GENETIC ANALYSES OF RESISTANCE TO LATE LEAF SPOT AND RUST *VIS-À-VIS* PRODUCTIVITY IN GROUNDNUT (*Arachis hypogaea* L.)

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By

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CERTIFICATE

This is to certify that the thesis entitled "Genetic analyses of resistance to late leaf spot and rust *vis-à-vis* productivity in groundnut (*Arachis hypogaea* L.)" submitted by Mr. B. N. MOTAGI. for the degree of DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING of the University of Agricultural Sciences, Dharwad, is a record of research work done by him during the period of his study in this University under my guidance and supervision and the thesis has not previously formed the basis of the award of any degree, diploma, associateship, fellowship or other similar titles.

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INTRODUCTION

I. INTRODUCTION

Groundnut (*Arachis hypogaea* L.) one of the major and important oilseed crops of the world is largely grown as a small hold crop, under rainfed conditions in semi-arid areas. In these areas, it is considered as a food and a cash crop. Groundnuts are crushed to provide vegetable oil for human consumption and protein-rich meal for livestock. The haulms are important source of fodder especially in developing countries.

Developing countries accounts for over 95 percent of world groundnut area and 94 percent of total production. Production is concentrated in Asia and Africa, with Asia accounting for about 60 percent of global area and 70 percent of production (Freeman *et al.*, 1999). Among groundnut producing nations, India sows the highest area (8.0 m.ha.) and is the second largest producer (7.3 m.t.; 28%) next to China (34%) [FAO, 2000]. Andhra Pradesh, Gujarat, Karnataka, Maharastra and Tamil Nadu account for about 89 percent of the total groundnut area of our country and contribute nearly 88 percent of the total groundnut production. Export performance in oilseeds indicate that India has been exporting only groundnuts and sesamum seeds in a significant quantity (Subramanian, 2000). Groundnut oil, meal and confectionary products are extensively used and traded. India exported 1,02,700 tons of shelled groundnuts during the period between 1994-96 as compared to meager 27,600 tons in 1989-91(Freeman *et al.*, 1999). India has a good opportunity to enhance its export of HPS (hand-picked selection) grade of groundnut to many Asian countries.

Though, India is a leading producer of groundnut, the productivity is very low (913 Kg ha^{-1}) as compared to USA (2981 Kg ha^{-1}) and China

(2789 Kg ha^{-1}) [FAO, 2000]. Groundnut suffers from several diseases, which cause wide fluctuations in annual production and productivity, particularly in the rainfed crop, which occupies 80 percent of total groundnut area in the country (Nigam, 2000). The crop loss due to foliar diseases viz., late leaf spot (*Phaeoisariopsis personata* Berk & Curt. V.Arx) and rust (*Puccinia arachidis* Speg.) is of paramount significance. In India, late leaf spot and rust diseases normally occur together and can cause yield loss up to 70 per cent (Subrahmanyam *et al.*, 1980). These diseases have an adverse influence on the recovery of pods, quality of seeds and haulms. Late leaf spot pathogen also produces dornithin, a potent mycotoxin that affects the fodder quality (Desai and Bandyopadhyay, 2000). Changes in ecological and economic conditions for agricultural production require zero pesticide-usage and the more intensive use of natural defense mechanism of plants to reduce losses due to various diseases. Generally, the non-genetic solution to disease management is uneconomical in rainfed agro-ecology due to low levels of groundnut yield obtained and resource limitations of the farmers. The genetic solution holds out a better promise in such situations. The research in breeding aims at evolving varieties with resistance to disease and tolerance to yield reduction, in addition to the improvement of yield potential, so that, yield reduction in presence of disease can be reduced. Resistant cultivars facilitate an economic and environmentally sound management of the diseases and thus promote sustainable productive agriculture.

In groundnut, erect bunch and early maturing Spanish types are most popular and widely cultivated because of ease in cultivation and harvesting. But, they are highly susceptible to foliar diseases and suffer heavy losses under epiphytotic conditions (Hegde *et al.*, 1995a). Most of the resistance sources are Valencia landraces with many undesirable features, viz., late maturity, thick shell, low productivity and poor adaptation, making them unsuitable for direct utilization (Hegde *et al.*, 1995b). Many of the wild *Arachis* species were found to be immune/highly resistant to rust and/or late leaf spot (Wynne *et al.*, 1991). Stable interspecific derivatives belonging to Virginia group with high yield and high level of resistance have been developed but they were late in maturity (Reddy *et al.*, 1991; Gowda *et al.*, 1995a). The hybridization efforts have met with limited success in combining the disease resistance with high productivity (Gowda *et al.*, 1995a). There is a strong negative association of disease resistance with desirable agronomic attributes (Gowda *et al.*, 1996). Identification of new sources of resistance in Spanish types is of great significance in resistance breeding in maintaining superior agronomic traits of Spanish types (Mehan *et al.*, 1996). Induced mutagenesis and extensive hybridization with interspecific derivatives were sought as alternative approaches to generate material combining desirable agronomic characters with disease resistance and high productivity.

Recently, attempts are being made to induce mutants and isolate cross-derivatives with high yield, good agronomic features and resistance to late leaf spot and/or rust in Spanish background (Motagi, *et al.*, 1996b; Liang *et al.*, 1999a and b; Packiaraj *et al.*, 1999; Motagi *et al.*, 2000a). Mutagenic treatment of Valencia 1 (VL 1) with EMS has resulted in isolation of a large number of early maturing, foliar disease resistant mutants with variation for other characters (Motagi, 1996). There is a need to assess other (morphological and productivity) characters in relation to late leaf spot and/or rust resistance in these mutants.

Incorporation of resistance against foliar diseases generally lead to reduction in yield potential of cultivars (Pixley *et al.*, 1990b; Wynne *et al.*, 1991; Knauft and Wynne, 1995). Poor partitioning of assimilates and inadequate translocation from source to sink could be the limiting factors for yield in the resistant genotypes. Physiological studies are required to gain better insight into the underlying mechanisms deterring the economics of genetic resistance. Coffelt *et al.* (1989) suggested that further increase in yield might be accomplished by developing resistant cultivars with a combination of high reproductive efficiency, high harvest index and high total flower count.

Quality of groundnut oil depends upon the proportion of oleic and linoleic acid, the two major fatty acids present in groundnut. Higher content of oleic acid is related to longer shelf life of oil, while higher content of linoleic acid is nutritionally desirable. Spanish bunch varieties have poor keeping quality with low O/L ratio (1.00). Late maturing spreading varieties are marginally superior in O/L ratio (~1.50). Various factors, viz., genotype, seasonal variation and foliar diseases affect the fatty acid make up of groundnut oil (Dwivedi *et al.*, 1993; Singh *et al.*, 2000). Foliar diseases considerably reduce the oil yield and affect quality also (Dwivedi *et al.*, 1993; Motagi *et al.*, 2000a and d). There is an urgent need to develop resistant genotypes with high oil recovery and also better oil quality in Spanish background.

Detailed assessment of various morphological traits based on IPGRI/ICRISAT descriptors has revealed overlapping of descriptor states without demarcations even for highly heritable traits (Rajgopal *et al.*, 2000). Intrinsic characteristics like isozymes, seed protein profiles and DNA markers would be more suitable for establishing identity of groundnut cultivars. Oxidative enzymes viz., peroxidase, catalase, superoxide dismutase, polyphenol oxidase etc. have often been implicated in disease resistance. Role of peroxidase and polyphenol oxidase enzymes in imparting resistance to rust (Velazhahan and Vidhyasekaran, 1994) and late leaf spot (Suryawanshi and Mayee, 1995) have been demonstrated clearly. Hence, under these situations, "Genetic analyses of resistance to late leaf spot and rust *vis-à-vis* productivity in groundnut (*Arachis hypogaea* L.) " were undertaken to investigate:

1. The variation in groundnut germplasm for resistance to late leaf spot and rust,
2. Diversity *in foliar disease resistant mutants,*
3. Genotypic responses for yield and quality in relation to disease resistance,
4. Genetics of resistance to late leaf spot and rust in induced mutants and inter-specific derivatives, and
5. Isozyme and protein variation for cultivar identification and its relation to foliar disease resistance.

REVIEW OF LITERATURE

II. REVIEW OF LITERATURE

Loss in crop yield due to diseases is one of the major constraints in meeting the demand of the world's ever increasing population. Though, crop losses due to diseases are being managed by use of chemicals and resistant cultivars, they are associated with limitations such as cost factor, health hazards and environmental pollution in the former, and time consuming laborious procedures and difficulty in ferrying the disease resistance genes in the latter. Nonetheless, Plant breeders have introgressed disease resistance genes from wild and cultivated plants to produce resistant varieties. In the recent years, integration of molecular techniques into conventional breeding program has facilitated marker-assisted selection, as an attractive strategy for simultaneously improving a multitude of complex agronomic traits.

The importance of rust and late leaf spot in groundnut production has made the researchers to increasingly concentrate on these diseases. The literature pertaining to these diseases, viz., host-plant resistance, undesirable associations with disease resistance, scope for breeding disease resistant and productive cultivars, physiological basis of yield variation in relation to resistance, effect of sowing dates, disease epidemiological components, genetic and biochemical (isozyme/protein, phytoalexins) basis of resistance in groundnut are presented hereunder.

2.1 Major Foliar diseases: Late leaf spot and Rust

The *Cercospora* or tikka leaf spots (early and late leaf spot) are the most important fungal diseases of groundnut. In India, late leaf spot is more predominant compared to early leaf spot because of its fast spreading nature. The late leaf spot caused by *Cercospora personatum* Berk and Curt. was first described in USA in 1875. The perfect stage *Mycosphaerella berkeleyii* was described by Jenkins (1938). But recently, it was renamed as *Phaeoisariopsis personata* (Berk and Curt) V. Arx.

The damage caused by leaf spots is by reducing the available photosynthetic area, lesion formation and premature leaflet abscission. However, lesions are not confined to the leaves but may occur also on petioles, stems and pegs leading to direct deterioration of the developing pods (Reys and Romasata, 1940). Generally, 10-50 per cent yield is reduced by late leaf spot disease (McDonald *et al.*, 1985). This disease is more prevalent during the rainy season in all groundnut-growing areas of India. Over 50 per cent loss in pod and fodder yield has been estimated due to this disease in the transitional tract of Karnataka state (Puranik *et al.*, 1973; Astaputre and Kulkarni, 1996).

Rust caused by *Puccinia arachidis* Speg. was first noted by Spegazzini (1884) in Paraguay. At present, rust is of economic importance in almost all groundnut growing areas of the world (Subrahmanyam and McDonald, 1983). The disease occurs in most of the groundnut growing Indian states and more intensively in south Indian states as condition favours the development and spread of the disease (Subrahmanyam and McDonald, 1982). Pod loss caused by rust may go up to 50-80 per cent in epidemic years (Sandhikar *et al.*, 1989).

The foliar diseases, viz., late leaf spot and rust, are commonly present wherever the groundnut is cultivated, but their incidence and severity vary between locations and seasons. Each disease alone is capable of causing substantial yield loss but when they occur together, losses are further increased. In India, late leaf spot and rust normally occur together and can cause yield losses up to 70 per cent (Subrahmanyam *et al.*, 1980). These diseases also have an adverse influence on the recovery of pods, quality of seeds and haulms.

2.2 Host-Plant Resistance

Effective control measures in the form of fungicides are available against the foliar diseases of groundnut. However, they are not cost-effective and cause environmental pollution. Host-plant resistance can be an acceptable proposition to combat these diseases. But, presently grown genotypes have only moderate resistance/tolerance to these diseases. A disease management program combining moderate resistance/tolerance and a reduction in fungicide application would be desirable and less costly (Gorbet *et al.*, 1982). A first step in this direction would be to ascertain the reaction of such varieties to the diseases and the control by fungicide(s).

Schiller and Sampagol (1981) reported the differential response of varieties to fungicide application. Gorbet *et al.* (1982) studied reactions of 12 genotypes and found highly significant differences among lines for susceptibility to late leaf spot in unsprayed plot, with Florunner recording highest lesion count. The relationship between remaining green leaf area at maturity and yield was linear in most genotypes and yield response to fungicide application varied with genotypes. Generally, the control of the disease resulted in smaller increase in resistant types and larger increase in susceptible types (Subrahmanyam *et al.*, 1984; Williams *et al.*, 1987). Varietal characteristics other than resistance influenced response to chemical control (Moraes *et al.*, 1994: Hegde *et al.*, 1995a).

Watson (1988) found that fungicide application reduced the rate of disease progress in Florunner, Southern Runner and UF 81206, especially in Florunner and resulted in higher yield than in Southern Runner. Chlorothalonil applied on a 21-days schedule provided control of late leaf spot that was sufficient to prevent yield losses in Southern Runner, a cultivar with moderate resistance (Culbreath *et al.*, 1992). Florunner gave highest yields and greatest adaptability over environments where diseases were well controlled. While, responses of Tatu and IAC-Caiapo to disease control were similar and they out yielded Florunner, when disease pressure was higher (Godoy *et al.*, 1999). The cultivar IAC-Caiapo, partially resistant to late leaf spot, had lower disease intensity under chemical control and disease progress was late (4-9 days) and slower than susceptible cultivar Tatu. Unsprayed IAC-Caiapo had higher yield than Tatu sprayed four times (Moraes *et al.*, 1994).

2.3 Sources of Resistance

Considerable efforts have been made in identifying the sources of resistance to major foliar diseases of groundnut. The elaborate screening programs in India and abroad have yielded germplasm lines with resistance to late leaf spot and/or rust (Table 1) but most of them were Valencia landraces originating in Peru, with a number of undesirable attributes like thick shell, low productivity, poor adaptation, late maturity, highly reticulated and constricted pods which are commercially unacceptable (Subrahmanyam *et al.*, 1982a and 1995; Ghewande *et al.*, 1983; Waliyar *et al.*, 1989 and 1993; Anderson *et al.*, 1993; Hegde *et al.*, 1995b; Singh *et al.*, 1997; Jiang *et al.*, 1998; Chen *et al.*, 1999). However, later, screening of the germplasm originating from secondary centers of diversity resulted in the identification of some resistant sources in good agronomic backgrounds (Singh *et al.*, 1997). Many of the wild *Arachis* species

Table 1: Sources of late leaf spot and/or rust resistance in groundnut

Germplasm/Accessions screened	**Resistant sources identified**	**Reference(s)**
_	Tarapoto (PI 259747) Rust	Mazzani and Hinojosa (1961)
-	PI 314817, 315608 (Israel line 136) Rust	Bromfield and Cevario (1970); Bromfield (1971)
-	PI 259744, PI 350680, EC 76446, NC Ac 17132, 17133, 17135 and 17090(LLS)	Subrahmanyam *et al.* (1982a)
3,655 entries	B 613 and PI 341839 (LLS and Rust)	Ghewande *et al.* (1983)
_	SO 850	Moraes and Godoy(1985)
-	UF 81206-1, UF 81206-2, PI 203396	Chiteka *et al.* (1988)
-	NC Ac 17127, 17500 Coll. 182, 58-295, PI 476143, 476176, 476033 and 476176.	Waliyar et *al.* (1989)
-	PI 259747, 405132, 215696, NC Ac 17132, 17135 and 17133 RF (LLS and Rust)	Muthusamy *et al.* (1991)
22 germplasm lines for 3 pathogens	NC Ac 17132, PI 476164 and 476168 (LLS)	Earnshaw *et al.* (1992)
500 peanut plant Introductions (PI)	PI 215695, 215396 and 215724 (LLS) but low pod yield	Anderson *et al.* (1993)
424 germplasm lines for three pathogens	ICG 1707, 6330 and USA-63	Waliyar *et al.* (1993)
13,000 accessions at ICRISAT Asia Center (IAC), 90 % Valencia and 70 % from Peru.	169 (Rust) ICG 1697 and 4747 69 (LLS), 42 (LLS and Rust)	Subrahmanyam *et al.* (1995)
979 germplasm accessions at ICRISAT	38 (Rust) 7(LLS); 4(LLS and Rust) - ICG 6843, 10890, 11567 and 12112. SB types - ICG 10881 and 11567.	Mehan *et al.* (1996)
54 accessions	PI 259747, ICG 7882, VG 78, VG 101, CS 16, GBFDS 272 and 273 (LLS), more yield potential.	Hegde *et al.* (1995a)
5,700 accessions of China and other countries	92 (Rust), 53 (LLS), 49(LLS and Rust)	Jiang *et al.* (1998)
104 accessions of Fuji	LLS resistance with high O/L ratio	Chen *et al.* (1999)

_ information not given

were found to be immune/highly resistant to rust and/or late leaf spot (Smart *et al.*, 1978; Subrahmanyam *et al.*, 1985; Wynne *et al.*, 1991). Those with multiple disease resistance include *A.cardenasii, A. chacoense* and *A. stenosperma*, which are cross compatible with cultivated types (Table 2). Thus resistance present both within the species and in related species of *Arachis* indicates considerable scope for breeding.

2.4 Association of Characters

There are several reports in India and abroad in which strong negative association of disease resistance with desirable agronomic attributes has been indicated (Arulshekar, 1972; Hammons, 1981; Gowda *et al.*, 1996). Stalker *et al.* (1979) reported linkage of several undesirable attributes (late maturity, small seeds, low yield) with late leaf spot resistance. Miller and Norden (1980) found that late leaf spot resistance was negatively correlated with pod yield and early maturity. High yield potential and high levels of resistance do not generally go together (Nigam *et al.*, 1991; Williams *et al.*, 1987). Multiple crosses have partially helped in breaking theses undesirable associations, but superior segregants isolated did not combine the expected level of resistance with high productivity (Gowda *et al.*, 1997; Angadi, 1999). Vasanthi *et al.* (1998 a and b) reported that the positive association of late leaf spot and rust severity with shelling per centage and haulm weight/plant would hinder the selection. On the contrary, Iroume and Knauft (1987) observed negative association between yield and leaf spot severity, which led the researchers to conclude that selection for yield under disease pressure in early generation may be effective in the development of high yielding genotypes with leaf spot resistance. Yield and foliar disease resistance were positively correlated in Virginia type and negatively in Valencia and Spanish types (Raju, 1982). This shows that disease resistance can easily be incorporated

Table 2: Resistance to late leaf spot and rust in wild *Arachis* species

Species	**Reaction to**	
	Late leaf spot	**Rust**
Section: Arachis		
A. stenosperma	Highly Resistant	Highly Resistant
A. duranensis	—	Immune
A. spegazzini	—	Immune
A. batizocoi	—	Immune
A. khulzianii	Resistant	Immune
A. correntiana	—	Immune
A. chacoense	Highly Resistant	Immune
A. cardenasii	Highly Resistant	Immune
A. villosa	Resistant	Immune
Section: Erectoides		
A. paraguaniensis	Moderately Resistant	—
A. benthamiia	Moderately Resistant	—
A. appressiplia	Resistant	Immune
Section: Extranervosae		
A. lutenseens	Highly Resistant	—
A. villosulicarpa	Highly Resistant	Immune
Section: Rhizomatosae		
A. glabrata	Moderately Resistant	—
A. hagenbeckii	Highly Resistant	Immune
Section: Triseminale		
A. pusilla	—	Immune

__ information not known

in Virginia types without deleterious effects, but one should be careful to alter character associations before disease resistance is incorporated in to Valencia and Spanish types. Motagi *et al.* (1997) reported negative and significant association of late leaf spot severity with productivity indicating desirable association of resistance with yield in Spanish bunch foliar disease resistant mutants.

2.5 Scope for breeding disease resistant productive cultivars

Hybridization

Attempts have been made to produce late leaf spot and/or rust resistant, productive cultivars through hybridization (Tables 3 and 4), but the lines developed either possessed only a moderate level of resistance or retained one or more undesirable features (Wynne *et al.*, 1991). Stable inter-specific hybrid derivatives belonging to *Virginia* group with high yield and high level of resistance have been developed but they were all late in maturity (Reddy *et al.*, 1991; Gowda *et al.*, 1995a). Late maturity could be very serious problem particularly in Semi Arid Tropics (SAT) where the groundnut season is short and the crop is raised in multiple cropping systems.

In groundnut, the erect bunch and early maturing Spanish types are most popular and widely cultivated because of ease in cultivation and harvesting. But, they are highly susceptible to foliar diseases and suffer heavy yield losses under epiphytotic conditions (Hegde *et al.*, 1995a and b).

The material developed with hybridization between resistant germplasm and high productivity lines tended to combine good agronomic features with moderate levels of resistance, while highly resistant types were deficient in one or more features. This was also

Table 3: Breeding lines/cultivars resistant to late leaf spot and/ or rust in groundnut

Lines/Cultivars Evaluated	Resistant lines/cultivars selected	Reference
33 genotypes	ACC 12, AH 334-5 and 61016 (LLS and Rust)	Hossain and Ali. (1990)
22 genotypes and standard cultivars (JL 24 and TMV 2)	PI 215696, NC Ac 927, EC 76446 (292), PI 350680 and PI 259747 (LLS and Rust)	Dinakaran *et al.* (1992)
7 lines selected for pod yield and resistance	5 lines with more pod and oil yield, high O/L ratio	Zullo *et al.* (1993)
56 genotypes (30 SB, 17 VB & 9 VR)	2 SB, 3 VB and 3 VR (LLS and Rust)	Gopal *et al.* (1993)
6 genotypes and 4 susceptible controls	R 8972 (Rust)	Gopal *et al.* (1994)
Elite bunch entries	ICGV 86590 and 87160 MR to LLS, low SP.	Gowda *et al.* (1995a)
44 entries of ICRISAT	ICG 2760, 6330 and 6284 (LLS and Rust)	Adiver *et al.* (1997)
20 cultivars	3 cultivars (LLS)	Ye *et al.* (1998)
25 genotypes	ICGV 87820, 87310, 87835, 87285, 89401, 91229, 91246 and 91251 (LLS and Rust)	Singh and Singh (1998)
65 foliar disease resistant lines	Lines with high yield, LLS and Rust resistance identified	Nasir *et al.* (1998)
Advanced Virginia breeding lines	PBS 20026, 21063 and 23007 (LLS and Rust), good yield	Samdur *et al.* (1999)
14 elite breeding lines and local cultivar CO 2	ICGV 88312, 88316, 91004, 92086 and 92088 (LLS and Rust)	Vimala *et al.* (1999)

Table 4: Late leaf spot and rust resistant lines selected from crosses in groundnut

Cross / Method	Resistant lines selected	Reference
400 single, triple and double crosses (12 S and 9 R). Mass pedigree method	30 lines (LLS and Rust), few 3000 kg ha^{-1} yield	Reddy *et al.* (1984)
Chico X Florigiant reciprocal crosses	High yield and more resistance than Florigiant	Coffelt and Porter (1986)
PI 203396 X Florunner derived $3F_6$ sister lines composite	Southern Runner (LLS) more yield	Gorbet *et al.* (1986)
20 populations in F_2 generation, M X N mating design	NC 6 and NC 7 (LLS) good agronomic traits	Jogloy *et al.* (1987)
X 14-4-B-19-B X NC Ac 17090 pedigree and bulk method.	Girnar 1	Reddy (1989)
Progenies of FESR X POL 2 cross	VG 80 and VG 81 (Rust and LLS) high yield	Muthusamy *et al.* (1991)
Argentine X PI 259747 (SB) (LLS & Rust)	ICGV 87157 (LLS and Rust) 23.5% more yield than JL 24	Nigam *et al.* (1992)
A. hypogaea X *A. cardenasii* selections	GP NCWS 1, 2,3 and 4 (LLS) high 100 seed mass	Stalker and Beute (1993)
Complex cross [(Ehua4 X TaishanSanlirou) F_2 X (EHua3 X Xiekargqing) F_2] Modified pedigree selection	Zhonghua 4 105 -125 days, MR-Rust, SP (72 %), oil (50.8 %), TW (65 g).	Tang *et al.* (1996)
Ah 1208 (large seeded) X Daekwangtangkong (high yield)	Daecheongtangkong (LLS)	Pae *et al.* (1998)
CO 1 X *A. cardenasii*	GP 9514 (LLS and Rust)	Varman (1999)
TMV 2 X *A. chacoense*	CS 19 (LLS)	Samdur *et al.* (1999)
F_2 of a cross Yueyou 116/PI381622// Yueyou 116/// Giuyou 28/ ICG 8641 using modified pedigree method.	Yueyou5 (LLS and Rust) 115 days	Liang *et al.* (1999a)
F_4 of a cross Shanyou 27//EC76446 (292)/Yueyou 431 using modified pedigree method	Yueyou 223 (Rust) 110 -115 days, SB type	Liang *et al.* (1999b)
F_4 population [R 33-2 X ICG (FDRS) 68] X [NC Ac 17090 X ALR 1]	ALG 63 / ALR 3 (Rust & LLS)	Packiaraj *et al.* (1999)
F_4 of cross KRG 1 X CS 16 JL 24 X ICGV 87165	SB type, early, high yield B 37c (LLS & Rust), D 39d / GPBD 4 (LLS & Rust) SB type, early, high yield, SP (78-80 %), Oil (49 %)	Motagi *et al.* (2000a and d)

evident from recently released resistant cultivars viz., ICG (FDRS) 4, ICG (FDRS) 10 and ICGV 86590 for cultivation in India indicating the limitation of the currently available resistant genotypes in the improvement of Spanish cultivars (Gowda *et al.*, 1996). Identification of sources of resistance in Spanish types is of great significance in resistance breeding in maintaining superior agronomic traits of Spanish types (Mehan *et al.*, 1996). Recently, cross derivatives with high yield potential, good agronomic features and resistance to late leaf spot and/or rust have been developed in Spanish background (Liang *et al.*, 1999b; Packiaraj *et al.*, 1999; Motagi *et al.*, 2000a and d).

Groundnut being an allotetraploid, the success in breeding efforts through conventional hybridization and selection suffers from undesirable linkages and genetic interactions. Artificial mutagenesis has been sought as the best alternative to break these linkages and to combine the desirable agronomic characters with disease resistance and high productivity.

Mutation Breeding for Disease Resistance

Groundnut is one of the few crops in which mutation breeding had played an important role not only in creating wide genetic variability and directly releasing cultivars for general cultivation but also in breeding for quantitative characters by utilizing the induced mutants in hybridization (Patil, 1974 and 1978; Balaiah and Reddy, 1975; Patil and Mouli, 1978; Qiu *et al.*, 1998).

Although, mutation-breeding program employed exclusively for disease resistance have been rather scarce in groundnut, few mutants resistant/tolerant to foliar diseases have been isolated (Marghitu *et al.*, 1982; Qiu, 1982; Motagi, 1996).

The release of NC 4X, a new high yielding, disease resistant variety developed by X-ray irradiation at North Carolina (Gregory, 1960) was a milestone in the history of use of mutation breeding in groundnut improvement. Cooper and Gregory (1960) irradiated groundnut seeds with 10,000 to 18,500 r X-rays, produced X_2 and X_3 progenies with both decreased and increased resistance to leaf spots.

Seeds of *A. hypogaea* were X-ray irradiated with 10-40 kR and 2453 M_2 seedlings obtained were inoculated thrice with spores of early and late leaf spot pathogen. However, after recurrent selection, only 3 M_3 lines were completely resistant. The disease resistant lines yielded almost twice as much as several commercial varieties (Soriano, 1988a and b).

Several lines resistant to late leaf spot and rust were isolated by utilizing the mutant obtained by gamma irradiation, in inter-specific crosses with *A. villosa* (Rathinaswamy *et al.*, 1986). Gopani and Vaishnani (1970) found spontaneous mutant "Gujarat Narrow Leaf Mutant" which showed potential for drought and *Cercospora* resistance.

Chemical mutagenesis has also paid dividends by release of a new high yielding, moderately resistant variety "CO 2" derived from EMS (0.2 %) treatment of POL 1 in M_5 generation (Sivaram *et al.*, 1989). A large number of foliar disease resistant mutants were isolated from recurrent mutagenesis of Valencia mutant (VL 1) derived from DER through EMS treatments. Among them, three mutants (28-2, 45 and 110) combined high yield potential and early maturity, besides multiple disease/pest resistance with desirable pod and kernel features (Motagi *et al.*, 1996b).

2.6 Physiological basis of yield variation in relation to resistance

Resistance to foliar diseases has been reported to be associated with low yield potential in groundnut. Further, there seems to be a "resistance/yield barrier" genetic mechanism (Williams *et al.*, 1987). Therefore, an understanding of physiology of this phenomenon will be useful to formulate breeding program for disease resistance.

Duncan *et al.* (1978) reported that the differences in the three physiological parameters viz., partitioning of assimilates between vegetative and reproductive parts, length of the pod filling period and rate of pod establishment are the three important physiological processes explaining most of the yield variation among groundnut cultivars. Of these, partitioning of assimilate had the greatest effect on pod yield. Williams *et al.* (1987) observed low dry matter partitioning in rust and late leaf spot resistant genotypes.

Pixley *et al.* (1990a) compared growth and partitioning characteristics of four peanut genotypes differing in resistance to late leaf spot. In fungicide treated plots, high partitioning (92%) of assimilate to the pods and early onset of pod filling enabled Florunner (susceptible genotype) to achieve high yield in 127 days. A combination of leaf spot resistance, low partitioning (77-80%) to pods (allowing leaf growth) and slightly longer pod filling resulted in satisfactory yields from Southern Runner and F 81206 (partially resistant genotypes) without leaf spot control.

Knauft and Gorbet (1990) reported that vegetative weights of disease susceptible cultivars did not exceed 165 g plant^{-1}, while many resistant lines exceeded 250 g plant^{-1}. Partitioning coefficients in susceptible cultivar generally exceeded 80 per cent, while in resistant lines it ranged from 20 to 80 per cent. Pod initiation in resistant lines lagged behind that of susceptible cultivars by 10 to 30 days, even if resistant lines had high partitioning coefficients.

Williams *et al.* (1993) studied the physiological response of cultivars differing in resistance and observed crop growth rate, pod growth and partitioning being influenced by both the variety and the chemical control of the foliar diseases. High partitioning and resistance to rust were not mutually exclusive, but differences in susceptibility to the leaf spots seem negatively associated with the partitioning.

Varman *et al.* (1993) studied relative efficiency of partitioning of dry matter in ten genotypes with varying reaction to foliar diseases. The accumulation of dry matter in stem and roots did not vary significantly among genotypes. In the susceptible and partially resistant genotypes, the partitioning of dry matter to pods was more. It was further concluded that poor partitioning of assimilates and inadequate translocation from source to sink could be the limiting factors for yield in the resistant genotypes. Coffelt *et al.* (1989) suggested that further increase in yield might be accomplished by developing cultivars with a combination of high reproductive efficiency, high harvest index and high total flower count.

Maximum leaf area (4-7 LAI) occurs during early to mid pod filling stage in groundnut and decreases there after depending on several factors, particularly, leaf spot disease (Boote *et al.*, 1980). Leaf area index is important for light interception, radiation use efficiency and plant growth.

Pixley *et al.* (1990a) studied disease progression and leaf area dynamics of four peanut genotypes differing in resistance to late leaf spot and indicated that maintenance of higher leaf area index by the resistant genotypes was associated with sustained leaf production until maturity. The combination of lower epidemic rates with continued leaf growth (compensating for diseased leaves) appeared to reduce the adverse effects of late leaf spot on assimilation and yield capability of the resistant lines.

Varman *et al.* (1995) reported higher crop growth rate, leaf area ratio and leaf area index, during pod filling and maturity stages in rust resistant and partially resistant genotypes indicating more partitioning of dry matter to leaf tissues rather than to pods. Seed yield was consistently lower in resistant genotypes, suggesting that partial resistance was preferable to both susceptibility and resistance. Valand *et al.* (1997) studied the effects of late leaf spot disease on groundnut cultivars TMV 2 and GAUG 2. TMV 2 was more susceptible than GAUG 2. Of the plant growth characters investigated, defoliation rate, leaf area, petiole weight and plant dry weight explained the differences in the disease intensity in these cultivars.

Patil *et al.* (1996) analyzed the growth and partitioning efficiency of late leaf spot resistant and susceptible lines and found that resistant germplasm had higher leaf area index (LAI), but were late maturing with low partitioning efficiency. On the contrary, susceptible genotypes were characterized by early maturity and high rates of partitioning, but suffered due to disease leading to significant reduction in LAI. Mutant VL 1-45 combined favourable characters by maintaining very high LAI, partitioning efficiency and also resistance.

Gowda *et al.* (1990) reported that per cent residual green leaf area was found to be important in determining the yield performance. It was confirmed by multiple regressions of all other traits on pod yield. They suggested that breeding program should take into account the performance status based on yield and disease severity, instead of pod yield alone.

Late leaf spot reduced photosynthesis and was major contributor to premature leaf drop, which had an adverse effect on yield. After 70 per cent plant maturity, leaf area lost had no significant effect on yield loss (Cole and Grimmer, 1977). Enyi (1975) reported that defoliation reduced the dry weight of stems, pods and seeds. The adverse effect of defoliation was more pronounced when defoliation was complete (59.7% reduction in yield) than when half the leaves (43.3% reduction in yield) were removed. The greatest reduction in seed yield occurred when the plants were defoliated during the early pod stage. Yield reduction ranged from 2 to 7, 7 to 21, 17 to 31, and 21 to 51 per cent from 25, 50, 75 and 100 per cent defoliation treatments, respectively (Nickle, 1977). Defoliation up to 25 per cent reduced seed yield by only 2 per cent, while 75 per cent defoliation reduced most by reduction in dry weight, chlorophyll, protein and sugar (Ghosh and Biswas, 1995). Photosynthesis is a major process affected by foliage removal (Boote *et al.*, 1980). Jones *et al.* (1982) reported reduction in canopy carbon dioxide exchange rate (CER) initially by 45 to 70 per cent after 75 per cent defoliation (LAI 1.00) but noticed subsequent CER recovery due to leaf area production and re-adaptation of previously shaded leaves to full sun. Gerlagh and Bokdam (1973) simulated the effects of late leaf spot infection by defoliation/shading and found that defoliation reduced the pod yield slightly, shading to a great extent and inoculation by 50 per cent had little effect on seed weight. In all the treatments, numerous underdeveloped pods were found. Similarly, bud removal caused low yield and low disease incidence and late maturity (Miller *et al.*, 1990). Ghosh and Biswas (1995) reported that removal of aerial flowers were more lethal than underground fruits in inducing whole plant senescence. Leaf senescence is uncoupled from fruit maturation under normal condition, possibly due to sink-limitation.

Waggoner and Berger (1987) showed that the simple concept of healthy leaf area duration (HAD) could be used to predict yield of manually defoliated and late leaf spot defoliated peanut. Aquino *et al.* (1992) developed regression models relating late leaf spot-healthy leaf area duration (HAD) and pod yield. Except for untreated control, HAD could explain the yield loss. Nutter and Littrell (1996) concluded that measurements of healthy leaf area (estimated as per cent reflectance at 800 nm) have better relationship with pod yield than defoliation per cent.

Boote *et al.* (1983) tried to couple the disease effect with PNUTGRO, a growth simulation model of groundnut. They coupled the late leaf spot into this model. They simulated the effect of disease on photosynthesis and other physiological processes. Using this, they could simulate seasonal peanut growth, vegetative growth and fruit growth rate in response to *Cercospora* leaf spot.

Savary and Zadoks (1992) conducted a series of experiments in groundnut rust-late leaf spot multiple pathosystem and tried to find the interrelations and effects on each other. The effects of rust and late leaf spot on damage were shown to be less than additive due to the difference in the mechanism of damage, i.e. late leaf spot causes damage mainly by defoliation and reduction in healthy leaf area, while rust damage was attributable to different mechanisms other than reduction in leaf area. They developed multiple regression models taking logarithmic transformed values of area under disease progress curve (AUDPC) of rust and late leaf spot and their interactions, as independent variables and yield loss as dependent variable. Bulbule and Mayee (1998) noticed the interaction between rust and late leaf spot pathogens and suggested a partial antagonistic relationship under simultaneous infection.

Das and Roy (1995) showed that late leaf spot severity and crop loss were highly correlated in groundnut. They used linear regression and obtained significant fit to the data collected. For every one per cent increase in disease severity, 6.08 g m^{-2} decrease in yield was observed. Benagi *et al.* (1998) developed yield loss models using AUDPC as the explanatory variable with highly significant coefficient of determination ($R^2 = 0.99$) in case of late leaf spot of groundnut.

