



OP 73

Sources of Resistance to Groundnut Fungal and Bacterial Diseases: an Update and Appraisal



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Abstract

Groundnut foliar fungal diseases, stem and pod rots, and wilt cause severe pod yield losses worldwide, while aflatoxin contamination causes serious quality problems. This information bulletin updates the list of sources of resistance to six important fungal and bacterial diseases and provides information on some of their agronomic traits and reaction to other diseases. Merits and demerits of these resistance sources that may influence their usage in different situations are highlighted.

Résumé

Sources de résistance aux maladies fongiques et bactériennes de l'arachide: le point de la recherche. Les maladies fongiques foliaires de l'arachide, la pourriture de la tige et des gousses, ainsi que le flétrissement bactérien causent des pertes importantes de rendement en grain et de graves problèmes de qualité chez l'arachide. Ce bulletin d'information met à jour la liste des sources de résistance à six maladies fongiques et bactériennes majeures en fournissant des informations utiles sur leurs traits agronomiques et leur réaction à d'autres maladies. Cet ouvrage met en relief les mérites et les démérites de ces sources de résistance dans le cadre de leur usage dans diverses situations.

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Sources of resistance to groundnut fungal and bacterial diseases: an update and appraisal

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**International Crops Research Institute for the Semi-Arid Tropics
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Foreword

Diseases are the most serious yield-reducing constraints of groundnut in the tropics and semi-arid tropics. Many of these diseases can be controlled effectively by the application of chemicals. However, host-plant resistance remains the most economical, sustainable, and environmentally friendly approach to manage these diseases. In certain situations a judicious combination of host-plant resistance and chemical control may be required. Several publications provide information on sources of resistance to many of these diseases. However, in most cases, the information is incomplete and details on the traits other than the resistance to specific diseases are lacking.

This information bulletin provides a comprehensive updated description of different sources of resistance to some of the most important diseases identified from the world collection of groundnut. Further, it discusses critically the merits and demerits that contribute to their effective use in resistance breeding. This bulletin should serve as a valuable reference source to groundnut scientists engaged in resistance breeding.

I compliment the authors for their exquisite endeavor in bringing out this information bulletin, and hope it will facilitate research efforts towards overcoming disease constraints, thereby sustaining and increasing yields of groundnut.

Y L Nene
Deputy Director General
ICRISAT

Introduction

Groundnut is attacked by several diseases caused by fungi and bacteria. However, only some of them are economically important. Of these economically important diseases, some are more widespread than others. Three foliar fungal diseases, late leaf spot [*Cercosporidium personatum* (Berk. & Curt.) Deighton = *Phaeoisariopsis personata* (Berk. & Curt.) v. Arx], early leaf spot (*Cercospora arachidicola* Hori), and rust (*Puccinia arachidis* Speg.), are the most widespread and destructive. Among the soilborne fungal pathogens, *Aspergillus flavus* Link ex Fries and *A. parasiticus* Speare, and *Sclerotium rolfsii* Sacc. are the most widespread. The infection by *A. flavus* and *A. parasiticus* and the consequent aflatoxin contamination of groundnut poses a serious quality problem that affects the trade in groundnut and groundnut products, and human and animal health. *Sclerotium rolfsii* causes stem and pod rots. The only bacterial disease of economic significance is bacterial wilt caused by *Pseudomonas solanacearum* (Smith) Smith.

Sources of genetic resistance to these fungal and bacterial diseases in the germplasm collection available in the genebank at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) have been documented in earlier publications. However, these publications contain little or no information on the other merits and demerits of such sources. In the absence of such analysis, there is only limited utilization of these resistance sources in breeding programs at ICRISAT and National Agricultural Research Systems (NARS). This publication updates the list of sources of resistance to six important diseases, and provides information on some of their agronomic traits and reactions to other diseases. The available data have been used to identify the uniqueness of an accession(s), and highlight such merits and demerits as may influence its usage in different situations.

Acknowledgment

The authors are grateful to Dr Y L Nene, Deputy Director General, ICRISAT for providing financial support and constant encouragement. They also wish to express their sincere thanks to Dr P J Bramel-Cox, Director, Genetic Resources Division, for her helpful suggestions. The excellent help extended by various NARS and ICRISAT scientists in providing information on certain special features of resistance sources is gratefully acknowledged.

Rust (*Puccinia arachidis*)

Rust (Fig. 1) can cause pod yield losses in excess of 50% (Subrahmanyam and McDonald 1987). However, when it occurs in combination with late leaf spot, losses in pod yield can be as high as 60-70%. Effective field and laboratory techniques for screening for resistance to rust have been developed (Subrahmanyam et al. 1995). To date over 13000 groundnut accessions originating from 89 countries have been screened for resistance to rust at ICRISAT Asia Center (IAC). Of these, 169 accessions with disease scores of 5 or less on a 1-9 scale (Subrahmanyam et al. 1995; Appendix I) have been reported as resistant (Table 1). These resistance sources include 135 landraces, of which 80% belong to *A hypogaea ssp fastigiata var peruviana* that originates predominantly from Peru, one of the secondary centers of diversity for groundnut. These resistance sources are likely to have similar genetic control and a narrow genetic base because of their common origin. Although many of them (e.g., ICGs 7896, 7897, 7899, 10014, 10030, 10052, 10053, 10067, 10933, 10939, 10940, and 10943) have low disease scores (<3), they have poor agronomic characters. They have low shelling outturns, thick pod shells, strong pod reticulation, and unacceptable seed coat colors. Of the 49 resistance sources used in rust resistance breeding



Figure 1. Groundnut rust disease caused by *Puccinia arachidis*.

program at IAC, only two lines (ICG 1697 and ICG 4747) have led to the release of such improved cultivars as ICG (FDRS 4), ICG (FDRS 10), and ICGV 86590 in India. These rust-resistant cultivars produce high pod yields under high disease pressure. However, their adoption has been limited, as their pods are poorly shaped and their shelling outturn is low. Some other sources of resistance identified later in accessions (ICGs 10056,

10567, 10925, 10932, 11108, 12059, 12112, and 12113) that originate from secondary centers of diversity in South America, i.e., Peru and Bolivia and the interspecific hybrids produced from introgression of genes (conferring resistance to rust) from wild *Arachis* species, particularly those involving *A batizocoi* and *A duranensis* [ICGs 11301 (CS 2), 11315 (CS 19), and 11321 (CS 26)], have high levels of resistance in

diverse botanical backgrounds, good agronomic potential, and resistance to other biotic stresses (Table 1). This suggests that the full spectrum of variability from secondary centers of diversity is yet to be explored. The use of the latter resistance sources in a breeding program is likely to produce more acceptable cultivars.

Resistance sources vary in the components of their resistance. However, these components that include infection frequency, lesion diameter, leaf area damage, incubation period, and sporulation index are not fully complementary in most genotypes. In only a few genotypes, e.g., ICGs 10881 and 10890, do these five components reinforce one another (Mehan et al. 1994a). Such genotypes are very useful in resistance breeding programs. Several other genotypes, including ICGs 10014, 10032, 10052, 10567, 10928, 10933, and 10940 should also prove useful resistance donors, as they have long incubation periods, low to medium sporulation indexes, and low leaf area damage. They also have low rust scores when screened in the field (Table 1).

Most of these resistant accessions when tested at locations in India, China, Taiwan, Trinidad, and USA showed stable resistance to rust, with the exception of ICG 1697 (NC Ac 17090), that was moderately resistant in China and susceptible in Taiwan (Subrahmanyam and McDonald 1987). The reasons for this change in the rust reaction of ICG 1697 at locations other than IAC have yet to be explained. Nevertheless, ICG 1697 is important in resistance breeding programs as it also has resistance to such insect pests as the groundnut leaf miner, *Aproaerema modicella* (Deventer) (Wightman and Ranga Rao 1994).

Resistance to rust in cultivated groundnut is recessive and appears to be governed by only a few genes. One-gene (Paramasivam et al. 1990) and two-gene models (Bromfield and Bailey 1972, Tiwari et al. 1984) have been proposed, but are unable to explain the segregation pattern for rust resistance in many crosses. In interspecific derivatives, rust resistance is governed by partially dominant gene (s) (Singh et al. 1984). In quantitative genetic analysis, both additive and non-additive gene effects are reported important (Tiwari et al. 1984, Paramasivam et al. 1990). Combining ability studies have reported ICGs 2716 [EC 76446 (292)], 4747 (PI 259747), 7013 [NC Ac 17133 (RF)], and 7882 (PI 314817) as good combiners for rust resistance (Tiwari et al. 1984, Anderson et al. 1990).

Table 1. Characteristics of sources of resistance to groundnut rust.

ICG ¹	Alternate identity	Origin	Bio. status ²	Bot. variety ³	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color ⁴	Score			Seed colon. ⁸ (%)	Bac. wilt ⁹ (%)
									RST ⁵	LLS ⁶	ELS ⁷		
1697	NC Ac 17090	Peru	LR	PRU	2220	67	47	Tan	4.1	6.6	7.0	38	63
1702	PI 275745	Peru	LR	PRU	-	-	56	Gasp(T+P)	4.7	5.0	7.0	-	-
1707	NC Ac 17132	Peru	LR	PRU	1610	63	62	Purple	4.0	4.0	8.0	43	65
1710	NC Ac 17135	Peru	LR	PRU	1610	48	63	Purple	4.0	4.0	8.0	38	59
2716	EC 76446(292)	Uganda	UN	FST	1540	60	47	Purple	4.4	3.7	8.0	37	88
3527	USA 63	USA	UN	FST	1860	66	60	Purple	4.3	4.7	7.0	71	-
4746	PI 298115	Israel	BL	HYB	990	60	90	Off-white	2.7	7.0	8.0	40	39
4747	PI 259747	Peru	LR	PRU	2050	64	46	Purple	3.7	4.0	7.0	39	56
4995	NC Ac 17506	Peru	UN	PRU	1610	58	66	Purple	4.3	4.3	7.0	-	-
5043	NC Ac 2240	USA	BL	HYR	860	67	45	Purple	5.0	9.0	8.0	-	-
5993	Peru No. 9 B	Peru	LR	FST	-	-	-	Tan	4.7	6.1	-	-	-
6022	NC Ac 927	Sudan	LR	FST	1980	60	70	Purple	4.0	4.0	9.0	43	67
6284	NC Ac 17500	Bolivia	LR	HYR	1030	57	75	Red	5.0	-	8.0	-	-
6330	PI 270806	Zimbabwe	BL	HYB	-	-	51	Tan	2.7	3.3	7.0	67	-
6340	PI 350680	Honduras	LR	FST	2040	66	52	Purple	4.1	4.5	8.0	64	56
6843	NC Ac 2382	USA	BL	FST	-	-	-	Tan	4.3	4.9	-	-	-
7013	NC Ac 17133(RF)	India	BL	FST	1990	58	61	Purple	3.3	4.0	7.0	40	58
7200	PI 270799	Zimbabwe	BL	FST	1915	68	48	Red	4.5	6.0	9.0	-	-
7205	PI 275692	Brazil	LR	FST	-	70	60	Tan	4.9	5.9	8.0	82	-
7296	203/66,WCG 190	Peru	LR	PRU	-	74	56	Tan	2.7	9.0	8.0	-	-
7320	NC Ac 17656	Unknown	BL	FST	-	-	-	Gasp(T+P)	4.3	9.0	7.0	-	-
7340	WCG 182,198/66	Peru	LR	PRU	-	-	72	Tan	4.3	9.0	8.0	-	-
7353	PI 262129	Peru	LR	PRU	-	-	45	Tan	4.0	9.0	8.0	-	-
7433	NC Ac 17518	Brazil	LR	FST	1280	62	65	Gasp(T+P)	4.7	9.0	7.0	-	-
7620	NC Ac 17505	Peru	LR	PRU	1340	58	61	Gasp(T+P)	4.7	9.0	7.0	60	-

Continued....

