pod constriction, pod reticulation, number of seeds per pod, and seed color pattern following IBPGR (now IPGRI) and ICRISAT descriptors (1992).

The peanut collection was first stratified by botanical variety within subspecies, i.e., subsp. *hypogaea* var. *hypogaea* and var. *hirsuta*, and subsp. *fastigiata* var. *fastigiata*, var. *peruviana*, var. *aequatoriana*, and var. *vulgaris*, followed by their country of origin. Accessions of the same botanical variety but from small and adjacent countries with similar agroclimates were grouped together (Brown, 1989a), providing 75 groups. In each group, data from 14 morphological descriptors were standardized using the range of each variable to eliminate scale differences (Milligan and Cooper, 1985). This was then subjected to the hierarchical cluster algorithm of Ward

(1963) at R^2 (squared multiple correlation) equal to 0.75, using SAS (SAS Inst., 1989).

From each cluster, approximately 10% of the accessions were randomly selected for inclusion into the core subset which consist of 1704 entries. This was 11.9% of the total number of accessions available. The core subset consists of 584 (34.3%) accessions belonging to variety *vulgaris*, 299 (17.5%) to *fastigiata*, 27 (1.6%) to *peruviana*, 6 (0.4%) *aequatoriana*, 784 (46.0%) *hypogaea*, and four (0.2%) *hirsuta*. Except for *aequatoriana* and *hirsuta* which have only 15 and 20 accessions, respectively, in the entire collection, the representation of botanical varieties in the core subset corresponded with their contribution to the entire collection. Mean comparisons using t-test and distributions using the chi-square test and Wilcoxon's (1945) rank-sum nonparametric test on different descriptors indicated that the genetic variation available for these traits in the entire collection had been preserved in the core. Shannon-Weaver's diversity index for different traits also was similar in the entire collection and core. Phenotypic correlations between different traits, which may be under the control of coadapted gene complexes, were preserved in the core collection. The core collection provides an effective mechanism to enhance the exploitation of groundnut germplasm resources for genetic improvement as well as simplifying aspects of genebank management. A preliminary evaluation of the core has resulted in the identification of 19 new sources of early maturity in the 1999/2000 rainy season (H.D. Upadhyaya, unpubl. data). Some of these sources are similar to the most widely cultivated, early maturing cultivar Chico, but have better pod and seed traits. Five of these lines have been included in the hybridization program at ICRISAT.

Conclusions

During the last two decades significant progress has been made in the collection, characterization, and evaluation of peanut germplasm at ICRISAT. There remains an urgent need to collect germplasm from areas of high diversity and early introduction. Although ICRISAT has supplied a large number of accessions for research and plant breeding throughout the world, progress in the utilization of genetic resources has been slow. Efforts are underway to enhance the utilization of the collection through core collection formation and making passport, characterization and evaluation data accessible through the world-wide web. Molecular techniques are being used increasingly to assess diversity and enhance the efficiency of plant breeding to broaden the genetic base of peanut cultivars. In conclusion, our challenge for the third millennium is to unlock the genetic potential contained in the genebank and use it, through crop improvement, to alleviate poverty and protect the environment.

Literature Cited

Brown, A.H.D. 1989a. Core collections: A practical approach to genetic resources management. Genome 31:818-824.

Brown, A.H.D. 1989b. The case for core collections, pp. 136-155. *In* A.H.D. Brown, O.H. Frankel, D.R. Marshall, and T.J. Williams (eds.) The Use of Plant Genetic Resources. Cambridge Univ. Press, Cambridge, England.

Dwivedi, S.L., S.N. Nigam, D.V.R. Reddy, A.S. Reddy, and G.V. Ranga Rao. 1995. Progress in breeding groundnut varieties with resistance to peanut bud necrosis virus and vector, pp. 35-40. *In* A.M.M. Buiel, J.E. Parlevliet, and J.M. Lenne, (eds.) Recent Studies on Peanut Bud Necrosis Disease. Dept. of Plant Breeding, Univ. of Wageningen/ICRISAT Center, India. Int. Crops Research Inst. for the Semi-Arid Tropics, Hyderabad, India.

Frankel, O.H. 1984. Genetic perspective of germplasm conservation, pp. 161-170. *In* W. Arber, K. Llimensee, W.J. Peacock, and P. Starlinger (eds.) Genetic Manipulations: Impact on Man and Society. Cambridge Univ. Press, Cambridge, England.

Frankel, O.H., and A.H.D. Brown. 1984. Current plant genetic resources—A critical appraisal, pp. 1-13. *In* Genetics: New Frontiers. Vol. IV. Oxford & IBH Publ. Co., New Delhi, India.

Gregory, W.C., and M.P. Gregory. 1976. Groundnut, pp. 151-154. *In* N. W. Simmonds (ed.) Evolution of Crop Plants. Longman Group Ltd., London.