Simple linear regression models of yield loss on disease variables revealed that yield loss was better explained by disease at 85-95 days after sowing. AUDPC models, polynomial and non-linear models could not explain the variations in yield loss more precisely than the models with single point disease variables. Multiple point linear regression models of yield loss on disease at different stages taken together, improved the explanatory value, but could not explain the variation precisely. Stepwise regression analysis on disease variable and physiological traits like leaf area index, harvest index, partitioning coefficient and growth rates improved the R^2 value of the models considerably in early and late sown experiments (Chandran, 2000).

2.7 Effect of sowing dates

Late leaf spot and rust become severe in particular period or season in a year. Hence in order to avoid the severe outbreak of the disease, change of date of sowing is considered as better way to escape from the infection and resulting yield loss.

Chevageon (1953) suggested that, large scale sowing of groundnut should be completed as quickly as possible as the late sown field become severely infected. The delay in sowing some time decreased the disease severity, but reduced the yield considerably (Nath and Kulkarni, 1967).

Shokes *et al.* (1983) reported that late plating resulted in a six-fold increase in number of lesions per leaflet and decrease in yield compared to early planting. The leaf spots were best avoided by early sowings in April when there is little inoculum present in the atmosphere. The early sown crop suffers least, whereas late sown crop suffers maximum because of high incoulum pressure in the atmosphere (Gupta, 1985).

Astaputre *et al.* (1994) studied the disease occurrence in four dates of sowing, 13th and 28th of June and July. Their study suggested that, early sowing (June) is better than late (July) in Dharwad conditions, since the disease occurrence and yield loss increased with the delay in sowing.

Naidu and Chandrika (1997) found that early sown (6th June) crop suffered least from late leaf spot and rust diseases due to low inoculum potential whereas late sown (11th August) crops suffered more because of ready availability of inoculum built in early sown crops. The best sowing times in southern zone of Andhra Pradesh to avoid late leaf spot and rust and to obtain maximum yields are early (6th June) and normal (15th July) *Kharif* sowing. Late *Kharif* sowing may be utilized for screening groundnut germplasm for disease resistance due to existence of maximum inoculum load on the late sown crop.

Hazarika *et al.* (2000) studied the effects of eight sowing dates from May 5 to July 14 on leaf spots and rust incidence and pod yield. The crop recorded least incidence of leaf spots and rust and highest pod yield when sown on May 5 (early) as against highest incidence of disease and least yield on June 24 and July 4 (late) sown crops.

2.8 Epidemiological components of resistance

Recognition of epidemiological components of rate reducing resistance has given a major strategy for the present day breeding efforts (Parlevliet, 1979; Anderson *et al.*, 1990b). Resistance to late leaf spot is partial not complete, as several components influence the resistance, it operates through prolonging incubation and latent periods and reducing infection frequency, lesion size, sporulation and defoliation (Subrahmanyam *et al.*, 1982b; Melouk *et al.*, 1984; Chiteka *et al.*, 1988; Chiyembeketa *et al.*, 1993).

Nevill (1981) reported that components of late leaf spot resistance, viz., longer latent periods, reduced sporulation and defoliation, are not fully complementary, are components of late leaf spot resistance. Moraes and Godoy (1985) reported that lesion number and diameter, infected leaf area, type of lesion and sporulation index as components of resistance. Culbreath *et al.* (1991) reported that incidence of stem lesions may be useful as a new parameter in evaluation and selection for resistance and/or tolerance to *C. personatum.* Leaf area damage, defoliation per cent were easily scorable at early stage and the components of late leaf spot, viz., lesions per leaflet, lesion size, lesions on petiole and main stem scored easily at/before harvest can be utilized profitably in evaluation (Motagi *et al.*, 1996a).

Savary and Zadoks (1989) reported highest predictive value of latency period duration because of inaccuracy in measurement and its correlation with other epidemiological variables (infection and sporulation efficiency). Aquino *et al.* (1995) found high correlation of both AUDPC and rate of infection (r) values with latent period (LP) and maximum percentage of lesions that sporulated and recommended them in evaluation of genotypes for late leaf spot resistance. Watson *et al.* (1998) studied the etiological mechanisms and observed slow disease progress in two resistant genotypes (Southern Runner and UF 81206) than in Florunner. Components different among these genotypes were lesion size, latent period, conidiophore production and sporulation. UF 81206 had longer latent period and had typically 10 per cent or less of its lesions with sporulation.

The rust resistance available at present in the cultivated groundnut is of "slow-rusting" type where resistant/tolerant genotypes have increased incubation period, decreased infection frequency and reduced pustule size, spore production and viability (Subrahmanyam *et al.*, 1983). Reduction in lesion size and duration of sporulation contribute to suppression of disease progress when infection occurs early in growing season (Anderson *et al.*, 1990a).

Rust resistant cultivars had longer incubation period (IP) and lower pustule densities and small pustules than susceptible ones (Reddy and Khare 1988). Mehan *et al.* (1994) studied the components of rust resistance in 144 groundnut genotypes using detached leaf technique. Components, viz., infection frequency, incubation period lesion diameter, percentage of leaf area damage and sporulation index were significantly correlated with each other and with mean field rust scores. However, the greatest variability among genotypes was observed for incubation period and sporulation index. Different components of resistance were not found in a single genotype. Complementation of components was evident in genotypes ICG 10890 and ICG 10881. They suggested the use of incubation period (IP) and sporulation index (SI) in selecting for rust resistance.

The effects of these components of resistance to rust and late leaf spot are cumulative over the course of disease epidemic. In general, on resistant genotypes, the disease appears late, builds up only slowly, and does little apparent damage to foliage as evident by the lower rates of disease development (r) and area under disease progress curve (AUDPC).

2.9 Inheritance of late leaf spot and rust resistance

The reports pertaining to inheritance of late leaf spot and rust resistance are controversial and inconclusive, as the findings differ from person to person. Both simple (two-gene model, Tiwari *et al.*, 1984) and complex (five-loci genetic model; Nevill, 1982) inheritance of resistance to late leaf spot with completely recessive alleles determining resistance is reported in the literature (Table 5). The triploid hybrids of crosses between resistant wild species and susceptible cultivars were susceptible, indicating that inheritance was recessive (Sharief *et al.*, 1978). Combining ability analysis for components of resistance to late leaf spot indicated the predominant role of additive gene effects for most of the components (Kornegay *et al.*, 1980; Anderson *et al.*, 1986).

Resistance to rust in cultivated groundnut is recessive and appears to be governed by only a few genes (Table 6). 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]. Quantitative genetic analysis revealed the importance of both additive and non-additive gene effects.

Table 5: Genetics of late leaf spot resistance in groundnut

Cross	Genetic nature of resistance	Remarks	Reference
A. hypogaea X *A. cardenasii*	Recessive	F_1 susceptible	Sharief *et al.* (1978)
Robut 33-1 X Krapovikas different crosses	Non-additive	Five recessive genes	Nevill (1980, 1982)
Crossed 6 resistant lines in diallel pattern	Non-additive, Maternal effect	NCGP 343, NC 5, NC Ac 3139 and NC 2 best general combiners	Kornegay *et al.* (1980)
Four crosses Robut 33-1 X EC 76446(292), J11 X EC 76446(292), GAUG1 X NC Ac 17090, TG17 X NC Ac 17090	Duplicate recessive	F_2 15 R: 1 S	Tiwari *et al.* (1984)
Crossed 5 resistant lines and 4 cultivars in M X N mating design	Additive (LN, LZ, DF, LP and (SP), Non-additive (SP)	Male: NC 6, NC 7, Tainan 9, CES 103. Female: NC Ac 17090, 17132, 17133, RF 17135, PI 259747; NC 7 best combiner	Walls and Wynne (1985)
—	Additive	GP NC 343 best combiner	Anderson *et al.* (1986)
Reciprocal cross of Chico X Florigiant	Additive	Cytoplasmic influence in F_2	Coffelt and Porter (1986)
Crossed 5 resistant lines as females and 4 cultivars as males	Additive	NC 6 and NC 7 best combiners Resistance low h^2 (0-0.13)	Jogloy *et al.* (1987)
γ-Ray induced resistant Pmu 2 and Pmu 8 were crossed with susceptible CES 3	Duplicate recessive	F_2 9 S: 7 R Genes ls_1 and ls_2	Soriano (1988a)
10 parental diallel cross	GCA and SCA significant	PI 341817 and ICGS 4 best combiners	Anderson (1990b)
3 susceptible varieties (KRG1, Dh 40 and JL 24) and 4 resistant germplasm (VG 101, CS 16, GBFDS 272 and PI 259747) crossed in L X T design	Additive, Additive X Additive	GBFDS 272 and CS 16 good combiners	Kuchanur *et al.* (1997)
5 crosses involving Kadiri 1 as female and EC 76446 (292), PI 393527B, PI 298115 and PI 41433 as males	Duplicate complementary recessive	3- 4 genes	Vasanthi and Reddy (1997)
EMS induced resistant mutant VL 1-45 crossed with its susceptible parent (VL 1) and grand parent (DER)	Duplicate complementary recessive	Suppressor element in DER, F_2 9 S: 7 R, Genes ls_1 and ls_2 I- Inhibitory locus	Motagi *et al.* (2000b)

— information not given

Table 6: Genetics of rust resistance in groundnut

Cross	Genetic nature of resistance	Remarks	Reference
PI 298115 X unknown male	Duplicate recessive	—	Bromfield and Bailey (1972)
—	More than 2 genes	Studied F_3 derived FESR lines	Nigam *et al.* (1980)
PI 298115 and PI 259747 reciprocally crossed with 2 susceptible cultivars	Duplicate recessive	Genes sr_1 and sr_2	Cook (1975)
Three susceptible X 3 resistant crosses	Digenic Trigenic	F_2 ratios: 15 S: 1 R 63 S: 1 R	Kishore (1981)
Two crosses UF 49-16-10-3 X PI 314817 and UF 49-16-10-3 X PI 350680	Duplicate recessive	—	Knauft and Norden (1983), Knauft (1987)
PI 315608 X UF 49-16-10-3	Multigenic	F_2 162 S: 1 R	Knauft and Norden (1983),
PI 315608 X PI 314817	—	Different F_2 ratios: genes in both lines non-allelic	Knauft (1987)
Crossed 7 susceptible and 4 resistant lines in L X T design	Recessive Non-additive	EC 76446(292), PI 259747 and NC Ac 17133 RF best combiners	Tiwari *et al.* (1983)
Crossed 2 susceptible and 2 resistant lines (EC76446, NC Ac17090)	Digenic	F_2 ratio 9 S: 6 I: 1R	Tiwari *et al.* (1984)
A hypogaea X *A batizocoi*	Dominant	F_1 resistant	Singh *et al.* (1984)
Phule Pragati X PI 259747	Monogenic	F_2 3 S: 1 R	Kalekar *et al.* (1984)
SB XI X NC Ac 17090 Phule Pragati X NC Ac 17090	Duplicate recessive	—	Deokar *et al.* (1986)
Crossed PI 259747, PI314817 and EC 76446 (292) with Shulamit and Virginia bunch	Partial resistant or dominant	—	Middleton and Shorter (1987)

— information not given

contd..

Table 6: Contd.,

Cross	Genetic nature of resistance	Remarks	Reference
Crossed 3 resistant (EC 76446 -292,NC Ac 17090 and PI 259747) and 2 susceptible (J 11 and Gangapuri) lines	Additive, Additive X Additive,Additive X dominance	2-3 duplicate recessive genes	Reddy *et al.* (1987)
Used 6 resistant lines in crosses with susceptible ones	Recessive	More than 2 genes	Zeng (1987)
Crossed 2 resistant (PI 298115 and EC 76446-292) with 2 susceptible lines in diallel	Recessive	Quantitative, high h^2, both GCA and SCA were high	Liao *et al.* (1988)
Three crosses involving CO 2 as female, and NC Ac 17090, PI 414331 and 414332 as males	Monogenic	F_2 ratio 3 S : 1 R	Paramasivam *et al.* (1990)
Ten parental diallel cross	GCA and SCA significant	PI 341817 good combiner	Anderson *et al.* (1990b)
Six crosses involving 3 susceptible (CO 2 and JL 24) as female cultivars and 3 resistant genotypes (NC Ac 17090, PI 414331 and 414332) as males	Additive and Non-additive (add X dom)	—	Varman *et al.* (1991)
Four crosses involving 2 susceptible cultivars (JL 24 and R 33-1) and 2 resistant lines (NC Ac 17090 and 17135)	Two recessive genes	—	Varman *et al.* (1993)
Five crosses involving Kadiri 1 as female and EC 76446 (292), PI 393527B, PI 298115 and PI 41433 as males	Duplicate recessive	2-3 genes	Vasanthi and Reddy (1997)

— information not given

2.10. Biochemical and Molecular Markers

In the era of Intellectual Property Rights there is an increasing emphasis on varietal identity for proprietary reasons. To meet this end, electrophoresis of storage and functional proteins has emerged as an efficient, simple and reliable tool supplementing traditionally used morphological parameters (Picket and Jarman, 1994). Isozyme techniques have been widely used because of their ease of visualization and low cost. Since the electrophoretic gel is stained for a specific enzyme activity, it is possible to distinguish allelic from non-allelic proteins after genetic analysis. Isozymes have been used to evaluate more than 30 crop species (Tanksley, 1983).

Enzyme polymorphism

Identification of up to 17 polymorphic isozymes among wild species by several workers suggested that, the isozymes have potential use as markers to follow introgression patterns in interspecific hybrids and to establish the phylogenetic relations in groundnut (Lacks *et al.*, 1991; Lu and Pickergill, 1993 and Stalker *et al.*, 1994). However, the cultivated species *Arachis hypogaea* showed polymorphism only for few isozymes. Galagaro and Lopes (1994) studied leucine amino peptidase (LAP), peroxidase (POX) and glutamate oxaloacetate transaminase (GOT) in five cultivars. LAP and POX were not discriminative and only GOT was polymorphic. Grieshammer and Wynne (1990) evaluated 25 isozymes and found only three, viz., GOT, isocitrate dehydrogenase (ICD) and phospho hexose isomerase (PHI) consistently polymorphic. Among them, GOT and PHI could distinguish botanical types. Similarly, Lacks and Stalker (1993) evaluated 18 isozymes and found that, only three (GOT, ICD and PHI) consistently variant and a specific PHI band pattern was associated with high yield, seed size and leaf spot resistance.

Enzymes and resistance

Plants defend themselves against pathogenic fungi by producing toxic substances such as phytoalexins, pathogenesis related (PR) proteins, oxidized phenols and several other components. Oxidative enzymes viz., peroxidase, catalase, super oxide dismutase, polyphenol oxidase, etc. have often been implicated in the resistance to different stresses. Role of peroxidase and polyphenol oxidase enzymes in imparting resistance to rust (Ekbote and Mayee, 1984; Velazhahan and Vidhyasekaran, 1994) and late leaf spot (Suryawanshi and Mayee, 1995) pathogen in groundnut have been demonstrated.

Subbarao *et al.* (1996) and Sankara *et al.* (1996) reported differential response of foliar disease resistant and susceptible genotypes for phytoalexin production. Isoflavanones were the major components of phytoalexin response whereas other phytoalexins viz., formononetin, diadzein and medicarpin comprised a minor component. Phytoalexins like hydroxy stilbenes and medicarpin (Subbarao *et al.*, 1988), dienol (Subbarao *et al.*, 1990a), alkyl bis phenyl ethers (Subbarao *et al.*, 1991) were isolated from groundnut leaves infected by rust. Edwards *et al.* (1995) reported three times more phytoalexin (medicarpin) production in rust resistant than susceptible cultivar. They emphasized the potential application of phytoalexins in screening germplasm.

In groundnut, attempts have been made to establish species relationships among both broad groups and among species of the section *Arachis* using seed protein profiles either in native form through poly acrylamide gel electrophoresis (Savoy, 1976; Basha, 1979 and Klozova *et al.*, 1983) or in denatured form using sodium dodecyl sulphate-poly acrylamide gel electrophoresis (Krishna *et al.*, 1986; Singh *et al.*, 1991; Lanham *et al.*, 1994 and Sheshagiri, 2000).

Salim (2000) used seed; root and hypocotyl protein profiles in combination for varietal identification and reported that, specific protein band(s) were absent in some mutants in response to moisture and temperature stress. On the contrary, there was no association between protein and host resistance to rust (Subbarao *et al.*, 1988).

DNA polymorphism

Though, considerable genetic and morphological diversity exists within the species, until recently, the cultivated groundnut was considered to be unique among crop species as the molecular techniques like restriction fragment length polymorphism (RFLP) and random amplified polymorphic DNA (RAPD) could find no variation among its genotypes (Halward *et al.*, 1991a; Halward *et al.*, 1992; Kochert *et al.*, 1991; Paik-Ro *et al.*, 1992). However, recent studies revealed polymorphism in *A. hypogaea* using DNA amplification finger printing (DAF) and amplified fragment length polymorphism (AFLP) [He and Prakash, 1997], random amplified polymorphic DNA (RAPD) [Bhagwat *et al.*, 1997; Subramanian *et al.*, 2000] and simple sequence repeats (SSRs) [Hopkins *et al.*, 1999]. A RAPD marker linked with large poded mutant (Bhagwat *et al.*, 1997) and three RAPD markers linked with nematode resistance (Burrow *et al.*, 1996) have been reported in groundnut.

MATERIAL AND METHODS

III. MATERIAL AND METHODS

The experimental material utilized and the methods adopted are given in this chapter.

3.1 MATERIAL

3.1.1 Variation for resistance to late leaf spot and rust

Forty-five groundnut germplasm comprising of inter-specific derivatives (9), advanced breeding lines (22), ruling cultivars (10) and mutants (4) and fifty-five Trombay genotypes were screened against late leaf spot and rust. Identity and pedigree of these genotypes are presented in Tables 7 and 8, respectively. Components of late leaf spot (lesion number, lesion size, lesions on petiole, lesions on mainstem, incubation period and latent period) and rust (pustule number, incubation period and latent period) resistance and their association with maturity were investigated.

3.1.2 Diversity in foliar disease resistant mutants

Eighteen mutants isolated from Valencia 1 (VL 1) upon Ethyl Methane Sulfonate (EMS @ 0.5%) mutagenesis were evaluated for morphological (number of primary branches, number of secondary branches, mainstem height, length of primary branches, leaflet length and width), productivity (pod yield and hundred seed mass) and disease (late leaf spot and rust) resistance parameters under diseased condition. Diversity of the material and association of resistance with other characters was ascertained.

Table 7: Pedigree of groundnut germplasm assessed for late leaf spot and rust resistance

Genotype	Bot. Group	Pedigree
Inter-specific derivatives		
1. ICGV 86699	VB	[(*A. batizocoi* X *A. duranensis*) X *A. hypogaea* (Cv. NC 2)] CS 29
2. ICGV 87165	VB	[*A. hypogaea var. fastigiata* (PI 261942) X *A. cardenasii*] CS 9
3. ICGV 88256	VB	(CS 9 X (Robut 33-1 X NC Ac 316)
4. ICGV 93023	SB	((Robut 33-1 X NC Ac 2214) X Cyto 213-2)
5. A 30b	VB	KRG 1 X ICGV 87165
6. B 31j	SB	JL 24 X ICGV 87165
7. B 37c	SB	JL 24 X ICGV 87165
8. D 39d	SB	KRG 1 X ICGV 86855
9. I 15e	SB	Dh 40 X VG 101
Advanced breeding lines		
1. ICGV 86031	SB	F 334 A-B-14 X NC Ac 2214
2. ICGV 87264	SB	Manfredi X NC Ac 17133RF
3. ICGV 87807	VL	((MK 374 X Rout 33-1) X FESR 2)
4. ICGV 90266	VB	(([J 11 X (M 13 X NC Ac 2214)] X ICG 2271)
5. ICGV 91173	VB	((NC Ac 343 X NC Ac 2214) X ICG 5240)
6. ICGV 91177	VB	(F 334 A-B-14 X NC Ac 2232) X ((TMV 7 X FSB 7-2) X NC Ac 214)
7. ICGV 91180	VB	((TMV 2 X FSB 7-2) X NC Ac 2232) X ((F 334 A-B-14 X NC Ac 32214)
8. ICGV 92188	VB	([Robut 33-1 X (M 13 X NC Ac 2214)] X JL 24)
9. ICGV 93008	SB	([Mani Pintar X (Robut 33-1 X NC Ac 2232)] X ICG 2320)
10. ICGV 93020	SB	[((Manfredi 68 X NC Ac 343) X ([Mani Pintar X (Robut 33-1 X NC Ac 2232)]
11. ICGV 93021	VB	((F 334 A-B-14 X NC Ac 2214) X 9/136)
12. ICG 2271	VB	NC Ac 343
13. ICG 1697	VL	NC Ac 17090
14. ICGV 96262	VB	89 R/ 52-8 X PI 270806
15. ICGV 96266	VB	ICGV 86577 X ICGV 86594
16. Dh 56	SB	Dh 3-30 X ICGV 86276
17. Dh 57	SB	Dh 3-30 X ICGV 86276
18. Dh 73	SB	Dh 3-30 X ICGV 87264
19. R 8972	SB	ICGS 59 X NC Ac 2240
20. R 9214	SB	(ICGS 7 X NC Ac 2214) X ICGV 86031
21. R 9227	SB	JL 24 X GBFDS 273
22. R 9248	SB	JL 24 X GBFDS 206
Mutants		
1. VL 1	VL	EMS mutant of Dharwad Early Runner (DER)
2. 28-2	SB	EMS mutant of Valencia 1 (VL 1)
3. 45	SB	EMS mutant of Valencia 1 (VL 1)
4. 110	SB	EMS mutant of Valencia 1 (VL 1)
Cultivars		
1. ICGV 86590	VL	X14-4-B-19-B X PI 259747
2. K 134	SB	Kadiri 3 X JL 24
3. KRG 1	SB	Selection from Argentina
4. JL 24	SB	Selection from EC 94943
5. TMV 2	SB	Mass selection from "Gudhiatham bunch"
6. Dh 8	SB	Selection from RS 144
7. Dh 40	SB	Dh 3-30 X TGE 2
8. R 8808	SB	ICGS 11 X Chico
9. TG 26	SB	BARCG 1 x TG 23
10. TAG 24	SB	TGS 2 x TGE 1

SB- Spanish bunch, VB - Virginia bunch, VL - Valencia

Table 8: Pedigree of the Trombay groundnut genotypes

Genotype	Bot. group	Year of devpt.	Pedigree	Salient feature
1. Spanish Improved (S.I.)	SB	-	Selection from Spanish Peanut	_
2. Somnath (TGS 1)	SB	-	TG 18A X M 13	Large seeded
3. TG 2	SB	1958	X- ray mutant of S.I. 75 kR	Small seeded
4. TG 3	SB	1958	X- ray mutant of S.I. 75 kR	More tertiary branches
5. TG 4	SB	1958	X- ray mutant of S.I. 75 kR	Short plant
6. TG 6	SB	1958	X- ray mutant of S.I. 75 kR	Short plant
7. TG7	SB	1963	TG 1 X Virescent	Dumble shape pods, 30 days dormancy
8. TG 9	SB	1963	TG 1 X Virescent	Dumble shape pod, 30 days dormancy, high oil
9. TG 10	SB	1963	TG 1 X Virescent	Dumble shape pod, 30 days dormancy, high oil
10. TG 13A	SB	1963	Virescent X TG 1	_
11. TG 14	SB	1969	Dark green X Virescent	_
12. TG 16	SB	1969	Virescent X TG 1	_
13. TG 17	SB	1969	Dark green X TG 1	Few branches
14. TG 18	VB	1969	Dark green X TG 1	Large seeded
15. TG 18A	SB	1969	γ-ray mutant of TG 18, 20 kR	Large seeded
16. TG 19	VB	1974	TG 17 X TG 1	Large seeded
17. TKG 19A	SB	1974	TG 17 X TG 1	Large seeded
18. TG 20	SB	1970	γ-ray mutant of S.I., 50 kR	Long pods
19. TG 22	SB	1980	Robut 33-1 X TG 17	Medium bold seeds
20. TG 23	SB	1981	TGS 2 X TGE 1	_
21. TAG 24	SB	1981	TGS 2 X TGE 1	Early, high harvest index
22. TAG 24 (M)	SB	-	Somaclonal variant of TAG 24	More biomass than TAG 24
23. TG 25	SB	1986	TGE 2 X TG 23	Early, compact pod setting
24. TG 26	SB	1986	BARCG 1 X TG 23	Early, 20 days dormancy compact pod setting
25. TG 27	SB	1986	BARCG 1 X TGE 1	_
26. TG 28	SB	1986	TAG 24 X BARCG 1	_
27. TG 28A	SB	1986	TAG 24 X BARCG 1	Medium bold seeded,
28. TG 29	SB	1986	TAG 24 X BARCG 1	_
29. TG 30	SB	1986	BARCG 1 X TGE 1	_
30. TG 31	SB	1988	TAG 24 X TG 9	_
31. TG 32	SB	1988	TAG 24 X ICGS 44	_
32. TG 33	SB	1990	Girnar 1 X TAG 24	_
33. TG 34	SB	1990	TAG 24 X GAUG 10	_

Contd..

Table 8: Contd.,

Genotype	Bot. group	Year of devpt.	Pedigree	Salient feature
34. TG 35	SB	1990	TAG 24 X TG 22	_
35. TG 36A	SB	1991	TAG 24 X TG 26	_
36. TG 36B	SB	1991	TG 26 X TAG 24	_
37. TG 36C	SB	1991	TG 26 X TAG 24	_
38. TG 37A	SB	1991	TG 25 X TG 26, γ - ray 30 kR	_
39. TG 37B	SB	1991	TG 25 X TG 26, γ - ray 30 kR	_
40. TG 37C	SB	1991	TG 25 X TG 26, γ - ray 30 kR	_
41. TG 37D	SB	1991	TG 25 X TG 26	_
42. TG 37E	SB	1991	TG 25 X TG 26	_
43. TG 37F	SB	1991	TG 25 X TG 26	_
44. TG 38A	SB	1991	Girnar 1 X TG 26	_
45. TG 38B	SB	1991	Girnar 1 X TG 26, γ-ray 30 kR	_
46. TG 38C	SB	1991	TG 26 X Girnar 1	_
47. TG 38D	SB	1991	Girnar 1 X TG 26, γ-ray 30 kR	_
48. TG 39	VB	-	TAG 24 X TG 19	Early, large seeded
49. TG 40	SB	-	TAG 24 X TG 19	Early, large seeded
50. TG 41	SB	-	TG 28A X TG 22	Early, large seeded
51. TG 42	SB	-	TG 19 X TG 26	Early, large seeded
52. TG 49	SB	-	TG 28A X TG 26	Early, large seeded
53. TGE 1	SB	1973	Tall X TG 9	Early, foliaceous stipule
54. TGE 2	SB	1972	TG 3 X Gujarat Dwarf Mutant	Early, red seeded
55. TGE 3	SB	1978	TG 17 X Chico	Early
56. BARCG 1	SB	-	γ-ray mutant of JL 24	Large poded

SB - Spanish bunch, VB - Virginia bunch

3.1.3 Agronomic performance in relation to resistance in selected genotypes

Ten genotypes comprising of foliar disease resistant inter-specific derivatives (D 39d, B 37c and ICGV 87165), late leaf spot resistant mutant (28-2), ruling but susceptible cultivars (JL 24, TMV 2 and TAG 24), a rust resistant cultivar (ICGV 86590) and moderately susceptible cultivars, viz., Dh 8 (late leaf spot) and R 8808 (rust), were evaluated for disease, productivity (yield/yield loss), physiological parameters at different growth stages in early and late sown experiments under diseased (UP) and fungicide sprayed (P) conditions during *Kharif*, 1998. Besides, detailed components of late leaf spot and/or rust resistance, fatty acid composition, effect of leaf/flower removal on incidence of disease and pod yield were also investigated.

3.1.4 Genetics of resistance

In order to discern the genetics of late leaf spot and rust resistance, crosses involving mutants [VL 1, 28-2, 45,110 and 45(S)] and inter-specific derivatives [ICGV 87165, D 39d and B 37c] viz., 110 × VL 1, 45 × 45 (S), VL 1 × ICGV 87165, 110 × ICGV 87165, 28-2 × D 39d, 28-2 × B 37c and B 37c × D 39d were made. Plants in F_1, F_2 and F_3 generations were assessed for reaction to fit and confirm appropriate segregation ratios.

3.1.5 Isozyme and protein variation

Seed protein, hypocotyl protein and Glutamate Oxaloacetate Transaminase (GOT) isozyme profiles of thirteen genotypes [consisting of 10 genotypes listed in section 3.1.3 and 28-2 (S), D 39d (S), and VL 1] were investigated in order to study the extent of biochemical diversity in these genotypes.

Late leaf spot resistant mutants (28-2, 45 and 110), inter-specific derivatives [D 39d, B 37c, I 15e and ICGV 86699] and an advanced breeding line (ICGV 2271), and their susceptible counterparts were investigated for resistance and polymorphism in oxidative enzymes, viz., Peroxidase (POX), Catalase (CAT) and Super Oxide Dismutase (SOD).

3.2 METHODOLOGIES ADOPTED

3.2.1 Experimental site

Experiments were conducted in the field unit of the Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad which is located in the transitional tract of Karnataka state at 15°13' N latitude, 75° 07' E longitude and at an altitude of 678 m above mean sea level.

3.2.2 Experimental details

Groundnut germplasm including Trombay genotypes were screened for reaction to late leaf spot and rust during *Kharif,* 1997 and summer, 1998 seasons. Each genotype was grown in two rows, 5 m long and 30 cm apart with seeds dibbled at 10 cm spacing with two replications.

Ten genotypes selected for detailed study were grown in a split-split plot design with three replications. The main plots consisted of two dates of sowing (early and late sown conditions with sowings done in first fortnight of June and July 1998, respectively), subplots with spray treatments (disease control by Chlorothalonil spray v/s no disease control, water spray) and the sub-subplots comprising of genotypes. A five-rows plot of 5 m length with a spacing of 30 × 10 cm was adopted. At 30 days after sowing (DAS), 1.15 Kg ha^{-1}

Chlorothalonil (Kavach®) in 800 liters water was applied using a knapsack sprayer. Subsequent sprayings were done at 15 days interval till harvest of the crop. Control plots were sprayed with 800 liters ha^{-1} water at the same intervals. The trials were protected against insect pests using appropriate insecticides. The recommended package of practices for groundnut crop was adopted.

The weather conditions of early and late sown experiments (rainy season, 1998) was characterized by more total rainfall (472.2 and 426.0 mm, respectively), more number of rainy days (52 and 40 days) and optimum range of temperature (>20° C) and high humidity (Appendix 1) which was ideal for the infection and development of late leaf spot and rust. However, there was heavy incidence of the disease in late sown experiment due to availability of inoculum from the early sown experiment.

All disease screening trails were conducted under high disease pressure of rust and late leaf spot using the infector row technique (Subrahmanyam et al., 1982a). Infector row of highly susceptible cultivar (TMV 2) was sown after every four rows of test entries. Inoculation was done with pure late leaf spot/rust pathogen suspension @ 20,000 spores mL^{-1} when crop was at 30 days old using atomizer. Scattering leaf debries collected from previous season's diseased crop along the infector rows provided additional late leaf spot/rust inoculum. To maintain optimum temperature (23-25° C) and long periods of leaf wetness with intermittent dry periods for at least 8-10 days, plants were sprinkled with water everyday in the evening hours. This resulted in early development and rapid build up of late leaf spot/rust (Plate 1) providing scope for meaningful screening of the material for disease under field conditions. Specific disease (late leaf spot/rust) condition was created with differential fungicide treatment. The plants were sprayed with Carbendazium and Tridemorph to control late leaf spot and rust, respectively.

LATE LEAF SPOT

RUST

Plate 1: Foliar diseases - field view and sympots

3.2.3 Collection of experimental data

The observations on following phenological and productivity characters were recorded on each genotype as per the "Groundnut descriptor" (IBPGR, 1988).

3.2.3.1 Classification of groundnut genotypes

The cultivated groundnut (*Arachis hypogaea* L.) a member of section *Arachis* can be divided into two subspecies based on morphological differences combined with physiological and genetic divergence (Table 9). Subspecies *hypogaea* is further subdivided into variety *hypogaea,* Virginia (bunch and runner) type and variety *hirsuta,* Peruvian runner type. Subspecies *fastigiata* is further subdivided into variety *fastigiata,* Valencia type and variety *vulgaris,* Spanish bunch type (Krapovikas, 1968).

3.2.3.2 Phenological characters

1. Growth habit (GH)
2. Branching pattern (BP)
3. Inflorescence type
4. Number of primary branches (NPB)
5. Number of secondary branches (NSB)
6. Mainstem height (MSH)
7. Length of primary branches (LPB)
8. Leaflet length (LL)
9. Leaflet width (LW)

3.2.3.3 Reproductive characters

Following characters were measured as the characters associated with the reproductive efficiency measures (REM) of the genotypes and calculated as the mean of five plants.

Table 9: Description of subspecies and botanical varieties of *Arachis hypogaea* L. (Krapovikas, 1968)

Subspecies	Variety	Botanical type	Floral axes on mainstem	Branching pattern	Growth habit	Inflorescence type	No. Seeds/pod	Fresh seed dormancy
hypogaea	***hypogaea***	Virginia Runner (VR)	Absent	Alternate	Prostrate	Simple	2 - 3	Present
		Virginia Bunch (VB)	Absent	Alternate	Erect	Simple	2 - 3	Present
	hirsuta	Peruvian Runner	Absent	Alternate	Prostrate	Simple	4	Present
fastigiata	***fastigiata***	Valencia (VL)	Present	Sequential	Erect	Simple	4	Absent
	vulgaris	Spanish Bunch (SB)	Present	Sequential	Erect	Compound	2	Absent

1. Number of flowers
2. Days taken for initiation of flowering (DIF)
3. Days taken for 50 per cent of flowering (DFF)
4. Days taken for accumulation of 25, 50, 75 and 100 flowers
5. Number of pegs

3.2.3.4 Physiological variables

1. Reproductive efficiency measures

Based on the flower count, pod number, etc., five reproductive efficiency measures were calculated as suggested by Coffelt *et al.* (1989), details of which are given below.

i) Harvest index (HI) or REM 1

Harvest index was calculated taking into account the energy consumption. Since, pod accumulation takes 1.67 times energy to that of vegetative mass accumulation.

$$\text{HI} = \frac{(\text{Pod yield} \times 1.67)}{(\text{Pod yield} \times 1.67 + \text{vegetative yield})} \times 100$$

ii) REM 2 = $$\frac{\text{Mature pod total}}{\text{Flower total}} \times 100$$

iii) REM 3 = $$\frac{\text{Pod total}}{\text{Flower total}} \times 100$$

iv) REM 4 = $$\frac{\text{Pod total + peg total}}{\text{Flower total}} \times 100$$

v) REM 5 = $$\frac{\text{Mature seed total}}{\text{2 (flower total)}} \times 100$$

2. Leaf area index (LAI)

Leaf area index was calculated at six growth stages using the leaf weight (LW) data, as suggested by Ma *et al.* (1992).

$$LA = 0.0234 \times (LW)^{0.97} \quad \text{and}$$

$$LAI = \frac{LA\ (m^2)}{\text{Land area}\ (m^2)}$$

3. Growth rates

As suggested by Pixley *et al.* (1990a) following growth rate measures were calculated.

i) Pod growth rate (PGR)

The linear regression coefficient of the linear phase of growth on time is taken as the growth rate. Accordingly seed growth rate (sgr) and shell growth rate (shgr) were calculated from the respective weights from 45 to 90 DAS at 15 days interval. Using these, pod growth rate was calculated as follows,

$$PGR = (sgr \times 2.47 + shgr \times 1.44)$$

ii) Vegetative growth rate (VGR)

The linear regression coefficient of vegetative biomass on time in the linear period of growth (30-75 DAS) at 15 days interval was calculated as vegetative growth rate (VGR).

iii) Crop growth rate (CGR)

It is sum of pod growth rate (PGR) and vegetative growth rate (VGR).

$$CGR = PGR + VGR.$$

4. **Partitioning coefficient (PC)**

Partitioning coefficient was calculated as the measure of how much energy is diverted to pod accumulation. It was calculated as

$$PC = \frac{PGR}{CGR}$$

5. **Pod and kernel accumulation (%) pattern**

In order to assess the pattern of pod and kernel accumulation (%) at different growth periods, pod and kernel weights (g) were recorded on five randomly selected plants at 15 days interval starting from 60 DAS till the date of harvest (DOH). Differences in the pod/kernel weights (g) between successive growth periods (up to 60 DAS, 60-75 DAS, 75-90 DAS and 90 DAS-DOH) were expressed as per cent of total pod/kernel weight recorded at harvest for each genotype.