Table 1. Continued....

ICG ¹	Alternate identity	Origin	Bio. status ²	Bot. variety ³	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color ⁴	Score			Seed colon. ⁸ (%)	Bac. wilt ⁹ (%)
									RST ⁵	LLS ⁶	ELS ⁷		
7621	NC Ac 17718	USA	BL	HYB	-	-	33	Tan	2.7	5.0	8.0	38	-
7630	WCG 190,204/66	Peru	LR	PRU	-	-	62	Tan	2.7	9.0	8.0	-	-
7881	PI 215696	Peru	LR	PRU	1700	61	41	D purple	4.3	3.7	7.0	48	49
7882	PI 314817	Peru	LR	PRU	1860	67	46	Tan	3.3	7.0	9.0	32	44
7883	PI 315608	Israel	BL	HYB	880	62	93	Off-white	3.0	7.0	7.0	40	100
7884	PI 341879	Israel	LR	FST	1690	60	50	Purple	3.0	3.7	7.0	33	82
7885	PI 381622	Honduras	LR	FST	1560	62	47	Purple	3.0	4.3	7.0	54	86
7886	PI 390593	Peru	LR	PRU	1810	64	46	Tan	2.7	-	8.0	57	54
7887	PI 390595	Peru	LR	PRU	1830	59	56	Purple	3.7	-	7.0	64	40
7888	PI 393516	Peru	LR	PRU	1110	50	39	White/Tan	4.7	3.3	8.0	-	-
7889	PI 393517	Peru	LR	PRU	2050	70	42	White	3.3	6.0	8.0	-	60
7890	PI 393526	Peru	LR	PRU	1650	67	48	Purple	2.3	-	8.0	40	-
7891	PI 393527	Peru	LR	HYR	-	67	63	Red	2.7	-	7.0	-	-
7892	PI 393527-B	Peru	LR	HYB	1570	54	70	D red	3.3	7.0	8.0	-	-
7893	PI 393531	Peru	LR	PRU	-	67	55	Gasp(T+P)	2.0	7.0	9.0	-	20
7894	PI 393641	Peru	LR	PRU	1710	64	53	Gasp(T+P)	4.0	4.7	8.0	-	20
7895	PI 393643	Peru	LR	PRU	1140	58	51	Tan	3.0	7.0	9.0	64	86
7896	PI 393646	Peru	LR	PRU	2040	70	43	L purple	3.0	7.0	8.0	46	40
7897	PI 405132	Venezuela	LR	FST	1640	56	52	Purple	2.7	4.0	8.0	62	80
7898	PI 407454	Ecuador	LR	AEQ	1920	63	51	Tan	3.3	7.0	8.0	-	65
7899	PI 414331	Honduras	BL	HYB	1000	54	46	Tan	2.7	7.0	7.0	53	-
7900	PI 414332	Honduras	BL	HYB	1510	71	63	Tan	2.7	7.0	8.0	-	25
8044	NC Ac 10034	South Africa	BL	FST	940	70	53	Tan	2.7	-	8.0	-	-
9185	PI 343419	Israel	BL	FST	-	-	74	Overo(O+R)	2.7	-	7.0	-	-
9294	58-295	Burkina Faso	LR	HYB	-	-	56	Tan	4.7	6.3	9.0	-	-

Continued....

Table 1. Continued....

ICG ¹	Alternate identity	Origin	Bio. status ²	Bot. variety ³	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color ⁴	Score			Seed colon. ⁸ (%)	Bac. wilt ⁹ (%)
									RST ⁵	LLS ⁶	ELS ⁷		
10003	SP 424 Gasp	Peru	LR	PRU	-	-	68	Gasp(T+P)	4.9	5.9	8.0	-	-
10005	SP 425 Flesh	Peru	LR	PRU	1520	67	58	Tan	4.7	6.6	8.0	-	-
10010	PI 476143	Peru	LR	PRU	1100	51	45	Gasp(T+P)	4.0	5.0	8.0	-	-
10013	SPZ 452 Flesh	Peru	LR	PRU	1723	76	48	Tan	4.5	6.7	9.0	-	-
10014	PI 476145	Peru	LR	PRU	1390	59	39	Tan	2.7	6.0	8.0	-	-
10020	PI 476149	Peru	LR	PRU	-	67	58	Tan	2.7	-	8.0	48	-
10021	PI 476149	Peru	LR	PRU	2120	63	55	D purple	2.3	9.0	9.0	-	-
10022	PI 476151	Peru	LR	PRU	2455	75	63	D purple	2.3	9.0	9.0	-	-
10023	PI 476152	Peru	LR	PRU	-	53	36	Tan	4.3	4.7	7.0	74	-
10025	PI 476162	Peru	LR	PRU	-	67	61	Tan	3.0	6.0	8.0	27	-
10028	PI 476163	Peru	LR	PRU	2470	72	59	Purple	4.7	5.0	8.0	-	-
10029	PI 476164	Peru	LR	PRU	-	-	-	Gasp(T+P)	4.3	5.0	8.0	-	-
10030	PI 476166	Peru	LR	PRU	1350	57	45	Gasp(T+P)	2.0	6.0	9.0	37	-
10031	PI 476168	Peru	LR	PRU	-	-	45	Tan	2.3	6.0	9.0	-	-
10032	PI 476168	Peru	LR	PRU	2430	74	48	Tan	3.0	6.0	8.0	-	-
10034	PI 476172	Peru	LR	PRU	1435	64	40	Tan	2.7	6.0	6.0	44	-
10035	PI 476172	Peru	LR	PRU	2500	69	75	Purple	4.0	3.7	7.0	-	-
10037	PI 476174	Peru	LR	PRU	2450	70	53	Tan	2.7	7.0	9.0	42	-
10039	PI 476174	Peru	LR	PRU	2270	65	60	Purple	2.7	6.0	8.0	50	-
10040	PI 476176	Peru	LR	PRU	-	-	46	Gasp(T+P)	4.7	-	8.0	-	-
10042	PI 476177	Peru	LR	PRU	1530	70	54	L purple	2.3	7.0	9.0	43	-
10043	SPZ 485 Flesh	Peru	LR	PRU	1383	69	50	Tan	4.7	6.6	9.0	-	-
10047	PI 476179	Peru	LR	PRU	1530	69	52	L purple	2.7	7.0	9.0	36	-
10048	PI 476179	Peru	LR	PRU	1170	69	54	Tan	2.7	7.0	8.0	48	-
10049	PI 476180	Peru	LR	PRU	1920	66	44	Tan	2.3	7.0	8.0	33	-

Continued....

Table 1. Continued....

ICG ¹	Alternate identity	Origin	Bio. status ²	Bot. variety ³	Pod		Shelling		100-seed			Score			Seed colon. ⁸ (%)	Bac. will ⁹ (%)
					yield (kg ha ⁻¹)	outturn (%)	mass (g)	Seed color ⁴	RST ⁵	LLS ⁶	ELS ⁷					
10051	PI 476180	Peru	LR	PRU	-	65	53	L purple	2.7	7.0	9.0	-	-			
10052	PI 476182	Peru	LR	PRU	-	64	54	Tan	2.3	7.0	7.0	-	-			
10053	PI 476183	Peru	LR	PRU	-	61	57	Tan	2.0	7.0	8.0	-	-			
10054	PI 476183	Peru	LR	PRU	1595	72	54	L red	2.7	7.0	8.0	44	-			
10055	PI 476183	Peru	LR	PRU	-	-	-	Striped	4.3	-	8.0	-	-			
10056	PI 476184	Peru	LR	PRU	2130	70	56	Tan	3.3	7.0	9.0	55	-			
10057	PI 476184	Peru	LR	PRU	-	73	53	L purple	2.7	7.0	9.0	45	-			
10058	PI 476185	Peru	LR	PRU	1535	73	55	Tan	2.7	7.0	9.0	42	-			
10059	PI 476185	Peru	LR	PRU	1590	71	43	L purple	3.0	7.0	9.0	36	-			
10060	PI 476186	Peru	LR	PRU	1995	69	61	Tan	3.0	7.0	9.0	50	-			
10061	PI 476186	Peru	LR	PRU	920	68	49	Purple	2.3	7.0	9.0	40	-			
10062	PI 476187	Peru	LR	PRU	1080	68	48	Purple	2.7	7.0	9.0	52	-			
10063	PI 476188	Peru	LR	PRU	1645	72	51	Purple	2.3	7.0	9.0	45	-			
10064	PI 476189	Peru	LR	PRU	1200	52	50	Tan	3.0	6.0	8.0	-	-			
10065	PI 476189	Peru	LR	PRU	-	65	66	Purple	2.3	7.0	8.0	32	-			
10067	PI 476191	Peru	LR	PRU	1340	60	48	Red	2.7	7.0	9.0	30	-			
10068	PI 476192	Peru	LR	PRU	1238	68	52	Red	2.3	7.0	8.0	39	-			
10069	PI 476193	Peru	LR	PRU	-	57	51	Tan	3.0	7.0	8.0	-	-			
10070	PI 476193	Peru	LR	PRU	1255	69	53	Purple	3.7	7.0	9.0	52	-			
10073	PI 476197	Peru	LR	PRU	1470	68	54	L purple	2.3	7.0	9.0	28	-			
10074	PI 476198	Peru	LR	PRU	2088	67	57	Purple	5.0	6.8	9.0	73	-			
10096	TGR 421	Zimbabwe	LR	VUL	-	-	57	Tan	5.0	6.5	-	-	-			
10286	75-137	Nigeria	BL	HYB	730	60	43	Tan	5.0	6.6	-	-	-			
10567	No. 2	Peru	LR	PRU	2050	72	56	Tan	4.0	6.2	9.0	-	-			
10881	BZC 372 Red	Bolivia	LR	VUL	-	-	-	D red	3.1	5.4	8.0	-	-			

Continued....

Table 1. Continued....