Halward, T.M., and J.C. Wynne. 1991. Generation means analysis for productivity in two diverse peanut crosses. Theor. Appl. Genet. 82:784-792.

Holbrook, C.C., and W.F. Anderson 1995. Evaluation of a core collection to identify resistance to late leafspot in peanut. Crop Sci. 35:1700-1702.

Holbrook, C.C., W.F. Anderson, and R.N. Pittman. 1993. Selection of a core collection from the U.S. germplasm collection of peanut. Crop Sci. 33:859-861.

Holbrook, C.C., P. Timper, and H.Q. Xue. 2000. Evaluation of the core collection approach to identifying resistance to *Meloidogyne arenaria* in peanut. Crop Sci. 40:1172-1175.

IBPGR, and ICRISAT. 1992. Descriptors for Groundnut. Int. Board of Plant Genetic Resources, Rome, Italy, and Int. Crops Research Inst. for the Semi-Arid Tropics, Patancheru, A.P., India.

Knauft, D.A., and D.W. Gorbet. 1989. Genetic diversity among peanut cultivars. Crop Sci. 29:1417-1422.

Krapovickas, A. 1969. The origin, variability, and spread of groundnut (*Arachis hypogaea*), pp. 427-440. *In* R.J. Ucko and C.W. Dimbleby (eds.) The Domestication and Exploitation of Plants and Animals. Duckworth, London.

Mehan, V.K. 1989. Screening of groundnuts for resistance to seed invasion by *Aspergillus flavus* and to aflatoxin production, pp. 323-334. *In* Aflatoxin Contamination of Groundnut: Proc. Int. Workshop, 6-9 Oct. 1989, ICRISAT Center, India. Patancheru, A.P. 502 324, India

Mehan, V.K., D. McDonald, and N. Ramakrishna. 1986. Varietal resistance in peanut to aflatoxin production. Peanut Sci. 13:7-10.

Mehan, V.K., P.M. Reddy, K. Vidyasagar Rao, and D. McDonald. 1994. Components of rust resistance in peanut genotypes. Phytopathology 84:1421-1426.

Milligan, G. W., and M. Cooper. 1985. An examination of procedures for determining the number of clusters in a data set. Psychometrika 50:159-179.

Nageswara Rao, R.C., A.K. Singh, L.J. Reddy, and S.N. Nigam. 1994. Prospects of utilization of genotypic variability for yield improvement in groundnut. J. Oilseeds Res. 11:259-268.

Prasad Rao, R.D.V.J., A.S. Reddy, S.K. Chakrabarty, D.V.R. Reddy, V.R. Rao, and J.P. Moss. 1991. Identification of peanut stripe virus resistance in wild *Arachis* germplasm. Peanut Sci. 18:1-2.

SAS Inst. 1989. SAS/STAT User's Guide. Vers. 6, 4th Ed. SAS Institute, Inc., Cary, NC.

Shannon, C.E., and W. Weaver. 1949. The mathematical theory of communication. Univ. Illinois Press, Urbana, IL.

Subrahmanyam, P., A. M. Ghanekar, B.L. Nolt, D.V.R. Reddy, and D. McDonald. 1985. Resistance to groundnut diseases in wild *Arachis* species, pp. 49-55. *In* J.P. Moss (ed.) Proc. Int. Workshop on Cytogenetics of *Arachis* Species, 31 Oct.-2 Nov. 1983, ICRISAT Center, India. Patancheru, A.P. 502 324, India.

Subrahmanyam, P., D. McDonald, F. Waliyar, L.J. Reddy, S.N. Nigam, R.W. Gibbons, V. Ramanatha Rao, A.K. Singh, S. Pande, P.M. Reddy, and P.V. Subba Rao. 1995. Screening methods and sources of resistance to rust and late leaf spot of groundnut. ICRISAT Info. Bull. No. 47, ICRISAT Patancheru, India.

Subrahmanyam P., R.A. Naidu, L.J. Reddy, P. Lava Kumar, and M.E. Ferguson. 2001. Resistance to groundnut rosette disease in wild *Arachis* species. Ann. Appl. Biol. 139:45-50.

Thakur, R.P., V.P. Rao, S.V. Reddy, and M. Ferguson. 2000. Evaluation of wild *Arachis* germplasm accessions for *in vitro* seed

colonisation and aflatoxin production by *Aspergillus flavus*. Int. *Arachis* Newslet. 20:44-46.
Upadhyaya, H.D., R. Ortiz, P.J. Bramel, and S. Singh 2001. Development of a groundnut core collection using taxonomical, geographical and morphological descriptors. Gene. Res. Crop Evol. 48:(in press).
Ward, J. 1963. Hierarchical grouping to optimize an objective function. J. Amer. Stat. Assoc. 38:236-244.
Wightman, J.A, and G.V. Ranga Rao. 1994. Groundnut pests, pp. 395-469. *In* J. Smartt (ed.) The Groundnut Crop: A Scientific Basis for Improvement. Chapman and Hall, London.
Wilcoxon, F. 1945. Individual comparisons by ranking methods. Biometrics Bull. 1:80-83.