3.2.3.5 Disease variables

The disease parameters were recorded at 10 days interval starting from 45 DAS till the harvest of the crop.

1. **Leaf area affected by late leaf spot/rust (LAA)**

Each leaf on main stem was compared with standard area diagrams showing the known percentage (0 to 100 %) of their area affected by late leaf spot/rust.

2. **Defoliation percentage (DF)**

$$DF\ (\%) = \frac{\text{Number of defoliated leaves}}{\text{Total number of leaves}} \times 100$$

3. **Remaining green leaf area percentage (RGLA)**

$$RGLA = (100-DF) - [(100-DF) \times (LLS + Rust)/100]$$

4. Disease severity (DS)

DS = (100 - RGLA)

5. Field Disease Score (FDS)

The modified 9-point scales for rust (Table 10a and Figure 1) and late leaf spot (Table 10b and Figure 2) as given by Subbarao *et al.* (1990b) were used for screening genotypes/germplasm. The visual scores (1-9) and the extent of leaf area destroyed (0-100 %) are linearly related. The field disease scores are mainly based on the extent of leaf area damage. For late leaf spot, the extent of defoliation is also incorporated into the scale (Subrahmanyam *et al.*, 1995).

6. Sporulation Score (SC)

Leaves were incubated in moist chamber for 48-72 h at 25° C and observed under stereomicroscope. SC was recorded by observing the percentage of lesion/pustule area covered with fascicles with conidia/urediospores on 1-9 scale (Table 11).

7. Area under disease progress curve (AUDPC)

Area under disease progress curve was calculated as suggested by Wilcoxson *et al.* (1975).

$$\text{AUDPC} = \sum_{i=1}^{k} \tfrac{1}{2} (S_i + S_{i-1}) \times d$$

Where, S_i = disease severity (100-RGLA) at the end of time i, k = the number of successive evaluations of late leaf spot and rust diseases, and d = interval between two evaluations.

8. Healthy leaf area duration (HAD)

HAD was calculated according to Waggoner and Berger (1987) to represent the severity of disease with a weightage to the time of

Table 10a: Modified 9-point scale used for field-screening groundnut genotypes for resistance to rust

Disease Score	Description	Disease severity (per cent)ψ
1	No disease	0
2	Pustules sparsely distributed, largely on lower leaves	1-5
3	Many pustules on lower leaves, necrosis evident; very few pustules on middle leaves	6-10
4	Number pustules on lower and middle leaves; severe necrosis on lower leaves	11-20
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 per cent damage to lower and middle leaves; pustules on top leaves, which are severely	61-80
9	Almost all leaves withered; bare stems seen	81-100

ψ Percentage leaf area damaged by rust

Table 10b: Modified 9-point scale used for field-screening groundnut genotypes for resistance to late leaf spot

Disease Score	Description	Disease severity (per cent)ψ
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 per cent defoliation of lower leaves	21-30
6	Severe lesions on lower and middle leave; lesions present but less severe on top leaves; extensive defoliation of lower leaves; defoliation of some leaflets 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

ψ Percentage leaf area damaged by late leaf spot Subbarao *et al.* (1990b)

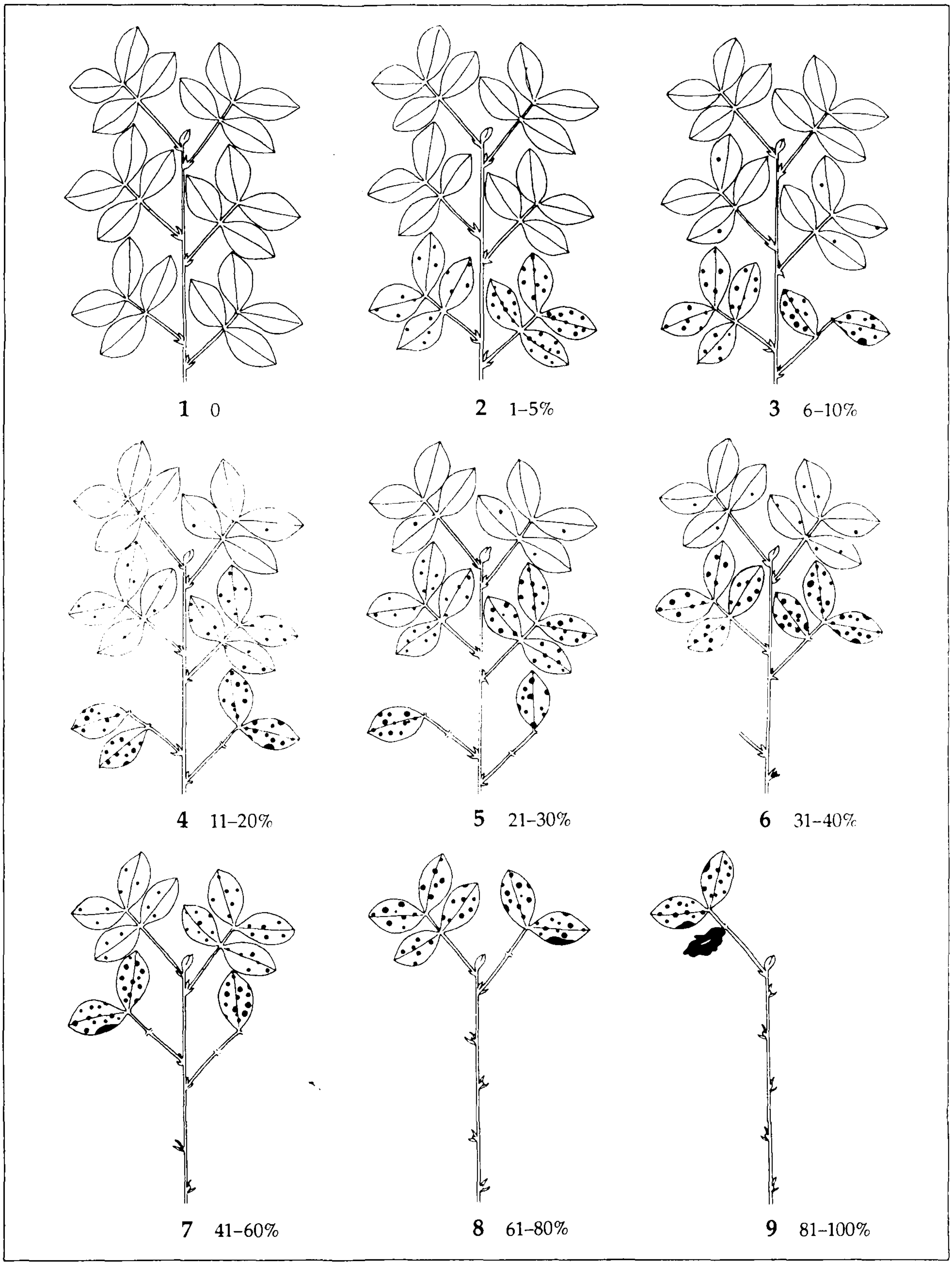
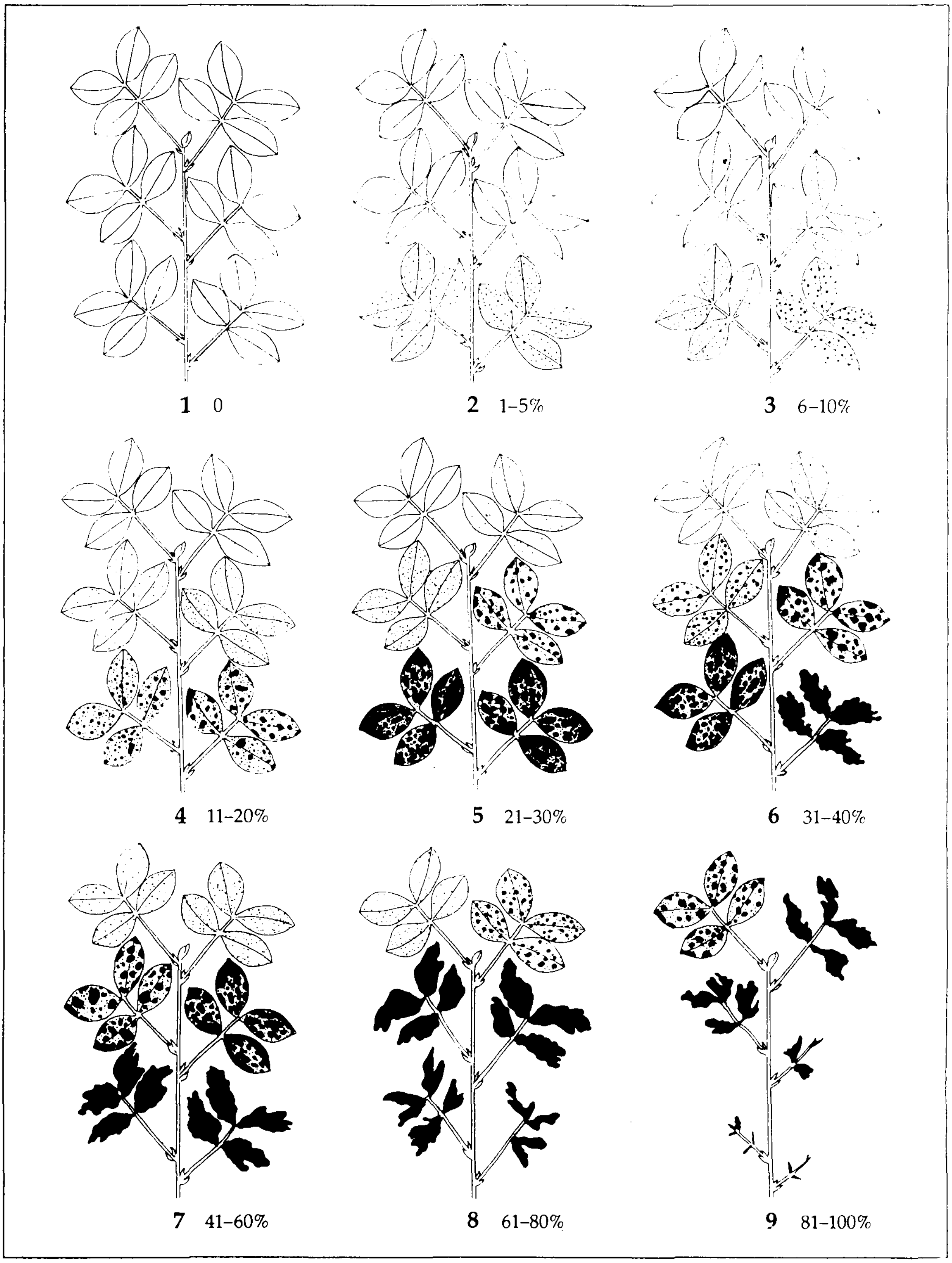


Figure 1: The modified 9-point scale for field evaluation of late leaf spot of groundnut


1 0

2 1-5%

3 6-10%

4 11-20%

5 21-30%

6 31-40%

7 41-60%

8 61-80%

9 81-100%

Figure 2: The modified 9-point scale for field evaluation of rust of groundnut

Table 11: Sporulation Score (1-9 Scale) for late leaf spot and rust resistance in groundnut

Rating	Reaction	Description	
		Late leaf spot	Rust
1	No Sporulation	Sporulation is completely absent	Sporulation is completely absent
2	Sparse	Up to 10 per cent of the lesion area covered with fascicles with conidia	Up to 10 per cent of the uredium is covered with urediospores and uredium is not ruptured
3	Slight	11 - 20 per cent of the lesion area covered with fascicles with conidia.	11 - 20 per cent of the uredium is covered with urediospores and uredium is not ruptured.
4	Moderate	21 - 30 per cent of the lesion area covered with fascicles with conidia	21 - 30 per cent of the uredium is covered with urediospores and uredium is not ruptured
5	Fair	31 - 40 per cent of the lesion area covered with fascicles with conidia	31 - 40 per cent of the uredium is covered with urediospores and Tip of the uredium is ruptured
6	Moderately High	41 - 50 per cent of the lesion covered with fascicles with conidia	41 - 50 per cent of the uredium is covered with urediospores and tip of the uredium is ruptured
7	High	51 - 60 per cent of the lesion covered with fascicles with conidia	51 - 60 per cent of the uredium is covered with urediospores and about 25 per cent uredium is ruptured
8	Very High	61 - 70 per cent of the lesion covered with fascicles with conidia	61 - 70 per cent of the uredium is covered with urediospores and about 50 per cent uredium is ruptured
9	Dense	81 - 100 per cent of the lesion covered with fascicles with conidia	81 - 100 per cent of the uredium is covered with urediospores and more than 50 per cent of the uredium is ruptured

Adopted from Pande and others, unpublished report from ICRISAT infection i.e., higher weightage is given to the area infected during early stages, by multiplying the area covered with time from last stage to the infection date.

HAD = $\Sigma[(1-Y_i)\ L_i + (1-Y_{i-1})\ (t_i-t_{i-1})/2]$ where,

Y_i = (100 - RGLA) at ith stage
L_i = leaf area index
t_i = time of ith stage.

9. Epidemiological components of resistance

The components of resistance were observed on five randomly selected plants. Leaflets from bottom, middle and upper strata of the plants were selected for counting the lesions/pustules and average was obtained.

1. Lesion (LN) / Pustule (PN) number per leaflet
2. Late leaf spot lesion size (LZ; mm^2)
3. Number of lesions on petiole (LPt)
4. Number of lesions on main stem (LM)
5. Incubation period (IP): measured as the number of days from inoculation to the appearance of the first lesion/speck.
6. Latent period (LP_{50}): defined as the time (days) from inoculation to the appearance of 50 per cent of lesions/pustules sporulating.

3.2.3.6 Oil content and fatty acid composition

Oil content (%) was determined by using the nuclear magnetic resonance (NMR) procedure (Jambunathan *et al.*, 1985). Fatty acid contents were estimated following the procedure described by Mercer et al. (1990). From the fatty acid estimates, the following oil quality characteristics were determined as described by Mozingo *et al* (1988).

i) O/L ratio = % oleic acid / % linoleic acid.

ii) Polyunsaturated (P)/Saturated (S) acids ratio

P/S ratio = % linoleic acid/Total saturated fat (TSF)

Where, TSF = % palmitic acid + % stearic acid + % arachidic acid + % behenic acid + % lignoceric acid.

3.2.3.7 Yield and yield components

i) Pod yield (PY)

The pod weight obtained from net plot (1.5 X 5 m^2) was used to calculate the pod yield per hectare as follows.

$$\text{PY (Kg ha}^{-1}) = \frac{\text{Net plot pod weight (Kg)}}{(1.5 \text{ X } 5)} \times 10000$$

ii) Shelling out-turn (SP)

Shelling out-turn was calculated, taking a sample of 100 g of pods and using the kernel weight obtained from that amount of pod.

$$\text{SP (\%)} = \frac{\text{Weight of kernel (g)}}{\text{Weight of pod (g)}} \times 100$$

iii) Kernel yield (KY)

Kernel yield (Kg ha^{-1}) = Pod yield (Kg ha^{-1}) × Shelling out-turn (%)

iv) Oil yield (OY)

Oil yield (Kg ha^{-1}) = Kernel yield (Kg ha^{-1}) × Oil content (%).

v) Fodder yield (FY)

Fodder mass obtained from net plot was used to calculate fodder yield/ha as follows.

$$\text{Fodder yield (t ha}^{-1}) = \frac{\text{Net plot fodder mass (Kg)}}{(1.5 \times 5)} \times 10$$

vi) Hundred seed mass (HSM; g)

The weight of 100 kernels was taken as test weight or HSM (g).

vii) Sound mature kernel percentage (SMK)

$$\text{SMK (\%)} = \frac{\text{Number of well-developed kernels}}{\text{Total number of kernels (Well-developed + shriveled kernels)}} \times 100$$

3.2.3.8 Yield loss variables

Yield values of protected and unprotected trials were used to find the yield loss for each genotype, replication wise, with regard to pod, kernel, oil and fodder. The difference of unprotected yield values from the mean of protected was calculated as the absolute yield loss. Since it was influenced greatly by the yield potential of the genotype, yield loss expressed, as the percentage of mean yield of the protected was considered more appropriate. It was calculated as,

$$\text{YL (\%)} = \frac{\text{Yp} - \text{Yup}}{\text{Yp}} \times 100$$

Where, YL = Yield loss (%), Yp = Mean yield (Kg ha^{-1}) in protected and Yup = Mean yield (Kg ha^{-1}) in unprotected conditions.

Yield loss was estimated for pod, kernel, oil and fodder separately.

3.2.4 Biochemical characterization (Isozyme and Protein)

3.2.4.1 Chemicals

All the chemicals used for the study were of analytical grade supplied by S.D. Fine Chemicals Ltd., Mumbai and Himedia, Mumbai.

3.2.4.2 Equipment

a. Pestle and mortar.
b. Centrifugation: Tabletop micro-centrifuge, Model Spinwin supplied by Tarson Private Limited, Kolkata.
c. Protein estimation: UV-VIS Spectrophotometer model SL 159 of ELICO, India.
d. Electrophoresis unit: Model GTV 100 of Ultra Violet Products, London.
e. Power pack: Model PSU 400/600 of Ultra Violet Products, London.
f. Transilluminator: White/UV Transilluminator of Ultra Violet Products, London.

3.2.4.3 Procedure

The analysis of proteins and isozyme, Glutamate Oxaloacetate Transaminase (GOT; E.C: 2.6.1.1), Peroxidase (POX; E.C: 1.11.1.7), Catalase (CAT; EC: 1.11.1.6), Super Oxide Dismutase (SOD; E.C: 1.15.1.1) was performed by poly acrylamide gel electrophoresis (PAGE) technique (Davis, 1964; Tanksley, 1983).

Seeds were germinated on a germination paper. Six day old seedlings were used for extraction. The hypocotyl portions were chopped into small pieces and were ground well by adding chilled phosphate buffer (0.2 M, pH 8.0) using pestle and mortar, kept on ice-cubes. About 1 mL of extraction buffer was used per gram of sample. The homogenate was filtered into an eppendorf tube using muslin cloth. The homogenate collected, centrifuged at 10,000 rpm for 15 minutes at 4° C. Supernatant so obtained was carefully transferred to another eppendorf tube and used as a source of protein/enzyme. For SDS-PAGE, seeds were ground under folds of Whatman No.1 filter paper and 40 mg of seed material was extracted for 1 hour at room temperature with 1 mL of extraction buffer. Samples were then boiled for 3 minutes and cooled for 30 minutes after which they were centrifuged briefly to remove particulate material and used as source of protein (Lanham *et al.*, 1994).

The protein sample was used for estimation of protein by Lowry's method. Based on protein content, working standards were prepared such that 1 mL has 8 mg of protein. All volume makeups were done with extraction buffer. Gels were prepared according to the methods of Hames and Rickwood (1984).

Stock solutions

1. Acrylamide–bis acrylamide monomer solution: It was prepared by dissolving 30.0 g of acryl amide and 0.8 g of bis-acrylamide in 100 mL water. The solution was then filtered through Whatman No. 1 filter paper and stored at 4° C in brown bottles.
2. Ammonium per sulphate
3. Tetramethyl Ethylenediamine (TEMED)

Electrophoresis buffers

1. Stacking gel buffer stock

0.5 M Tris-HCl (pH 6.8): 6.0 g of Tris base was dissolved in 40.0 mL of water and pH was adjusted to 6.8 with HCl and final volume was made to 100 mL.

2. Resolving gel buffer stock

3.0 M Tris-HCl (pH 8.3): 36.3 g of Tris base was dissolved in 40 mL of water and pH was adjusted to 8.3 with HCl and final volume was made to 100 mL.

3. Tank buffer (Electrode buffer: 24.8 mM Tris + 0.19 M Glycine, pH 8.3)

Three g of Tris base and 14.4 g of Glycine were dissolved in water and pH was adjusted to 8.3 and volume was made up to 1000 mL. For SDS-PAGE, 1 g of SDS was added to 1000 mL of electrode buffer.

4. Extraction buffer

For Native Page: Phosphate buffer M, pH 8.0 with 1% PVP.

For SDS-PAGE: 65mM Tris-HCl, pH 6.8 with 2% SDS W/V, 1% PVP W/V, 5% β-mercaptoethanol V/V.

Recipe for gel preparation

Component	**Resolving gel (20 mL)**		**Stacking gel (10 mL)**
	(7.5%)	(12.5%)	(2.5%)
Monomer Solution	5.0 mL	8.4 mL	1.25 mL
Resolving gel buffer	2.5 mL	2.5 mL	---
Stacking gel buffer	---	---	2.5 mL
Distilled water	12.5 mL	9.16 mL	6.25 mL
TEMED @ 0.5μL/mL	10.0 μL	10.0 μL	5.0μL
APS @ 0.75 mg/mL	15 mg	15 mg	7.5 mg

For SDS-PAGE, 12.5% gels were used and 0.2 mL and 0.1 mL of 10% SDS W/V was added to resolving and stalking gels respectively (Laemmli, 1970).

Preparation of slab gels

Glass plate sandwich was prepared using clean glass plates with spacers coated with a thin film of Vaseline and gel sandwich was finally assembled using the adhesive tape.

Appropriate resolving gel mixture was prepared by adding correct volumes of all components except TEMED and APS, which were added just before use. The assembled plate was held vertically in the gel casting unit and the resolving gel mixture was poured into the space between the glass plates up to 3/4th level and was over laid with water to avoid contact with atmospheric oxygen. The assembly was left undisturbed. After the polymerization, the top water layer was blotted and the stacking gel solution was poured and the comb was inserted avoiding air bubbles. For isozyme analysis, stacking gel was not used. After polymerization the comb was carefully removed and wells were washed with the reservoir buffer and fixed to electrophoresis apparatus. Tank buffer (200 mL) was poured in the gel apparatus. 50-100 µg of protein sample along with 5 µl of Bromophenol blue (tracking dye) was mixed well and loaded into the wells. After loading of samples was complete, voltage clamps were attached and the gel apparatus was connected to power pack set at 70 volts. The gel was run till the tracking-dye was ½ - 1 cm away from bottom of the gel.

Once the run was over, gel sandwich was detached and placed in distilled water to avoid exposure to air. Right hand side was marked by cutting piece of gel at the end. Later, the gel was transferred to suitable staining solution.

Staining

i) <u>Protein</u>: 0.1 % Coummassie brilliant blue R 250 in Methanol: Acetic acid: Water (5:2:5 v/v/v)

Staining recipe

Methanol	100 mL
Acetic acid	40 mL
Distilled water	100 mL
CBB R 250	240 mg

CBB R 250 was dissolved completely and filtered through Whatman No. 1 filter paper.

Destainer Solution (1000 mL)

Methanol 30 % V/V	300 mL
Acetic acid 10 % V/V	100 mL
Distilled water	600 mL

Gel was incubated in stain for 8 h and non-specific stain was removed by destaining.

ii) <u>Peroxidase</u> (POX); E.C: 1.11.1.7

A. Na-Acetate buffer (0.2 M pH 5.6)	100 mL
B. Benzidine	100 mg
C. H_2O_2	0.1 mL

Solution A was boiled with B and cooled and filtered. H_2O_2 was added just before incubation. Gel was incubated (in dark) till brown bands appear and rinsed in 7 % acetic acid. Gel was stored in 2 % acetic acid.

iii) <u>Glutamate Oxaloacetate Transaminase</u> (GOT); E.C: 2.6.1.1

A. Tris 0.1 M, pH 8.5	100 mL
ά- Keto glutarate	100 mg
Aspartic acid	200 mg
B. Pyridoxal 5' phosphate	10 mg
Fast Blue BB salt	150 mg

Solution A was mixed 15 minutes in advance, as the acids are not readily soluble. Solution A was poured into flask containing B reagents just before use. Gels were incubated in dark at 30° C for 2 to 4 hours or until blue bands appear.

iv) <u>Super Oxide Dismutase</u> (SOD); E.C: 1.15.1.1

50 Mm Tris-HCl, pH 8.0	50 mL
Riboflavin	2 mg
EDTA	1 mg
NBT	10 mg

Ingredients were poured over gel and incubated for 30 minutes. Later, gel was illuminated on a light box. Zones of SOD activity were revealed as achromatic regions on a dark blue background. Gels were rinsed with water and fixed in 2 per cent acetic acid.

v) <u>Catalase</u> (CAT); E.C: 1.11.1.6

H_2O_2 (0.01 % v/v)	50 mL
H_2O	50 mL
Ferric Chloride	500 mg
Potassium Ferricynide	500 mg

H_2O_2 was poured on gel slice and left for 5 minutes; meanwhile, the remaining ingredients were mixed. Peroxide was poured off and the stain solution was added. The gel was swirled gently until bands were developed. Catalase activity was revealed as achromatic bands on green background. Gel was rinsed with water and fixed in 2 per cent acetic acid.

3.2.5 Statistical Analysis

The data were subjected to statistical analyses i.e. ANOVA in Randomized Complete Block Design (RCBD), Split-plot and Split-split plot designs as detailed by Panse and Sukathme (1995). Further, from these analyses parameters of variation, viz., phenotypic coefficient of variation, heritability and genetic advance were derived using appropriate procedures. Z-transformation of yield and yield-loss variables was performed to get normal distribution.

Correlation and path coefficients were worked out (Singh and Chaudhury, 1979) to determine the degree of association among characters. Mahalanobis D^2-statistic was used for assessing the genetic divergence between genotypes (Rao, 1952).

Chi-square for goodness of fit was used to confirm the genetic hypothesis for segregation in F_2 and F_3 generations for late leaf spot and rust resistance.

EXPERIMENTAL RESULTS

IV. EXPERIMENTAL RESULTS

The experiments conducted in the present study included the assessment of variation in germplasm for resistance to late leaf spot and rust, diversity in foliar disease resistant mutants, genotypic responses in terms of yield and quality in relation to resistance, and genetic and biochemical (isozyme and protein) analysis of resistance. The results obtained from these experiments are presented here under.

4.1 Variation for resistance to late leaf spot and rust

Germplasm

A total of 45 groundnut germplasm comprising of inter-specific derivatives (9), advanced breeding lines (22), mutants (4), and ruling cultivars (10) were screened against late leaf spot and rust during *Kharif*, 1997 and summer, 1998. The components of late leaf spot (leaf area affected, lesion number, lesion size, lesions on mainstem and lesions on petiole) and rust (leaf area affected and pustule number), field disease score (FDS), defoliation (DF), remaining green leaf area (RGLA) and days to maturity (DM) were recorded in both the seasons. Incubation (IP) and latent (LP_{50}) periods of late leaf spot and rust were recorded during *Kharif*.

Pooled analysis of variance revealed highly significant seasonal and genotypic variation for all the parameters (Table 12). The significant interactions between the seasons and genotypes for all the parameters except for lesion size and field disease score of late leaf spot indicated the need for screening germplasm over seasons. However, the incidence of late leaf spot was more during *Kharif* and that of rust in summer.

Table 12: Pooled (*Kharif* and summer, 1998) ANOVA for late leaf spot and rust resistance parameters in groundnut germplasm

Source of variation	d.f.	Late leaf spot								Rust					DF	RGLA	DM
		IP	LP_{50}	LAA	LN	LZ	LPt	LM	FDS	IP	LP_{50}	LAA	PN	FDS			
Season	01	-	-	210.8**	163.0**	416.2**	343.3**	281.5**	17.4**	-	-	19.5**	170.5**	5.0**	19130.4**	15105.4**	8778.3*
Genotype	44	6.4**	78.9**	61.1**	15.6**	15.4**	10.1**	6.9**	6.4**	30.6**	107.1**	79.2**	135.1**	9.1**	637.2**	628.8**	187.0**
Genotype × Season	44	-	-	5.3**	1.5*	0.3^{NS}	3.2**	3.0**	0.3^{NS}	-	-	48.6**	2.6*	0.5**	143.3**	96.9**	48.8**
Error	88	0.1	0.5	1.4	0.8	0.2	0.6	0.4	0.2	0.1	0.3	1.1	1.4	0.2	18.3	16.9	0.7

*, ** denotes significance at 5% and 1% level of probability, respectively NS - not significant –: observations recorded in *Kharif* 1998 season o

IP - Incubation period LP_{50} - Latent period LAA - Leaf area affected (%) LN - Lesion number PN - Pustule number
LPt - Lesions on petiole LM - Lesions on mainstem FDS - Field disease score DF - Defoliation (%) DM - Days to maturity
RGLA - Remaining green leaf area (%) LZ – Lesion size (mm^2)

Many components of late leaf spot (incubation period, lesions on mainstem and petiole) and rust (pustule number, incubation period and latent period) had high genetic advance and heritability compared to field disease scores, defoliation per cent and remaining green leaf area (Table 13). Similarly, some components of late leaf spot (lesions on mainstem and lesions on petiole) and rust (pustule number and incubation period) had higher phenotypic coefficient of variation than field disease score.

Mean and range of variation in groundnut germplasm revealed the high magnitude of variation for components of late leaf spot and rust resistance in advanced breeding lines and mutants; and that of days to maturity in advanced breeding lines and inter-specific derivatives indicating the scope for selection (Table 14). Frequency of resistant genotypes in each group revealed that, most of the inter-specific derivatives were resistant to late leaf spot and rust but they matured later than ruling cultivars. Many advanced breeding lines (40 %) were resistant to rust. Mutants were early maturing and resistant to either late leaf spot (75 %) or rust (25 %). All the ruling cultivars except ICGV 86590 were susceptible to late leaf spot and rust. The cultivar ICGV 86590 was resistant to rust but matured late.

Correlation coefficients indicated highly significant association among components of late leaf spot (incubation period, latent period, lesion number, lesion size, lesions on petiole, lesions on mainstem and field disease score) and rust (incubation period, latent period, pustule number and field disease score) resistance revealing the possibility of common genetic control (Table 15). However, the strength of association between components of late leaf spot and rust was rather low. The association of incubation period of late leaf spot with pustule number; incubation period of rust with lesion number was non-significant. The low strength of association between the components of rust and late leaf spot was due to different kinds of

Table13: Parameters of variation for late leaf spot and rust resistance components in groundnut germplasm (Pooled over *Kharif* and summer,1998 seasons)

	Late leaf spot							Rust				DF	RGLA	DM
	IP	LP_{50}	LN	LZ	LPt	LM	FDS	IP	LP_{50}	PN	FDS			
Minimum	04.4	15.7	04.0	04.24	01.0	00.1	04.0	04.7	15.9	02.6	02.8	34.7	12.0	99.0
Maximum	11.3	39.0	12.0	10.91	08.0	05.6	08.3	17.0	39.0	22.0	08.0	86.4	63.3	122.0
Mean	06.1	29.3	08.6	07.90	04.2	02.4	06.6	10.9	28.4	11.4	05.1	60.4	35.7	111.1
Phenotypic Coefficient of Variation (%)	29.4	21.5	24.3	25.20	36.5	47.7	20.0	36.0	25.8	51.5	30.1	19.7	34.3	08.0
Heritability (%)	97.9	98.7	80.9	94.80	84.2	82.3	80.9	99.4	99.5	95.8	89.2	80.1	88.7	99.2
Genetic Advance over Mean (GA_m ; %)	58.7	43.7	40.7	49.4	54.8	70.8	36.4	73.4	93.8	101.8	56.9	35.4	62.8	16.3

IP - Incubation period
LP_{50} - Latent period
LAA - Leaf area affected (%)
LN - Lesion number
PN - Pustule number
LPt - Lesions on petiole
LM - Lesions on mainstem
FDS - Field disease score
DF - Defoliation (%)
DM - Days to maturity
RGLA - Remaining green leaf area (%)
LZ – Lesion size (mm^2)

Table 14: Variation for components of late leaf spot and rust resistance in groundnut germplasm

		Late leaf spot								Rust					DF	RGLA	DM
		IP	LP_{50}	LAA	LN	LZ	LPt	LM	FDS	IP	LP_{50}	LAA	PN	FDS			
Interspecific derivatives (9)	Min	05.5	31.2	02.3	04.0	04.71	1.0	0.5	4.0	12.4	31.5	00.9	02.6	2.8	34.7	34.2	110.
	Max	10.3	39.0	04.2	07.8	07.41	4.1	3.1	6.5	16.7	39.0	02.2	06.8	4.3	63.3	63.3	122.
	Mean	08.2	36.8	03.6	07.3	05.81	2.3	1.8	5.1	14.4	36.3	01.5	04.8	3.3	51.8	45.8	119.
Advanced breeding lines (22)	Min	04.6	20.7	02.0	04.6	05.64	2.5	0.8	5.0	05.1	15.5	00.7	04.3	3.0	36.8	15.2	101.
	Max	11.3	35.8	12.8	11.6	10.32	8.0	5.3	7.8	13.8	35.8	08.4	19.5	7.5	83.0	59.6	122.
	Mean	05.6	29.1	05.84	08.8	08.2	4.2	2.3	6.9	11.4	27.6	03.0	10.4	5.0	60.8	36.6	113.
Mutants (4)	Min	05.1	27.9	04.4	05.9	05.48	2.4	1.1	4.8	05.9	12.3	01.4	07.0	3.0	35.9	12.0	101.
	Max	08.3	39.0	12.6	11.3	10.91	5.4	3.5	8.3	17.0	34.5	12.2	22.0	7.5	86.4	53.2	106.
	Mean	07.3	34.6	06.3	07.4	06.93	3.4	2.0	5.8	10.4	23.1	16.3	17.1	5.0	53.1	39.5	104.
Cultivars (10)	Min	04.4	15.7	03.5	08.5	05.64	4.3	1.3	6.8	04.7	15.5	00.8	07.5	3.5	61.4	12.2	100.
	Max	08.6	26.2	15.2	12.0	11.36	7.6	5.6	8.3	14.3	32.5	14.2	21.3	8.0	85.5	3.0	115.
	Mean	05.1	21.4	10.7	09.9	09.43	5.9	3.8	7.9	06.7	19.5	10.0	18.8	7.1	69.8	24.4	100.
Grand Mean (45 genotypes)		06.1	29.3	06.5	08.6	07.9	4.2	2.4	6.6	10.9	28.4	04.7	11.4	5.1	60.1	35.7	111.