ICG ¹	Alternate identity	Origin	Bio. status ²	Bot. variety ³	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color ⁴	Score			Seed colon. ⁸ (%)	Bac. wilt ⁹ (%)
									RST ⁵	LLS ⁶	ELS ⁷		
10884	PI 475981	Bolivia	LR	HYB	1080	68	65	Overo(R+W)	2.7	-	8.0	84	-
10887	KSSc 402 Red	Bolivia	LR	HYB	-	72	66	D red	3.8	6.3	8.0	-	-
10888	PI 476015	Peru	LR	PRU	-	66	52	Gasp(T+P)	2.7	7.0	8.0	-	-
10889	PI 476016	Peru	LR	FST	920	63	45	D red	3.3	4.3	8.0	76	-
10890	SPA 406 Red	Peru	LR	FST	-	70	59	Red	3.8	4.9	8.0	-	-
10915	PI 476148	Peru	LR	PRU	1510	68	49	Gasp(T+P)	2.3	5.0	6.0	54	-
10916	SPZ 457 Gasp	Peru	LR	PRU	1395	59	55	Gasp(T+P)	4.9	6.0	7.0	-	-
10918	PI 476151	Peru	LR	PRU	1900	65	43	Tan	2.7	-	9.0	-	-
10919	PI 476151	Peru	LR	PRU	1880	71	57	L purple	3.3	7.0	7.0	63	-
10925	PI 476159	Peru	LR	PRU	2350	71	49	Tan	3.0	7.0	7.0	23	-
10927	PI 476160	Peru	LR	PRU	880	66	43	Gasp(T+P)	2.7	7.0	8.0	45	-
10928	PI 476160	Peru	LR	PRU	1895	72	50	Tan	2.7	7.0	8.0	49	-
10932	PI 476165	Peru	LR	PRU	2170	70	47	Tan	2.7	7.0	7.0	25	-
10933	PI 476166	Peru	LR	PRU	1830	63	47	Tan	2.7	9.0	7.0	23	-
10935	PI 476168	Peru	LR	PRU	2040	67	53	Purple	2.3	7.0	7.0	31	-
10936	PI 476168	Peru	LR	PRU	-	70	83	Purple	4.3	4.0	8.0	-	-
10937	PI 476169	Peru	LR	PRU	1710	71	58	Purple	3.0	7.0	7.0	53	-
10939	PI 476172	Peru	LR	PRU	1190	52	50	Gasp(T+P)	2.3	7.0	8.0	-	-
10940	PI 476173	Peru	LR	PRU	978	49	49	Gasp(T+P)	2.3	5.0	8.0	-	-
10941	PI 476174	Peru	LR	PRU	1018	55	52	G orange	4.7	4.7	6.0	67	-
10943	PI 476175	Peru	LR	PRU	1530	63	44	Purple	2.7	7.0	6.0	28	-
10945	PI 476175	Peru	LR	PRU	1650	60	47	Rose	3.0	8.0	7.0	-	-
10954	PI 476180	Peru	LR	PRU	1630	71	53	Purple	3.0	7.0	7.0	29	-
10962	PI 476186	Peru	LR	PRU	1750	58	44	L purple	2.7	7.0	8.0	-	-
10963	PI 476186	Peru	LR	PRU	1290	60	48	L purple	2.7	7.0	8.0	47	-

Continued....

Table 1. Continued....

ICG ¹	Alternate identity	Origin	Bio. status ²	Bot. variety ³	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color ⁴	Score			Seed colon. ⁸ (%)	Bac. wilt ⁹ (%)
									RST ⁵	LLS ⁶	ELS ⁷		
10964	PI 476188	Peru	LR	PRU	1870	68	48	L purple	2.3	7.0	8.0	44	-
10966	PI 476188	Peru	LR	PRU	1255	67	53	Tan	3.0	7.0	7.0	47	-
10969	PI 476190	Peru	LR	PRU	1830	70	50	L purple	2.3	7.0	8.0	33	-
10974	PI 476195	Peru	LR	PRU	1190	63	46	L purple	2.3	7.0	8.0	-	-
10978	PI 476197	Peru	LR	PRU	-	75	52	L purple	4.1	6.5	8.0	-	-
11073	PI 476151	Peru	LR	PRU	1285	71	56	L purple	3.0	-	7.0	67	-
11080	PI 476169	Peru	LR	PRU	1710	54	55	Tan	2.7	6.0	8.0	48	-
11088	PI 476196	Peru	LR	PRU	1400	63	51	L red	2.7	7.0	7.0	43	-
11094	ZFA 3186-1	Zambia	LR	HYR	-	-	79	Tan	4.6	5.3	-	-	-
11108	PI 476195	Peru	LR	PRU	1930	70	56	L red	2.7	7.0	8.0	46	-
11182	PI 476015	Peru	LR	PRU	-	-	58	Tan	2.7	5.0	8.0	65	-
11183	PI 476020	Peru	LR	PRU	1043	56	50	L purple	2.7	7.0	7.0	35	-
11269	RM 70-1	Tanzania	LR	HYB	-	-	-	Tan	4.5	5.9	9.0	-	-
11270	RM 70-2	Tanzania	LR	HYB	-	-	52	Red	4.8	6.8	-	-	-
11282	SPA 411	Peru	LR	FST	1048	72	56	Red	4.5	6.4	7.0	-	-
11285	SPZ 473 Gasp	Peru	LR	PRU	-	-	53	Gasp(T+P)	4.3	6.9	7.0	-	-
11292	ZM 2617-1	Zambia	LR	HYB	-	-	60	D tan	4.3	6.6	-	-	-
11295	Blakeslee 4-1	Ecuador	LR	AEQ	-	-	63	Rose	4.8	6.6	-	-	-
11301	CS 2	India	ID	VUL	3440	-	-	Tan	1.7	8.0	-	-	-
11303	CS 4	India	ID	VUL	2300	-	-	Tan	4.7	5.8	9.0	-	-
11310	CS 14	India	ID	VUL	3600	-	-	Red	2.0	7.0	-	-	-
11312	CS 16	India	ID	VUL	5430	-	-	Red	4.0	4.5	-	-	-
11315	CS 19	India	ID	VUL	2290	-	-	Red	2.0	8.0	7.0	-	-
11317	CS 22	India	ID	VUL	3150	-	-	D red	2.0	4.0	8.0	-	-
11321	CS 26	India	ID	VUL	3110	-	-	D red	2.0	4.0	8.0	-	-

Continued....

Table 1. Continued....

ICG ¹	Alternate identity	Origin	Bio. status ²	Bot. variety ³	Pod		Shelling outturn (%)	100-seed mass (g)	Seed color ⁴	Score			Seed colon. ⁸ (%)	Bac. wilt ⁹ (%)
					yield (kg ha ⁻¹)	yield (%)				RST ⁵	LLS ⁶	ELS ⁷		
11325	CS 30	India	ID	VUL	4890	-	-	56	Red	2.0	3.4	-	-	-
11337	CS 46	India	ID	VUL	5280	74	-	60	D red	3.0	2.9	9.0	-	-
11341	CS 52	India	ID	VUL	3260	-	-	-	Tan	3.0	5.0	8.0	-	-
11485	PI 393530	Peru	LR	PRU	-	64	-	68	Purple	5.0	3.7	9.0	50	-
11567	Non-nod	India	BL	VUL	-	-	-	43	D purple	3.9	5.0	-	-	-
11899	RS 033-3-1	Mali	LR	HYB	-	-	-	50	Tan	4.8	6.9	9.0	-	-
11992	RS 122-2 Rose	Mali	LR	HYB	-	-	-	49	Tan	4.3	6.5	8.0	-	-
12059	BZCJ 392 Tan	Bolivia	LR	HYR	-	-	-	112	Tan	4.7	5.5	-	-	-
12112	SPZ 485 LPL	Peru	LR	PRU	-	-	-	-	Purple	4.7	5.1	8.0	-	-
12113	SPZ 496 Gasp	Peru	LR	PRU	2190	60	-	53	Gasp(T+P)	4.0	6.1	7.0	-	-
12724	KSSc 805-1 Tan	Bolivia	LR	HYR	-	-	-	-	Tan	4.9	-	-	-	-
12726	KSSc 818-1	Bolivia	LR	HYB	-	-	-	-	Gasp(R+T)	3.9	6.5	-	-	-
12727	KSSc 818-2 Pink	Bolivia	LR	HYB	-	-	-	-	L red	4.2	-	-	-	-
13916	CS 9	India	ID	VUL	3510	-	-	-	Red	3.0	4.0	-	-	-
13919	799	India	ID	-	2340	-	-	-	Red	2.0	3.0	-	-	-
13920	838	India	ID	-	3180	-	-	-	Red	2.0	4.0	-	-	-
13921	856	India	ID	-	3110	-	-	-	Red	2.0	5.0	-	-	-
13922	2245	India	ID	-	3080	-	-	-	Red	2.0	4.0	-	-	-
13923	2256	India	ID	-	3270	-	-	-	Red	2.0	6.0	-	-	-

1. ICRISAT groundnut accession number.

2. Biological status: LR = Landrace, BL = Breeding line, UN = Unknown; RC = Released cultivar, ID = Interspecific derivative.

3. Botanical variety: VUL = *vulgare*, FST = *fastigiata*, HYB = *hypogaea* (bunch), HYR = *hypogaea* (runner), PRU = *peruviana*, AEC = *aequatoriana*.

4. D = Dark, L = Light, G = Greyed, T = Tan, P = Purple, R = Red, W = White, O = Rose, Gasp = Flecks of color, Overo = Blotch.

5. RST = Rust.

6. LLS = Late leaf spot.

7. ELS = Early leaf spot.

8. Seed colonization by *A. niger*.

9. Bacterial wilt incidence.

See Appendix 1 for 1-9 scale used for RST, LLS, and ELS resistance.

Tabulated ELS scores are from screening in Malawi.

Source: ICRISAT 1986, Mehan et al. 1996, Subrahmanyam et al. 1995.

Late leaf spot (*Phaeoisariopsis personata*)

Late leaf spot (LLS) (Fig. 2) can cause up to 55% losses in pod yield (Subrahmanyam and McDonald 1987). Screening over 13000 accessions at IAC led to the identification of 69 genotypes with resistance (disease score ranging between 3 and 5 on a 1-9 scale) to LLS (Subrahmanyam et al. 1995, ICRISAT 1986, Mehan et al. 1996). Forty-nine of these resistance sources are landraces, mainly from Peru var *peruviana*. Most have low pod yields, and low shelling outturn. Like the rust resistance sources, most of them have red, purple, or variegated seeds that are not acceptable colors. Of the 69 LLS-resistant sources, only 19 have been used in resistance breeding programs at IAC. Only one of them (ICG 4747 with a disease score of 4) has resulted in the release of such resistant cultivars as ICG (FDRS 4) and ICGV 86590 from IAC, and Girnar 1 from the Indian national program. But, these cultivars have only low levels of resistance to LLS (disease scores 6.0 to 7.5), probably because of the emphasis laid on maintaining or increasing pod yield potential rather than on disease resistance during the selection process. The other commonly used resistance source is ICG 2716 [EC 76446 (292)], but this has not yet resulted in the release of any resistant cultivar. Pod and seed characteristics, and yield potential limit the use of most sources of resistance. Nevertheless, some resistant accessions (ICGs 10920, 11182, 12720) from Peru and Ecuador, and interspecific derivatives (Fig. 3) bred after incorporating genes that confer resistance from such wild *Arachis* species as *A cardenasii* (ICGs 11317, 11325, 11337, 13917, 13919), besides being of diverse origin, offer high levels of resistance in different botanical backgrounds with good agronomic potential (Table 2). The use of such sources should help to develop lines with high levels of resistance in good agronomic backgrounds, and to overcome the limitations of sources identified in the early stages of screening.