Use of Plant Introductions in Peanut Cultivar Development

T. G. Isleib[1]*, C. C. Holbrook[2], and D. W. Gorbet[3]

ABSTRACT

The genetic base of peanut (*Arachis hypogaea* L.) in the U.S.A. has at times been extremely narrow, particularly in specific production areas where a single cultivar may be grown in near-monoculture. Because peanut is not a native North American species, all U.S. cultivars necessarily trace their ancestry to plant introductions (PIs), but most of the genetic base of current cultivars rests on selections from farmer-stock peanuts of obscure origin. The objectives of this study were to (a) summarize and document the use of introduced genetic resources in cultivar development and (b) estimate the resulting economic impact. Different PIs were used as parents in early breeding programs. B.B. Higgins used Gambian line Basse as a parent of the GA 207 cross that gave rise to selections used in Georgia, Florida, and North Carolina as the basis for further improvement. PI 121067 was one of seven parents used by W.C. Gregory to initiate the program in North Carolina. A different set of PIs including PI 121070, PI 161317, PI 168661, and *A. monticola* Krapov. & Rigoni were used in the Texas and Oklahoma programs. Recycling of lines as parents and exchange of germplasm among breeding programs proliferated these PIs in the pedigrees of cultivars released since 1960. Over the past 20 yr, there have been concerted efforts to incorporate additional germplasm into U.S. breeding populations, usually with the purpose of improving resistance to diseases or pests, but also with the objective of broadening the genetic base. These efforts have had a significant economic impact on U.S. peanut farmers, the largest from the development of cultivars with resistance to Sclerotinia blight (*Sclerotinia minor* Jagger), root-knot nematodes (*Meloidogyne* spp.), and tomato spotted wilt virus. Use of these resistant cultivars has an economic impact of more than $200 million annually for U.S. peanut producers. In the runner and virginia market types, the average PI ancestry of all cultivars was 17.9%. There are several examples of successful cultivars with up to 25% ancestry from a single PI, including Georgia Green and NC-V11. In the spanish market type, most successful cultivars have derived 50% or more of their ancestry from PIs. Several recent or impending releases incorporate PI germplasm but have not yet been proven in the U.S. seed market.

Key Words: *Arachis hypogaea* L., coancestry, disease resistance, genetic vulnerability, genetic resources.

As of July 2000, 119 peanut (*Arachis hypogaea* L.) cultivars had been released in the U.S. (Table 1), 53 released prior to 1961 when the Crop Science Society of America (CSSA) began to register crop cultivars and germplasm (Isleib and Wynne, 1992) and 66 registered with the CSSA after 1960 (registered cultivars, germplasm lines, parental lines, and genetic stocks can be obtained from the National Plant Germplasm System web site at www.ars-grin.gov/npgs) or with the Plant Variety Protection Office. Forty-eight were protected under Plant Variety Protection certificates, 24 of them current, eight expired, and 16 pending. One hundred twenty-eight additional lines have been released as germplasm, parental lines, or genetic stocks (Table 2).

In spite of the large number of cultivars available to growers, the U.S. peanut crop has been characterized as being genetically vulnerable to diseases and insect pests (Hammons, 1972, 1976; Knauft and Gorbet, 1989). This has been due to the commercial success of specific cultivars grown in particular production areas. For example, the runner-type cultivar Florunner dominated production in the southeastern U.S. (Georgia, Florida, and Alabama) from 1972 to 1993, occupying over 60% of the acreage in those years, over 80% from 1974 through 1987, and over 95% from 1976 through 1984. Currently, southeastern production is dominated by the cultivar Georgia Green. The Virginia-Carolina (VC) production area has had less tendency toward monoculture. The most dominant cultivar of the past 40 yr in the VC area was Florigiant which averaged over 60% of the area's acreage from 1974 through 1985, and with a maximum of over 80% in 1979. Since the decline of Florigiant, no cultivar in the VC area has occupied more than 50% of the acreage in a given year. In the southwestern (SW) production area (Texas and Oklahoma) where spanish-type cultivars were the main type produced through the 1970s, there was near-monoculture of Starr in the late 1960s and early 1970s. Over the past 20 yr. there has

[1]Dept. of Crop Science, North Carolina State Univ., Raleigh, NC 27695-7629.
[2]USDA-ARS, Coastal Plain Exp. Sta., Tifton, GA 31793-0748.
[3]Univ. of Florida, N. Florida Res. and Educ. Ctr., 3925 Hwy. 71, Marianna, FL 32446-7906.
*Corresponding author (email: tisleib@cropserv1.cropsci.ncsu.edu).