IP - Incubation period
LP_{50} - Latent period
LAA - Leaf area affected (%)
LN - Lesion number
PN - Pustule number
LPt - Lesions on petiole
LM - Lesions on mainstem
FDS - Field disease score
DF - Defoliation (%)
DM - Days to maturity
RGLA - Remaining green leaf area (%)
LZ – Lesion size (mm^2)

Table 15: Correlation coefficients for disease resistance parameters, components of resistance and days to maturity in groundnut germplasm (Pooled over *Kharif* and summer, 1998 seasons)

	Late leaf spot							Rust				DF	RGLA	DM
	IP	LP_{50}	LN	LZ	LPt	LM	FDS	IP	LP_{50}	PN	FDS			
Late leaf spot														
IP	1.000	0.710**	-0.626**	-0.722**	-0.653**	-0.565**	-0.849**	0.413**	0.371**	-0.247	-0.427**	-0.647**	0.642**	0.369**
LP_{50}		1.000	-0.794**	-0.695**	-0.832**	-0.730**	-0.879**	0.526**	0.589**	-0.445**	-0.663**	-0.775**	0.795**	0.539**
LN			1.000	0.735**	0.855**	0.871**	0.818**	-0.299	-0.378*	-0.309*	0.351*	0.798**	-0.840**	-0.423**
LZ				1.000	0.786**	0.785**	0.879**	-0.338*	-0.354*	0.308*	0.402**	0.605**	-0.638**	-0.570**
LPt					1.000	0.927**	0.942**	-0.516**	-0.595**	0.536**	0.711**	0.747**	-0.826**	-0.639**
LM						1.000	0.945**	-0.469**	-0.542**	0.533**	0.647**	0.778**	-0.886**	-0.666**
FDS							1.000	-0.389*	-0.475**	0.348*	0.508**	0.863**	-0.875**	-0.679**
Rust														
IP								1.000	0.920**	-0.855**	-0.883**	-0.367**	0.455**	0.436**
LP_{50}									1.000	-0.887**	-0.897**	-0.457**	0.547**	0.633**
PN										1.000	0.892**	0.215*	-0.370*	-0.655**
FDS											1.000	0.367**	-0.498**	-0.762**
DF												1.000	-0.983**	-0.464**
RGLA													1.000	0.585**
DM														1.000

*, ** denotes significance at 5% and 1% level of probability, respectively

IP - Incubation period	LP_{50} - Latent period	LAA - Leaf area affected (%)	LN - Lesion number	PN - Pustule number
LPt - Lesions on petiole	LM - Lesions on mainstem	FDS - Field disease score	DF - Defoliation (%)	DM - Days to maturity
RGLA - Remaining green leaf area (%)		LZ – Lesion size (mm^2)		

material i.e., resistant to late leaf spot or rust, resistant/susceptible to both the diseases. Remaining green leaf area, an integrated measure of defoliation and leaf area affected by late leaf spot and rust diseases was highly significantly and negatively associated with defoliation. Defoliation was negatively associated with resistance components (incubation and latent periods) and positively with disease components (lesion number, lesion size, lesions on petiole, lesions on mainstem, pustule number and field disease score). But, the strength of association was more with components of late leaf spot than rust revealing the importance of late leaf spot as defoliating disease. Days to maturity had strong positive association with resistance (incubation period, latent period of late leaf spot and rust, remaining green leaf area) and negative association with disease (lesion number, lesion size, lesions on petiole, lesions on mainstem, pustule number, field disease score and defoliation) components indicating the late maturing nature of the resistant germplasm.

Based on lower values for field disease score and longer incubation and latent periods, inter-specific derivatives (ICGV 86699, ICGV 87165, D 39d and B 37c) and advanced breeding lines (ICGV 87264 and ICGV 96266) were categorized as late leaf spot and rust resistant; mutants, viz., 28-2, 45 and 110 as late leaf spot resistant and advanced breeding lines (ICGV 93008, ICGV 93023 and R 8972), mutant (VL 1) and cultivar (ICGV 86590) as rust resistant (Table 16). Among the germplasm lines, inter-specific derivatives, D 39d followed by ICGV 96266 and B 37c had highest green leaf area present at harvest. While, mutants (VL 1, 28-2, 45 and 110), advanced breeding line (R 8972) and inter-specific derivative (D 39d) had desirable combination of early maturity (100-110 days) with late leaf spot and/or rust resistance.

Table 16: Components of late leaf spot and rust resistance in selected groundnut germplasm

Genotype	Late leaf spot			Rust			RGLA	DM†
	IP	LP_{50}	FDS	IP	LP_{50}	FDS		
LLS and Rust resistant								
ICGV 86699	09.9^{b}	39.0^{a}	4.0^{a}	15.9^{b}	39.0^{a}	2.8^{a}	49.5^{bc}	122.0^{e}
ICGV 87165	10.6^{b}	39.0^{a}	4.5^{ab}	16.8^{a}	39.0^{a}	2.8^{ab}	46.0^{bc}	122.0^{e}
ICGV 87264	11.3^{a}	32.5^{c}	5.0^{ab}	13.8^{cd}	33.0^{d}	4.3^{bc}	46.2^{b}	118.0^{d}
ICGV 96266	06.2^{d}	32.0^{c}	5.0^{ab}	12.7^{cd}	33.4^{b}	4.5^{bc}	59.6^{b}	121.0^{e}
D 39d	10.3^{b}	39.0^{a}	4.0^{a}	16.7^{a}	39.0^{a}	2.8^{a}	63.3^{a}	110.0^{bc}
B 37c	07.5^{cd}	39.0^{a}	4.8^{ab}	14.4^{c}	39.0^{a}	2.8^{a}	54.4^{ab}	115.0^{d}
LLS resistant								
28 - 2	08.3^{c}	39.0^{a}	4.8^{ab}	06.6^{f}	17.2^{e}	6.3^{d}	53.2^{b}	106.0^{b}
45	07.9^{c}	35.5^{b}	5.0^{ab}	06.3^{fg}	18.0^{e}	6.8^{de}	47.9^{b}	106.0^{b}
110	07.9^{c}	36.0^{b}	5.0^{ab}	05.9^{fg}	16.9^{e}	7.0^{de}	45.0^{bc}	106.0^{b}
Rust resistant								
ICGV 86590	05.6^{d}	23.7^{f}	7.8^{d}	14.3^{c}	32.5^{d}	4.5^{bc}	22.2^{e}	115.0^{d}
ICGV 93008	05.3^{d}	29.5^{d}	6.3^{c}	16.8^{a}	35.8^{bc}	3.0^{ab}	39.2^{bc}	121.0^{e}
ICGV 93023	05.7^{d}	29.8^{d}	6.3^{c}	12.4^{e}	34.5^{c}	3.8^{bc}	34.2^{d}	121.0^{e}
VL 1	05.1^{d}	27.9^{e}	8.3^{e}	17.0^{a}	34.5^{c}	3.5^{ab}	12.0^{f}	101.0^{a}
R 8972	05.2^{d}	27.5^{e}	7.3^{d}	16.0^{b}	34.8^{bc}	4.0^{bc}	40.3^{bc}	101.0^{a}
Susceptible Check								
TMV 2	04.6^{e}	15.7^{g}	8.3^{e}	04.7^{h}	15.9^{f}	8.0^{f}	23.1^{e}	101.0^{a}
Mean (45 genotypes)	06.1	29.3	6.6	10.9	28.4	5.1	35.7	111.1
C.D. (5%)	00.5	01.4	00.7	00.6	01.0	00.6	05.8	001.6
C. V. (%)	04.3	02.4	7.2	02.7	01.8	9.0	11.5	00.73

† days to maturity recorded in *Kharif* 1998 season Figures with same subscript (s) do not differ significantly at 5% level probability

IP - Incubation period LP_{50} - Latent period FDS - Field disease score RGLA - Remaining green leaf area (%)

Trombay groundnuts

Fifty-five Trombay genotypes were assessed for reaction to late leaf spot and rust. Pooled analysis of variance indicated highly significant variation for season, genotype and their interactions for all the parameters except for days to maturity where interaction effect was non-significant, revealing differential response of genotypes to season for late leaf spot and rust resistance (Table 17).

Parameters of variation for disease resistance components revealed higher magnitude of variation for rust than late leaf spot. Components of late leaf spot, viz., incubation period, lesion size and lesions on mainstem and rust viz., incubation and latent periods had high coefficient of variation, heritability and genetic advance compared to corresponding field disease scores implying the utility of these components in evaluating the Trombay genotypes (Table 18). Low mean (98.2 days) and narrow range (94.5 - 99.0 days) for days to maturity indicates the early maturing nature of Trombay genotypes especially under epiphytotic conditions.

Correlation coefficients revealed highly significant association among many components of late leaf spot and rust resistance (Table 19). However, there was lack of association among some components of late leaf spot (incubation period with lesions on mainstem; latent period with lesion size and lesions on mainstem) and rust (incubation period with pustule number) and between many components of late leaf spot and rust. The strength of association of components of resistance with defoliation and remaining green leaf area was stronger in late leaf spot compared to rust. However, lesions on leaflet, petiole and mainstem of late leaf spot, and latent period and pustule number of rust had much stronger association with defoliation and remaining green leaf area implying their utility in the evaluation. Days to maturity had either non-significant or low magnitude of positive

Table 17: Pooled (*Kharif* and summer, 1998) ANOVA for late leaf spot and rust resistance parameters in Trombay groundnut genotypes

Source of variation	d.f.	Late leaf spot								Rust					DF	RGLA	DM
		IP	LP_{50}	LAA	LN	LZ	LPt	LM	FDS	IP	LP_{50}	LAA	PN	FDS			
Season	01	-	-	387.0**	196.5**	144.1**	1453.0**	1460.6**	205.4**	-	-	708.2**	215.5**	16.6**	57215.1**	39865.8**	18144.0**
Genotype	55	9.72**	9.2**	2.7**	13.6**	6.2**	3.3**	5.5**	1.2**	9.2**	20.8**	27.0**	18.7**	5.5**	631.8**	519.6**	6.6**
Genotype × Season	55	-	-	30.9**	3.5**	0.3**	1.7**	3.6**	0.9**	-	-	20.0**	2.1**	2.4**	213.1**	192.4**	0.1^{NS}
Error	110	0.5	0.1	2.8	1.5	0.3	0.4	0.3	0.1	0.1	0.3	1.7	1.3	0.5	22.9	16.6	0.3

*, ** denotes significance at 5% and 1% level of probability, respectively NS - not significant -: observations recorded in *Kharif* 1998 season only

IP - Incubation period
LP_{50} - Latent period
LAA - Leaf area affected (%)
LN - Lesion number
PN - Pustule number
LPt - Lesions on petiole
LM - Lesions on mainstem
FDS - Field disease score
DF - Defoliation (%)
DM - Days to maturity
RGLA - Remaining green leaf area (%)
LZ – Lesion size (mm^2)

Table18: Parameters of variation for components of late leaf spot and rust resistance in Trombay groundnut genotypes (Pooled Over *Kharif* and summer, 1998 seasons)

	Late leaf spot							Rust				DF	RGLA	DM
	IP	LP_{50}	LN	LZ	LPt	LM	FDS	IP	LP_{50}	PN	FDS			
Minimum	04.6	16.5	06.3	05.5	03.1	02.1	05.9	05.2	15.9	02.9	02.0	23.3	18.3	94.5
Maximum	08.5	27.3	14.1	11.3	07.5	07.6	08.0	15.8	32.5	12.5	06.5	77.7	64.2	99.0
Mean	06.5	21.6	10.7	09.2	04.9	03.8	06.7	08.1	21.0	06.7	04.7	45.3	46.3	98.2
Phenotypic Coefficient of Variation (%)	17.4	12.6	18.3	33.1	17.7	22.8	06.1	28.4	16.3	13.9	22.6	23.8	22.7	01.4
Heritability (%)	96.6	90.4	62.7	81.8	60.2	68.4	54.2	98.8	97.5	76.6	63.7	80.0	83.1	84.4
Genetic Advance over Mean (GA_m; %)	34.9	23.7	23.6	39.4	17.7	27.5	05.7	57.9	32.7	31.4	30.6	32.2	38.8	02.3

IP - Incubation period
LP_{50} - Latent period
LAA - Leaf area affected (%)
LN - Lesion number
PN - Pustule number
LPt - Lesions on petiole
LM - Lesions on mainstem
FDS - Field disease score
DF - Defoliation (%)
DM - Days to maturity
RGLA - Remaining green leaf area (%)
LZ – Lesion size (mm^2)

Table 19: Correlation coefficients for late leaf spot and rust resistance parameters, components of resistance and days to maturity in Trombay groundnut genotypes (Pooled over *Kharif* and summer, 1998 seasons)

	Late leaf spot							Rust				DF	RGLA	DM
	IP	LP_{50}	LN	LZ	LPt	LM	FDS	IP	LP_{50}	PN	FDS			
Late leaf spot														
IP	1.000	0.756**	-0.296*	-0.352**	-0.114	-0.164	-0.658**	0.513**	0.510**	-0.325*	-0.273*	-0.577**	0.570**	0.193
LP_{50}		1.000	-0.445**	-0.222	-0.306*	0.013	-0.884**	0.409**	0.642**	-0.515**	-0.245	-0.541**	0.548**	0.315**
LN			1.000	0.497**	0.941**	0.416**	0.677**	-0.241	-0.275*	0.507**	0.573**	0.634**	-0.713**	-0.485**
LZ				1.000	0.409**	0.504**	0.677**	-0.434**	-0.387**	0.408**	0.849**	0.439**	-0.364**	-0.162
LPt					1.000	0.582**	0.606**	-0.142	-0.141	0.581**	0.347**	0.805**	-0.918**	-0.331*
LM						1.000	0.876**	-0.001	0.090	0.475**	0.167	0.710**	-0.671**	-0.163
FDS							1.000	-0.090	-0.428**	0.757**	0.525**	0.744**	-0.778**	-0.677**
Rust														
IP								1.000	0.736**	-0.133	-0.608**	-0.113	0.129	0.159
LP_{50}									1.000	-0.328*	-0.583**	-0.342**	0.385**	0.405**
PN										1.000	0.377**	0.233*	-0.510**	-0.101
FDS											1.000	0.095	-0.197	-0.155
DF												1.000	0.994**	-0.596**
RGLA													1.000	0.677**
DM														1.000

*, ** denotes significance at 5% and 1% level of probability, respectively

IP - Incubation period	LP_{50} - Latent period	LAA - Leaf area affected (%)	LN - Lesion number	PN - Pustule number
LPt - Lesions on petiole	LM - Lesions on mainstem	FDS - Field disease score	DF - Defoliation (%)	DM - Days to maturity
RGLA - Remaining green leaf area (%)		LZ - Lesion size (mm^2)		

association with resistance (incubation period, latent period and remaining green leaf area) and negative association with disease (lesion number, lesion size, lesions on petiole, lesions on mainstem, pustule number, field disease score and defoliation) parameters indicating undesirable association of maturity with late leaf spot and rust resistance even in early maturing Trombay genotypes.

Based on lower values for disease components (lesion number, lesion size, lesions on petiole, lesions on mainstem, pustule number and field disease score), and longer incubation and latent periods, some genotypes were superior for late leaf spot and rust (Spanish Improved, Somnath, TG 33 and TG 38D); late leaf spot (TG 20, TG 32, TG 35, TG 36B and TG 37D and TGE 2), and rust (TG 3, TG 4, TG 37F, TG 38A, TG 38B, and TG 38C) compared to susceptible check, JL 24 (Table 20). The genotypes, TG 32, TG 20 followed by TG 36B, Spanish Improved, and TG 35 had highest green leaf area at harvest. The frequency of genotypes superior for late leaf spot (5.4 %) was very low compared to rust (46 %) indicating better scope for selection for rust resistance. Mean values for components of late leaf spot and/or rust in Trombay genotypes approached the susceptible check, JL 24 (Tables 18 and 20). The means of superior lines revealed very low and moderate level of resistance to late leaf spot and rust, respectively. However, these values were far lower as compared to resistant check indicating the need for further improvement for disease resistance.

4.2 Diversity in foliar disease resistant mutants

Induced mutants

Eighteen mutants isolated from VL 1 were screened for reaction to late leaf spot and rust. They were also characterized for morphological and productivity parameters. The genetic diversity and

Table 20: Mean values for late leaf spot and rust resistance parameters and days to maturity in selected Trombay groundnut genotypes (Pooled over *Kharif* and summer, 1998 seasons)

Genotype	Late leaf spot							Rust				RGLA	D M†
	IP	LP$_{50}$	LN	LZ	LPt	LM	FDS	IP	LP$_{50}$	PN	FDS		
Superior for LLS and rust													
Spanish Improved	06.7^{de}	22.9^{d}	09.0^{bc}	06.8^{b}	04.8^{bc}	04.3^{cd}	5.9^{bc}	10.3^{f}	23.4^{d}	04.6^{bc}	04.5^{c}	59.4^{b}	98.0^{b}
Somnath	07.9^{bc}	27.3^{b}	08.9^{bc}	05.5^{a}	03.9^{bc}	04.1^{cd}	5.9^{bc}	15.8^{b}	30.5^{b}	02.9^{b}	02.0^{a}	54.7^{b-d}	98.0^{b}
TG 33	08.8^{b}	25.4^{bc}	08.8^{bc}	10.0^{e}	04.0^{bc}	04.3^{cd}	5.9^{bc}	15.2^{c}	29.9^{b}	04.7^{bc}	02.8^{ab}	55.5^{b-d}	98.0^{b}
TG 38D	08.2^{bc}	21.9^{d}	09.8^{bc}	08.3^{cd}	04.5^{bc}	03.6^{b-d}	6.5^{bc}	13.7^{d}	22.3^{de}	03.1^{b}	02.0^{a}	49.1^{cd}	95.5^{a}
Superior for LLS													
TG 20	07.3^{d}	26.2^{bc}	08.1^{ab}	08.4^{cd}	03.6^{b}	02.9^{bc}	6.3^{bc}	06.4^{ij}	18.3^{gh}	06.6^{cd}	05.8^{cd}	63.0^{b}	98.0^{b}
TG 32	08.8^{b}	26.8^{bc}	09.1^{bc}	07.1^{b}	04.3^{bc}	03.3^{b-d}	6.5^{bc}	06.9^{ij}	20.2^{f}	06.2^{cd}	05.5^{cd}	64.2^{b}	96.0^{a}
TG 35	07.9^{bc}	21.2^{d}	09.6^{bc}	08.3^{cd}	04.4^{bc}	02.6^{bc}	6.5^{bc}	08.0^{h}	22.3^{de}	08.6^{e}	05.8^{cd}	58.6^{b}	98.0^{b}
TG 36B	06.4^{de}	20.5^{d-f}	09.0^{bc}	09.5^{cd}	03.9^{bc}	03.1^{bc}	6.3^{bc}	06.6^{ij}	18.4^{gh}	07.7^{cd}	05.3^{cd}	60.6^{b}	98.0^{b}
TG 37D	08.0^{bc}	20.2^{d-f}	10.0^{bc}	08.1^{cd}	04.4^{bc}	02.1^{b}	6.4^{bc}	06.7^{i}	19.1^{fg}	06.3^{cd}	05.8^{cd}	56.0^{bc}	98.0^{b}
TGE 2	07.1^{d}	20.5^{d-f}	06.3^{a}	09.2^{cd}	04.1^{bc}	03.6^{b-d}	6.1^{bc}	08.6^{g}	19.0^{fg}	05.4^{b-d}	04.8^{cd}	52.6^{cd}	99.0^{b}
Superior for Rust													
TG 3	06.7^{de}	22.8^{d}	10.0^{bc}	11.3^{f}	05.2^{bc}	03.8^{cd}	6.6^{bc}	09.0^{g}	25.3^{c}	05.6^{b-d}	04.0^{b}	57.9^{bc}	98.0^{b}
TG 4	06.7^{de}	22.4^{d}	10.3^{bc}	08.9^{cd}	04.4^{bc}	04.0^{cd}	6.6^{bc}	08.1^{h}	25.5^{c}	06.2^{cd}	03.0^{ab}	55.8^{b-d}	98.0^{b}
TG 37F	05.9^{ef}	19.2^{f}	12.9^{c}	10.1^{e}	06.3^{c}	04.1^{cd}	7.3^{de}	11.4^{e}	23.5^{d}	03.6^{bc}	04.0^{b}	50.2^{cd}	98.0^{b}
TG 38A	07.9^{bc}	22.5^{d}	10.0^{bc}	08.0^{c}	04.8^{bc}	03.1^{bc}	7.3^{de}	08.0^{h}	23.1^{de}	04.1^{bc}	02.5^{ab}	49.3^{cd}	96.0^{a}
TG 38B	07.6^{bc}	18.5^{f}	13.3^{c}	09.8^{e}	06.3^{c}	03.4^{b-d}	7.5^{de}	07.1^{i}	20.0^{fg}	05.4^{b-d}	03.3^{b}	47.4^{cd}	95.5^{a}
TG 38C	07.1^{d}	19.7^{d-f}	10.4^{bc}	11.0^{ef}	04.6^{c}	03.6^{b-d}	6.8^{cd}	11.2^{e}	20.8^{f}	04.9^{bc}	03.0^{ab}	48.6^{cd}	98.0^{b}
Susceptible checks													
JL 24	05.2^{h}	20.2^{d-f}	11.6^{bc}	10.2^{ef}	05.3^{bc}	04.9^{cd}	7.6^{de}	05.1^{k}	18.7^{g}	06.8^{cd}	07.5^{e}	46.7^{d}	98.0^{b}
TG 26	06.1^{ef}	20.2^{d-f}	10.0^{bc}	08.7^{cd}	05.0^{bc}	03.5^{b-d}	6.9^{cd}	07.1^{i}	25.5^{c}	06.7^{cd}	05.8^{cd}	54.0^{b-d}	98.0^{b}
TAG 24	04.6^{g}	16.5^{g}	12.8^{c}	10.1^{e}	06.3^{c}	05.9^{e}	7.6^{de}	05.2^{k}	17.5^{gh}	06.4^{cd}	05.0^{cd}	18.3^{e}	96.0^{a}
Resistant check													
ICGV 87165	10.9^{a}	39.0^{a}	05.0^{a}	05.2^{a}	02.3^{a}	01.0^{a}	3.0^{a}	17.8^{a}	39.0^{a}	00.6^{a}	01.0^{a}	75.7^{a}	125.0^{c}
Mean	06.3	20.3	11.0	09.4	05.1	04.0	7.0	07.6	19.9	07.0	04.9	43.8	98.2
C.D. (5%)	00.4	01.6	01.8	00.8	01.0	00.8	0.4	00.4	01.0	01.6	01.0	05.7	01.4
C. V. (%)	03.2	03.9	11.2	05.9	12.5	14.7	4.5	03.1	02.6	16.0	13.6	09.3	00.8

† days to maturity recorded in *Kharif* 1998 season Figures with same subscript (s) do not differ significantly at 5% level probability
IP - Incubation period LP$_{50}$ - Latent period LAA - Leaf area affected(%) LN - Lesion number PN - Pustule number
LPt - Lesions on petiole LM - Lesions on mainstem FDS - Field disease score DF - Defoliation (%) DM - Days to maturity
LZ – Lesion size (mm^2)

character association among mutants was assessed by using Mahalanobis D^2 and correlation analyses, respectively.

Analysis of variance revealed significant variation for all the parameters. Diversity analysis grouped the 18 mutants into three clusters (Tables 21 and 22a). Cluster I comprised of nine mutants resistant to rust but susceptible to late leaf spot and the VL 1 parent. They were characterized by broad leaves with moderate pod yield and test weight. Cluster II included five mutants highly resistant to late leaf spot but susceptible to rust. They had more number of primary and secondary branches, short main stem and primary branches, small leaves with high pod yield and test weight. Four mutants with moderate resistance to late leaf spot and rust were clustered separately (cluster III). They had long main stem and primary branches with intermediate leaf size. Cluster II was equidistant from cluster I (6.011) and cluster III (6.675). While, cluster III and I (4.670) were more closely related (Table 21).

Late leaf spot resistance in the mutants was highly associated with rust susceptibility. Its strong association was also observed with increased number of primary and secondary branches; hundred seed mass and pod yield and reduced leaflet length and width (Table 22b). In contrast, an opposite trend in interrelationships was evident with rust resistance revealing distinct nature of rust and late leaf spot resistant mutants.

Spontaneous mutants

Spontaneously occurring susceptible counterparts were isolated from resistant mutants (28-2, 45 and 110), inter-specific derivatives (D 39d, B 37c, I 15e and ICGV 86699) and an advanced breeding line

Table 21: Clustering pattern and inter-cluster distance in groundnut mutants

Cluster		Groundnut mutants	Inter-cluster distances	
			II	**III**
I	**(9 + 1)**	1-1, 2-1, 2-2, 27-1, 78-1, 78-2, 109-1, 139-1, 171 and VL 1	6.011	4.670
II	**(5)**	28-1, 28-2, 45, 98 and 110	-	6.675
III	**(4)**	3-1, 29-1, 121 and 161	-	-

Values in parenthesis indicate the number of groundnut mutants included in the cluster

Table 22a: Cluster means for morphological, productivity and disease resistance parameters in groundnut mutants

	NPB	NSB	MSH	LPB	LL	LW	PY	HSM	LLS	Rust
Cluster I	4.00	1.50	33.42	37.89	6.20	3.09	24.41	43.58	7.05	1.93
Cluster II	5.00	5.40	29.85	31.66	5.12	2.56	31.89	58.83	4.20	6.40
Cluster III	3.25	3.12	43.65	48.60	5.65	3.04	23.90	32.38	6.25	5.25

Table 22b: Correlation coefficients for morphological, productivity and disease resistance parameters in groundnut mutants

	NPB	NSB	MSH	LPB	LL	LW	PY	HSM	LLS	Rust
LLS	-0.64**	-0.63**	0.23	0.44	0.85**	0.97**	-0.62**	-0.58**	1.00	-
Rust	0.36	0.47*	0.10	0.03	-0.73**	-0.60**	0.35	0.30	-0.75**	1.00

*, ** denotes significance at 5% and 1% level of probability, respectively

NPB - Number of primary branches
NSB - Number of secondary branches
MSH - Mainstem height
LL - Leaf let length
LW - Leaf let width
PY - Pod yield
HSM - Hundred seed mass
LLS - Late leaf spot.

(ICG 2271). The resistant and susceptible counterparts of these genotypes were screened for components of late leaf spot and rust resistance in two seasons. Besides, they were also investigated for their polymorphism in oxidative enzymes viz., peroxidase, catalase and superoxide dismutase. The results on isozyme analysis are presented in section 4.5.

The data on components of late leaf spot and rust resistance was subjected to split-split plot analysis with seasons as main plots, resistant (R)/susceptible (S) group as sub-plots and genotypes as sub-sub plots. The analysis of variance indicated significant variation among the genotypes for all the parameters (Table 23). Seasonal variation was non-significant for most of the components except lesion number, lesion size and lesions on mainstem. The resistant and susceptible counterparts significantly differed for all the components of late leaf spot, and latent period and field disease score of rust, defoliation, remaining green leaf area and days to maturity. R/S group × genotype interaction effect was significant for all the parameters.

Mean values for components of late leaf spot and rust resistance in the resistant and their susceptible counterparts indicated that they differed mainly for late leaf spot and not for rust (Table 24). The resistant genotypes maintained very high remaining green leaf area as compared to their susceptible counterparts but they matured late.

4.3 Agronomic performance in relation to resistance

A total of ten genotypes comprising of late leaf spot and rust resistant inter-specific derivatives (D 39d and B 37c and ICGV 87165), late leaf spot resistant mutant (28-2), ruling but susceptible cultivars (JL 24, TMV 2 and TAG 24), rust resistant cultivar (ICGV 86590) and moderately susceptible cultivars, Dh 8 (late leaf spot) and R 8808 (rust) were evaluated in early and late sown experiments, under

Table 23: Analysis of variance for late leaf spot and rust resistance parameters and days to maturity in spontaneous mutants of groundnut

Source of variation.	d.f	Late leaf spot								Rust					DF	RGLA	DM
		IP	LP_{50}	LAA	LN	LZ	LPt	LM	FDS	IP	LP_{50}	LAA	PN	FDS			
Factor A (Season)	1	-	-	63.6^{NS}	72.0*	9.8*	40.1^{NS}	33.9*	6.6^{NS}	-	-	6.3^{NS}	30.3^{NS}	0.1^{NS}	1609.9*	1380.9*	1827**
Factor B (R/S group)	1	79.7**	1831.8**	786.0**	893.5**	176.7**	433.0**	378.1**	192.1**	06.7^{NS}	311.7**	0.4^{NS}	78.6^{NS}	19.1*	17579.9**	16478.4**	649.1*
Factor C (Genotype)	9	03.6**	23.6**	31.0**	11.9**	11.5**	7.0**	10.3**	2.9**	26.5**	212.2**	168.5**	355.3**	16.2**	418.2**	408.9**	68.0**
Interactions																	
AB	9	-	-	0.1^{NS}	1.6^{NS}	0.5^{NS}	0.3^{NS}	0.1^{NS}	0.4^{NS}	-	-	0.0^{NS}	2.0^{NS}	0.1^{NS}	97.9^{NS}	144.6^{NS}	266.1**
AC	9	-	-	1.4^{NS}	0.5^{NS}	0.3^{NS}	2.2**	0.9**	2.2**	-	-	4.4**	3.3**	0.4^{NS}	80.3**	77.6**	48.1**
BC	9	02.2**	33.3**	21.7**	8.8**	6.1**	9.2**	11.9**	9.2**	10.0**	18.5**	19.5**	31.7**	1.2**	320.5**	254.6**	98.9**
ABC	9	-	-	1.4^{NS}	0.4^{NS}	0.2^{NS}	0.6^{NS}	0.6^{NS}	0.6^{NS}	-	-	4.3**	1.7^{NS}	0.2^{NS}	38.6**	31.2**	13.3**
Error	72	0.1	0.4	0.8	0.6	0.2	0.6	0.3	0.2	0.2	2.0	0.9	1.0	0.3	9.2	9.4	0.6
C.V. (%)		5.0	2.3	12.8	7.9	4.6	16.6	17.2	6.9	3.3	5.0	18.1	8.9	10.1	5.0	8.7	0.7

*, ** denotes significance at 5% and 1% level of probability, respectively

NS - Not significant

IP - Incubation period

LP_{50} - Latent period

LAA - Leaf area affected (%)

LN - Lesion number

PN - Pustule number

LPt - Lesions on petiole

LM - Lesions on mainstem

FDS - Field disease score

DF - Defoliation (%)

DM - Days to maturity

RGLA - Remaining green leaf area (%)

LZ – Lesion size (mm^2)

Table 24: **Mean values for late leaf spot and rust resistance parameters and days to maturity in spontaneous mutants of groundnut (Pooled over *Kharif* and summer, 1998 seasons)**

Genotype	Late leaf spot														Rust								RGLA		DM	
	IP		LP_{50}		LN		LZ		LPt		LM		FDS		IP		LP_{50}		PN		FDS					
	R	S	R	S	R	S	R	S	R	S	R	S	R	S	R	S	R	S	R	S	R	S	R	S	R	S
28-2	08.3	5.4	39.0	15.3	6.2	13.4	5.61	10.72	2.4	08.5	1.3	7.0	4.8	8.3	06.5	09.4	17.2	17.3	20.1	19.3	6.3	7.3	53.2	13.4	106	101
45	07.9	6.1	35.5	19.8	5.9	11.3	5.70	10.14	2.8	05.6	1.4	3.9	5.0	7.8	06.3	10.8	18.0	17.7	21.5	20.3	6.8	6.5	47.9	23.0	106	101
110	07.9	4.8	36.0	20.3	6.3	10.8	5.48	10.04	3.0	05.1	1.8	2.8	5.0	7.5	05.9	09.3	16.9	17.3	22.0	22.7	7.0	7.3	44.5	31.3	106	101
D 39d	10.3	5.4	39.0	24.0	4.0	12.5	4.65	08.99	1.0	05.0	0.5	3.6	3.8	8.0	16.7	11.4	39.0	29.5	05.5	06.4	3.0	3.0	63.2	20.4	109	106
B 37c	07.6	5.6	39.0	23.5	7.2	11.5	4.78	08.66	2.2	05.1	0.8	3.4	4.5	8.0	14.4	12.8	39.0	28.5	02.7	05.3	2.3	4.0	54.4	27.2	115	105
B 31j	09.0	5.7	32.8	23.8	5.5	16.0	7.76	10.06	2.6	06.0	1.8	6.0	6.0	8.3	14.5	11.8	33.5	31.5	06.0	10.2	5.0	6.0	34.0	07.4	110	110
I 15e	09.4	5.1	34.5	23.5	7.1	14.8	9.52	09.60	1.8	11.0	0.1	8.4	5.8	8.5	15.8	12.0	36.5	27.5	04.1	13.5	4.0	5.3	51.3	21.5	110	110
ICGV 86699	09.9	5.4	39.0	23.5	6.7	11.6	5.09	06.82	2.5	08.0	1.7	3.8	4.0	8.0	15.9	12.9	39.0	33.6	04.6	08.3	2.8	5.0	49.5	34.2	122	112
ICG 2271	05.2	4.9	24.0	22.8	9.1	15.4	6.27	09.10	3.8	06.6	2.0	6.0	7.0	8.5	12.4	11.1	30.0	25.9	11.8	12.5	5.8	6.3	31.6	14.0	110	110
ICGV 96266	06.2	4.7	32.0	20.5	7.5	11.0	8.95	09.59	3.1	06.6	1.0	9.5	5.0	9.0	12.7	12.8	33.4	24.5	10.1	04.5	4.5	5.3	59.6	13.9	121	111
Mean	08.2	5.3	35.1	21.7	6.5	12.8	6.60	09.44	2.6	06.8	1.2	5.4	5.1	8.1	12.1	11.4	30.2	24.8	10.8	12.3	4.7	5.6	48.9	20.6	112	110
C.D(5%)	00.8	0.8	01.3	01.6	1.1	01.1	0.64	0.51	1.3	01.5	0.9	1.1	0.9	0.6	00.7	01.0	00.7	1.4	1.7	2.0	1.0	0.6	09.4	04.4	2.8	1.6
C.V (%)	04.4	6.4	01.6	03.3	11.1	6.0	6.9	3.8	20.0	14.4	19.8	13.4	12.3	4.9	02.5	03.8	01.1	2.4	11.[illegible]	11.1	14.0	6.8	13.3	14.6	1.1	0.6

IP - Incubation period
LPt - Lesions on petiole
R - Resistant
LP_{50} - Latent period
LM - Lesions on mainstem
S - Susceptible
LAA - Leaf area affected (%)
FDS - Field disease score
RGLA - Remaining green leaf area (%)
LN - Lesion number
DF - Defoliation (%)
PN - Pustule number
DM - Days to maturity
LZ - Lesion size (mm^2)

unprotected (UP) and protected (P) conditions. The parameters included disease [disease severity at five different growth stages, area under disease progress curve], productivity [pod, kernel, oil and fodder yield/yield loss, and yield components, viz., shelling out-turn, sound mature kernel per cent, hundred seed mass and oil content], physiological (harvest index, reproductive efficiency measures, leaf area index, healthy leaf area duration, growth rates and partitioning coefficient) and oil quality (fatty acid composition, O/L and P/S ratios) variables. Association/effect of disease and physiological parameters on yield/yield loss was investigated using correlation and path analysis. Besides, effect of leaf/flower removal on incidence of disease and pod yield; interaction effects of late leaf spot and rust diseases were also investigated.

4.3.1 Yield and yield loss in relation to resistance

Different regression models were applied to know the critical resistance and physiological parameters determining yield/yield loss in ten genotypes (Chandran, 2000). Simple linear regression models indicated area under disease progress curve (AUDPC) and disease severity at 85 days after sowing (DS 5) as critical in explaining yield (pod, kernel and fodder) loss and at 65 days after sowing (DS 3) for oil yield loss in early sown experiment. While, disease severity at 95 days after sowing (DS 6) explained yield/yield loss in late sown experiment. Stepwise regression incorporating disease and physiological variables improved the explanatory power of the model considerably both in early and late sown experiments.