Resistance to rust and LLS is reported to be correlated ($r = 0.48-0.60$) (Anderson et al. 1990). The

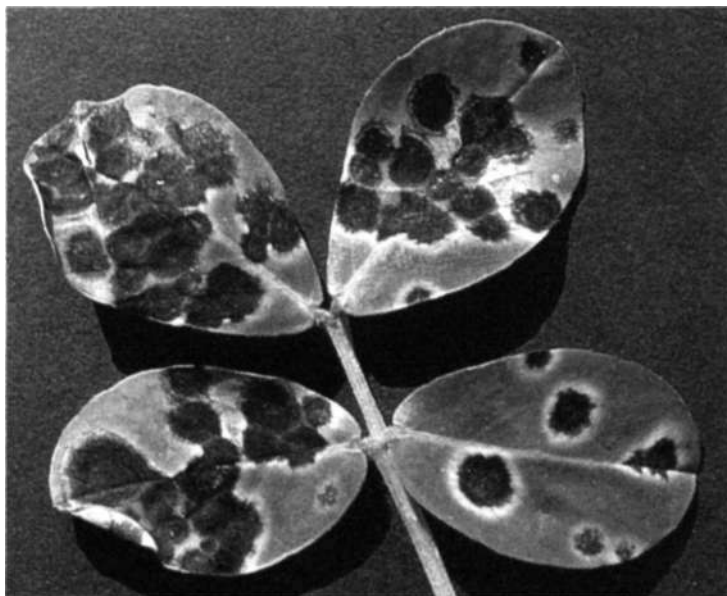


Figure 2. Groundnut late leaf spot disease caused by *Phaeoisariopsis personata*.



Figure 3. An interspecific derivative, ICG 11325 showing resistance to rust and late leaf spot compared to a susceptible cultivar.

interspecific derivative, ICG 13917 [259-2 (red)], that has shown a high level of stable LLS resistance across several locations in southeast Asia and Africa, and also has resistance to ELS and rust should be particularly useful in breeding for multiple resistance.

There is an additional important set of 42 LLS-resistance sources that are also resistant to rust. Their use (particularly those with good agronomic traits) in breeding programs should prove advantageous.

Resistance to LLS is partial (not complete, as several components influence the resistance) and is similar to the 'slow rusting' type of resistance. Genetic variability for the various components of LLS resistance exists in resistance sources. The extent of sporulation, lesion size, and latent period are highly correlated with each other, and with the percentage of necrotic area in infected leaves. Sporulation, lesion size, lesion number, and latent period are important components that contribute to low field scores for LLS (Chitekwa et al. 1988, Anderson et al. 1990). ICGs 2716 and 4747 have fewer lesions, longer incubation periods, and lower sporulation rates than susceptible cultivars in India (Nevill 1981).

Most of these sources of LLS resistance, when tested at locations within India and worldwide, were generally stable with some occasional minor changes in their relative disease scores. Such variation in disease scores probably reflects differences in the time of onset of disease, inoculum pressure, environmental conditions, and the stage of disease scoring rather than differences in the LLS pathogen or genotypes.

Both simple (Tiwari et al. 1984) and complex (Nevill 1982) inheritance of resistance to LLS are reported in the literature. While Tiwari et al. (1984) reported a two-gene control of resistance, Nevill (1982) proposed a five-loci genetic model to explain the inheritance of resistance with the completely recessive alleles determining resistance. The triploid hybrids of crosses between resistant wild species and susceptible cultivars were susceptible, indicating that resistance was recessive (Sharief et al. 1978). Narrow-sense heritability estimates in crosses involving ICG 2716 [EC 76446 (292)] ranged from 0.18 to 0.74 (Anderson et al. 1991). Combining ability analysis for components of resistance to LLS indicated the predominant role of additive gene effects for most of the components (Kornegay et al. 1980, Anderson et al. 1986). GP-NC 343, FESR 5-P2-B1, NC Ac 17090, NC 5, NC Ac 3139, Florigiant, and NC 2 were reported to be good combiners for LLS resistance in USA, but they have either not expressed LLS resistance at IAC, or are not available in the world collection at IAC. GP-NC 343, NC 5, and FESR 5-P2-B1 were also found to be good combiners for ELS resistance in these studies.

Table 2. Characteristics of sources of resistance to groundnut late leaf spot.¹

ICG	Alternate identity	Origin	Bio. status	Bot. variety	Pod		Shelling		100-seed mass (g)	Seed color	Score			Seed colon. (%)	Bac. wilt (%)
					yield (kg ha ⁻¹)	outturn (%)	LLS	RST			ELS				
1702	PI 275745	Peru	LR	PRU	-	-	-	-	56	Gasp(T+P)	5.0	4.7	7.0	-	-
1703	NC Ac 17127	Peru	LR	PRU	1190	51	-	-	57	Gasp(T+P)	5.0	4.7	7.0	42	15-20
1705	NC Ac 17130	Peru	LR	PRU	1150	50	-	-	54	Tan	4.7	-	7.0	42	10-15
1707	NC Ac 17132	Peru	LR	PRU	1610	63	-	-	62	Purple	4.0	4.0	8.0	43	65
1710	NC Ac 17135	Peru	LR	PRU	1610	48	-	-	63	Purple	4.0	4.0	8.0	38	59
2716	EC 76446(292)	Uganda	UN	FST	1540	60	-	-	47	Purple	3.7	4.4	8.0	37	88
3527	USA 63	USA	UN	FST	1860	66	-	-	60	Purple	4.7	4.3	7.0	71	-
4747	PI 259747	Argentina	LR	PRU	2050	64	-	-	46	Purple	4.0	3.7	7.0	39	56
4790	Krapovickas16	Peru	LR	FST	2080	65	-	-	61	Purple	4.3	9.0	8.0	65	80
4995	NC Ac 17506	Sudan	UN	PRU	1610	58	-	-	66	Purple	4.3	4.3	7.0	-	-
6022	NC Ac 927	Zimbabwe	LR	FST	1980	60	-	-	70	Purple	4.0	4.0	9.0	43	67
6330	PI 270806	Honduras	BL	HYB	-	-	-	-	51	Tan	3.3	2.7	7.0	67	-
6340	PI 350680	India	LR	FST	2040	66	-	-	52	Purple	4.5	4.1	8.0	64	56
6843	NC Ac 2382	Peru	BL	FST	-	-	-	-	-	Tan	4.9	4.3	-	-	-
7013	NC Ac 17133(RF)	Peru	BL	FST	1990	58	-	-	61	Purple	4.0	3.3	7.0	40	58
7232	PI 262127	USA	LR	PRU	-	-	-	-	-	Purple	4.3	9.0	8.0	-	-
7406	PI 262121	Peru	LR	PRU	-	-	-	-	36	Purple	4.7	9.0	8.0	74	-
7621	NC Ac 17718	Peru	BL	HYB	-	-	-	-	33	Tan	5.0	2.7	8.0	38	-
7628	PI 275747	Unknown	LR	PRU	-	56	-	-	48	D purple	5.0	9.0	8.0	-	-
7712	NC Ac 16167	Peru	LR	PRU	-	-	-	-	-	Tan	5.0	9.0	8.0	74	-
7777	Sam col 186	Israel	LR	FST	-	-	-	-	52	Red	5.0	-	8.0	-	-
7881	PI 215696	Honduras	LR	PRU	1700	61	-	-	41	D purple	3.7	4.3	7.0	48	49
7884	PI 341879	Peru	LR	FST	1690	60	-	-	50	Purple	3.7	3.0	7.0	33	82
7885	PI 381622	Venezuela	LR	FST	1560	62	-	-	47	Purple	4.3	3.0	7.0	54	86
7888	PI 393516	Peru	LR	PRU	1110	50	-	-	39	White/Tan	3.3	4.7	8.0	-	-

Continued....

Table 2. Continued....

ICG	Alternate identity	Origin	Bio. status	Bot. variety	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color	Score			Seed colon. (%)	Bac. wilt (%)
									LLS	RST	ELS		
7894	PI 393641	Peru	LR	PRU	1710	64	53	Gasp(T+P)	4.7	4.0	8.0	-	20
7897	PI 405132	Peru	LR	FST	1640	56	52	Purple	4.0	2.7	8.0	62	80
10010	PI 476143	Peru	LR	PRU	1100	51	45	Gasp(T+P)	5.0	4.0	8.0	-	-
10016	PI 476146	Peru	LR	PRU	-	56	42	Gasp(T+P)	4.7	-	7.0	60	-
10023	PI 476152	Peru	LR	PRU	-	53	36	Tan	4.7	4.3	7.0	74	-
10028	PI 476163	Peru	LR	PRU	2470	72	59	Purple	5.0	4.7	8.0	-	-
10029	PI 476164	Peru	LR	PRU	-	-	-	Gasp(T+P)	5.0	4.3	8.0	-	-
10035	PI 476172	Peru	LR	PRU	2500	69	75	Purple	3.7	4.0	7.0	-	-
10038	PI 476174	Peru	LR	PRU	2350	66	72	Purple	4.0	6.0	8.0	-	-
10075	PI 476204	Peru	LR	FST	-	58	81	Red	5.0	-	7.0	69	-
10450	PI 215724	Peru	LR	PRU	1100	71	53	Purple	4.7	-	7.0	-	-
10889	PI 476016	Peru	LR	FST	920	63	45	D red	4.3	3.3	8.0	76	-
10890	SP 406 Red	Peru	LR	FST	-	70	59	Red	4.9	3.8	8.0	-	-
10891	PI 476018	Peru	LR	PRU	-	-	-	Red	5.0	-	8.0	-	-
10903	PI 476036	Peru	LR	FST	-	-	90	Tan	4.3	7.0	8.0	-	-
10915	PI 476148	Peru	LR	PRU	1510	68	49	Gasp(T+P)	5.0	2.3	6.0	54	-
10920	PI 476152	Peru	LR	PRU	-	65	58	Tan	4.0	-	8.0	-	-
10931	PI 476164	Peru	LR	PRU	1725	73	44	L tan	3.7	7.0	8.0	48	-
10936	PI 476168	Peru	LR	PRU	-	70	83	Purple	4.0	4.3	8.0	-	-
10940	PI 476173	Peru	LR	PRU	978	49	49	Gasp(T+P)	5.0	2.3	8.0	-	-
10941	PI 476174	Peru	LR	PRU	1018	55	52	G orange	4.7	4.7	6.0	67	-
10949	PI 476178	Peru	LR	PRU	1660	64	66	D purple	4.3	-	7.0	-	-
10951	PI 476178	Peru	LR	PRU	-	62	74	Purple	4.0	7.0	8.0	-	-
10975	PI 476195	Peru	LR	PRU	1470	66	63	D purple	3.7	-	8.0	-	-
10979	PI 476199	Peru	LR	FST	-	67	60	Tan	4.7	-	8.0	-	-

Continued....

Table 2. Continued....

ICG	Alternate identity	Origin	Bio. status	Bot. variety	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color	Score			Seed colon. (%)	Bac. wilt (%)
									LLS	RST	ELS		
10980	PI 476200	Peru	LR	FST	-	72	38	Red	5.0	-	8.0	-	-
11075	PI 476158	Peru	LR	PRU	1175	68	72	Gasp(T+P)	5.0	-	8.0	-	-
11182	PI 476015	Peru	LR	PRU	-	-	58	Tan	5.0	2.7	8.0	65	-
11185	PI 476167	Peru	LR	PRU	1710	72	61	Gasp(T+P)	4.3	6.0	7.0	71	-
11186	PI 476180	Peru	LR	PRU	-	60	67	Gasp(T+P)	5.0	-	7.0	-	-
11312	CS 16	India	ID	VUL	5430	-	-	Red	4.5	3.0	-	-	-
11317	CS 22	India	ID	VUL	3150	-	-	D red	4.0	2.0	8.0	-	-
11321	CS 26	India	ID	VUL	3110	-	-	D red	4.0	2.0	8.0	-	-
11325	CS 30	India	ID	VUL	4890	-	56	Red	3.4	2.0	-	-	-
11331	CS 39	India	ID	VUL	3660	-	-	D red	4.3	6.0	8.0	-	-
11337	CS 46	India	ID	VUL	5280	74	60	D red	2.9	3.0	9.0	-	-
11485	PI 393530	Peru	LR	PRU	-	64	68	Purple	3.7	5.0	8.0	50	-
11567	Non-nod	India	BL	VUL	-	-	43	D purple	5.0	3.9	-	-	-
12720	BPZ 691	Ecuador	BL	AEQ	-	-	61	Purple	4.1	5.9	-	-	-
13916	CS 9	India	ID	VUL	3510	-	-	Red	4.0	3.0	-	-	-
13917	259-2 Red	India	ID	VUL	-	-	37	Red	3.6	5.5	4.0	-	-
13919	799	India	ID	-	2340	-	-	Red	3.0	2.0	-	-	-
13920	838	India	ID	-	3180	-	-	Red	4.0	2.0	-	-	-
13922	2245	India	ID	-	3080	-	-	Red	4.0	2.0	-	-	-

1. For abbreviations see Table 1.

See Appendix 1 for 1-9 scale used for RST, LLS, and ELS resistance. Tabulated ELS scores are from screening in Malawi.

Source: ICRISAT 1986, Mehan et al. 1996, Subrahmanyam et al. 1995.

Early leaf spot (*Cercospora arachidicola*)

Early leaf spot (ELS) (Fig. 4) is the most serious of the three foliar diseases in several countries of southern Africa, and in the USA. Yield losses due to ELS can exceed 50%. Presently known sources of resistance to ELS identified in collaboration with scientists of ICRISAT Asia Region working at IAC are listed in Table 3. Field screening for resistance to ELS is in progress at the SADC/ICRISAT Groundnut Project, at Chitedze Agricultural Research Station, Lilongwe, Malawi, where the natural disease pressure is very high. Screening more than 7000 accessions has so far resulted in the identification of four sources with moderate levels of resistance to ELS (disease scores less than 6 on a 1-9 scale). Similarly, screening a large number of accessions at Bengou, Niger, over three rainy seasons, resulted in the identification of a further 18 accessions resistant to ELS (disease scores 3.3-5.0) (Waliyar et al. 1993a). Limited screening in some Asian countries [Nepal and India (ICRISAT Asia Center and Pantnagar)] by ICRISAT scientists in collaboration with NARS, has also led to the identification of a few additional sources of resistance (Waliyar et al. 1990). Like rust and LLS resistance sources, most of the ELS resistance sources originated from secondary centers of diversity in South America. But, they have a broader genetic base as several sources of resistance belong to var *hypogaea*, var *fastigiata*, and var *peruviana*. However, none of the sources of resistance is of the Spanish type (var *vulgaris*).

Most of these sources show differential disease reactions at different locations, indicating the possible existence of variation in the ELS pathogen. Sources of ELS resistance reported from the USA, were found susceptible when tested at IAC in India and Chitedze in Malawi (Nigam and Bock 1985). Environmental factors, particularly temperature, also affect the stability of the components of resistance to ELS.

However, several genotypes [91 PA 150, NC Ac 17894 (ICG 6902), PI 274194 (ICG 11476), NC Ac 18045 (ICG 8298), and 91 PA 131], have expressed stable resistance across several temperature regimes (Waliyar et al. 1994).

Resistance sources ICGs 6284, 6902, 7878, 10000,



Figure 4. Groundnut early leaf spot caused by *Cercospora arachidicola*.

10948, and 13917 show some level of resistance at more than one location (Table 3). They are thus more useful in ELS resistance breeding programs. Nevertheless, it is important that ELS resistance sources are first screened to verify their resistance before they are used in resistance breeding at any location.

In multiple foliar disease resistance breeding, such sources as ICG 1703, 4995, 10920, and 13917 can play an important role, since they have resistance to more than one foliar disease. ICG 13917, an interspecific derivative is particularly useful as it has stable ELS resistance in Malawi, and at three locations in Asia, and also has resistance to LLS and rust.

Most of the ELS resistance sources show significant differences among the components of their resistance. ELS resistance sources, ICGs 1703, 6284, 6902, 7878, 8298, 9989, 10900, and 10920, have longer incubation periods, reduced sporulation, smaller lesion diameter, and lower infection frequencies than susceptible accessions (Waliyar et al. 1993b). Lesion size and sporulation ratings are moderately correlated for both leaf spots, indicating a genetic, and/or physiological relationship within the host that involves lesion development (Anderson et al. 1990).

Most of the inheritance studies related to ELS resistance have been reported from USA. Resistance to ELS is quantitative and controlled predominantly by additive gene effects (Kornegay et al. 1980, Anderson et al. 1986). Narrow-sense heritability estimates have been reported to vary from low to high.

Table 3. Characteristics of sources of resistance to groundnut early leaf spot.¹

ICG	Alternate identity	Origin	Bio. status	Bot. variety	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color	Score			Seed colon. (%)	Bac. wilt (%)
									ELS	LLS	RST		
Sources identified in Malawi													
5501	AH 7759	India	LR	VUL	-	-	40	Tan	5.0	9.0	9.0	-	-
9988	PI 475872	Bolivia	LR	FST	-	-	59	L tan	5.3	-	-	-	-
10900	PI 476033	Peru	LR	FST	1380	64	40	Red	5.3	-	-	-	-
10904	PI 476037	Peru	LR	FST	-	-	65	D red	5.3	-	-	-	-
Sources identified in western Africa													
1707	NC Ac 17132	Peru	LR	PRU	1610	63	62	Purple	5.7	4.0	4.0	-	65
2711	NC 5	USA	RC	HYR	-	-	70	Tan	5.3	9.0	9.0	-	-
3527	USA 63	USA	UN	FST	1860	66	60	Purple	5.4	4.7	4.3	71	-
6280	NC Ac 17124	Peru	LR	PRU	1260	55	49	Gasp(T+P)	5.5	-	-	-	-
6284	NC Ac 17500	Bolivia	LR	HYR	1030	57	75	Red	3.6	-	5.0	-	-
6330	PI 270806	Zimbabwe	BL	HYB	-	-	51	Tan	5.6	3.3	2.7	67	-
6902	NC Ac 17894	USA	BL	HYB	-	66	69	Tan	6.0	9.0	9.0	-	-
7756	RMP 49/5	Malawi	BL	HYB	-	-	-	D red	4.5	9.0	9.0	-	-
7878	NC Ac 10811 A	USA	BL	HYB	-	-	70	Tan	3.6	9.0	9.0	-	-
8298	NC Ac 18045	USA	BL	HYB	-	-	-	Tan	3.9	-	-	-	-
8339	NC Ac 18091	USA	BL	HYB	-	-	91	Tan	4.5	-	-	-	-
9989	PI 476015	Peru	LR	FST	-	-	46	D red	5.3	-	-	-	-
10000	PI 476030	Peru	LR	FST	-	-	-	Red	4.9	-	-	-	-
10450	PI 215724	Peru	LR	PRU	1100	71	53	Purple	5.3	4.7	-	-	-
10883	PI 475959	Bolivia	LR	HYR	-	-	68	Tan	5.3	-	-	-	-
10900	PI 476033	Peru	LR	FST	1380	64	46	Red	4.0	-	-	-	-

Continued....

Table 3. Continued....

ICG	Alternate identity	Origin	Bio. status	Bot. variety	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color	Score			Seed colon. (%)	Bac. wilt (%)
									ELS	LLS	RST		
10948	PI 479177	Peru	LR	PRU	2120	71	51	Rose	5.3	-	-	-	-
10954	PI 476180	Peru	LR	PRU	1630	71	53	Purple	4.9	7.0	3.0	29	-
Sources identified in India													
1703	NC Ac 17127	Peru	LR	PRU	1190	51	57	Gasp(T+P)	5.0	5.0	4.7	42	20
1710	NC Ac 17135	Peru	LR	PRU	1610	48	63	Purple	6.0	4.0	4.0	-	59
2711	NC 5	USA	RC	HYR	-	-	70	Tan	6.3	9.0	9.0	-	-
4995	NC Ac 17506	Peru	UN	PRU	1610	58	66	Purple	6.0	4.3	4.3	-	-
6284	NC Ac 17500	Bolivia	LR	HYR	1030	57	75	Red	5.0	-	5.0	-	-
6330	PI 270806	Zimbabwe	BL	HYB	-	-	51	Tan	6.3	3.3	2.7	67	-
6709	NC Ac 16163	Peru	LR	FST	-	62	52	Red	4.3	9.0	9.0	-	-
6902	NC Ac 17894	USA	BL	HYB	-	66	69	Tan	5.6	9.0	9.0	-	-
7878	NC Ac 10811 A	USA	BL	HYB	-	-	70	Tan	5.0	9.0	9.0	-	-
9294	58-295	Burkina Faso	LR	HYB	-	-	56	Tan	5.3	6.3	4.7	-	-
10040	PI 476176	Peru	LR	PRU	-	-	46	Gasp(T+P)	5.0	-	4.7	-	-
10756	TGR 997	Zimbabwe	LR	HYB	2070	69	80	Red	6.0	-	-	-	-
10920	PI 476152	Peru	LR	PRU	-	65	58	Tan	6.0	4.0	-	-	-
10946	PI 476176	Peru	LR	PRU	-	-	54	Tan	5.2	-	-	-	-
11099	ZFA 3525	Zambia	LR	HYB	-	-	77	Tan	5.3	-	-	-	-

i. For abbreviations see Table 1.