Analysis of variance

The data on yield and yield components were subjected to split-split plot analysis. Treatment and genotypic effects were significant for yield/yield components and/or their losses (Table 25). However, the

Table 25: Analysis of variance for yield/yield loss and its components as influenced by genotype, disease pressure and dates of sowing

Source of variation	d.f.	PY	PYL	KY	KYL	OY	OYL	FY	FYL	SP	SPL	SMK	SMKL	HSM	HSML	OC	OCL
Factor A (Date of sowing	1	325.9^{NS}	1.7^{NS}	285.7*	26.2^{NS}	157.7*	179.2**	80.3**	214.9**	59.7*	47.2^{NS}	8.47^{NS}	61.8**	277.6**	21.8^{NS}	518.0**	156.6**
Factor B (Disease contro UP & P)	1	3019.3**	-	1828.7**	-	448.9**	-	508.3**	-	305.5**	-	3688.2**	-	2720.3**	-	255.4**	-
Factor C (Genotype)	9	276.5**	698.6**	190.7**	828.3**	57.0**	818.9**	333.9**	1444.8**	328.1**	118.2**	43.8**	249.7**	753.4**	2529.9**	69.0**	780.8**
<u>Interactions</u>																	
AB	1	11.3*	-	4.5^{NS}	-	1.1^{NS}	-	0.1^{NS}	-	11.8**	-	26.0**	-	0.1^{NS}	-	10.1**	-
AC	9	5.0**	90.3**	4.9**	150.9**	1.4**	150.9**	2.52**	124.7**	9.1**	170.9**	8.7**	132.1**	19.6**	4055.0**	11.2**	408.4**
BC	9	47.6**	-	30.3**	-	4.1**	-	19.4**	-	2.9**	-	13.6**	-	36.6**	-	7.6**	-
ABC	9	7.2**	-	8.9**	-	2.0**	-	2.8**	-	5.4**	-	7.0**	-	8.1**	-	4.5**	-
Error	72	1.4	3.2	0.7	2.3	0.2	3.2	0.1	3.0	0.8	1.1	0.8	0.4	1.3	4.2	0.1	0.6
C.V. (%)		3.3	7.3	3.4	5.5	4.2	5.5	2.6	6.1	1.3	20.0	1.0	5.5	2.6	10.7	0.8	11.5

*, ** denotes significance at 5% and 1% level of probability, respectively

NS - not significant

PY and PYL -Pod yield and its loss

KY and KYL-Kernel yield and its loss

OY and OYL - Oil yield and its loss

FY and FYL - Fodder yield and its loss

SP and SPL - Shelling percentage and its loss

OC and OCL - Oil content and its loss

HSM and HSML - Hundred seed mass and its loss effect of sowing dates was non-significant for pod yield, pod yield loss, kernel yield loss, shelling out-turn loss, sound mature kernel per cent and hundred seed mass loss. All the interaction effects involving factor C (genotype) were significant indicating the major role of genotypes in determining the yield than sowing dates and disease control. Pooled analysis of variance for yield/yield loss, disease and physiological variables also indicated significant genotypic effects. Interaction effect (sowing date × genotype) was significant for all the parameters indicating the differential response of genotypes to sowing dates (Table 26a and b). Effect of date of sowing was significant on most of the disease and physiological parameters (reproductive efficiency measures 2 and 5, healthy leaf area duration, vegetative, crop and pod growth rates, and partitioning coefficient), but non-significant on yield/yield loss variables (except fodder yield and its loss) and some physiological parameters (harvest index, reproductive efficiency measure 4, leaf area index at 85 and 95 days after sowing).

Correlation and path analysis

Based on the results of regression models, disease (disease severity at 65, 85 and 95 days after sowing; area under disease progress curve) and physiological parameters (harvest index, reproductive efficiency measure, leaf area index, healthy leaf area duration, vegetative, crop and pod growth rates, and partitioning coefficient) were selected to assess their association/effect on yield/yield loss using correlation and path analysis (Tables 27, 28 and 29) in early and late sown experiments separately and together (pooled analysis).

Correlation coefficients in early sown experiment revealed highly significant and negative association of disease parameters (disease severity at 65, 85 and 95 days after sowing; area under disease progress curve) with yield and positive association with yield loss

Table 26a: Pooled analysis of variance for yield/ yield loss and disease parameters in selected groundnut genotypes

Source of variation	d.f.	PY	PYL	KY	KYL	OY	OYL	FY	FYL	DS 3	DS 5	DS 6	AUDPC
Factor A (Date of sowing)	1	10377.6^{NS}	31.6^{NS}	83307.2^{NS}	6.3^{NS}	583.0^{NS}	49.0^{NS}	39.1**	273.5**	5579.5**	1264.7**	2396.8**	2059328.0**
Factor B (Genotype)	9	24438.4**	760.9**	15664.6**	798.5**	394.0**	777.7**	184.8**	1516.9**	1609.4**	2025.6**	2312.6**	2636952.9**
Interaction													
A X B	9	613.1**	92.8**	364.0**	135.7**	216.7**	203.6**	1.9**	96.6**	76.1**	53.4**	63.6**	310288.7**
Error	36	161.5	9.4	94.2	11.3	17.9	17.3	0.2	9.5	0.7	0.9	2.0	1737.2

PY and PYL - Pod yield and its loss
FY and FYL - Fodder yield and its loss
KY and KYL-Kernel yield and its loss
OY and OYL - Oil yield and its loss
AUDPC - Area under disease progress curve
DS 3, 5 and 6 - Disease severity at 65, 75, and 85 days after sowing

Table 26b: Pooled analysis of variance for physiological parameters in selected groundnut genotypes

Source of variation	d.f	HI	REM 2	REM 3	REM 4	REM 5	LAI 5	LAI 6	HAD	VGR	CGR	PGR	PC
Factor A (Date of sowing)	1	29.8^{NS}	667.9**	671.5**	90.6^{NS}	1070.4**	0.1^{NS}	1.3^{NS}	9470.3**	63.3**	107.4**	5.8**	0.1**
Factor B (Genotype)	9	258.9**	168.9**	220.3**	920.0**	189.6**	12.6**	23.1**	15935.8**	100.2**	132.6**	25.4**	0.1**
Interaction													
A X B	9	37.8**	8.7**	28.3**	126.2*	16.0**	2.6**	5.5**	483.6**	14.0**	25.5**	5.8**	0.1**
Error	36	7.8	2.2	6.0	44.9	4.4	0.6	0.3	1.2	0.1	0.1	0.1	0.1

*,** denotes significance at 5% and 1% level of probability, respectively
HI - Harvest index
HAD - Healthy leaf area duration
PGR - Pod growth rate
REM - Reproductive efficiency measure
VGR - Vegetative growth rate
PC - Partitioning coefficient
NS-not significant
LAI 5 and 6 - Leaf area index at 85 and 95 days after sowing
CGR - Crop growth rate

Table 27: Correlation coefficients relating yield/yield-loss variables with disease/physiological parameters in early and late sown experiments

Yield/ Yield loss	DS 3	DS 5	DS 6	AUDPC	HI	REM 2	REM 3	REM 4	REM 5	LAI 5	LAI 6	HAD	VGR	CGR	PGR	PC
Early sown																
PY	-0.95**	-0.97**	-0.96**	-0.95**	-0.38*	-0.30^{NS}	-0.49**	-0.58**	-0.34^{NS}	0.44*	0.51**	0.79**	0.40*	0.45*	0.32^{NS}	-0.26^{NS}
KY	-0.93**	-0.92**	-0.93**	-0.93**	-0.28^{NS}	-0.34^{NS}	-0.52**	-0.63**	-0.43*	0.35^{NS}	0.32^{NS}	0.68**	0.20^{NS}	0.33^{NS}	0.40*	-0.07^{NS}
OY	-0.95**	-0.92**	-0.94**	-0.94**	-0.31^{NS}	0.30^{NS}	-0.48**	-0.56**	-0.40*	0.35*	0.31^{NS}	0.69**	0.17^{NS}	0.35^{NS}	0.47**	-0.01^{NS}
FY	-0.79**	-0.84**	-0.81**	-0.82**	-0.64**	-0.26^{NS}	-0.34^{NS}	-0.47**	-0.33^{NS}	0.62**	0.82**	0.89**	0.77**	0.72**	0.19^{NS}	0.64**
PYL	0.87**	0.87**	0.87**	0.86**	0.12^{NS}	0.22^{NS}	0.47**	0.54**	0.27^{NS}	-0.16^{NS}	-0.25^{NS}	-0.57**	-0.17^{NS}	-0.17^{NS}	-0.16^{NS}	0.09^{NS}
KYL	0.65**	0.62**	0.64**	0.61**	-0.15^{NS}	0.02^{NS}	0.32^{NS}	0.33^{NS}	0.13^{NS}	0.22^{NS}	0.05^{NS}	-0.23^{NS}	0.01^{NS}	0.14^{NS}	0.18^{NS}	0.04^{NS}
OYL	0.73**	0.71**	0.74**	0.70**	0.01^{NS}	-0.01^{NS}	0.26^{NS}	0.34^{NS}	0.15^{NS}	0.08^{NS}	-0.03^{NS}	-0.34^{NS}	0.03^{NS}	0.07^{NS}	0.02^{NS}	-0.01^{NS}
FYL	0.78**	0.82**	0.79**	0.79**	-0.02^{NS}	-0.34^{NS}	0.56**	0.66**	0.42*	-0.15^{NS}	-0.18^{NS}	-0.54**	-0.15^{NS}	-0.15^{NS}	-0.15^{NS}	0.08^{NS}
Late sown																
PY	-0.88**	-0.88**	-0.93**	-0.60**	-0.66**	-0.15^{NS}	-0.27^{NS}	-0.40*	-0.02^{NS}	0.69**	0.77**	0.81**	0.56**	0.70**	0.49**	-0.44*
KY	-0.87**	-0.85**	-0.87**	-0.67**	-0.55**	-0.26^{NS}	-0.37^{NS}	-0.48**	-0.21^{NS}	0.51**	0.56**	0.71**	0.35^{NS}	0.52**	0.51**	-0.25^{NS}
OY	-0.88**	-0.84**	-0.82**	-0.71**	-0.61**	-0.19^{NS}	-0.32^{NS}	-0.40*	-0.14^{NS}	0.52**	0.54**	0.75**	0.41*	0.58**	0.52**	-0.31^{NS}
FY	-0.72**	-0.69**	-0.68**	-0.65**	-0.73**	-0.22^{NS}	-0.37*	-0.39*	-0.03^{NS}	0.92**	0.85**	0.93**	0.96**	0.85**	0.05^{NS}	-0.94**
PYL	0.59**	0.58**	0.65**	0.24^{NS}	0.59**	-0.16^{NS}	-0.05^{NS}	0.08^{NS}	-0.12^{NS}	-0.40*	-0.52**	-0.53**	-0.29^{NS}	-0.40*	-0.29^{NS}	0.27^{NS}
KYL	0.64**	0.63**	0.66**	0.34^{NS}	0.66**	0.02^{NS}	0.15^{NS}	0.25^{NS}	-0.01^{NS}	-0.49**	-0.55**	-0.63**	-0.35^{NS}	-0.46**	-0.31^{NS}	0.34^{NS}
OYL	0.60**	0.57**	0.56**	0.26^{NS}	0.75**	-0.11^{NS}	0.06^{NS}	0.12^{NS}	-0.08^{NS}	-0.44*	-0.51**	-0.58**	-0.34^{NS}	-0.43**	-0.30^{NS}	0.32^{NS}
FYL	0.79**	0.82**	0.92**	0.50**	0.62**	0.13^{NS}	0.28^{NS}	0.41*	0.08^{NS}	-0.71**	-0.86**	-0.75**	-0.62**	-0.67**	-0.30^{NS}	0.52**

*, ** denotes significance at 5% and 1% level of probability, respectively

NS - not significant

PY, KY, OY and FY - Pod, kernel, oil and fodder yield

PYL, KYL, OYL and FYL - Pod, kernel, oil and fodder yield loss

DS - Disease severity

AUDPC - Area under disease progress curve

REM - Reproductive efficiency measure

LAI - Leaf area index

HAD - Healthy leaf area duration

VGR - Vegetative growth rate

CGR - Crop growth rate

PGR - Pod growth rate

PC - Partitioning coefficient

Table28: Correlation coefficients relating yield/yield-loss variables with disease/physiological parameters (Pooled over early and late sowings)

	DS 3	DS 5	DS 6	AUDPC	HI	REM 2	REM 3	REM 4	REM 5	LAI 5	LAI 6	HAD	VGR	CGR	PGR	PC
Yield																
PY	-0.998**	-0.959**	-0.996**	-0.911**	-0.663**	-0.247^{NS}	-0.480**	-0.639**	-0.192^{NS}	0.763**	0.864**	0.843**	0.604**	0.719**	0.442*	-0.420*
KY	-0.995**	-0.928**	-0.974**	-0.933**	-0.550**	-0.357*	-0.565**	-0.709**	-0.369^{NS}	0.605**	0.645**	0.750**	0.377*	0.565**	0.556**	-0.174^{NS}
OY	-0.999**	-0.929**	-0.976**	-0.953**	-0.615**	-0.292^{NS}	-0.473**	-0.612**	-0.296^{NS}	0.639**	0.665**	0.778**	0.405*	0.637**	0.662**	-0.174^{NS}
FY	-0.786**	-0.774**	-0.776**	-0.799**	-0.836**	-0.217^{NS}	-0.362*	-0.527**	-0.188^{NS}	0.966**	0.999**	0.947**	0.990**	0.970**	0.210^{NS}	-0.896**
Yield loss																
PYL	0.869**	0.835**	0.922**	0.761**	0.567**	0.062^{NS}	0.296^{NS}	0.483**	0.046^{NS}	-0.526**	-0.675**	-0.632**	-0.418*	-0.463**	-0.232^{NS}	0.352*
KYL	0.918**	0.898**	0.993**	0.800**	0.645**	0.094^{NS}	0.317^{NS}	0.506**	0.055^{NS}	-0.619**	-0.797**	-0.681**	-0.433*	-0.504**	-0.299^{NS}	0.336^{NS}
OYL	0.984**	0.933**	0.989**	0.855**	0.768**	-0.012^{NS}	0.210^{NS}	0.436*	-0.022^{NS}	-0.673**	-0.796**	-0.738**	-0.420*	-0.548**	-0.432*	0.294^{NS}
FYL	0.858**	0.855**	0.963**	0.699**	0.490**	0.164^{NS}	0.388*	0.626**	0.266^{NS}	-0.579**	-0.777**	-0.676**	-0.425*	-0.498**	-0.284^{NS}	0.272^{NS}

*,** denotes significance at 5% and 1% level of probability, respectively

NS - not significant

DS - Disease severity

AUDPC - Area under disease progress curve

REM - Reproductive efficiency measure

LAI - Leaf area index

HAD - Healthy leaf area duration

VGR - Vegetative growth rate

CGR - Crop growth rate

PGR - Pod growth rate

PC - Partitioning coefficient

Table 29: Path analysis indicating the direct effects of selected disease/physiological parameters on yield/yield-loss variables

	Rank in early sown experiment				Rank in late sown experiment				Rank in pooled analysis			
	I	II	III	IV	I	II	III	IV	I	II	III	IV
Yield												
PY	-0.910 (DS 5)	0.545 (REM 5)	0.420 (HAD)	0.417 (REM 2)	-2.008 (DS 6)	-1.711 (DS 5)	1.157 (VGR)	0.940 (HAD)	25.709 (CGR)	21.558 (VGR)	10.919 (PGR)	3.088 (HAD)
KY	-8.664 (AUDPC)	-6.065 (DS 6)	-2.605 (DS 3)	1.210 (CGR)	-2.146 (DS 6)	1.707 (VGR)	-1.658 (DS 5)	1.400 (HAD)	21.219 (VGR)	20.605 (CGR)	08.804 (PGR)	-4.896 (DS 6)
OY	6.234 (AUDPC)	-4.475 (DS 6)	-2.383 (DS 3)	0.972 (CGR)	-1.832 (VGR)	-1.676 (DS 6)	-1.368 (DS 5)	1.235 (CGR)	18.624 (VGR)	15.705 (CGR)	06.630 (PGR)	-5.384 (DS 6)
FY	-1.433 (DS 5)	-1.071 (AUDPC)	0.814 (HAD)	0.764 (DS 3)	-0.615 (DS 5)	-0.494 (DS 6)	0.439 (PGR)	0.433 (CGR)	06.991 (CGR)	06.600 (VGR)	02.992 (PGR)	0.856 (REM 2)
Yield loss												
PYL	1.269 (AUDPC)	0.829 (DS 5)	-0.577 (REM 3)	-0.575 (REM 5)	3.054 (DS 6)	2.983 (DS 5)	-2.087 (HAD)	-0.957 (CGR)	-48.761 (CGR)	-46.515 (VGR)	-19.889 (PGR)	-4.076 (HAD)
KYL	4.849 (AUDPC)	3.939 (DS 6)	1.383 (DS 3)	0.651 (DS 5)	3.558 (DS 5)	2.983 (DS 6)	-2.704 (HAD)	-0.517 (CGR)	-38.456 (CGR)	-38.208 (VGR)	-15.484 (PGR)	4.273 (DS 6)
OYL	6.361 (AUDPC)	4.824 (DS 6)	2.000 (DS 3)	0.592 (DS 5)	3.369 (DS 5)	2.246 (DS 6)	-2.217 (HAD)	-1.378 (CGR)	-42.969 (VGR)	-39.830 (CGR)	-15.889 (PGR)	5.763 (DS 6)
FYL	6.935 (AUDPC)	4.542 (DS 6)	2.448 (DS 5)	-1.265 (LAI 6)	-2.222 (CGR)	2.169 (DS 6)	1.273 (DS 5)	-0.990 (VGR)	-16.915 (VGR)	-16.120 (CGR)	-06.616 (PGR)	2.316 (DS 5)

PY, KY, OY and FY - Pod, kernel, oil and fodder yield PYL, KYL, OYL and FYL - Pod, kernel, oil and fodder yield loss
DS - Disease severity AUDPC - Area Under disease progress curve REM - Reproductive efficiency measure
HAD - Healthy leaf area duration VGR - Vegetative growth rate CGR - Crop growth rate
PGR - Pod growth rate

variables (Table 27). However, physiological parameters (reproductive efficiency measures 3 and 4, leaf area index at 85 days after sowing and healthy leaf area duration) were significantly associated with yield variables only. The results thus indicated, the role of disease parameters in explaining the variation in both yield and yield loss, but physiological parameters in yield variation in early sown experiment.

In late sown experiment, disease (disease severity at 65, 85 and 95 days after sowing) physiological (harvest index, leaf area index at 95 days after sowing, vegetative, crop and pod growth rates) parameters were significantly associated with both yield and yield loss. Area under disease progress curve and reproductive efficiency measure 4, were significantly and negatively associated with yield only (Table 27).

In pooled analysis all the disease and physiological parameters except reproductive efficiency measures 2 and 5, pod growth rate and partitioning coefficient were significantly associated with yield and yield loss. However, the magnitude of association was more with disease than physiological parameters (Table 28).

Path analysis indicated the highest direct effects of area under disease progress curve, followed by disease severity at 65, 85 and 95 days after sowing in early sown experiment; disease severity at 95 days after sowing followed by disease severity at 85 days after sowing, healthy leaf area duration and crop growth rate in late sown experiment and vegetative, crop and pod growth rates, and disease severity at 95 days after sowing in pooled analysis (Table 29 and Appendices 2 to 7).

Based on correlation and path analysis, it is clear that most of the yield and yield loss variation was explained by disease parameters in early sown experiment; while both disease and physiological parameters explained the yield and yield loss variation in late sown and pooled analysis.

4.3.2 Performance of genotypes

Disease and physiological parameters

Genotype, D 39d followed by B 37c, ICGV 87165 and mutant 28-2 were superior for disease resistance as they recorded significantly lower values for disease severity at different growth stages and area under disease progress curve in both early and late sown experiments (Table 30 and Appendix 8). Genotypes Dh 8, R 8808 and ICGV 86590 recorded moderate values for disease severity and area under disease progress curve, indicating moderate/partial resistance to foliar diseases. On the contrary, TAG 24 followed by TMV 2 and JL 24 were susceptible by recording highest values for disease severity and area under disease progress curve. Overall, disease severity in late sown experiment was high compared to early sown experiment in all most all the genotypes (Appendix 8).

Mean values for physiological parameters revealed that resistant genotype D 39d had high pod growth rate (23.8), while ICGV 87165 followed by B 37c had high healthy leaf area duration, vegetative and crop growth rates, and partitioning coefficient. Moderately susceptible genotypes (Dh 8 and ICGV 86590) had higher reproductive efficiency measures 3 and 5. TAG 24 was either superior or comparable to other susceptible genotypes (JL 24 and TMV 2) for reproductive efficiency measures 3 and 5, crop and pod growth rates, and partitioning coefficient (Table 30 and Appendix 8).

Yield components

All the genotypes had lower values for yield components (shelling out-turn, sound mature kernel per cent, hundred seed mass

Table 30: Overall performance of groundnut genotypes for disease and physiological parameters (Pooled over early and late sowings)

Genotype	DS 3	DS 5	DS 6	AUDPC	REM 3	REM 5	HAD	VGR	CGR	PGR	PC
D 39d	18.78^{a}	39.18^{a}	46.30^{a}	1199.3^{a}	32.61^{cd}	24.41^{cd}	210.4^{c}	14.20d	38.40^{c}	24.20^{a}	63.07^{a}
B 37c	23.90^{b}	41.50^{b}	50.56^{c}	1442.3^{b}	22.26^{e}	18.00^{e}	243.5^{b}	19.00^{b}	42.30^{b}	23.30^{b}	54.49^{c}
Dh 8	55.16^{h}	73.93^{f}	79.60^{e}	2965.2^{i}	45.56^{a}	31.58^{b}	124.0^{f}	11.30g	29.65g	18.35^{g}	61.93^{ab}
R 8808	43.401^{e}	57.74^{d}	67.23^{d}	2327.0^{d}	28.45^{d}	20.34^{de}	167.4^{de}	12.15e	33.40^{g}	21.25^{c}	63.69^{a}
Mutant (28-2)	31.04^{d}	45.41^{c}	51.24^{c}	1713.3^{c}	30.81^{cd}	23.41^{cd}	178.7^{d}	12.05ef	31.50f	19.95^{d}	63.57^{a}
JL 24	53.44^{g}	73.56^{f}	87.81^{f}	2411.6^{e}	34.53^{bc}	27.16^{c}	148.2^{e}	11.75ef	31.60f	19.85^{de}	62.84^{ab}
TMV 2	56.98^{i}	78.61^{g}	91.92^{g}	2565.4^{f}	34.55^{bc}	22.20^{d}	157.6^{de}	12.30e	31.80^{f}	19.50^{e}	62.50^{ab}
TAG 24	65.86^{j}	89.94^{h}	96.32^{h}	2904.4^{h}	35.35^{bc}	23.10^{ed}	095.5^{g}	11.05g	30.60g	19.55^{de}	63.79^{a}
ICGV 86590	51.05^{f}	69.39^{e}	80.76^{e}	2709.9^{g}	37.52^{b}	37.11^{a}	157.3^{de}	14.55c	35.80^{d}	21.25^{c}	59.81^{ab}
ICGV 87165	26.23^{c}	41.39^{b}	48.30^{b}	1413.2^{b}	34.47^{bc}	24.88^{c}	262.3^{a}	25.70^{a}	44.65^{a}	18.95^{f}	42.48^{d}
Mean	42.59	61.07	70.00	2165.2	33.51	25.12	174.5	14.85	35.20	20.35	59.82
C.D. (5%)	1.00	1.14	1.64	48.9	2.86	2.46	12.9	00.30	00.36	00.32	3.29
C.V. (%)	2.01	1.58	2.00	01.9	7.29	8.34	06.3	01.18	00.68	00.94	2.95

Figure(s) with same superscript(s) do not differ significantly at 5% level of probability

DS - Disease severity
LAI - Leaf area index
CGR - Crop growth rate
AUDPC - Area under disease progress curve
HAD - Healthy leaf area duration
PGR - Pod growth rate
REM - Reproductive efficiency measure
VGR - Vegetative growth rate
PC - Partitioning coefficient

and oil content) under diseased condition compared to protected (P) condition in both early and late sown experiments (Appendices 9 and 10). The resistant genotypes viz., D 39d and B 37c (shelling out-turn); D 39d and 28-2 (sound mature kernel per cent); B 37c, 28-2 and ICGV 87165 (hundred seed mass), and D 39d and ICGV 87165 (oil content) were superior by recording higher values and least reduction due to disease (Table 31 and Appendices 9 and 10). JL 24 even though susceptible to foliar diseases recorded least reduction in shelling out-turn and oil content.

Productivity

All the genotypes recorded significantly higher (pod, kernel, oil and fodder) yield under early sown experiment compared to late sown experiment and yield levels were significantly high in fungicide sprayed condition than diseased condition (Appendices 11 and 12). Genotypes did not differ much for pod, kernel and oil yield under protected condition. Overall performance of genotypes across dates of sowing for productivity indicated that, genotypes D 39d and B 37c were superior for pod, kernel and oil yield and ICGV 87165 and B 37c for fodder yield by recording higher values and least reduction due to disease (Table 32). On the contrary, TMV 2, JL 24 and TAG 24 had lower values and highest reduction due to disease for all the productivity parameters. However, TAG 24 even though highly susceptible to foliar diseases recorded relatively higher pod and kernel yield, and lower reduction in pod, kernel, and fodder yield and early maturing compared to other susceptible genotypes (JL 24 and TMV 2).

Genotypes differed for maturity and hence, an attempt was made to asses per day productivity. Overall, per day productivity of the genotypes was higher in early sown experiment compared to late sown experiment. Fungicide spray resulted in enhanced per day productivity especially in susceptible genotypes (Appendix 13 and

Table 31: Overall performance of groundnut genotypes for yield components (Pooled over early and late sowings)

Genotype	Shelling out-turn (%)			Sound Mature kernel (%)			Hundred seed mass (g)			Oil content (%)		
	UP	P	% R	UP	P	% R	UP	P	% R	UP	P	% R
D 39d	75.31^{a}	76.23^{a}	02.9^{ab}	86.53^{a}	94.70^{ab}	08.6^{a}	36.50^{de}	40.63^{d}	10.1^{a}	45.32^{a}	46.77^{a}	03.1^{ab}
B 37c	70.87^{b}	73.73^{b}	03.8^{a}	84.09^{ab}	95.20^{ab}	11.7^{ab}	54.56^{a}	60.79^{a}	10.3^{a}	40.97^{bc}	43.71^{b}	06.3^{ab}
Dh 8	64.64^{cd}	69.03^{c}	06.3^{ab}	81.92^{ab}	91.33^{ab}	10.2^{ab}	28.53^{f}	34.40^{e}	17.0^{b}	38.77^{c}	40.46^{c}	04.2^{a}
R 8808	67.08^{c}	69.91^{c}	04.0^{ab}	81.87^{ab}	95.60^{ab}	13.3^{b}	42.72^{c}	51.04^{b}	16.3^{b}	37.66^{cd}	40.60^{c}	07.2^{ab}
Mutant (28-2)	68.14^{c}	70.24^{c}	03.0^{a}	86.60^{a}	95.83^{a}	09.8^{a}	49.23^{b}	58.71^{a}	16.4^{b}	40.11^{bc}	45.06^{ab}	11.3^{bc}
JL 24	67.07^{c}	69.66^{c}	02.8^{a}	84.78^{ab}	95.72^{a}	11.4^{ab}	40.42^{c}	50.29^{b}	19.6^{b}	41.10^{bc}	42.05^{bc}	02.4^{a}
TMV 2	65.92^{cd}	69.23^{c}	04.8^{ab}	81.22^{bc}	96.13^{a}	15.5^{bc}	33.62^{de}	46.47^{bc}	27.5^{c}	39.34^{bc}	40.78^{c}	03.5^{ab}
TAG 24	64.32^{cd}	69.46^{c}	07.4^{b}	82.93^{ab}	96.18^{a}	13.8^{bc}	35.15^{de}	50.24^{b}	30.0^{c}	35.11^{e}	40.74^{c}	14.0^{c}
ICGV 86590	56.59^{f}	60.07^{d}	05.8^{ab}	79.00^{bc}	90.89^{c}	12.9^{bc}	35.61^{de}	48.60^{bc}	26.4^{c}	38.61^{cd}	42.69^{bc}	09.4^{bc}
ICGV 87165	59.27^{e}	62.01^{e}	04.4^{ab}	83.38^{ab}	92.63^{ab}	10.0^{ab}	47.38^{b}	57.79^{a}	18.0^{b}	42.03^{b}	45.31^{ab}	07.3^{ab}
Mean	65.98	69.16	04.6	83.33	94.42	11.7	40.37	49.90	19.2	39.90	42.82	06.9
C.D. (5%)	02.37	02.12	02.4	02.70	02.67	02.3	02.81	03.12	03.7	01.73	01.48	05.6
C.V. (%)	03.10	02.65	44.4	02.80	02.43	16.8	06.00	05.39	16.6	03.74	02.97	45.1

Figure(s) with same superscript(s) do not differ significantly at 5% level of probability

UP - Unprotected condition P - Protected condition %R - Percent reduction over protected condition

Table 32: Overall performance of groundnut genotypes for productivity (Pooled over early and late sowings)

Genotype	Pod yield ($q\ ha^{-1}$)			Kernel yield ($q\ ha^{-1}$)			Oil yield ($q\ ha^{-1}$)			Fodder yield ($t\ ha^{-1}$)		
	UP	P	% R	UP	P	% R	UP	P	% R	UP	P	% R
D 39d	38.69^{a}	44.00^{ab}	12.0^{a}	29.17^{a}	34.65^{a}	15.9^{ab}	13.36^{a}	16.14^{a}	17.6^{a}	12.05^{c}	14.23^{cd}	15.8^{b}
B 37c	38.49^{a}	43.28^{ab}	09.1^{a}	27.28^{b}	31.59^{ab}	12.3^{a}	11.19^{b}	13.86^{b}	17.7^{a}	16.70^{b}	19.81^{b}	15.8^{b}
Dh 8	28.95^{cd}	35.53^{c}	18.0^{b}	18.70^{f}	24.47^{c}	23.3^{bc}	07.26^{d}	09.91^{c}	25.6^{b}	06.98^{h}	09.71^{de}	28.0^{c}
R 8808	30.48^{c}	43.74^{ab}	30.4^{d}	20.48^{e}	30.5^{ab}	33.1^{d}	07.79^{d}	12.45^{bc}	38.0^{c}	09.12^{f}	10.89^{de}	16.3^{b}
Mutant (28-2)	35.6^{b}	42.92^{ab}	17.0^{b}	24.31^{c}	30.03^{ab}	19.0^{ab}	09.85^{c}	13.53^{b}	28.1^{b}	10.77^{d}	12.74^{cd}	15.6^{b}
JL 24	23.30^{ef}	38.22^{dc}	39.0^{c}	15.77^{g}	27.06^{ab}	40.5^{e}	06.26^{ef}	11.19^{bc}	41.9^{cd}	08.02^{g}	15.72^{c}	48.6^{e}
TMV 2	22.40^{ef}	38.66^{dc}	42.0^{e}	14.77^{gh}	28.64^{ab}	48.0^{f}	05.83^{ef}	11.67^{c}	50.4^{d}	06.81^{h}	15.84^{c}	56.2^{f}
TAG 24	24.54^{e}	36.40^{c}	32.6^{d}	15.68^{gh}	25.03^{c}	37.4^{e}	05.55^{f}	10.21^{c}	46.1^{cd}	05.57^{i}	09.02^{de}	38.5^{d}
ICGV 86590	29.73^{cd}	40.52^{bc}	26.6^{c}	16.81^{g}	24.29^{c}	30.8^{d}	06.51^{e}	10.42^{c}	37.1^{c}	09.71^{e}	15.69^{c}	38.0^{d}
ICGV 87165	37.98^{a}	47.02^{a}	19.4^{b}	22.53^{d}	29.17^{ab}	22.9^{bc}	09.48^{c}	13.24^{b}	28.5^{b}	23.90^{a}	27.34^{a}	11.8^{a}
Mean	31.02	41.03	24.6	20.55	28.55	28.3	08.33	12.26	33.1	10.96	15.10	28.5
C.D. (5%)	01.49	03.22	03.6	01.14	04.39	03.94	00.49	01.68	04.9	00.53	02.32	03.61
C.V. (%)	04.10	03.47	12.4	04.72	06.80	11.89	05.08	06.05	12.6	04.07	06.79	10.8

Figure(s) with same superscript(s) do not differ significantly at 5% level of probability

UP - Unprotected condition P - Protected condition % R - Percent reduction over protected condition

Table 33). Genotypes D 39d, B 37c, mutant 28-2 and R 8808 had higher pod, kernel and oil productivity, while, B 37c and ICGV 87165 had higher fodder production in both diseased and protected conditions. D 39d and mutant 28-2 recorded higher per day fodder yield under diseased condition. TAG 24 exhibited superiority over other susceptible genotypes (JL 24 and TMV 2) for pod and kernel yield under diseased condition while the reverse was true for oil and fodder yield under fungicide sprayed condition.

Flower, pod and kernel accumulation pattern

Pod and kernel accumulation (%) pattern of selected genotypes at different growth periods (60 days after sowing, 60-75 days after sowing, 75-90 days after sowing and between 90 days after sowing to date of harvest) revealed varied response of genotypes under dates of sowing rather than disease control treatments (Appendix 14). Genotypes R 8808, JL 24 and TAG 24 were stable for pod and kernel accumulation pattern over dates of sowing. Genotypes Dh 8 and ICGV 86590 recorded more pod and kernel accumulation at 75-90 days after sowing in early sown but at 60 days after sowing in late sown condition. ICGV 87165 accumulated most at 75-90 days after sowing in early sown and between 90 days after sowing to date of harvest in late sown condition, thus revealing their sensitive nature. Genotypes TAG 24, JL 24, TMV 2 and D 39d accumulated nearly 70-80 per cent of their pod and kernel yield by the end of 75 days after sowing. Similarly, R 8808 and mutant 28-2 accumulated 75 per cent of their pod yield by 75 days after sowing. However, TAG 24 was significantly early by accumulating 55-60 per cent of its pod and kernel yield by 60 days after sowing (Table 34). On the contrary, B 37c, ICGV 87165 and Dh 8 accumulated nearly 20 per cent of their pod and kernel yield during later part of growth period (between 90 days after sowing to date of harvest). This contrasting response was evident in flowering behaviour also. Initiation and attainment of fifty per cent flowering

Table 33: Per day productivity (gm^{-2} d^{-1}) and days to maturity of groundnut genotypes (Pooled over early and late sowings)

Genotype	Pod yield		Kernel yield		Oil yield		Fodder yield		Days to maturity	
	UP	P	UP	P	UP	P	UP	P	UP	P
D 39d	3.60^{a}	4.04^{ab}	2.71^{a}	3.18^{ab}	1.24^{a}	1.48^{a}	11.21^{c}	13.06^{de}	107.5^{d}	109.0^{d}
B 37c	3.45^{ab}	3.81^{ab}	2.47^{b}	2.78^{ab}	1.01^{b}	1.22^{b}	14.98^{b}	17.45^{b}	111.5^{e}	113.5^{e}
Dh 8	2.92^{bc}	3.54^{b}	2.06^{c}	2.43^{ab}	0.80^{c}	0.99^{cd}	07.05^{cd}	09.66^{e}	099.0^{b}	100.5^{b}
R 8808	3.08^{b}	4.35^{a}	2.07^{c}	3.03^{ab}	0.79^{c}	1.24^{b}	09.21^{d}	10.84^{de}	099.0^{b}	100.5^{b}
Mutant (28-2)	3.53^{a}	4.13^{ab}	2.41^{b}	2.89^{ab}	0.98^{b}	1.30^{b}	10.66^{c}	12.25^{de}	101.0^{c}	104.0^{c}
JL 24	2.35^{b}	3.80^{ab}	1.59^{d}	2.69^{ab}	0.66^{cd}	1.17^{b}	08.10^{d}	15.61^{cd}	099.0^{b}	100.5^{b}
TMV 2	2.26^{d}	3.85^{ab}	1.49^{d}	2.85^{ab}	0.58^{cd}	1.16^{b}	06.88^{cd}	15.76^{cd}	099.0^{b}	100.5b
TAG 24	2.65^{bc}	3.81^{ab}	1.70^{d}	2.62^{ab}	0.61^{cd}	1.07^{c}	06.02^{e}	09.45^{e}	092.5^{a}	095.5^{a}
ICGV 86590	2.62^{c}	3.48^{b}	1.48d	2.08^{b}	0.58^{cd}	0.89^{cd}	08.56^{d}	13.47^{cd}	113.5^{f}	116.5^{f}
ICGV 87165	3.19^{ab}	3.89^{ab}	1.94^{c}	2.41^{ab}	0.80^{c}	1.10^{c}	19.94^{a}	22.39^{a}	119.0^{g}	121.0^{g}
Mean	2.97	3.87	1.99	2.69	0.80	1.16	10.26	13.98	104.1	106.2
C.D. (5%)	0.31	0.37	0.23	0.44	0.17	0.17	01.61	02.37	1.55	3.04
C.V. (%)	4.66	4.25	5.15	7.21	9.17	6.64	06.95	07.48	0.66	1.27

Figure(s) with same superscript(s) do not differ significantly at 5% level of probability
UP - Unprotected condition P - Protected condition % R - Percent reduction over protected condition

Table 34: Pod and kernel accumulation (%) and flowering pattern in groundnut genotypes across disease pressure and dates of sowin

Genotype	Pod accumulation pattern (%)				Kernel accumulation pattern (%)				Flowering pattern					
	60 DAS	60-75 DAS	75-90 DAS	90 DAS -DOH	60 DAS	60-75 DAS	75-90 DAS	90 DAS -DOH	DIF	DFF	D 25FA	D 50FA	D 75FA	TFC
D 39d	34.8^{c}	41.8^{ab}	16.8^{ab}	06.7^{ab}	20.8^{c}	50.5^{a}	22.9^{ab}	05.8^{b}	26.7^{b}	29.7^{bc}	06.7^{b}	12.6^{ab}	17.5^{ab}	80.4^{b}
B 37c	15.5^{d}	47.3^{a}	15.6^{ab}	21.7^{a}	06.2^{d}	42.3^{a}	28.0^{ab}	33.6^{a}	27.2^{b}	29.8^{bc}	07.5^{bc}	13.0^{ab}	20.8^{c}	96.1^{a}
Dh 8	32.2^{c}	32.7^{ab}	20.2^{ab}	14.8^{ab}	24.1^{c}	42.6^{a}	22.9^{ab}	10.9^{ab}	29.7^{d}	32.5^{d}	07.7^{c}	15.0^{c}	21.5^{c}	54.4^{cd}
R 8808	40.1^{bc}	37.7^{ab}	14.9^{ab}	07.4^{ab}	23.1^{c}	47.6^{a}	20.5^{ab}	08.9^{b}	26.7^{b}	29.7^{bc}	07.7^{c}	13.3^{ab}	18.8^{ab}	83.1^{b}
Mutant (28-2)	38.3^{bc}	35.3^{ab}	15.7^{ab}	11.9^{ab}	24.4^{c}	41.7^{a}	23.2^{ab}	10.8^{ab}	28.0^{c}	31.0^{d}	06.5^{b}	13.0^{ab}	21.3^{c}	62.1^{c}
JL 24	49.5^{b}	38.1^{ab}	06.8^{ab}	05.7^{ab}	35.3^{b}	49.4^{a}	08.7^{b}	06.6^{b}	27.0^{b}	29.5^{bc}	06.9^{bc}	12.3^{a}	16.7^{a}	53.7^{de}
TMV 2	46.3^{bc}	36.3^{ab}	10.8^{ab}	06.7^{ab}	36.9^{b}	41.7^{a}	15.4^{ab}	06.2^{b}	27.2^{b}	28.8^{bc}	06.4^{bc}	11.3^{a}	17.3^{a}	59.2^{cd}
TAG 24	63.7^{a}	23.0^{b}	08.5^{ab}	04.9^{b}	55.6^{a}	27.5^{b}	11.0^{b}	05.9^{b}	23.3^{a}	27.7^{a}	05.6^{a}	11.0^{a}	17.0^{a}	60.6^{cd}
ICGV 86590	32.0^{c}	47.3^{a}	13.1^{ab}	07.8^{ab}	17.6^{c}	45.2^{a}	31.1^{ab}	08.1^{b}	27.0^{b}	29.2^{bc}	11.3^{d}	20.3^{d}	22.0^{c}	50.6^{de}
ICGV 87165	07.4^{d}	42.8^{ab}	30.5^{a}	19.3^{ab}	03.8^{d}	38.2^{ab}	39.2^{a}	18.8^{ab}	29.5^{d}	34.2^{e}	14.9^{e}	23.9^{e}	29.9^{d}	69.2^{cd}
Mean	34.0	38.2	15.3	10.7	24.8	42.7	22.3	10.6	27.2	30.2	08.1	14.6	20.3	66.6
C.D. (5%)	08.2	12.7	15.1	09.2	07.1	11.4	13.7	08.2	0.6	0.8	0.7	1.5	1.4	8.1
C.V. (%)	15.9	18.0	20.0	200	20.0	18.7	19.1	19.6	1.8	2.3	6.9	8.7	5.8	10.4

Figure(s) with same superscript(s) do not differ significantly at 5% level of probability
DAS - Days after sowing DIF and DFF - Days to initiation and fifty percent flowering TFC - Total flower count
D 25, 50 and 75 FA - Days taken for 25, 50 and 75 flower accumulation

was very early in TAG 24, and very late in ICGV 87165 and Dh 8. Days taken for accumulation of 25, 50, and 75 flowers were early in TAG 24 followed by JL 24 and TMV 2. Total flower count was highest in B 37c followed by R 8808 and D 39d. In general, there was early initiation and attainment of 50 per cent of flowering, accumulation of 25, 50 and 75 flowers and more number of flowers produced in late sown compared to early sown condition (Appendix 15). Resistant genotypes were late in initiation, attainment of 50 per cent flowering and days taken for 25, 50, 75 flower accumulation besides in pod and kernel accumulation. However, D 39d and mutant 28-2 were comparable to susceptible genotypes in pod and kernel, and pod accumulation, respectively.