See Appendix I for 1-9 scale used for RST, LLS, and ELS resistance. Tabulated ELS scores are from screening in Malawi.

Source: P Subrahmanyam (pers. communication), Waliyar et al. 1990, Waliyar et al. 1993a.

Aflatoxin contamination (*Aspergillus flavus*)

Aspergillus flavus infection and the consequent aflatoxin contamination of groundnut present a serious quality problem worldwide (Fig. 5). Field infection by the aflatoxigenic fungus can lead to serious postharvest aflatoxin contamination. *Aspergillus flavus* infection mainly occurs before the crop is harvested in the semi-arid tropics, particularly under late-season drought stress conditions. In wet and humid areas infection predominantly occurs postharvest. Around 2000 groundnut accessions have been screened for their resistance to *A. flavus* seed infection in a sick plot under imposed drought stress conditions at IAC. Twenty-one genotypes have been identified as resistant ($\leq 2\%$ seed infection) (Table 4). Significant genotype \times environment interactions for seed infection are reported. However, some accessions (ICGs 1326, 3263, 3336, 3700, 4749, and 7633) have shown consistent resistance reactions to seed infection in India and Senegal (Mehan et al. 1991). Most of these lines have also been evaluated for resistance to seed colonization by *A. flavus* under artificial inoculation conditions in the laboratory. The ability to resist seed colonization has significance

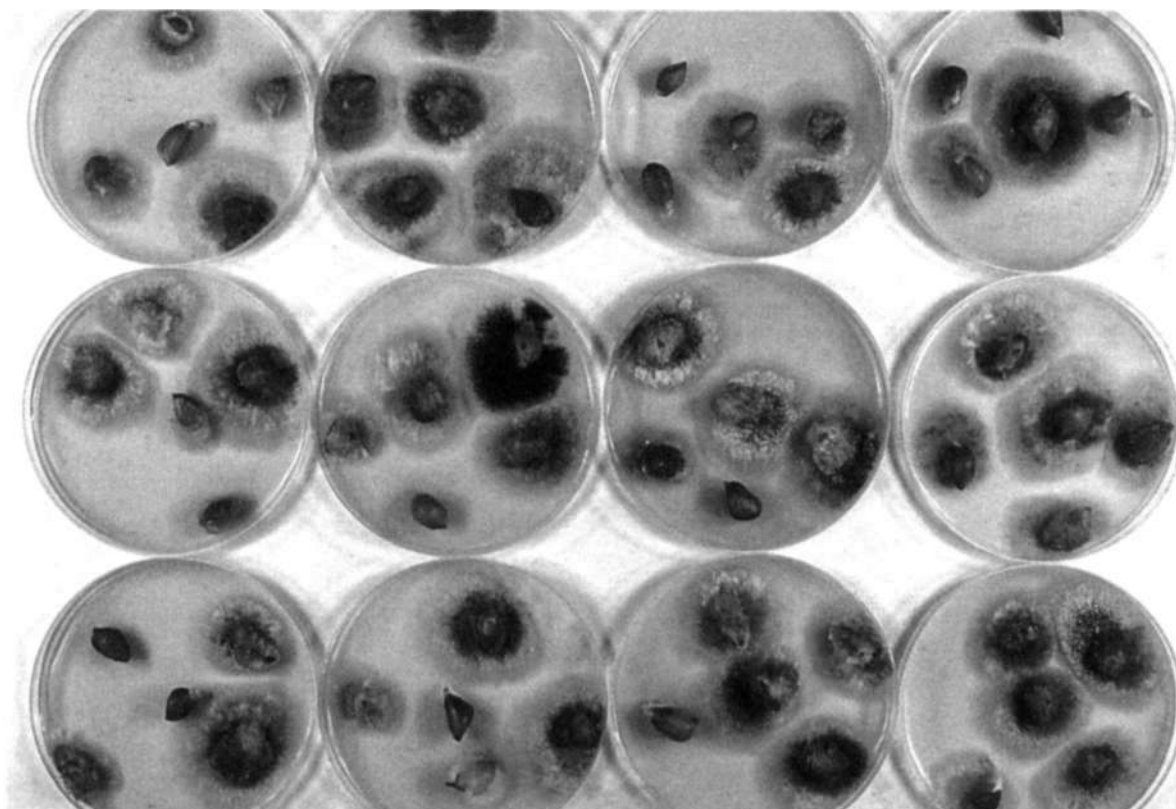


Figure 5. *Aspergillus flavus* seed infection in ICG 2716, a source of resistance to rust and late leaf spot.

during postharvest field drying and storage. Several accessions (ICGs 1326, 3263, 3700, 4749, 4888, 7633, and 9407) possess resistance to both seed infection and seed colonization, and are of special significance in breeding programs that combine pre- and postharvest resistance to the aflatoxigenic fungus.

Over 80% of the *A. flavus* resistance sources belong to *A. hypogaea* ssp *fastigiata* var *vulgaris*, but they are of diverse origins. Several of these sources, including ICGs 1326, 1994, 1323, and 8666 are high-yielding released cultivars with superior seed and pod characteristics; these should be preferred in breeding programs that target high yield and resistance (Figs. 6 and 7). Such genotypes could also be considered for direct introduction to areas where the aflatoxin problem is serious.

The accessions, ICGs 8666, 10020, and 10933 that are resistant to *A. flavus* seed infection are also resistant to other diseases. The latter two are resistant to rust, while ICG 8666 is also resistant to bacterial wilt. These three lines should be used in multiple resistance breeding programs. ICGs 1326, 4749, and 7633 have been commonly used as resistance donors in India, Senegal, and Thailand.

Several structural and biochemical components of resistance to seed colonization have been identified. Most resistance sources have compact palisade cellular arrangements, small hila, extensive surface wax, deposition of tannin-like compounds, and low contents of such amino acids as glycine, arginine, aspergin, and aspartic acid.

Genotypes vary in their ability to support aflatoxin production. U 4-7-5 and VRR 245 support only low levels of aflatoxin production, but are susceptible to seed colonization by *A. flavus*.

There is very limited information available on the genetics of resistance to *A. flavus* seed infection, seed colonization, and aflatoxin production. Only one study (Utomo et al. 1990) has highlighted the lack of correlation between the three types of resistance and the probability that they are governed by different genes. This provides an opportunity to combine these three resistances to give genotypes reinforced defence against this pathogen. The broad-sense heritability reported for these three resistances varies from low to high (Upadhyaya et al. 1997, Utomo 1990). Preliminary studies on combining ability indicate that ICGs 3700, 4749, and 7633 are good combiners for resistance to seed colonization. Significant maternal effects are also noticed in some crosses for seed-coat resistance, perhaps because there is significant maternal influence on testa structure.

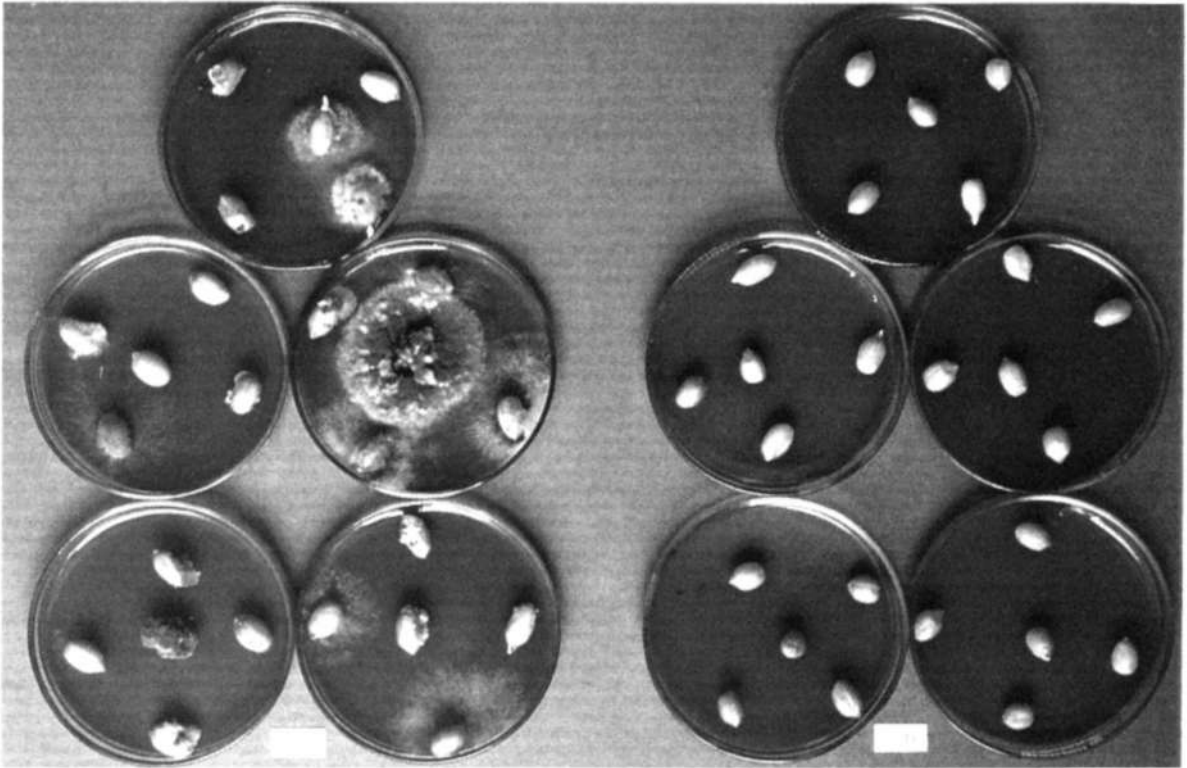


Figure 6. Cultivar J 11 showing resistance to seed infection by *Aspergillus flavus* in comparison to susceptible cultivar JL.. 24.

Figure 7. Lines resistant to seed colonization by *Aspergillus flavus*: J 11 (left), and ICG 4749 (center), compared to a highly susceptible line (right).