4.3.3 Fatty acid composition and oil quality

Analysis of variance for fatty acid composition (palmitic, stearic, oleic, linoleic, arachidic, ecosenic, behenic and lignoceric acids) and oil quality (O/L and P/S ratios) parameters indicated significant genotypic effects for all the parameters (Table 35). Date of sowing had significant effect on linoleic acid, arachidic acid content and O/L ratio. While, disease control treatment significantly affected all the parameters except linoleic acid and arachidic acid content. However, the margin of change was less as a result of date of sowing and disease control on fatty acid composition and oil quality as compared to genotypes (Table 35 and Appendix 16). All the interaction effects involving genotype were highly significant for all the parameters indicating the importance of genotypic effects in determining fatty acid composition and oil quality. Date of sowing and disease control interaction effect was non-significant for oleic, linoleic and arachidic acid content and O/L ratio.

Among the genotypes, D 39d followed by ICGV 87165 had higher oleic acid (46-48 %) content and O/L ratio (1.5-1.7) across

Table 35: Analysis of variance for fatty-acid composition as influenced by genotype, disease pressure and dates of sowing

Source of variation	d.f.	Palmitic acid (16:0)	Stearic acid (18:0)	Oleic acid (18:1)	Linoleic acid (18:2)	Arachidic acid (20:0)	Ecosenic acid (20:1)	Behanic acid (22:0)	Lignoceric acid (24:0)	O/L ratio	P/S ratio
Factor A (Date of sowing)	1	0.21^{NS}	0.01^{NS}	4.00^{NS}	1.69**	0.06**	0.01^{NS}	1.62^{NS}	0.08^{NS}	0.03*	0.01^{NS}
Factor B (Disease control)	1	5.17**	0.02**	21.42**	0.16^{NS}	0.02^{NS}	0.08**	4.86**	0.19**	0.01*	0.16**
Factor C (Genotype)	9	9.07**	5.30**	265.56**	180.43**	0.85**	0.57**	3.74**	0.61**	0.89**	0.35**
Interactions											
AB	1	0.15**	0.33**	0.10^{NS}	0.61^{NS}	0.02^{NS}	0.02*	0.20*	0.04**	0.01^{NS}	0.01**
AC	9	0.17**	0.13**	2.23**	3.97**	0.02**	0.02**	0.47**	0.05**	0.02**	0.02**
BC	9	0.45**	0.20**	3.21**	0.83**	0.05**	0.03**	0.45**	0.06**	0.01**	0.01**
ABC	9	0.08**	0.24**	1.75**	1.36**	0.03**	0.01**	0.41**	0.06**	0.01**	0.01**
Error	72	0.03	0.13	0.42	0.32	0.01	0.01	0.08	0.01	0.01	0.01

*, ** denotes significance at 5 % and 1 % level of probability, respectively NS - not significant
O - Oleic acid L- Linoleic acid P- Polyunsaturated fatty acid S - Saturated fatty acid

sowing dates and disease pressure indicating the improved shelf-life and nutritional quality of oil in these cultivars (Appendix 16 and Table 36). Linoleic acid content was highest in R 8808 (40.2 %) followed by ICGV 86590 (39.1 %) and mutant 28-2 (38.8 %). Unsaturated fatty acid content was highest in Dh 8 (80.6 %) and D 39d (78.8 %). While, P/S ratio was highest in R 8808 (1.85) followed by ICGV 86590 (1.75) and Dh 8 (1.73).

4.3.4 Effect of leaf/flower removal on disease development and pod yield

To gain insight into the physiology of disease development and pod loss due to disease, genotypes were evaluated for the effects of artificial removal of leaves and flowers. Analysis of variance revealed significant treatment (leaf/flower removal) and genotypic effects for disease components and pod yield. Treatment × genotypic interaction effect was also significant indicating the differential response of genotypes to leaf/flower removal (Table 37).

In all the genotypes, flower removal significantly enhanced the resistance to late leaf spot and rust by reducing the lesion number and size, lesions on petiole and mainstem, pustule number, and field disease score and increasing the remaining green leaf area as compared to normal and leaf removal treatments (Tables 38 and 39). But, the enhanced resistance was at the cost of pod yield (40 %). The effect of flower removal in enhancing resistance and reducing yield was more in susceptible (JL 24, Dh 8, TMV 2 and TAG 24) than in resistant genotypes.

Artificial leaf removal significantly reduced the lesions on petiole (35.5 %) and mainstem (33.3 %) but its effect on other components (lesion number, lesion size and pustule number) was only marginal (Table 39). Leaf removal reduced the pod yield to the extent of 25 per cent. The yield reduction due to leaf removal was more in resistant

Table 36: Overall performance of groundnut genotypes for fatty acid composition

Genotype	Palmitic acid (16:0)	Stearic acid (18:0)	Oleic acid (18:1)	Linoleic acid (18:2)	Arachidic acid (20:0)	Ecosenic acid (20:1)	Behenic acid (22:0)	Lignoceric acid (24:0)	USF	SF	O/L ratio	P/S ratio
D 39d	10.55^{g}	2.38^{de}	48.54^{a}	28.82^{g}	1.45^{c}	1.45^{ab}	4.86^{bc}	1.94^{c}	78.8^{b}	21.2^{cd}	1.68^{a}	1.37^{g}
B 37c	11.79^{e}	2.40^{de}	43.11^{d}	33.29^{e}	1.40^{d}	1.29^{cd}	4.64^{bc}	2.05^{b}	77.7^{bc}	22.3^{bc}	1.30^{d}	1.49^{e}
Dh 8	10.74^{f}	1.96^{f}	45.93^{c}	33.36^{e}	1.12^{g}	1.30^{c}	3.74^{d}	1.84^{d}	80.6^{a}	19.4^{e}	1.38^{c}	1.73^{b}
R 8808	12.70^{ab}	1.70^{g}	36.51^{fg}	40.23^{a}	1.05^{h}	1.50^{a}	4.58^{bc}	2.14^{a}	78.3^{bc}	21.8^{cd}	0.91^{h}	1.85^{a}
Mutant (28-2)	12.84^{a}	2.40^{de}	36.96^{fg}	38.77^{b}	1.32^{e}	1.05^{e}	4.80^{bc}	1.76^{e}	76.8^{cd}	23.2^{bc}	0.95^{g}	1.68^{c}
JL 24	12.64^{ab}	2.84^{c}	37.34^{ef}	38.64^{b}	1.47^{c}	0.98^{f}	4.56^{bc}	1.56^{f}	77.0^{c}	23.0^{bc}	0.97^{g}	1.68^{c}
TMV 2	12.48^{bc}	3.90^{a}	37.67^{ef}	35.45^{d}	1.98^{a}	0.96^{f}	6.02^{a}	1.60^{f}	74.1^{e}	26.0^{a}	1.06^{e}	1.37^{g}
TAG 24	12.61^{a-c}	3.31^{b}	37.98^{e}	37.41^{c}	1.60^{b}	0.90^{g}	4.71^{bc}	1.46^{g}	76.3^{cd}	23.9^{b}	1.02^{f}	1.58^{d}
ICGV 86590	12.28^{d}	1.96^{f}	37.10^{f}	39.05^{b}	1.20^{f}	1.40^{ab}	5.00^{b}	1.97^{c}	77.6^{bc}	22.4^{bc}	0.96^{g}	1.75^{b}
ICGV 87165	10.86^{f}	2.53^{d}	46.38^{b}	30.79^{f}	1.48^{c}	1.24^{cd}	4.78^{bc}	1.95^{c}	78.4^{bc}	21.6^{cd}	1.51^{b}	1.43^{f}
Mean	11.91	2.54	40.75	35.58	1.41	1.21	4.77	1.83	77.6	22.5	1.17	1.59
C.D. (5%)	0.14	0.13	0.53	0.46	0.04	0.05	0.23	0.05	0.9	1.0	0.03	0.03
C.V. (%)	1.43	6.27	1.60	1.59	3.58	4.59	5.99	3.06	0.8	3.0	3.08	2.57

Figure(s) with same superscript(s) do not differ significantly at 5% level of probability
O - Oleic acid L- Linoleic acid P- Polyunsaturated S - Saturated fatty acid
USF - Unsaturated fatty acid SF - Saturated fatty acid

Table 37: ANOVA for late leaf spot and rust resistance parameters and pod yield in groundnut genotypes as influenced by season and treatment (leaf/flower removal)

Source of variation	d.f.	Late leaf spot						Rust			DF	RGLA	PY
		LAA	LN	LZ	LPt	LM	FDS	LAA	PN	FDS			
Factor A (Season)	1	50.4*	33.9*	5.3*	39.5*	50.1*	6.1^{NS}	14.9^{NS}	05.2*	0.08^{NS}	842.2^{NS}	806.0^{NS}	174.7*
Factor B (Treatment N, LR&FR)	2	162.1**	115.4**	30.1**	50.5**	44.6**	82.7**	209.1**	589.2**	67.20**	49969.3**	43440.1**	248.4**
Factor C (Genotype)	9	76.8**	82.8**	53.7**	17.2**	7.7**	31.0**	166.4**	500.4**	39.20**	666.6**	931.6**	44.3**
Interaction													
A.B	2	3.5*	0.68^{NS}	0.3^{NS}	4.2**	11.1**	0.1^{NS}	00.5^{NS}	05.2*	0.03^{NS}	11.2^{NS}	5.0^{NS}	2.5^{NS}
A.C	9	4.5*	0.7^{NS}	0.1^{NS}	4.4**	3.2**	0.2^{NS}	0.7^{NS}	05.0*	0.06^{NS}	29.4**	19.9**	5.1**
B.C	18	5.4*	3.1**	0.3**	2.1**	3.5**	1.7**	11.6**	32.9**	0.97**	123.6**	154.2**	3.7**
A.B.C	18	0.8^{NS}	0.3^{NS}	0.1^{NS}	1.3**	2.1**	0.2^{NS}	0.3^{NS}	02.6^{NS}	0.06^{NS}	08.5^{NS}	6.7^{NS}	0.9^{NS}
Error	54	1.0	0.8	0.1	0.4	0.3	0.2	01.2	02.2	0.30	09.2	7.2	0.9
C.V. (%)		18.1	14.7	5.2	19.2	20.0	8.2	19.6	14.1	9.2	06.2	5.8	8.4

*, ** denotes significance at 5% and 1% level of probability, respectively

NS - Not significant

N - Normal	LR - Leaf removal	FR - Flower removal	FDS - Field disease score
LN - Lesion number	PN - Pustule number	LPt - Lesions on petiole	LM - Lesions on mainstem
DF - Defoliation	PY - Pod yield	RGLA - Remaining green leaf area	LAA - Leaf area affected by late leaf spot/rust

Table 38: Mean performance of groundnut genotypes for late leaf spot resistance as influenced by leaf/flower removal

Genotype	LN			LZ			LPt			LM			FDS		
	N	LR	FR	N	LR	FR	N	LR	FR	N	LR	FR	N	LR	FR
D 39d	03.3	3.2 (-3.0)	2.6 (-21.2)	04.7	4.5 (-4.3)	3.3 (-29.8)	0.8	0.5 (-25.0)	0.5 (-37.5)	0.5	0.4 (-20.0)	0.2 (-60.0)	3.8	5.8 (52.6)	2.7 (-28.9)
B 37c	04.0	4.0 (0.0)	2.4 (-40.0)	04.4	4.2 (-4.5)	3.1 (-29.6)	1.6	1.4 (-12.5)	0.7 (-56.3)	1.0	0.8 (-20.0)	0.5 (-50.0)	3.8	5.8 (52.6)	2.8 (-26.3)
Dh 8	07.4	7.1 (-4.1)	4.9 (-33.8)	06.4	6.0 (-6.3)	4.6 (-28.1)	3.1	2.1 (-32.3)	0.5 (-83.9)	1.8	1.4 (-22.2)	0.5 (-72.2)	7.3	8.3 (13.7)	5.3 (-27.4)
R 8808	08.1	8.0 (-1.2)	4.5 (-44.4)	07.6	7.3 (-3.9)	6.3 (-17.1)	3.5	3.3 (-05.7)	0.8 (-77.1)	2.1	1.5 (-28.6)	0.5 (-76.2)	8.0	8.4 (05.0)	4.5 (-43.8)
28 2	04.5	4.4 (-2.2)	2.5 (-44.4)	05.4	5.0 (-7.4)	3.0 (-27.6)	1.6	1.1 (-31.3)	0.5 (-68.8)	1.3	0.9 (-30.8)	0.5 (-61.5)	5.0	6.5 (30.0)	3.8 (-24.0)
JL 24	09.8	9.3 (-5.1)	4.0 (-59.8)	09.6	9.2 (-4.2)	7.9 (-17.7)	5.5	3.3 (-40.0)	1.9 (-65.5)	4.6	2.1 (-54.3)	0.8 (-82.6)	8.0	8.3 (03.8)	6.5 (-18.8)
TMV 2	11.0	8.9 (-19.1)	7.5 (-31.8)	10.0	9.3 (-7.0)	8.1 (-19.0)	5.6	3.9 (-30.4)	1.8 (-67.9)	4.8	2.1 (-56.3)	0.6 (-87.5)	8.3	8.6 (03.6)	7.0 (-15.7)
TAG 24	09.6	8.9 (-07.3)	7.3 (-24.0)	08.0	7.5 (-6.3)	5.6 (-30.0)	4.5	2.5 (-44.4)	0.9 (-80.0)	3.0	2.0 (-33.3)	0.6 (-80.0)	8.0	8.3 (03.8)	5.0 (-37.5)
ICGV 86590	09.3	9.2 (-01.1)	4.8 (-48.4)	7.8	7.3 (-6.4)	6.7 (-14.1)	3.8	2.1 (-44.8)	0.9 (-76.3)	2.9	1.6 (-44.8)	0.5 (-82.8)	7.8	8.5 (09.0)	5.3 (-32.1)
ICGV 87165	03.1	2.9 (-06.5)	1.9 (-38.7)	3.8	3.5 (-7.8)	2.9 (-23.7)	0.6	0.5 (-16.7)	0.4 (-33.3)	0.3	0.2 (-33.3)	0.1 (-66.7)	3.3	6.0 (81.8)	2.5 (-24.2)
Mean	07.0	6.7 (-4.3)	3.9 (-44.3)	6.8	6.4 (-5.9)	5.1 (-25.0)	3.1	2.0 (-35.5)	0.8 (-74.2)	2.1	1.4 (-33.3)	0.1 (-81.0)	6.3	7.3 (15.9)	4.4 (-30.2)
C.D. (5%)	1.4	1.5	1.3	0.6	0.7	0.5	1.5	1.2	1.1	1.6	1.4	0.8	0.7	0.7	1.0
C.V. (%)	13.9	15.2	15.2	6.4	7.0	6.2	20.7	17.4	20.2	18.0	19.9	25.0	7.7	6.7	14.6

Figures in parenthesis indicate percentage over normal condition N - Normal LR - Leaf removal FR - Flower removal
LN - Lesion number LZ - Lesion size LPt - Lesions on petiole LM - Lesions on mainstem
FDS - Field disease score

Table 39: Mean performance of groundnut genotypes for rust resistance and pod yield as influenced by leaf/flower removal

Genotype	PN			FDS			RGLA			PY		
	N	LR	FR	N	LR	FR	N	LR	FR	N	LR	FR
D 39d	02.8	2.5 (-10.7)	01.9 (-28.6)	3.0	4.5 (50.0)	2.5 (-16.7)	76.4	14.8 (-80.6)	84.7 (10.9)	16.4	12.8 (-22.0)	10.9 (-33.5)
B 37c	03.4	3.2 (-06.6)	02.3 (-32.4)	3.0	4.5 (50.0)	2.5 (-16.7)	74.8	12.8 (-82.9)	82.9 (10.8)	17.0	13.3 (-21.8)	12.4 (-27.1)
Dh 8	22.1	21.4 (-03.2)	09.0 (-59.3)	7.5	7.8 (04.0)	4.5 (-40.0)	34.8	03.7 (-89.4)	63.1 (81.3)	12.7	09.6 (-24.4)	06.9 (-45.7)
R 8808	18.1	17.1 (-05.5)	07.5 (-58.6)	7.0	7.5 (07.1)	4.5 (-39.7)	54.6	05.5 (-89.9)	72.5 (32.8)	14.5	12.1 (-16.6)	11.3 (-22.1)
28-2	22.0	21.1 (-04.1)	08.3 (-62.3)	6.3	7.5 (19.1)	4.5 (-02.9)	59.9	10.3 (-82.8)	68.7 (14.7)	15.6	10.2 (-34.6)	10.0 (-35.9)
JL 24	20.5	19.4 (-05.4)	09.4 (-54.1)	7.8	8.0 (02.6)	6.3 (-19.2)	45.4	08.2 (-81.9)	72.3 (59.3)	12.3	09.9 (-19.5)	06.3 (-48.8)
TMV 2	20.1	18.5 (-08.0)	11.0 (-45.3)	7.5	7.8 (04.0)	6.3 (-16.0)	47.4	08.7 (-81.6)	61.8 (30.4)	10.4	09.1 (-12.5)	06.0 (-42.3)
TAG 24	10.4	08.6 (-17.3)	05.6 (-46.2)	7.8	8.0 (02.6)	6.0 (-23.1)	47.7	07.7 (-83.9)	71.2 (49.3)	10.7	08.5 (-20.6)	06.2 (-42.1)
ICGV 86590	07.9	06.8 (-13.2)	04.0 (-49.4)	4.0	5.5 (37.5)	3.0 (-25.0)	46.8	07.5 (-84.0)	70.4 (50.4)	13.7	10.7 (-21.9)	8.0 (-41.6)
ICGV 87165	03.5	03.0 (-09.1)	02.0 (-39.4)	3.0	4.8 (60.0)	2.2 (-26.7)	77.5	16.8 (-78.3)	83.6 (07.9)	17.5	11.6 (-33.7)	10.8 (-40.6)
Mean	13.0	12.4 (-04.6)	06.1 (-53.1)	5.7	6.6 (15.8)	4.0 (-29.8)	56.5	09.6 (-83.0)	73.1 (29.4)	14.1	10.7 (-24.1)	08.2 (-41.8)
C.D. (5%)	02.3	02.5	01.3	0.6	0.7	00.6	7.5	05.5	6.0	2.0	01.6	01.5
C.V. (%)	11.9	13.6	13.6	6.9	7.6	10.0	8.9	19.7	5.5	9.8	10.3	11.1

Figures in parenthesis indicate percentage over normal condition
FR - Flower removal
PY - Pod yield
N - Normal
PN - Pustule number
RGLA - Remaining green leaf area
LR - Leaf removal
FDS - Field disease score

genotypes (28-2 and ICGV 87165) than in susceptible genotypes. Flower removal treatment had more pronounced effect on yield reduction (40 %) than leaf removal (25 %) revealing importance of sink rather than source in the genotypes (Table 39).

4.3.5 Interaction between late leafspot and rust

In order to study the effect of incidence of one disease (late leaf spot/rust) on the other, the components of late leaf spot (incubation and latent periods, leaf area affected, lesion number and size, lesions on petiole and mainstem, defoliation, sporulation and field disease scores) were assessed in the presence/absence of rust disease in genotypes with varying level of resistance to late leaf spot and/or rust (Tables 40 and 41). Similarly, components of rust (incubation and latent periods, leaf area affected, pustule number, defoliation, sporulation and field disease scores) disease in the presence/absence of late leaf spot were also investigated (Tables 42 and 43).

Analysis of variance indicated significant effect of rust on most of the components of late leaf spot (latent period, leaf area affected, lesion size, lesions on petiole, defoliation, sporulation and field disease scores). While, incubation period, lesion number and lesions on mainstem were not affected by rust disease, revealing the partial antagonistic effect of rust on late leaf spot at later stage of disease development (Table 40). Genotypes differed significantly for all the components of late leaf spot. The genotype × rust disease (presence/absence) interaction effects were significant for all the components except sporulation and field disease scores indicating the differential response of genotypes for components of late leaf spot *vis-à-vis* rust.

Rust disease increased the leaf area affected (22 %) and defoliation (7 %) by late leaf spot and reduced the latent period (13 %)

Table 40: Analysis of variance for components of late leaf spot resistance in relation to rust disease in groundnut genotypes

Source of variation	d.f.	IP	LP_{50}	LAA	LN	LZ	LPt	LM	DF	RGLA	SC	FDS
Factor A (+/- Rust)	1	1.51^{NS}	179.92**	35.41*	4.76^{NS}	7.08*	16.80*	1.60^{NS}	1599.81**	2494.73**	1.20*	0.42*
Factor B (Genotype)	9	33.72**	577.16**	159.58**	56.27**	29.25**	57.80**	59.51**	1819.22**	1794.93**	54.12**	30.33**
A × B interaction	9	3.13**	13.12**	10.52**	5.84**	0.88**	5.63**	1.62**	79.58**	62.73**	0.12^{NS}	0.18^{NS}
Error	36	0.4	0.6	0.5	0.8	0.1	0.3	0.3	2.8	1.7	0.2	0.1
C. V. (%)		9.14	3.34	9.46	10.99	4.26	13.78	18.13	2.69	3.68	9.29	5.10

*, ** denotes significance at 5% and 1% level of probability, respectively

NS - not significant

IP - Incubation period
LN - Lesion number
LM - Lesion on mainstem
SC - Sporulation score

LP_{50} - Latent period
LZ - Lesion size
DF - Defoliation
FDS - Field disease score

LAA - Leaf area affected by late leaf spot
LPt - Lesions on petiole
RGLA - Remaining green leaf area

of late leaf spot, making the plants more sensitive to late leaf spot (Table 41). At the same time rust disease decreased the lesion size and lesions on petiole.

As revealed by ANOVA, presence of late leaf spot significantly affected the components of rust (incubation period, latent period, leaf area affected, pustule number and defoliation) but not sporulation and field disease scores, indicating the antagonistic effect of late leaf spot on rust at early stage of disease development. Genotypic and interaction effects were significant for all the components of rust (Table 42).

Late leaf spot pathogen significantly increased the defoliation (78 %) and reduced the pustule number (47 %), incubation period (21 %), latent period (14 %) and leaf area affected (10 %) [Table 43]. The antagonistic effect of late leaf spot on rust disease components was clearly evident in susceptible (JL 24, TMV 2 and TAG 24) and moderately susceptible (R 8808 and Dh 8) genotypes than in resistant genotypes (Tables 41 and 43).

4.3.6 Yield performance of 28-2 and D 39d

Two promising foliar disease resistant genotypes mutant III (28-2) and D 39d (GPBD 4) were evaluated along with checks (JL 24 and Dh 3-30) for yield performance in multi location trails of zone 8 (Northern transitional tract of Karnataka) where the incidence of foliar diseases is very high. The evaluation was done at three locations (Dharwad, Nippani and Sankeshwar) over three (1996, 1997 and 1998) and two (1999 and 2000) rainy seasons for mutant III and D 39d, respectively. Overall, the mutant III and D 39d out yielded the national check, JL 24 for pod (20.6 and 16.0 %), kernel (18.1 and 18.0 %), oil (16.8 and 18.0 %) and fodder (16.3 and 19.2 %) yield,

Table 41: Components of late leaf spot resistance as influenced by rust disease

Genotype	IP		LP$_{50}$		LAA		LZ		LP		DF	
	-R	+R	-R	+R	-R	+R	-R	+R	-R	+R	-R	+R
D 39d	11.0^{a}	09.9^{a} (-10.0)	34.5^{c}	34.0^{a} (-01.4)	02.5^{a}	03.1^{ab} (24.0)	05.7^{c}	5.4^{bc} (-05.3)	00.7^{ab}	0.5^{a} (-28.6)	37.1^{ab}	42.1^{b} (13.5)
B 37c	10.5^{b}	07.2^{bc} (-31.4)	33.3^{d}	32.7^{ab} (-01.8)	02.5^{a}	02.6^{ab} (04.0)	04.9^{b}	4.8^{b} (-02.0)	01.2^{ab}	1.0^{a} (-16.7)	32.4^{a}	45.4^{c} (09.3)
Dh 8	05.9^{e}	05.0^{de} (-15.3)	26.2^{e}	16.7^{c} (-36.3)	04.4^{ab}	04.8^{c} (09.1)	06.6^{d}	6.1^{cd} (-07.6)	03.7^{c}	3.5^{b} (-05.4)	74.2^{f}	83.4^{f} (12.4)
R 8808	05.2^{ef}	05.1^{de} (-01.9)	23.9^{f}	18.3^{c} (-23.4)	06.0^{bc}	07.5^{d} (25.0)	08.2^{f}	7.6^{de} (-07.3)	03.5^{c}	2.7^{b} (-22.9)	62.3^{d}	65.2^{d} (04.7)
Mutant (28-2)	08.3^{d}	07.9^{bc} (-04.8)	36.5^{b}	32.0^{a} (-06.9)	03.7^{ab}	04.2^{c} (13.5)	06.0^{c}	5.7^{bc} (-05.0)	03.7^{c}	2.8^{b} (-24.3)	34.1^{ab}	41.0^{a} (20.2)
JL 24	05.3^{ef}	04.8^{de} (-09.4)	14.3^{h}	12.7^{d} (-11.2)	10.0^{d}	16.5^{f} (65.0)	10.1^{g}	8.9^{f} (-11.9)	08.5^{d}	5.0^{c} (-41.2)	65.6^{e}	66.3^{d} (01.1)
TMV 2	04.9^{ef}	04.5^{de} (-08.2)	14.2^{h}	11.7^{d} (-17.6)	13.0^{e}	19.2^{g} (47.7)	12.4^{h}	9.9^{g} (-20.2)	10.0^{e}	6.7^{d} (-33.0)	57.3^{c}	69.6^{e} (21.5)
TAG 24	04.1^{f}	03.8^{de} (-07.3)	14.1^{h}	11.6^{d} (-17.7)	13.0^{e}	13.5^{e} (03.9)	08.1^{f}	6.7^{cd} (-17.3)	11.0^{f}	7.0^{d} (-36.4)	84.3^{g}	92.5^{h} (09.7)
ICGV 86590	05.7^{ef}	04.5^{de} (-21.1)	16.8^{g}	14.2^{e} (-15.5)	07.3^{bc}	08.5^{d} (14.1)	07.2^{e}	7.2^{de} (-01.4)	04.3^{c}	3.7^{b} (-14.0)	75.7^{f}	87.2^{g} (15.2)
ICGV 87165	10.0^{b}	08.9^{b} (-11.1)	36.5^{a}	31.0^{ab} (-15.1)	01.7^{a}	02.0^{a} (17.6)	03.8^{a}	3.4^{a} (-10.5)	00.4^{a}	0.3^{a} (-25.0)	39.2^{b}	42.5^{b} (08.4)
Mean	06.8	06.5 (-04.4)	25.1	21.7 (-13.5)	06.6	08.1 (22.7)	07.3	6.6 (-09.6)	04.5	3.4 (-24.4)	56.5	60.8 (07.6)
C.D. (5%)	00.7	1.3	1.0	1.6	01.3	1.1	00.3	0.6	00.9	1.0	02.9	02.8
C.V. (%)	06.1	11.6	02.4	4.3	11.6	7.6	02.7	5.6	11.6	16.5	03.0	02.4

Figures in parenthesis indicate percentage over presence of late leaf spot only

+R and -R indicate presence and absence of rust, respectively

IP - Incubation period

LP$_{50}$ - Latent period

LAA - Leaf area affected by late leaf spot;

LZ - Lesion size

LPt - Lesions on petiole

DF - Defoliation

Table 42: Analysis of variance for components of rust resistance in relation to late leaf spot disease in groundnut genotypes

Source of variation	d.f.	IP	LP_{50}	LAA	PN	DF	RGLA	SC	FDS
Factor A (+/- Late leafspot)	1	86.40**	171.03*	13.07*	1088.86**	16150.72**	15617.07**	1.07^{NS}	0.94^{NS}
Factor B (Genotype)	9	152.27**	531.29**	243.22**	344.90**	1031.58**	1213.32**	64.69**	39.44**
A × B interaction	9	1.33*	31.47**	3.06**	71.79**	194.58**	178.56**	0.77**	1.23**
Error	36	0.5	2.3	0.3	2.4	2.6	2.5	0.2	0.1
C. V. (%)		7.32	6.75	6.04	11.16	3.20	3.52	7.94	5.87

*, ** denotes significance at 5% and 1% level of probability, respectively

NS - not significant

IP - Incubation period

LP_{50} - Latent period

LAA - Leaf area affected by rust

PN - Pustule number

DF - Defoliation

RGLA - Remaining green leaf area

SC - Sporulation score

FDS - Field disease score

Table 43: Components of rust resistance as influenced by late leaf spot

Genotype	IP		LP_{50}		PN		LAA		DF	
	-LLS	+LLS	-LLS	+LLS	-LLS	+LLS	-LLS	+LLS	-LLS	+LLS
D 39d	17.0^{b}	15.2^{b} (-10.6)	36.0^{ab}	33.0^{a} (-08.3)	04.8^{a}	03.0^{a} (-37.5)	02.6^{b}	02.3^{b} (-11.5)	18.3^{a}	42.1^{b} (130.1)
B 37c	16.5^{b}	13.7^{b} (-17.0)	33.7^{ab}	33.5^{a} (-00.6)	05.7^{a}	05.0^{a} (-12.3)	03.8^{c}	02.6^{d} (-31.6)	22.9^{a}	45.4^{c} (098.3)
Dh 8	05.8^{ef}	05.0^{d} (-13.8)	15.1^{cd}	12.3^{e} (-18.5)	26.3^{e}	12.3^{bc} (-53.2)	11.5^{f}	08.4^{d} (-27.0)	53.1^{g}	83.4^{g} (057.1)
R 8808	09.2^{d}	04.9^{d} (-46.8)	16.4^{cd}	16.3^{d} (-00.6)	20.0^{c}	10.7^{b} (-46.5)	08.6^{d}	06.4^{c} (-25.6)	37.1^{d}	62.3^{d} (067.9)
Mutant (28-2)	07.9^{e}	05.0^{d} (-36.7)	18.2^{c}	16.0^{d} (-12.1)	22.6^{d}	18.0^{cd} (-20.4)	10.6^{e}	09.9^{e} (-06.6)	29.8^{c}	41.0^{a} (057.7)
JL 24	07.5^{ef}	05.6^{d} (-25.3)	15.1^{cd}	13.4^{e} (-11.3)	28.0^{e}	10.7^{b} (-61.8)	16.4^{h}	15.9^{g} (-03.0)	41.7^{de}	66.3^{e} (059.0)
TMV 2	06.8^{ef}	04.4^{d} (-35.3)	14.8^{cd}	13.3^{e} (-10.1)	31.5^{f}	15.0^{b-d} (-52.4)	19.0^{i}	18.0^{h} (-05.3)	39.9^{de}	69.6^{f} (074.4)
TAG 24	07.8^{e}	04.7^{d} (-39.7)	15.9^{cd}	13.1^{e} (-17.6)	27.0^{e}	12.0^{bc} (-55.6)	13.7^{g}	11.4^{f} (-16.8)	49.0^{f}	92.5^{i} (088.8)
ICGV 86590	13.2^{c}	10.9^{c} (-17.4)	38.8^{a}	23.0^{c} (-40.7)	09.0^{b}	03.0^{a} (-66.7)	02.3^{b}	00.4^{a} (-82.6)	25.7^{c}	87.2^{h} (239.3)
ICGV 87165	19.5^{a}	17.7^{a} (-09.2)	35.2^{ab}	31.0^{b} (-11.9)	06.0^{a}	04.0^{a} (-33.3)	01.0^{a}	00.4^{a} (-60.0)	24.7^{b}	42.5^{b} (072.1)
Mean	11.1	08.7 (-21.6)	23.9	20.5 (-14.2)	18.1	09.6 (-47.0)	08.8	7.9 (-10.2)	34.0	60.8 (078.8)
C.D. (5%)	0.8	1.6	3.2	1.7	1.9	3.2	0.6	1.1	2.8	2.8
C.V. (%)	4.3	10.4	7.9	4.8	6.3	19.5	4.1	7.8	4.8	2.4

Figures in parenthesis indicate percentage over presence of rust only
+LLS and -LLS indicate presence and absence of late leaf spot, respectively
IP - Incubation period LP_{50} - Latent period   LAA - Leaf area affected by rust   PN - Pustule number   DF - Defoliation

respectively (Tables 44 and 45). These genotypes are under adaptive trials.