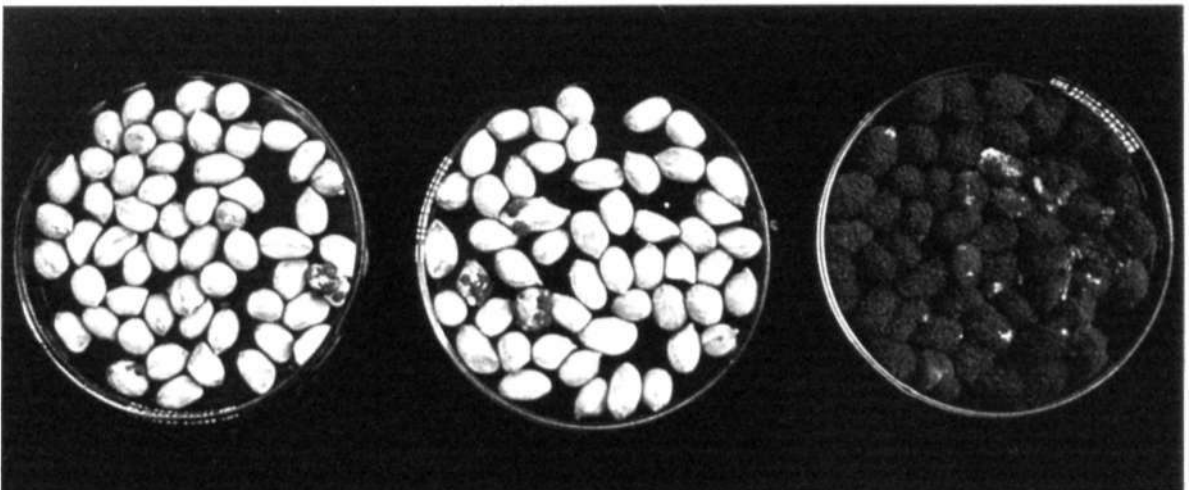


Table 4. Characteristics of sources of resistance to *Aspergillus flavus* seed infection and seed colonization.¹

ICG	Alternate identity	Origin	Bio. status	Bot. variety	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color	Seed inf. (%)	Seed colon. (%)	Score			Bac. wilt (%)
											LLS	RST	ELS	
1122	Lin Yuch Tsao	China	LR	VUL	810	68	49	Tan	1.3	32	9.0	9.0	8.0	-
1173	AH 61	India	UN	VUL	1640	71	37	Tan	1.0	-	9.0	9.0	8.0	-
1323	HG 1	India	RC	VUL	-	-	47	Tan	1.3	-	9.0	9.0	8.0	-
1326	J 11	India	RC	VUL	1630	70	47	Tan	1.3	8-15	9.0	9.0	9.0	-
1859	EC 6902	Unknown	UN	VUL	1570	81	40	Tan	1.0	-	9.0	9.0	-	-
1994	TG 6	India	RC	VUL	-	70	44	Tan	1.0	-	9.0	9.0	9.0	-
3263	U 4-47-7	Uganda	LR	VUL	1550	79	42	Tan	1.7	15-20	9.0	9.0	8.0	-
3267	U 4-47-14	USA	LR	VUL	1330	68	42	Tan	1.3	-	9.0	9.0	-	-
3336	Exotic 6	Unknown	UN	VUL	1035	80	40	L.Tan	1.7	15-25	9.0	9.0	-	-
3700	AH 7223	Nigeria	UN	VUL	1280	73	38	Tan	1.7	10-15	9.0	9.0	9.0	-
4589	Exotic 2	Unknown	UN	VUL	-	-	-	L.Tan	1.3	24	9.0	9.0	-	-
4749	PI 337394 F	Argentina	LR	VUL	1710	69	39	Tan	2.0	11-15	9.0	9.0	-	-
4888	AH 7827	China	UN	VUL	-	66	37	Tan	1.7	15-20	9.0	9.0	8.0	-
7412	277/71	Zimbabwe	LR	FST	-	-	43	Tan	1.0	-	9.0	9.0	8.0	-
7633	UF 71513	USA	BL	FST	1440	71	39	Tan	1.7	10-15	9.0	9.0	-	-
8666	Schwarz 21	Indonesia	LR	VUL	-	76	60	Tan	2.0	25	9.0	9.0	-	15
9407	61-40	Senegal	UN	VUL	-	62	54	Tan	1.7	10-15	-	-	9.0	-
9610	VRR 538	India	LR	VUL	-	61	42	Tan	1.0	-	-	-	9.0	-
10020	PI 476149	Peru	LR	PRU	-	67	58	Tan	2.0	48	-	2.7	8.0	-
10094	S 4	Zimbabwe	LR	VUL	-	-	43	Tan	1.3	-	-	-	9.0	-
10933	PI 476166	Peru	LR	PRU	1830	63	47	Tan	1.3	23	9.0	2.7	7.0	-

1. For abbreviations see Table 1.

See Appendix I for 1-9 scale used for RST, LLS, and ELS resistance. Tabulated ELS scores are from screening in Malawi.

Source: Mehan et al. 1987, Mehan et al. 1991.

Stem and pod rots (*Sclerotium rolfsii*)

Stem and pod rots are major constraints to production in several countries of Asia, Africa, and the Americas (Figs. 8 and 9). Yield losses of over 25% have been reported from India (Mayee and Datar 1988). Only limited resistance screening of germplasm has been attempted. There are very few reports of clear varietal differences in resistance and no genotype is known to be immune or highly resistant to *S. rolfsii*. Most of the genotypes identified as resistant only show field resistance (Smith et al. 1989, Grichar and Smith 1992, Branch and Brennenman 1993, Mehan et al. 1995).



Figure 8. Groundnut plant showing advanced symptoms of stem rot caused by *Sclerotium rolfsii*.

Most of the limited screening has been done in USA using disease 'hot spots', or by adding inoculum to the soil under high disease pressure conditions in the field. Based on the percentage of disease incidence resistant genotypes have been identified (Table 5). Among stem and pod rot resistant lines, 80-95% survive infection compared to a <40% survival rate in susceptible lines. Some interspecific hybrid derivatives (*A. hypogaea* x *A. cardenasii*) have also shown consistently lower percentages of disease incidence in multilocational trials in India (Table 5). Certain genotypes



Figure 9. Groundnut pods showing symptoms of pod rot caused by *Sclerotium rolfsii*.

(e.g., ICG 12083) have shown resistance in the field, but are less resistant in greenhouse tests.

The resistance sources identified in USA—a released cultivar (NC 2), and breeding lines [NC Ac 18016 (ICG 12083) and NC Ac 18416 (ICG 12087)]—have superior agronomic features, but are susceptible to other fungal diseases. The resistance sources identified from interspecific derivatives have resistance to foliar diseases, but have poor pod yields, low shelling outturn, and low seed masses.

Resistance to stem and pod rots has been attributed mainly to the presence in resistant genotypes of a thick impervious cuticle, thick-walled cortical cells, and cork cambium activity. Differences in susceptibility to stem rot have also been related to growth habit; semi-decumbent or bunch types being more susceptible than runners (Grichar and Smith 1992). A few Spanish types have also been reported resistant.

Table 5. Characteristics of sources of resistance to stem and pod rots.¹

ICG	Alternate identity	Origin	Bio. status	Bot. variety	Pod yield (kg ha ⁻¹)	Shell-ing (%)	100-seed mass (g)	Seed color	Stem and pod rot incidence (%)			Seed colon. (%)
									ELS	LLS	RST	
4477	NC 2	USA	RC	HYB	2360	74	68	Tan	<10	9.0	9.0	-
5125	NC 2	USA	RC	VUL	-	-	34	Tan	<10	9.0	9.0	-
5175	NC 2	USA	BL	FST	-	69	59	Red	<10	9.0	9.0	-
12083	NC Ac 18016	USA	BL	HYB	1920	73	64	Tan	<10	-	-	-
12087	NC Ac 18416	USA	BL	HYB	-	-	-	Tan	<10	-	-	-
15233	326	India	ID	FST	-	81	58	D red	<10	-	-	-
15234	1019	India	ID	VUL	-	65	20	Tan	<10	-	-	-
15235	1267	India	ID	VUL	-	74	35	Tan	<10	-	-	-
15236	1367	India	ID	VUL	-	73	26	D red	<10	-	-	-

1. For abbreviations see Table 1.

See Appendix 1 for 1-9 scale used for RST, LLS, and ELS resistance.

Tabulated ELS scores are from screening in Malawi.

Source: Mehan et al. 1995.

Bacterial wilt (*Pseudomonas solanacearum*)

Bacterial wilt (BW) is a major constraint to groundnut production in southeastern and eastern Asia (Fig. 10). Extensive screening of germplasm, largely based on field evaluation at hot spots in Indonesia and China by national programs has resulted in the identification of many BW-resistant germplasm lines. Lines are considered resistant when 80-95% of the plants do not show wilt symptoms (Naixiong et al. 1993, Yeh 1990, Mehan et al. 1994b). Of these resistance sources, 24 are available in the gene bank at IAC. Most sources are varieties of subspecies *fastigiata*. The use of several of these BW-resistance sources in breeding programs has resulted in the release of many BW-resistant cultivars in Indonesia and China (Mehan et al. 1994b).

Most of the wilt resistance sources are of Chinese or Indonesian origin, probably because the main selection for gene(s) conferring resistance occurred in this region, where the disease pressure is greatest (Fig. 11). However, there are lines of Peruvian origin (ICGs 1703, 7893, and 7894) indicating the presence of gene(s) conferring resistance to bacterial wilt in the initial material that evolved in the secondary centers of diversity. Some of these lines (ICGs 1703, 1705, 7893, and 7894) are of special significance as they also have resistance to rust and/or LLS (Table 6). These lines could be used in breeding programs to develop high-yielding varieties with multiple disease resistance. Recent screening has resulted in the identification of wilt resistance in an interspecific derivative (ICG 11325) that has high levels of resistance to both LLS and rust; such sources are important in broadening the genetic base.



Figure 10. Groundnut plants infected by bacterial wilt caused by *Pseudomonas solanacearum*.

Isolates of *P. solanacearum* have been classified into five races, biovars, and strains. Race 1 affects groundnut; within this race, biovar 1 is associated with groundnut in America, while biovars 3 and 4 affect groundnut crops in southeast and east Asia.

The disease reaction of some accessions has been found to vary at different locations. For example, ICGs 5272, 5273, and 5276 were resistant in Indonesia, but were only moderately resistant in some areas of China (Yeh 1990). Such variation in BW reaction may be due to inoculum pressure, pathogen virulence, environmental factors, and host x pathogen x environmental interactions. In most cases, disease ratings in the field are not correlated to those from greenhouse tests. However, ICGs 1609, 5313, 7343, 7968, and 8666 are reported to be resistant both in field and greenhouse tests (Yeh 1990).

Very little is known about the components of resistance to BW. Resistant types have shorter latent periods, less vascular browning, and lower wilting rates than susceptible genotypes. Information on the genetics of BW resistance is not conclusive. Liao et al. (1986) reported BW resistance to be partially dominant, involving three pairs of major genes and some minor genes, while Wang et al. (1985) reported that the genes conferring resistance are recessive in nature. In Indonesia, Schwarz 21 or its derivatives (Gajah and Kidang) have been extensively used as resistance donors, while in China, two BW-resistant accessions with good general combining ability, Xiekangging (ICG 15230) and Taishan Zhengzhu have been used as resistance donors (Liao et al. 1990).