4.4 Genetics of resistance

In order to discern the genetic basis of late leaf spot and rust resistance and to test for allelic relation between mutational and inter-specific sources, crosses involving mutants (VL 1, 28-2, 45, 45 (S) and 110) and inter-specific derivatives (ICGV 87165, D 39d and B 37c), viz., 110 × VL 1, 45 × 45 (S), VL 1 × ICGV 87165, 110 × ICGV 87165, 28-2 × D 39d, 28-2 × B 37c and B 37c × D 39d were made. Mutant VL 1 is resistant to rust but susceptible to late leaf spot, mutants 28-2, 45 and 110 are resistant to late leaf spot but susceptible to rust. While, 45 (S) is susceptible to both late leaf spot and rust. Inter-specific derivatives, ICGV 87165, D 39d and B 37c are resistant to both late leaf spot and rust. The parents, F_1, F_2 and F_3 generations were assessed for their reaction to late leaf spot and rust using field disease scores recorded at one week before harvest.

F_1 hybrids of the crosses 110 × VL 1, VL 1 × ICGV 87165, 110 × ICGV 87165, 28-2 × D 39d and 28-2 × B 37c, i.e. involving mutants and inter-specific derivatives had moderately susceptible reaction to late leaf spot and rust. While, F_1's of B 37c × D 39d cross were resistant to late leaf spot and rust (Table 46).

Based on parental and near-bimodal distribution in F_2 generation, individual plants showing 1.0 - 5.0 field disease score were taken as resistant (R) and those between 5.1 - 9.0 as susceptible (S). Hypotheses were formulated on F_2 and confirmed through F_3 breeding behaviour (Tables 47 and 48).

F_2 segregation ratio for late leaf spot resistance in crosses involving resistant (R) and susceptible (S) mutants, viz., 110 × VL 1, 45 × 45 (S) revealed duplicate complementary recessive genes (9 S: 7

Table 44: Performance of Mutant III (28-2) in multi location trials of zone 8 (Northern Transitional Tract of Karnataka)

Entry	Pod Yield (q ha^{-1})									Mean Kernel Yield (q ha^{-1})	Mean Oil Yield (q ha^{-1})	Mean Fodder Yield (t ha^{-1})
	Dharwad				Nippani			Sankeshwar	Overall Mean			
	1996	1997	1998	Mean	1997	1998	Mean	1998				
Mutant III (28-2)	45.4	38.0	24.0	35.8 (16.7)	34.0	17.5	24.2 (1.5)	20.5 (11.4)	28.8 (20.6)	18.9 (18.1)	08.9 (16.8)	08.12 (16.3)
<u>Checks</u>												
JL 24	44.4	31.1	19.7	31.7	27.5	20.9	21.7	18.4	23.9	15.5	07.4	06.99
Dh 3-30	37.0	34.5	27.6	33.0	30.0	17.3	23.7	14.5	23.7	14.7	07.1	06.07
Mean (10 genotypes)	42.8	34.2	23.6	33.1	35.1	19.4	27.7	22.3	26.0	21.2	10.02	07.06
C.D. (5%)	08.1	07.4	08.0	-	09.1	05.1	-	06.1	-	-	-	-
C.V. (%)	10.9	13.6	18.0	-	14.5	13.9	-	20.1	-	-	-	-

Figures in parenthesis indicate per cent increase over national check JL 24

Table 45: Performance of D 39d (GPBD 4) in multi location trials of zone 8 (Northern Transitional Tract of Karnataka)

Entry	Pod Yield (q ha^{-1})										Mean Kernel Yield (q ha^{-1})	Mean Oil Yield (q ha^{-1})	Mean Fodder Yield (t ha^{-1})
	Dharwad			Nippani			Sankeshwar			Overall Mean			
	1999	**2000**	**Mean**	**1999**	**2000**	**Mean**	**1999**	**2000**	**Mean**				
D 39d (GPBD 4)	60.2	25.1	42.6 (13.6)	38.4	29.7	34.5 (7.8)	55.7	27.4	41.6 (26.1)	39.4 (16.0)	26.9 (18.0)	13.0 (19.2)	08.72 (21.5)
Checks													
JL 24	54.5	20.6	37.5	35.6	27.6	31.6	40.4	25.6	33.0	34.0	22.1	10.5	07.18
Dh 3-30	48.3	16.2	32.2	33.5	26.6	30.1	43.4	16.3	29.9	30.7	19.0	09.1	06.36
Mean (10 genotypes)	56.8	22.4	39.6	34.9	29.2	31.8	41.5	25.6	33.5	35.7	14.0	4.93	06.44
C.D. (5%)	08.0	05.9	-	09.0	08.4	-	08.8	04.5	-	-	01.4	6.52	01.20
C.V. (%)	08.6	17.0	-	15.2	18.3	-	13.2	10.0	-	-	08.0	8.01	14.60

Figures in parenthesis indicate per cent increase over national check JL 24

Table 46: Mean field disease score in parents and F_1 hybrids of groundnut crosses

Parents/ Hybrids (F_1)	Field Disease Score (Modified 1-9 scale)	
	Late leaf spot	Rust
Parents		
Mutants		
VL 1	9.0	4.0
28 - 2	5.0	7.0
45	5.0	7.0
45 (S)	8.0	8.0
110	5.0	7.0
Inter-specific derivatives		
ICGV 87165	4.0	3.0
D 39d	4.0	3.0
B 37c	4.0	3.0
F_1Hybrids		
110 × VL 1	7.0	6.0
45 × 45 (S)	7.0	8.0
VL 1 × ICGV 87165	7.0	5.0
110 × ICGV 87165	6.0	6.0
28-2 × D 39d	6.0	6.0
28-2 × B 37c	6.0	6.0
B 37c × D 39d	4.0	3.0

Table 47: F_2 segregation pattern for late leaf spot and rust field disease scores in groundnut crosses

Cross	Disease	F_2 ratio	Number of F_2 plants					Chi-square	Probability
			Susceptible*		$^{\Psi}$ Resistant		Total		
			Oi	Ei	Oi	Ei			
1. 110 × VL 1	LLS	9:7	92	81.0	52	63.0	144.0	1.707	0.10-0.20
	Rust	9:7	94	81.0	50	63.0		2.384	0.10-0.20
2. 45 × 45 (S)	LLS	9:7	88	83.2	60	64.8	148.0	0.316	0.50-0.60
	Rust	-	144	148.0	04	0.0		0.054	-
3. VL 1 × ICGV 87165	LLS	9:7	126	135.0	114	105.0	240.0	0.457	0.40-0.50
	Rust	81:175	84	75.9	156	164.1		0.421	0.50-0.60
4. 110 × ICGV 87165	LLS	81:175	66	89.1	210	192.9	282.0	2.918	0.05-0.10
	Rust	9:7	174	158.4	108	123.6		1.168	0.20-0.30
5. 28-2 × D 39d	LLS	81:175	60	72.0	168	156.0	228.0	0.975	0.30-0.40
	Rust	9:7	132	128.1	96	99.9		0.091	0.70-8.00
6. 28-2 × B 37c	LLS	81:175	90	77.2	154	166.8	244.0	1.552	0.20-0.30
	Rust	9:7	150	137.2	94	106.8		1.364	0.20-0.30
7. B 37c × D 39d	LLS	-	06	00.0	150	156.0	156.0	0.154	0.90-0.95
	Rust	-	03	00.0	153	156.0		0.039	0.80-0.90

$^{\Psi}$Resistant: 1 - 5 field disease score
O_i - Observed value

* Susceptible: 5.1 - 9 field disease score
E_i - Expected value

LLS - Late leaf spot

Table 48: F_3 breeding behaviour for late leaf spot and rust resistance in groundnut crosses

Cross			Frequencies of families under each class of F_3 of different F_2 ratios						Total	Chi-square	Probability
			0:1(BTR)	3:1	9:7	27:37	81:175	1:0 (BTD)			
1. 110 × VL 1	LLS	O_i	52.0	34.0	44.0	-	-	14.0	144.0		
	(9:7)	E_i	63.4	36.0	36.0	-	-	08.6		3.665	0.3
	Rust	O_i	50.0	40.0	42.0	-	-	10.0	144.0		
	(9:7)	E_i	63.4	36.0	36.0	-	-	08.6		2.252	0.5-0.6
2. 45 × 45 (S)	LLS	O_i	60.0	42.0	30.0	-	-	16.0	148.0		
	(9:7)	E_i	64.0	37.0	37.0	-	-	16.8		4.071	0.2-0.3
	Rust	O_i	04.0	-	-	-	-	144.0	148.0		
	(BTD)	E_i	00.0	-	-	-	-	148.0		0.054	0.8-0.5
3. VL 1 × ICGV 87165	LLS	O_i	114.0	51.0	51.0	-	-	18.0	240.0		
	(9:7)	E_i	105.6	60.0	60.0	-	-	14.4		1.423	0.7-0.8
	Rust	O_i	156.0	03.0	27.0	39.0	03.0	06.0	240.0		
	(81:175)	E_i	163.2	04.8	24.0	31.2	04.8	02.4		3.581	0.6-0.7
4. 110 × ICGV 87165	LLS	O_i	210.0	06.0	24.0	24.0	03.0	06.0	282.0		
	(81:175)	E_i	191.7	05.7	28.2	36.6	05.7	27.0		4.865	0.4-0.5
	Rust	O_i	105.0	78.0	66.0	28.8	-	18.0	282.0		
	(9:7)	E_i	124.4	70.5	70.5		-	16.8		3.223	0.3-0.4
5. 28-2 × D 39d	LLS	O_i	168.0	06.0	18.0	18.0	04.0	06.0	228.0		
	(81:175)	E_i	155.1	04.5	22.8	29.7	04.6	02.4		6.476	0.2-0.3
	Rust	O_i	096.0	60.0	54.0	-	-	18.0	228.0		
	(9:7)	E_i	100.2	57.0	57.0	-	-	13.8		0.591	0.8-0.09
6. 28-2 × B 37c	LLS	O_i	154.0	10.0	20.0	32.0	11.0	06.0	244.0		
	(81:175)	E_i	166.0	04.8	25.8	31.8	07.3	02.4		5.524	0.3-0.4
	Rust	O_i	094.0	56.0	68.0	-	-	20.0	244.0		
	(9:7)	E_i	107.4	61.0	61.0	-	-	14.6		2.442	0.4-0.5
7. B 37c × D 39d	LLS	O_i	150.0	-	-	-		06.0	156.0		
	(BTR)	E_i	1056.0	-	-	-		00.0		0.154	0.8-0.9
	Rust	O_i	153.0	-	-	-		03.0	156.0		
	(BTR)	E_i	156.0	-	-	-		00.0		0.039	0.8-0.9

BTR and BTD: Bred true for recessive (resistance) and dominant (susceptibility) character, respectively

LLS - Late leaf spot O_i - Observed value E_i - Expected value

R) controlling late leaf spot resistance. A similar result was evident in the cross involving late leaf spot susceptible mutant (VL 1) and resistant inter-specific derivative (ICGV 87165). However, four complementary recessive genes (81 S: 175 R) control the late leaf spot resistance in the crosses involving resistant (110 and 28-2) mutants and inter-specific (ICGV 87165, D 39d and B 37c) derivatives viz., 110 × ICGV 87165, 28-2 × D 39d and 28-2 × B 37c revealing two independent duplicate complementary recessive genes for late leaf spot resistance in mutational and inter-specific sources (Table 47). There was no segregation in B 37c × D 39d cross indicating the common gene control for resistance. The crosses 110 × VL 1, 45 × 45 (S) and VL 1 × ICGV 87165 exhibited the following breeding behaviour [7 (Bred true for resistance); 4 (3 S: 1 R); 4 (9 S: 7 R) and 1 (Bred true for susceptibility)] in F_3 generation confirming the hypothesis. Similarly, breeding behaviour [175 (Bred true for resistance); 6 (3 S: 1 R); 24 (9 S: 7 R); 32 (27 S: 37 R); 16(81 S: 175 R) and 3 (Bred true for susceptibility)] in F_3 generation of the crosses 110 × ICGV 87165, 28-2 × D 39d and 28-2 × B 37c confirmed proposed hypotheses (Table 48).

Segregation in F_2 generation of the crosses involving the rust resistant (VL 1)/ susceptible (110 and 28-2) mutants, and resistant inter-specific (ICGV 87165, D 39d and B 37c) derivatives viz., 110 × VL 1, 110 × ICGV 87165, 28-2 × D 39d and 28-2 × B 37c revealed duplicate complementary recessive genes (9 S: 7 R) conferring resistance to rust. Allelic test cross involving rust resistant mutant and inter-specific derivative VL 1 × ICGV 87165 recorded 81 S: 175 R segregation ratio in F_2 generation (four complementary recessive genes) indicating independent duplicate complementary recessive genes in mutant and inter-specific source (Table 47). F_3 breeding behaviour confirmed the proposed F_2 segregation ratios (Table 48). Based on these results, a four-locus model was formulated (Table 49).

Table 49: Genetic constitution of groundnut genotypes for late leafspot and rust resistance

Genotype	Late leaf spot	Rust
Mutants		
VL 1	$LS_1 LS_1 LS_2 LS_2 LS_3 LS_3 LS_4 LS_4$	$r_1 r_1 r_2 r_2 R_3 R_3 R_3 R_4 R_4$
45 (S)	$LS_1 LS_1 LS_2 LS_2 LS_3 LS_3 LS_4 LS_4$	$R_1 R_1 R_2 R_2 R_3 R_3 R_4 R_4$
28-2, 45 and 110	$ls_1\ ls_1\ ls_1\ ls_1\ LS_3 LS_3 LS_4 LS_4$	$R_1 R_1 R_2 R_2 R_3 R_3 R_4 R_4$
Inter-specific derivatives		
ICGV 87165, D 39d and B 37c	$LS_1 LS_1 LS_2 LS_2\ ls_3\ ls_3\ ls_4\ ls_4$	$R_1 R_1 R_2 R_2 r_3 r_3 r_4 r_4$

LS - Late leaf spot   R - Rust

4.5 Isozyme and protein variation

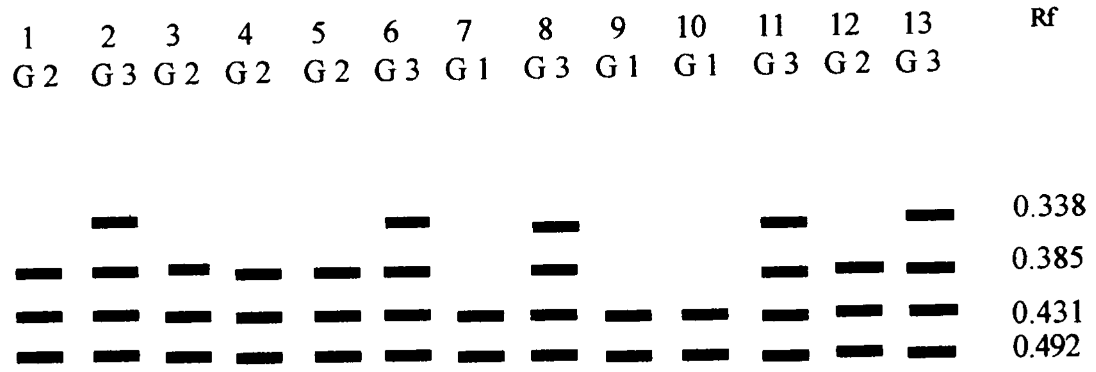
4.5.1 Isozyme profiles of genotypes

Of the four enzymes studied, only Glutamate Oxaloacetate Transaminase (GOT) was polymorphic. Catalase (CAT), Peroxidase (POX) and Super Oxide Dismutase (SOD) were monomorphic. The isozyme-banding pattern of GOT for 13 genotypes is presented in the form of zymograms (Figure 3). Four bands with Rf values 0.338, 0.385, 0.431 and 0.492 were observed. The third (Rf=0.431) and fourth (Rf=0.492) polymorphs were present in all the genotypes. The first two bands (Rf=0.338 and 0.385) displayed three patterns through their presence/absence. The pattern I (G 1) comprised of the genotypes JL 24, TMV 2 and Dh 8 having only two bands (3rd and 4th); the pattern II (G 2) with the genotypes VL 1, 28-2(S), D 39d, D 39d (S) and ICGV 86590 had three (2nd, 3rd and 4th) bands; and the Pattern III (G 3) consisted of mutant 28-2, B 37c, R 8808, TAG 24 and ICGV 87165 having all the four bands.

4.5.2 Protein profiles

Native total proteins of hypocotyl

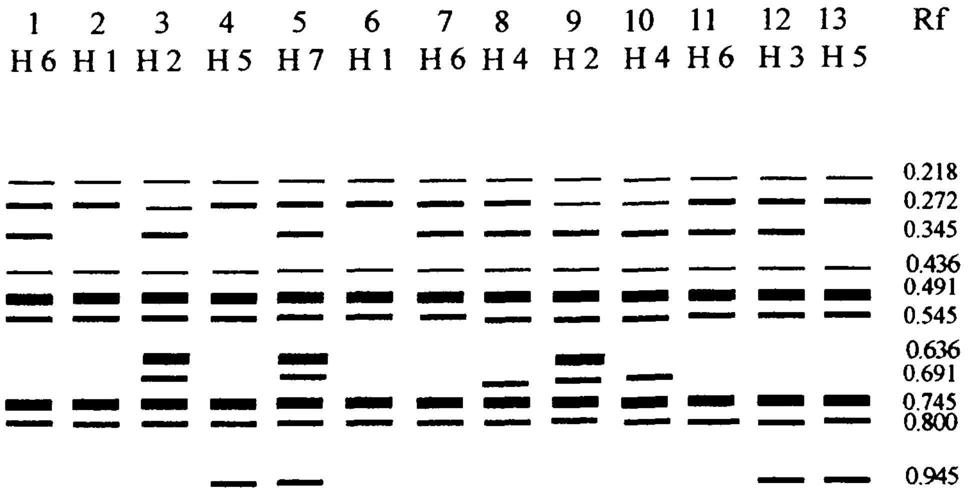
The native protein profiles of 13 genotypes are presented in the form of zymograms (Figure 4). A total of 11 bands with Rf value ranging from 0.218 to 0.945 were resolved. Of these four bands were polymorphic corresponding to Rf values 0.345, 0.636, 0.691 and 0.945. Based on presence or absence of these bands, seven electrophoretic phenotypes (H 1 - H 7) were identified.



G 1-G 3 - Electrophoretic phenotype for GOT Rf- Relative front value

1. VL 1 2. Mutant (28-2) 3. 28-2 (S) 4. D 39d 5. D 39d (S) 6. B 37c 7. Dh 8
8. R 8808 9. JL 24 10. TMV 2 11. TAG 24 12. ICGV 86590 13. ICGV 87165

Figure 3: Glutamate Oxaloacetate Transaminase (GOT) isozyme profiles of groundnut genotypes



H 1-H 7 - Electrophoretic phenotype for hypocotyl protein Rf - Relative front value

1. VL 1 2. Mutant (28-2) 3. 28-2 (S) 4. D 39d 5. D 39d (S) 6. B 37c
7. Dh 8 8. R 8808 9. JL 24 10. TMV 2 11. TAG 24 12. ICGV 86590
13. ICGV 87165

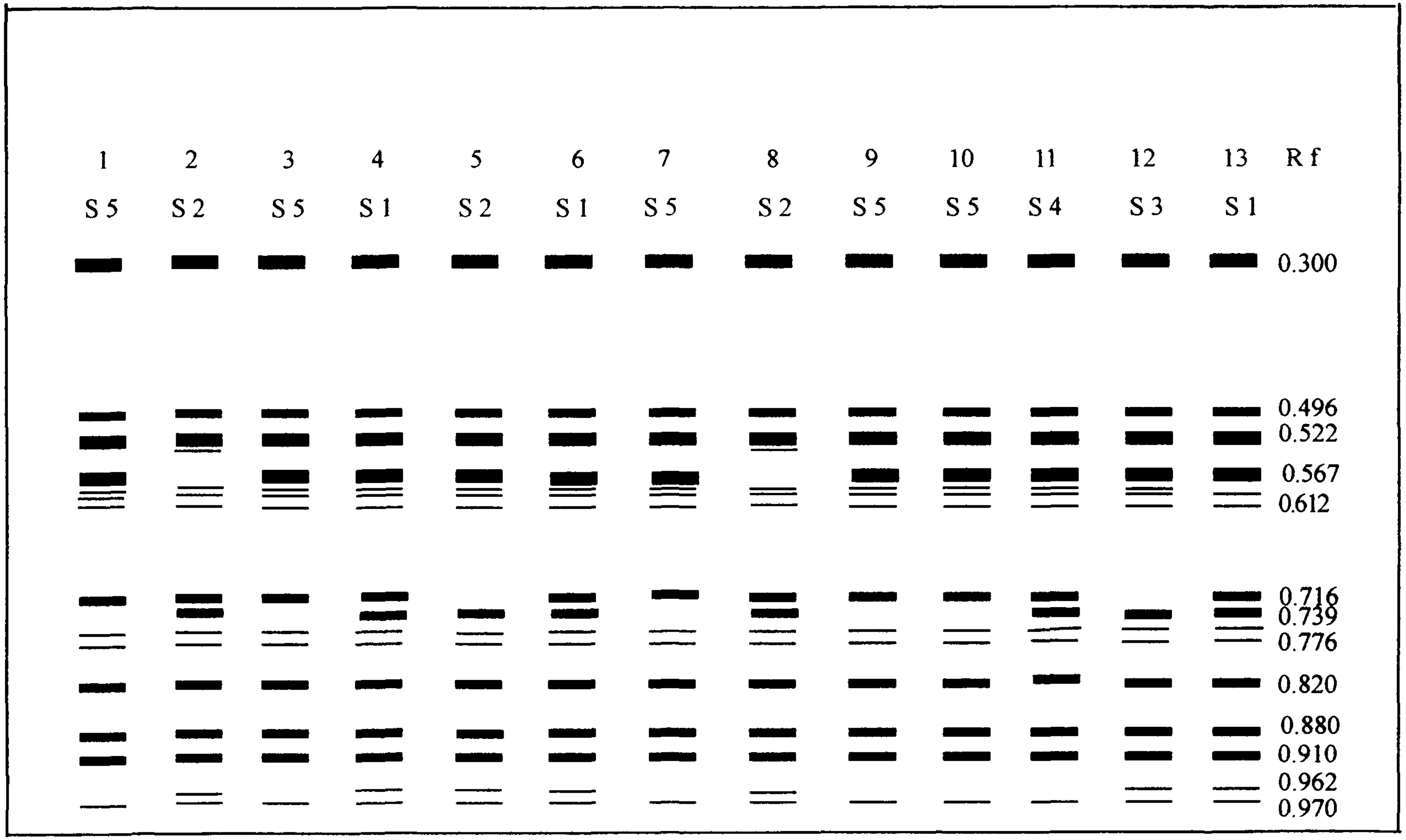
Figure 4: Hypocotyl protein profiles of groundnut genotypes

Electrophoretic Phenotype	Characteristics	Varieties
H 1	All the four polymorphic bands were absent	28-2 and B 37c
H 2	Out of the four polymorphic bands, only band of Rf value 0.436 was absent	28-2 (S) and JL 24
H 3	The bands of Rf value 0.636 and 0.691 were absent	ICGV 86590
H 4	The bands of Rf value 0.636 and 0.945 were absent	R 8808 and TMV 2
H 5	The bands of Rf value 0.345, 0.636 and 0.691 were absent	D 39d and ICGV 87165
H 6	The bands of Rf value 0.636, 0.691 and 0.945 were absent	VL 1, Dh 8 and TAG 24
H 7	All the four bands were present	D 39d (S)

Seed protein profiles

The seed protein profiles of 13 genotypes are presented as zymograms in Figure 5. A total of 17 bands were resolved in these genotypes with Rf values ranging from 0.300 to 0.970. Of these, five bands were polymorphic. These polymorphic bands corresponded to Rf values 0.529, 0.567, 0.716, 0.739 and 0.962. Based on these polymorphic bands, five electrophoretic phenotypes (S 1 - S 5) have been identified among the 13 genotypes.

Electrophoretic Phenotype	Characteristics	Varieties
S 1	Out of the five polymorphic bands, the band of Rf value 0.529 was absent	D 39d, B 37c and ICGV 87165
S 2	Out of 5 bands, only band of Rf value 0.567 was absent	28-2 and R 8808
S 3	The bands of Rf value 0.529 and 0.716 were absent	D 39d (S) and ICGV 86590
S 4	The bands of Rf value 0.529 and 0.962 were absent	TAG 24
S 5	The bands of Rf value 0.529, 0.739, and 0.962 were absent	VL 1, 28-2 (S), Dh 8, JL 24 and TMV 2



S 1 - S 5 Electrophoretic phonotype for seed protein Rf - Relative front value

1. VL 1 2. Mutant (28-2) 3. 28-2 (S) 4. D 39d 5. D 39d (S) 6. B 37c 7. Dh 8
8. R 8808 9. JL 24 10. TMV 2 11. TAG 24 12. ICGV 86590 13. ICGV 87165

Figure 5: Seed protein profiles of groudnut genotypes

4.5.3 Cultivar identification using Protein and GOT isozyme polymorphism

A total of five electrophoretic (S 1 - S 5) phenotypes were observed using denaturating electrophoresis of seed proteins and seven electrophoretic phenotypes (H 1 - H 7) were found using native PAGE of hypocotyl proteins. By combining both the seed and hypocotyl protein profiles, ten different groups have been identified. Three groups had two cultivars each (D 39d and ICGV 87165; VL 1 and Dh 8; 28-2 (S) and JL 24) with protein profiles; all the thirteen genotypes could be uniquely identified (Figure 6). The protein and GOT key for identification of the cultivars are as follows.

Electrophoretic phenotype	Genotype
S 1H 1G 3	B 37c
S 1H 5G 2	D 39d
S 1H 5G 3	ICGV 87165
S 2H 1G 3	28-2
S 2H 4G 3	R 8808
S 3H 3G 2	ICGV 86590
S 3H 7G 2	D 39d (S)
S 4H 6G 3	TAG 24
S 5H 2G 1	JL 24
S 5H 2G 2	28-2 (S)
S 5H 4G 1	TMV 2
S 5H 6G 1	Dh 8
S 5H 6G 2	VL 1

4.5.4 Isozyme variation in relation to resistance

The late leaf spot resistant mutants (28-2, 45 and 110), inter-specific derivatives (D 39d, B 37c, I 15e and ICGV 86699) and a germplasm line, ICG 2271 were studied along with their susceptible variants/counterparts for the oxidative enzymes viz., Peroxidase (POX), Catalase (CAT) and Super Oxide Dismutase (SOD) by native PAGE in the hypocotyl and/or leaf tissues. In the hypocotyl tissue, the resistant I 15e showed an additional band for all the three oxidative

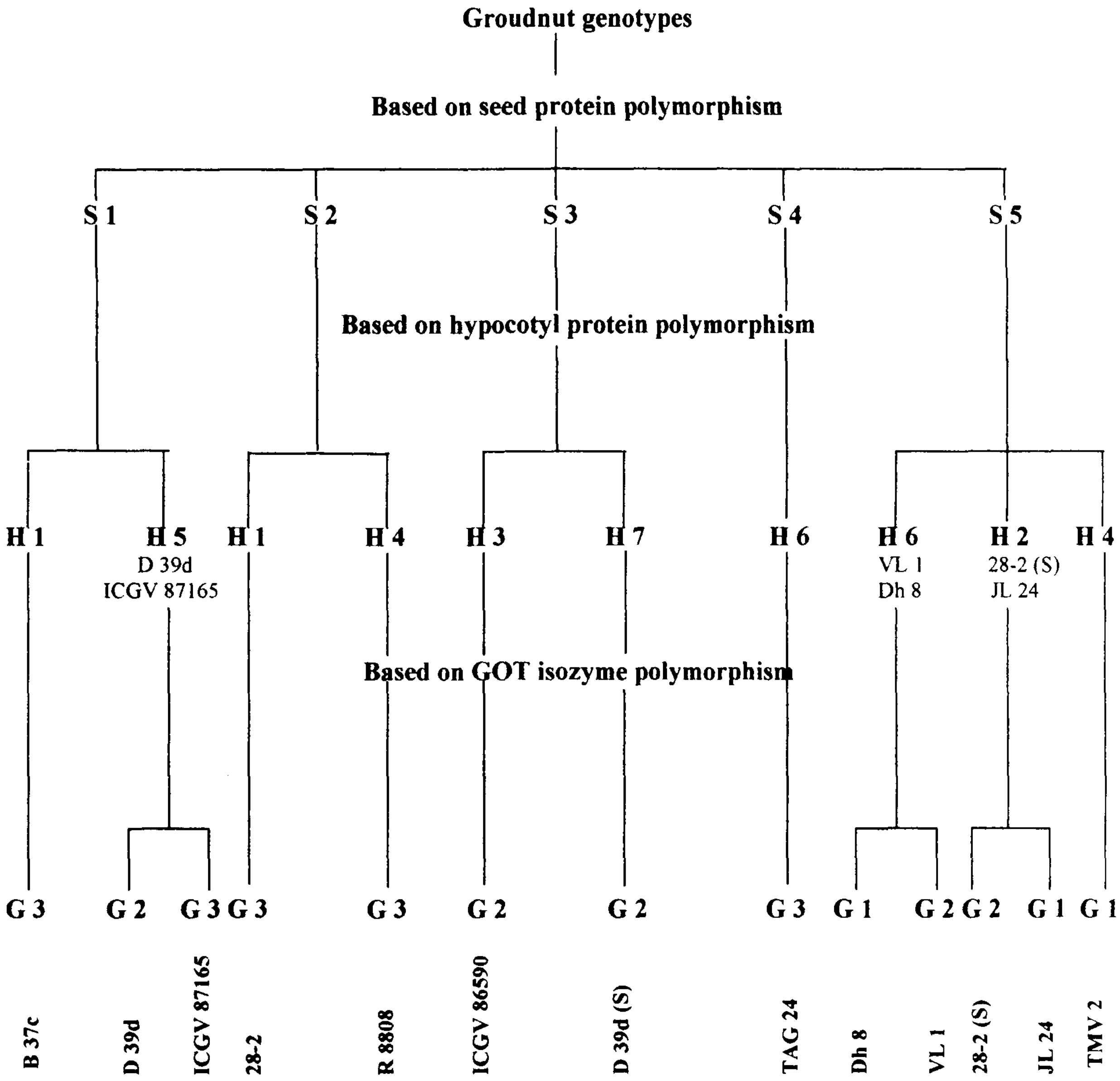


Figure 6: Individualization of groundnut genotypes based on seed and hypocotyl proteins and GOT isozyme polymorphism

enzymes as compared to its susceptible counterpart. While the other resistant genotypes showed either presence of an additional band or more intense bands for peroxidase as compared to their susceptible counterparts. A total of four peroxidase bands with Rf value 0.058 (POX 1), 0.116 (POX 2), 0.686 (POX 3) and 0.872 (POX 4) were observed. POX 4 was present in resistant mutants (45 and 110) and inter-specific derivative (ICGV 86699) and an advanced breeding line (ICG 2271) but was absent in their susceptible counterparts. Similarly, there was only intensity variation in POX 2 band in these genotypes. However, POX 3 was present only in I 15e resistant genotype but absent in its susceptible counterpart and other genotypes (Figure 7). Super oxide dismutase profile had only two bands of Rf value 0.757 (SOD 1) and 0.909 (SOD 2), SOD 1 is polymorphic only in I 15e genotype i.e. present in resistant and absent in susceptible counterpart (Figure 8).

The resistant mutant VL 1-45 and inter-specific derivative, D 39d showed inducible and constitutive expression, respectively when analyzed for peroxidase in the leaf tissue challenged with late leaf spot pathogen (Table 50).