Figure 11. Bacterial wilt resistance sources compared to a susceptible cultivar in a field trial in China.

Table 6. Characteristics of sources of resistance to bacterial wilt.¹

ICG	Alternate identity	Origin	Bio. status	Bot. variety	Pod yield (kg ha ⁻¹)	Shelling outturn (%)	100-seed mass (g)	Seed color	Bac. wilt ² (%)	Score			Seed colon. (%)
										LLS	RST	ELS	
1609	Schwarz 21	Indonesia	RC	VUL	-	-	56	Tan	10-20	9.0	9.0	9.0	-
1703	NC Ac 17127	Peru	LR	PRU	1190	51	57	Gasp(T+P)	15-20	5.0	4.7	7.0	42
1705	NC Ac 17130	Peru	LR	PRU	1150	50	54	Tan	10-15	4.7	-	7.0	42
5272	Gajah	Indonesia	RC	VUL	-	54	48	Tan	15-30	9.0	9.0	-	-
5273	Matjan	Indonesia	BL	VUL	-	63	54	Tan	15-20	9.0	9.0	9.0	-
5276	Kidang	USSR	RC	VUL	-	-	-	Tan	15-25	9.0	9.0	9.0	-
5313	Schwarz 21	Indonesia	RC	VUL	-	-	-	Tan	5-10	9.0	9.0	9.0	-
7343	Schwarz 21	Indonesia	RC	VUL	-	-	59	Tan	10-15	9.0	9.0	-	-
7893	PI 393531	Peru	LR	PRU	-	67	55	Gasp(T+P)	10-20	7.0	2.0	9.0	-
7894	PI 393641	Peru	LR	PRU	1710	64	53	Gasp(T+P)	10-20	4.7	4.0	8.0	-
7968	Schwarz 21	Indonesia	RC	VUL	-	-	56	Tan	10-15	-	-	-	-
8666	Schwarz 21	Indonesia	RC	VUL	-	-	-	Tan	10-15	-	-	-	-
11325	CS 30	India	ID	VUL	4890	-	56	Red	15-20	3.4	2.0	-	-
15222	Gouliaozhong	China	RC	HYR	-	71	72	Rose	16	-	-	-	-
15224	Jiangtianshong	China	RC	HYR	-	78	94	Rose	14	-	-	-	-
15227	Taishan Zhengzhu	China	RC	VUL	-	72	61	Tan	13	-	-	-	-
15232	Zhong Hua 2	China	RC	VUL	-	74	54	.	5	-	-	-	-
15230	Xiekangging	China	RC	VUL	-	-	-	Tan	10	-	-	-	-
15220	E Hua 5	China	RC	VUL	-	-	-	Tan	10	-	-	-	-
15228	Yue You 92	China	RC	VUL	-	-	-	Tan	10-15	-	-	-	-
15221	Gui You 28	China	RC	VUL	-	-	-	Tan	10-15	-	-	-	-
15226	Lu Hua 3	China	RC	VUL	-	-	-	Tan	10-15	-	-	-	-

1. For abbreviations see Table 1.

2. Range of bacterial wilt incidence at different locations/countries.

See Appendix I for 1-9 scale used for RST, LLS, and ELS resistance.

Tabulated ELS scores are from screening in Malawi.

Source: Mehan et al. 1994b, Nausing et al. 1993.

Conclusions

Significant variability for rust, LLS, and ELS resistance exists among the sources identified in cultivated groundnut. Most of the sources identified in the earlier stages of screening have undesirable pod and seed characteristics. However, later screening of the germplasm originating from secondary centers of diversity resulted in the identification of some resistant sources in good agronomic backgrounds. This emphasizes the need for evaluation of additional germplasm from such areas, particularly for LLS and ELS resistance. Further, more emphasis should be placed on the use of such accessions as ICGs 10056, 10567, 10920, 10925, 10932, 11094, 11182, 12059, and 12720 that have scores of 2 to 4 on a 1-9 scale for resistance to LLS or rust. They also have superior agronomic backgrounds and thus overcome the limitations of previously used sources. For combined resistance to LLS and rust, ICGs 6330, 7884, 10023, 10035, and 11182 that possess resistance to both diseases, together with good agronomic potential and are of diverse origins should be used.

Interspecific derivatives that have recorded a score of 2 to 4 on a 1-9 scale for resistance to both LLS and rust (ICGs 11312, 11317, 11321, 11325, 11337, 13916, 13917, 13919, 13920, and 13922) and in some cases to ELS as well (ICG 13917) in good agronomic backgrounds are rich sources of resistance to these foliar pathogens. The resistance of most of these sources has remained stable across locations. The presence of relatively high levels of resistance in these sources, particularly in the interspecific derivatives, suggests that their use in breeding programs would reduce the 'dilution effect' on resistance in populations selected for high pod yields and agronomic quality. The stability of ELS resistance across locations is variable. Nevertheless, ICGs 6284, 6902, 7878, 10000, 10948, and 13917 should be useful because their resistance has been proved stable at more than one location.

The variability in resistance to *A. flavus* seed colonization and infection, and to stem and pod rot is limited, and no single genotype is immune or highly resistant to all these constraints. The available sources can be used to improve levels of resistance in good agronomic backgrounds, and genetic resistance could be part of an integrated disease management strategy. There is much scope for the exploitation of such wilt-resistant sources as ICGs 1703, 7893, and 7894 in southeast and east Asia, since they also possess resistance to rust and/or LLS, which occur together with BW in the region.

From the available information, it is evident that although most of the foliar disease resistance sources are susceptible to *A. flavus* invasion, it would be prudent to select those sources that are least susceptible in foliar disease resistance breeding programs.

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Appendix 1

9-point scale used for field screening groundnut genotypes for resistance to rust disease.

Disease score	Description	Disease severity
1	No disease	0
2	Pustules sparsely disturbed, largely on lower leaves	1-5
3	Many pustules on lower leaves; necrosis evident; very few pustules on middle leaves	6-10
4	Numerous pustules on lower and middle leaves; severe necrosis on lower leaves	21-30
5	Severe necrosis of lower and middle leaves; pustules may be present on top leaves, but less severe	21-30
6	Extensive damage to lower leaves; middle leaves necrotic, with dense distribution of pustules; pustules on top leaves	31-40
7	Severe damage to lower and middle leaves; pustules densely distributed on top leaves	41-60
8	100% damage to lower and middle leaves; pustules on top leaves, which are severely necrotic	61-80
9	Almost all leaves withered; bare stems seen	81-100

9-point scale used for field screening groundnut genotypes for resistance to late and early leaf spot diseases.

Disease score	Description	Disease severity (%)>
1	No disease	0
2	Lesions present largely on lower leaves; no defoliation	1-5
3	Lesions present largely on lower leaves, very few on middle leaves; defoliation of some leaflets evident on lower leaves	6-10
4	Lesions on lower and middle leaves but severe on lower leaves; defoliation of some leaflets evident on lower leaves	11-20
5	Lesions present on all lower and middle leaves; over 50% defoliation of lower leaves	21-30
6	Severe lesions on lower and middle leaves; lesions present but less severe on top leaves; extensive defoliation of lower leaves; defoliation of some leaflet evident on middle leaves	31-40
7	Lesions on all leaves but less severe on top leaves; defoliation of all lower and some middle leaves	41-60
8	Defoliation of all lower and middle leaves; severe lesions on top leaves; some defoliation of top leaves evident	61-80
9	Almost all leaves defoliated, leaving bare stems; some leaflets may remain, but show severe leaf spots	81-100

1. Leaf area damaged (%).

Source: Subrahmanyam et al. 1995.

Appendix II

Agreement on ICRISAT Germplasm Exchange

ICRISAT signed an agreement with the United Nations Food and Agriculture Organization (FAO) on 26 Oct 1994, placing germplasm collections maintained by ICRISAT under the auspices of the FAO, as part of the International Network of *ex situ* collections provided for in Article 7 of the International Undertaking on Plant Genetic Resources, to be held in trust by ICRISAT. The materials covered by the Agreement are listed as 'designated germplasm'.

ICRISAT has traditionally adhered to a policy of unrestricted availability of germplasm held in its genebanks. In the interest of keeping this material available for future research and utilization, ICRISAT has undertaken, under Article 3(b) of the Agreement with FAO, not to claim legal ownership over 'designated germplasm', or to seek any intellectual property rights over that germplasm or related information. To ensure continued free availability of that germplasm, ICRISAT has also agreed to pass on these obligations to all future recipients of 'designated germplasm'.

Accordingly, no 'designated germplasm' will be released in future unless the recipient signs a Standard Germplasm Order Form reproduced overleaf.

Rules for future exchange of germplasm for food and agriculture are currently being debated in the FAO Commission on Plant Genetic Resources in coordination with the Conference of the Parties to the Convention on Biological Diversity. ICRISAT and the Consultative Group on International Agricultural Research (CGIAR) are actively participating in this debate to ensure that any future regime will facilitate exchange and utilization of this precious global resource, and the fair and equitable sharing of the benefits derived from the commercial or other utilization of the germplasm.



ICRISAT

Standard Germplasm Order Form

I/we order the following material:

Insofar as this material is "designated germplasm" under the 26 Oct 1994 Agreement between ICRISAT and the Food and Agriculture Organization of the United Nations (FAO) placing collections of plant germplasm under the auspices of FAO¹,

I/we agree

- not to claim ownership over the material received, nor to seek intellectual property rights over that germplasm or related information.
- to ensure that any subsequent person or institution to whom I/we make samples of the germplasm available, is bound by the same provision.

Place and date _____

Name of person or institution requesting the germplasm _____

Address _____

Shipping address (if different from the above) _____

Authorized signature _____

1. "Designated germplasm" will be indicated by an asterisk (*) on the Shipment Notice.

About ICRISAT

The semi-arid tropics (SAT) encompasses parts of 48 developing countries including most of India, parts of southeast Asia, a swathe across sub-Saharan Africa, much of southern and eastern Africa, and parts of Latin America. Many of these countries are among the poorest in the world. Approximately one-sixth of the world's population lives in the SAT, which is typified by unpredictable weather, limited and erratic rainfall, and nutrient-poor soils.

ICRISAT's mandate crops are sorghum, pearl millet, finger millet, chickpea, pigeonpea, and groundnut; these six crops are vital to life for the ever-increasing populations of the semi-arid tropics. ICRISAT's mission is to conduct research which can lead to enhanced sustainable production of these crops and to improved management of the limited natural resources of the SAT. ICRISAT communicates information on technologies as they are developed through workshops, networks, training, library services, and publishing.

ICRISAT was established in 1972. It is one of 16 nonprofit, research and training centers funded through the Consultative Group on International Agricultural Research (CGIAR). The CGIAR is an informal association of approximately 50 public and private sector donors; it is co-sponsored by the Food and Agriculture Organization of the United Nations (FAO), the United Nations Development Programme (UNDP), the United Nations Environment Programme (UNEP), and the World Bank.



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