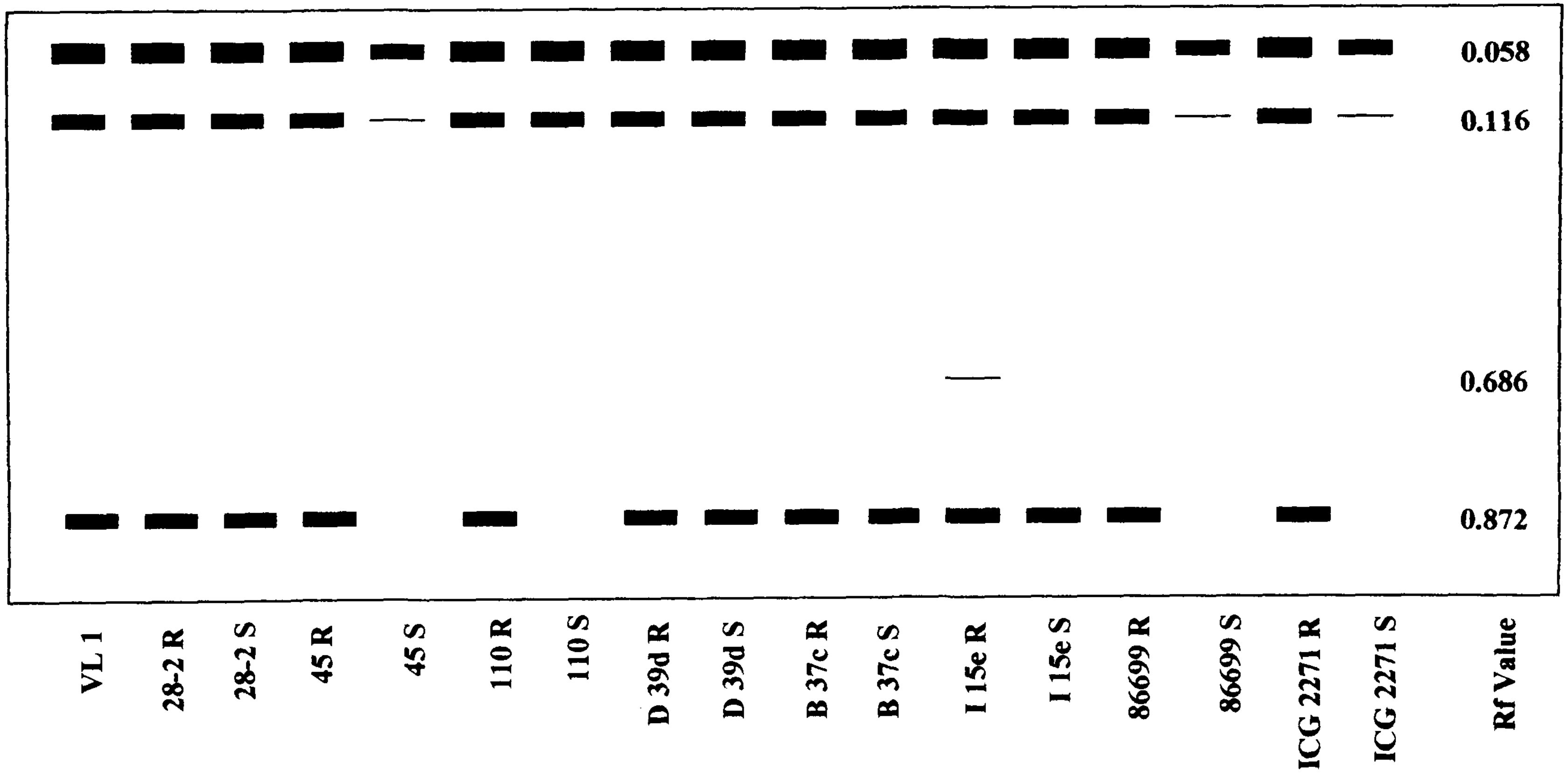


Figure 7:Hypocotyl peroxidase (POX) isozyme profile of groundnut genotypes

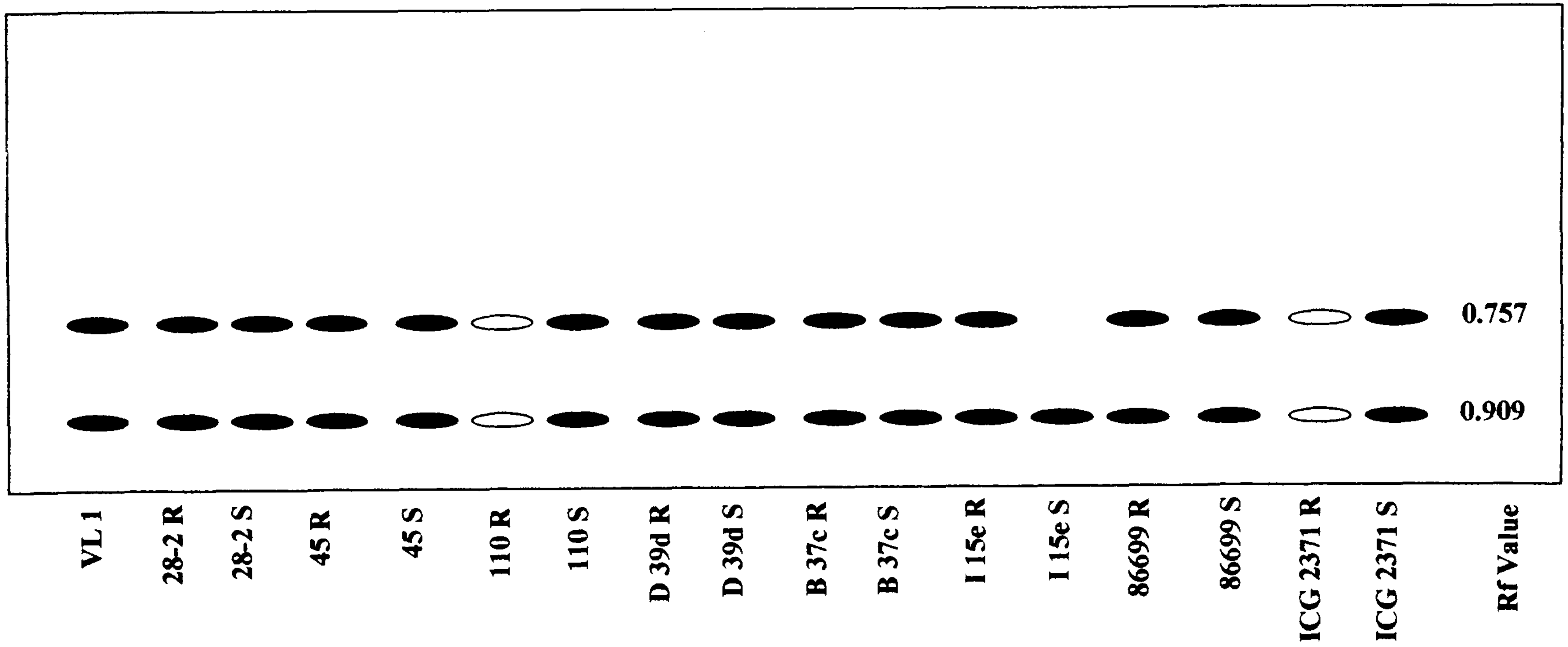


Figure 8: Hypocotyl super oxide dismutase (SOD) isozyme profile of groundnut genotypes

Table 50: Response of groundnut genotypes for peroxidase (POX) in leaf tissue (45 days after sowing) challenged with late leaf spot pathogen

Genotype	Intensity of POX band	
	Unchallenged	Challenged
VL 1	+	+
45	+	+++
45 (S)	++	+
D 39d	++	++
D 39d (S)	+	+
KRG 1	+	+

+ indicate intensity of peroxidase band

DISCUSSION

V. DISCUSSION

The role of diseases in reducing agricultural production was evident even at the beginning of modern agriculture and ever since there has been efforts to reduce the loss, both in quantitative and qualitative terms. Rust and late leaf spot are the most serious fungal diseases of groundnut worldwide (Subrahmanyam *et al.,* 1985; McDonald *et al.,* 1985). Yield losses are generally substantial when the crop is attacked by rust and late leafspot together (Subrahmanyam *et al.,* 1984). Efforts to breed varieties with multiple disease resistance is an important focus on research. Such varieties could greatly increase yield stability and contribute to the sustainability of cropping systems under various conditions.

Screening of large number of accessions led to the identification of genotypes with resistance to late leaf spot and/or rust. Most of these resistance sources are landraces belonging 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. They have poor agronomic features viz., low shelling out-turn, thick pod shells, high reticulation and unacceptable seed coat colours (Subrahmanyam *et al.*, 1989). However, this germplasm was poorly understood and least used in improvement programs. Only two disease resistant parents (NC Ac 17090 and PI 259747) appear in the parentage of cultivars released in India (Nigam, 2000). A cursory analysis of improved groundnut cultivars revealed that, out of 100 varieties released so far in the country, only Girnar 1, ICG (FDRS) 4, ICG (FDRS) 10 and ICGV 86590 are resistant to foliar diseases. However, these cultivars suffer from inferior agronomic traits such as low shelling out-turn, long duration and poor pod shape. Because of this, and in spite of their higher pod yield under disease epidemic conditions, these cultivars have not been popular with the farmers (Nigam, 2000).

Spanish bunch cultivars are most popular in India as they mature early and facilitate double cropping under rainfed conditions besides possessing desirable pod and kernel features. But, they are highly susceptible to foliar diseases and suffer heavy losses under diseased condition (Hegde *et al.,* 1995a). Nevertheless, some other sources of resistance identified later in accessions that originate from secondary centers of diversity in south America i.e. Peru, Ecuador and Bolivia, and inter-specific derivatives bred after incorporating genes that confer resistance from such wild species *A. cardenasii, A. batizocoi, A. duranensis* have high levels of resistance in diverse botanical backgrounds, good agronomic potential and resistance to other biotic stresses. The use of such sources should help in developing lines with high levels of resistance in good agronomic backgrounds, and to overcome the limitations of previously used sources (Singh *et al.*, 1997). This also emphasizes the need for evaluation of additional germplasm. Identification of new sources of resistance in Spanish types is of greater significance in maintaining superior agronomic traits of Spanish types (Mehan *et al.,* 1996). Induced mutagenesis and extensive hybridization with inter-specific derivatives were sought as an alternative approach to generate material combining desirable agronomic characters with disease resistance and high productivity.

The present investigation was undertaken to assess the variation in germplasm for resistance to late leaf spot and rust, diversity in foliar disease resistant mutants, genotypic responses for yield and quality in relation to resistance, genetic and biochemical analyses of resistance. The results are discussed here under.

5.1 Current germplasm status for resistance to late leaf spot and rust

A total of forty-five groundnut germplasm comprising of inter-specific derivatives (9), advanced breeding lines (22), mutants (4) and ruling cultivars (10), and fifty-five genotypes developed at Bhabha Atomic Research Centre, Trombay, Mumbai were assessed for reaction to late leaf spot and rust in two (*Kharif* and summer) seasons.

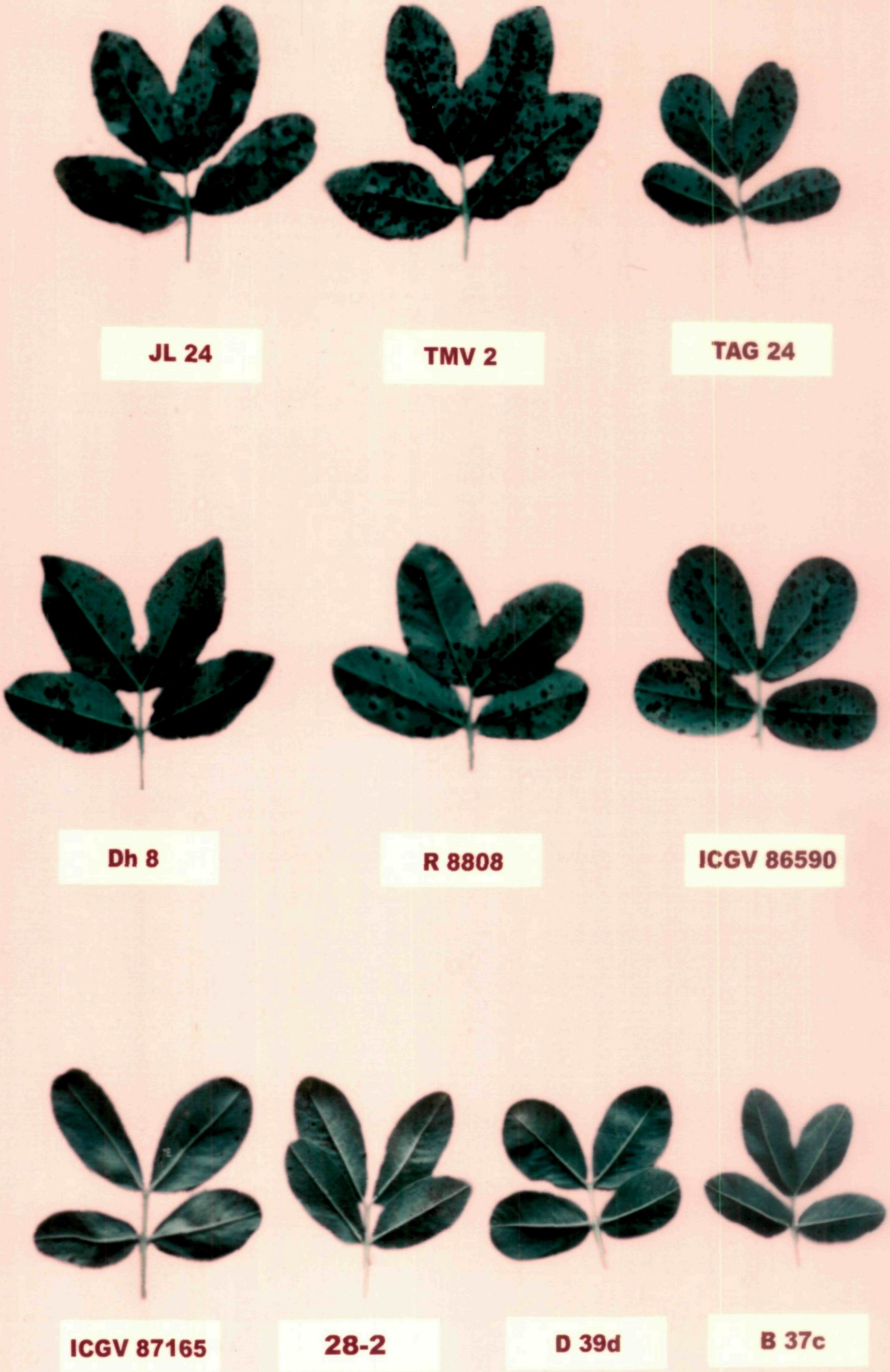
Pooled analysis of variance revealed highly significant variation for season, genotype and their interactions for all the parameters except lesion size and field disease score of late leaf spot in germplasm and days to maturity in the Trombay genotypes indicating the need for screening the germplasm over seasons (Tables 12 and 17). Most of the resistance sources, when tested over seasons were generally stable with some occasional minor changes in their relative disease scores. Such variation probably reflects differences in the time of onset of disease, inoculum pressure and environmental conditions prevailing in the season rather than differences in the pathogen or genotypes (Singh *et al.*, 1997). However, the incidence of late leaf spot was more during *Kharif* and that of rust in summer.

The effective selection for disease resistance can be practiced if the variability available in the germplasm is wider, and the heritability and genetic advances are more for components of resistance. In addition, if components have a strong positive association, the selection for one component could be expected to advance the other (Chiteka *et al.*, 1988). Field disease score of late leaf spot and rust had low coefficient of variation, heritability and genetic advance than components revealing the need to look at the components. Components of late leaf spot viz., lesions on mainstem and petiole, and rust, viz., incubation period and pustule number in germplasm; and incubation period, lesion size and lesions on mainstem (Late leaf spot), and incubation and latent periods (Rust) in Trombay genotypes had high heritability, genetic advance and coefficient of variation compared to the field disease score, defoliation and remaining green leaf area (Tables 13 and 18). These components had strong association with field disease score, defoliation and remaining green leaf area (Tables 15 and 19) implying the utility of any of these components in assessing genotypes for foliar disease resistance. The results are in agreement with Motagi *et al.* (1996a) who reported strong association of area under disease progress curve, an overall indicator of disease resistance with per cent necrotic leaf area, defoliation and remaining green leaf area easily scoreable at early stage and components of late leaf spot (lesion number, lesion size, lesions on mainstem and petiole) scored at/before harvest and suggested their utility in evaluation of induced mutants.

Remaining green leaf area, an integrated measure of defoliation and leaf area affected by both late leaf spot and rust diseases, had strong association with all the components of late leaf spot and rust and all the components were significantly associated with each other perhaps indicating their common genetic control. Remaining green leaf area and defoliation had high magnitude of association with components of late leaf spot than rust revealing the importance of late leaf spot as defoliating disease. Late leaf spot cause damage mainly by defoliation and reduction in healthy leaf area, while rust damage was attributed to different mechanism other than reduction in leaf area (Savary and Zadoks, 1992). These results are in confirmation with Nevill (1981) who reported a high correlation among components of resistance and proposed a similar polygenic system acting to control the expression of all the components.

Association of maturity with components of late leaf spot and rust indicated the late maturity of most of the resistance sources in germplasm. There are several reports in the country and abroad indicated the strong negative association of disease resistance with desirable agronomic attributes (Arulshekar, 1972; Hammons, 1981; Williams *et al.,* 1987; Gowda *et al.,* 1996). Stalker *et al.* (1979) reported linkage of several undesirable characters viz., late maturity, small seeds and low yield with leaf spot resistance. Miller and Norden (1980) found negative association of resistance to late leaf spot with yield and early maturity. On the contrary, Iroume and Knauft (1987) observed negative correlation between yield and leaf spot severity in advanced breeding lines. Motagi *et al.* (1997) reported negative association of late leaf spot severity with productivity indicating desirable association of resistance with yield in Spanish bunch resistant mutants.

All the inter-specific derivatives were resistant to late leaf spot and rust but matured late (except D 39d and B 37c) than ruling cultivars. Most of the advanced breeding lines (55 %) were rust resistant. Mutants were either resistant to rust (25 %) or late leaf spot (75 %) with early maturity. Ruling cultivars were early maturing but highly susceptible to late leaf spot and rust (Plate 2 and Figure 9), except ICGV 86590, which was rust resistant but matured late (Table 10). Mutants (28-2, 45 and 110) and cross derivatives (D 39d and B 37c) had desirable combination of foliar disease resistance, early maturity, acceptable pod and kernel features with high yield and are proved to be superior over existing resistant germplasm (Patil, 1996;



JL 24

TMV 2

TAG 24

Dh 8

R 8808

ICGV 86590

ICGV 87165

28-2

D 39d

B 37c

Plate 2: Genotypic differences for late leaf spot development

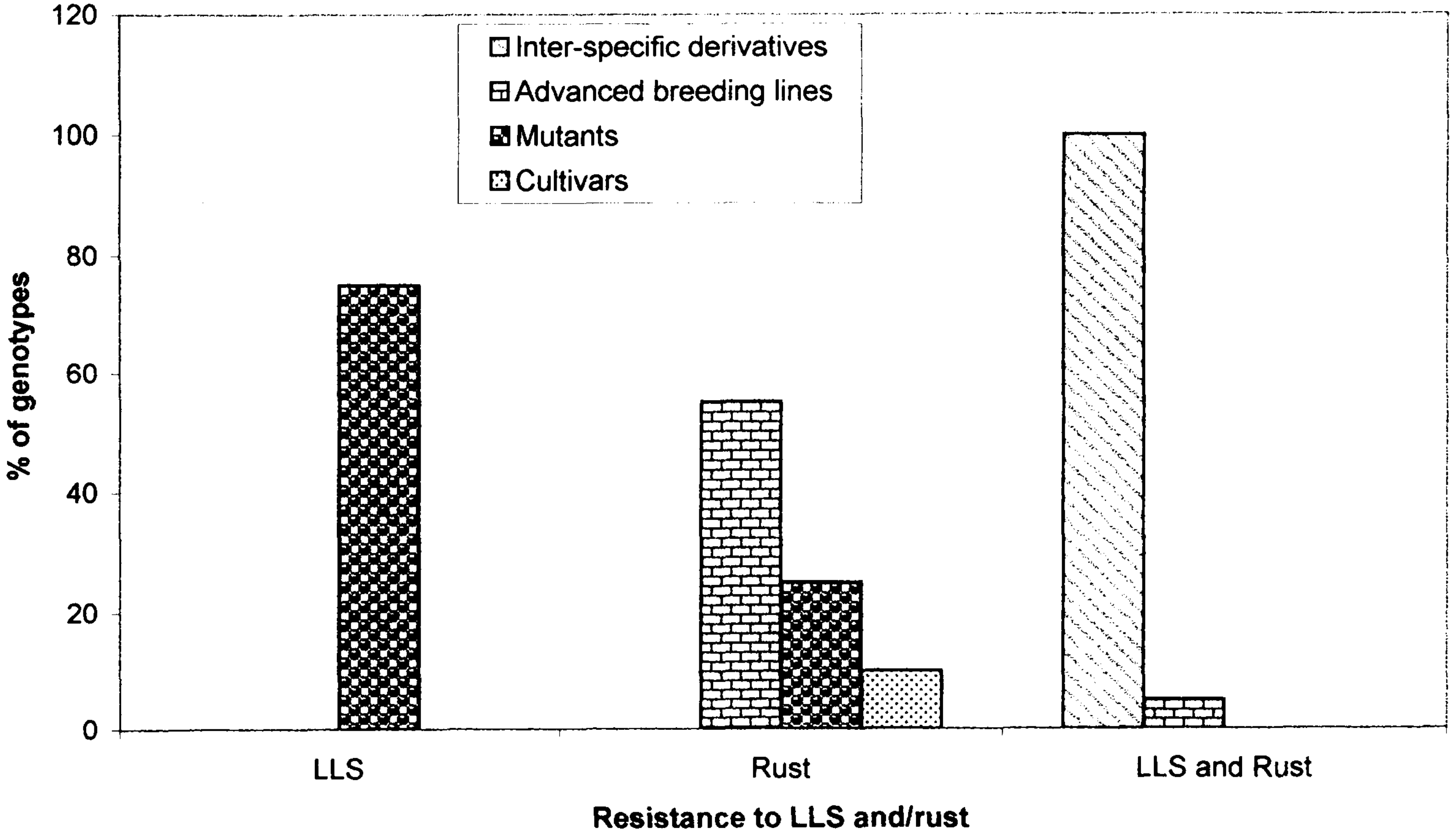


Figure 9: Pattern of distribution of late leaf spot and rust resistance in different categories of groundnut germplasm

Gowda *et al.*, unpublished data) they could be profitably utilized in resistance breeding to improve Spanish bunch groundnuts.

A cursory analysis of pedigree of resistant genotypes indicated that late leaf spot and rust resistant inter-specific derivatives viz., ICGV 86699 (CS 29), ICGV 87165 (CS 9), and ICGV 93023 shared wild species viz., *A duranensis, A batizocoi* and *A cardenasii* which were highly resistant/immune to late leaf spot and rust, as one of their parents (Table 7). Cross derivatives viz., D 39d and B 37c had inter-specific derivatives, CS 16 (Plate 6) and CS 9 as their parents respectively. Late leaf spot and rust resistance in advanced breeding lines ICGV 87624 and ICGV 96266 traced back to NC AC 17133 RF; ICGV 86577 and ICGV 86594 in their pedigree. Similarly, rust resistance in ICGV 96266 and R 8972 to NC Ac 2232 and NC Ac 2240, respectively. Rust resistant cultivar ICGV 86590 had PI 259747 as its parent. PI 259747 and NC Ac 17133 RF were found to be good combiner for late leaf spot and/or rust resistance (Tiwari *et al.,* 1984; Anderson *et al.,* 1990b). Late leaf spot (28-2, 45 and 110) resistance in the mutants was due to elimination of suppressor through EMS mutagenesis in original parent DER and gain of function mutation in VL 1 (Motagi *et al.*, 2000b).

Although late leaf spot resistance is predominantly governed by additive gene action, the very low to medium heritability levels render this character relatively difficult to select in early generations. Moreover, presence of an unspecified number of modifier genes and linkage of resistance with undesirable features makes the task of breeding late leaf spot resistant cultivars difficult (Reddy and Murthy, 1994). On the contrary, rust resistance has high heritability with considerable additive component, it is possible to select for rust resistance in early segregating generations (Reddy and Murthy, 1994).

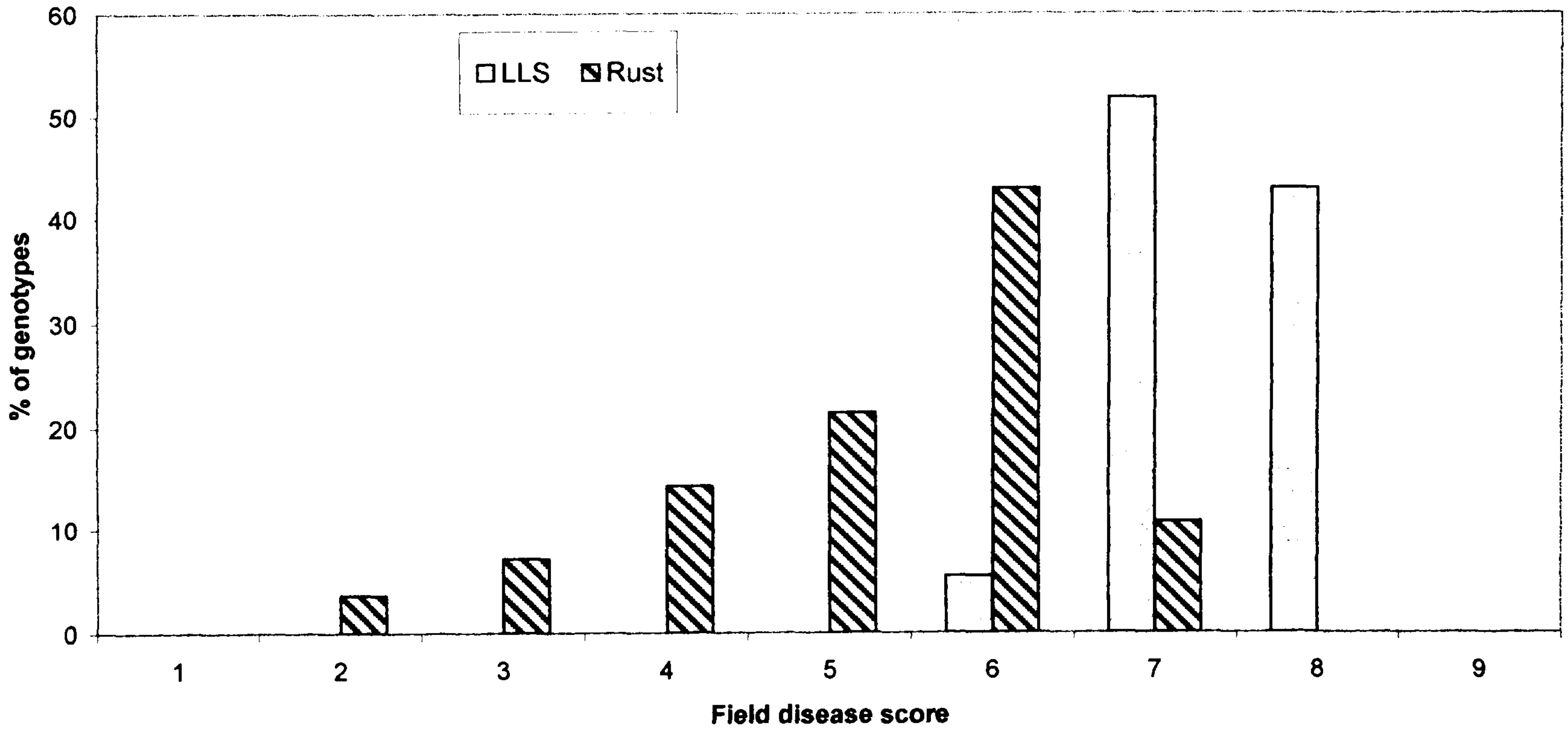
Most of the landraces/advanced breeding lines were rust resistant but had less tolerance to late leaf spot. Early maturing *fastigiata* mutants comprised new source of late leaf spot resistance but they lacked rust resistance. Inter-specific derivatives even though highly resistant to late leaf spot and rust had undesirable features like late maturity and poor agronomic attributes (Reddy *et al.*, 1991; Gowda *et al.*, 1995a). Late leaf spot and/or rust resistant mutants, landraces and inter-specific derivatives should be exploited to diversify the resistance sources. Wild *Arachis* species, which are not only excellent sources of resistance but they also, provide 'new' genes for yield and yield related attributes (Guok *et al.*, 1986; Halward *et al.*, 1991b). Recurrent selection program in inter-specific population resulted in significant improvement in pod yield (Stalker and Moss, 1987). Introgression of both the genomes of groundnut could be the reason for high levels of resistance found in selected inter-specific derivatives (Garcia and Stalker, 1995). Alternatively, high levels of resistance could result from the change of gene expression in new genetic background (Smartt *et al.*, 1978). Inter-specific derivatives that have recorded field disease score of 3.0 - 5.0 for resistance to both late leaf spot and rust in good agronomic backgrounds are rich sources of resistance to foliar diseases. The presence of high level of resistance in these sources, suggests that their use in breeding programmes would reduce the "dilution effect" on resistance in populations selected for high yield potential and agronomic quality. Cross derivatives D 39d and B 37c, which are products of second cycle of mating from inter-specific derivatives, had desirable combination of early maturity, pod and kernel features, and foliar disease resistance besides high yield in Spanish background. From this discussion, it can be concluded that extensive hybridization programmes involving ruling but susceptible Spanish bunch cultivars and inter-specific derivatives as parents in cycles of mating could be advantageously utilized to generate desirable types.

The Trombay genotypes had low resistance at field level but there was large variation in some of the components of resistance. Based on lower values for field disease score and other disease components, Spanish Improved, Somnath, TG 33 and TG 38D were superior for late leaf spot and rust; TG 20, TG 32, TG 35, TG 36B, TG 37D and TGE 2 for late leaf spot and TG 3, TG 4, TG 37F, TG 38A, TG 38B and TG 38C for rust compared to susceptible check JL 24 (Tables 18 and 20). The genotypes TG 32 followed by TG 20, TG 36B and Spanish Improved had highest remaining green leaf area at harvest. Pedigree analysis of Trombay genotypes (Table 8) revealed that, the genotypes TG 38A, TG 38B, TG 38C, TG 38D and TG 33 had Girnar 1 as one of their parents, which was late leaf spot/rust resistant cultivar released in India. Girnar 1 had NC Ac 17090, a rust resistant Valencia land race as its parent. Somnath had Mungfali 13 (M 13), a Virginia runner tolerant to late leaf spot with waxy leaves, which was inturn selection from NC 13. Other superior genotypes especially TG 20 and TG 35 either had Spanish Improved or TG 26 as one of their parents, which had least defoliation due to disease.

A perfect blend of mutagenesis and hybridization of mutants has. been used in the genetic improvement of groundnut by the scientists at Bhabha Atomic Research Centre through which a series of cultivars have been released. These cultivars with novel plant types are very popular among farmers in different states of the country because of their high productivity, early maturity, bold kernels, high harvest index and fresh seed dormancy (Kale *et al.*, 2000), but most of them are highly susceptible to late leaf spot. Nonetheless, there was lot of variation in components like defoliation, lesion size and lesions on mainstem that could be exploited in future breeding. Incidence of stem lesions caused by late leaf spot may be useful as new parameter to be considered in evaluation and selection for resistance and/or tolerance to late leaf spot (Culbreath *et al.*, 1991). The frequency of genotypes superior for late leaf spot (5.4 %) was very low compared to rust (46 %) indicating the scope for selecting genotypes resistant to rust (Figure 10). The extent of resistance in the Trombay mutants and mutant derivatives was very low compared to resistant check revealing the need for accumulation of resistance retaining optimum agronomic features in future breeding programs.

5.2 Diversity in foliar disease resistant mutants

Cultivated groundnut germplasm shows limited genetic variability for many important characteristics. This has led to the exploration of different methods for improving variability including induced mutagenesis. At the University of Agricultural Sciences, Dharwad mutagenesis with ethyl methane sulfonate (EMS) of Dharwad Early Runner (DER) resulted in early maturing and erect



Fifure 10: Frequency distribution of Trombay groundnuts for resistance to late leaf spot (LLS) and rust

bunch mutants (Nadaf, 1993). On subsequent mutagenesis with EMS, mutant 1 (VL 1) yielded 18 mutants (6.3 X 10^{-2} on M_2 family basis) with wide spectrum of variability for foliar disease resistance and other morphological traits (Sheshagiri, 1994). In the present study, VL 1 and its mutants were evaluated for morphological and productivity parameters in relation to late leafspot and/or rust resistance to gain insight into the nature of origin and genetic diversity. Foliar disease resistant mutants and their susceptible variants were also used in crossing programmes in order to discern the genetic basis of late leaf spot and rust resistance and to test for allelism with resistant inter-specific derivatives, which will be discussed in section 5.4.

Analysis of variance for morphological, productivity and disease resistance parameters revealed significant variation for all the parameters in the induced mutants. Diversity analysis grouped the 18 mutants into three clusters (Tables 21 and 22a). Cluster I comprised of nine mutants resistant to rust but susceptible to late leaf spot and VL 1 parent. Cluster II included five mutants highly resistant to late leaf spot but susceptible to rust. Four mutants with moderate resistance to late leaf spot and rust were clustered separately (Cluster III). Cluster II was equidistant from cluster III and I. While cluster III and I were more closely related (Table 21). Although, all the mutants originated from the same source (VL 1) their grouping into three different clusters indicated wide genetic variability induced through mutagenesis, which is comparable to the working germplasm reserves maintained by the breeders. Gowda *et al.* (1995b) isolated very high frequency of mutants resembling all four botanical types through EMS mutagenesis of DER, which confirmed the importance of mutations in creating genetic diversity.

Late leaf spot resistance was strongly associated with rust susceptibility and its strong association was also observed with increased number of primary and secondary branches, hundred seed mass, pod yield and reduced leaflet length and width. In contrast, an opposite trend in interrelationship was evident with rust resistance revealing distinct nature of rust and late leaf spot resistant mutants (Table 22a and b). Most of the resistant mutants were *fastigiata* types. The majority of rust and late leaf spot resistant peanuts in the germplasm collections are primitive *fastigiata* (Valencia) types originating from Peru. Such types have been under cultivation since about 200 B.C. Human selection following spontaneous mutation was earlier thought to be responsible for the evolution of resistance (Subrahmanyam *et al.*, 1989). The present study also gives the credence to such hypothesis. The mutants genetically differed from VL 1 parent for various disease resistance, morphological and productivity parameters. The changes in many but same set of characters leading to phenotypic syndromes are often implicated in mutations at regulatory loci. Regulatory mutations generally were assumed to have large phenotypic effects. The shifts in many characters in mutants could also be due to pleiotropic nature of resistant genes (Gowda *et al.*, 2000).

The mutants VL 1 (from DER), VL 1-28-2, 45 and 110 (from VL 1) were all recovered as homozygous mutations with changes in as many as 8-10 characters (Plate 3) viz., growth habit, leaf shape and color, number of primaries and secondaries, pod features besides,

DER → **VL 1** → **28-2**

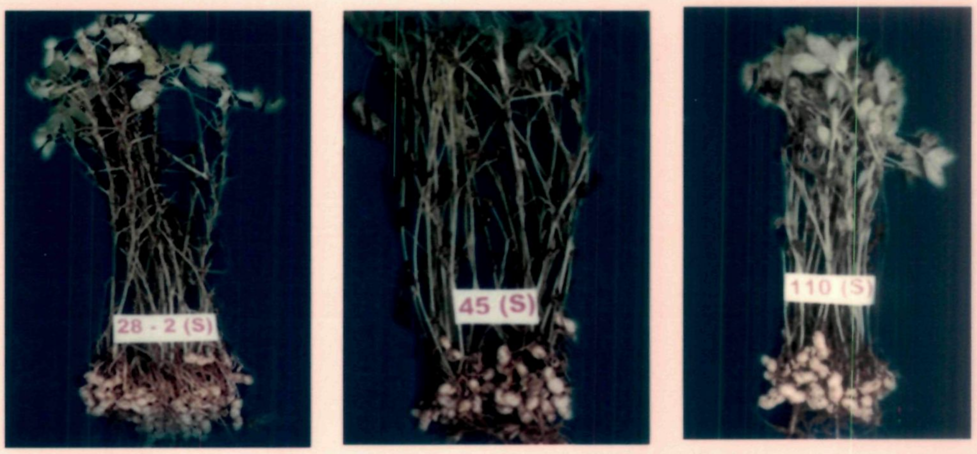
Susceptible to rust and LLS

Resistant to rust

Resistant to LLS

Resistant to late leaf spot

↓ ↓ ↓



Susceptible to late leaf spot

Plate 3: Mutants resistant to foliar diseases

resistance to rust, late leaf spot, *Spodoptera* and *Sclerotium* damage (Motagi *et al.,* 1996b; Gowda *et al.,* 2000; Rajendraprasad *et al.,* 2000; Sheshagiri, 2000). The unusual features like high frequency of mutations and reversions, non-random mutations, segregation distortions, somatic mutations, multiple character mutations, multiple alternate forms, homozygous mutations and mutation outbursts were associated with these mutants (Gowda *et al.*, 1995b). These unusual features indicate the role of non-Mendelian genomic turnover mechanisms as the possible modulators (Rasmusson and Phillips, 1997) in generating the mutants. Various stresses to genome like EMS treatment in the present study could activate such genetic mechanisms (McClintock, 1984). Resistant genes often occur in clusters and evolve rapidly through duplication and diversification (Ronald, 1998). Recombinogenic events viz., unequal crossing over, gene conversion, intra-genic recombination, besides transpositions were the great prime movers in generating both spontaneous and induced variation in resistance genes (Hulbert, 1998). EMS with its effect on base pairing could have lead to mispairing driven recombination in resistance genes.

In the present investigation, number of susceptible counterparts from late leaf spot and/or rust resistant mutants (28-2, 45 and110; Plate 3), inter-specific derivatives (D 39d, B 37c, I 15e and ICGV 86699) and an advanced breeding line (ICG 2271) were isolated. Detailed analysis of these along with their resistant counterparts revealed that they differ mainly for late leaf spot and not for rust. The resistant types had very high remaining green leaf area but matured late (Tables 23 and 24).

The material forms an additional source to investigate the mechanisms of their occurrence, genetic basis of late leaf spot resistance since many of them differ only for resistance and some associated with other characters and are cogenic. Mutagenesis constitutes an important approach to gain insight into the resistance genes. Two complementary genetic approaches viz., mutagenesis of homozygous *R* gene-containing plant genotypes to identify susceptible mutants and the identification of plant mutations that abolish specific defense-related events have been extensively used. Although some mutations will lie in the *R* gene itself, others may define additional genes (non *R*-genes) whose products function in resistance. Most genes whose products are required for resistance are also essential at certain times in development (Li and Chory, 1997). Indeed, second-site mutations that disrupt resistance to various pathogens have been identified in several crops including barley (Torp and Jorgensen, 1986; Jorgensen, 1988). The *ror1* and *ror2* mutations affect the function of the recessive resistant *mlo* gene in barley which mediates resistance to all powdery mildew isolates (Freialdenhouen *et al.*, 1996). They compromise the induction of several classes of PR proteins in Mla_{12} mediated resistance. Clearly these second-site mutations provide powerful tools for defining steps in the resistance process in order to separate the different defense-related responses and to define distinct signal transduction pathways.

5.3 Agronomic performance in relation to resistance

A total of ten genotypes comprising of late leaf spot and rust resistant inter-specific derivatives (D 39d and B 37c and ICGV 87165), late leaf spot resistant mutant (28-2), ruling but susceptible cultivars (JL 24, TMV 2 and TAG 24), rust resistant cultivar (ICGV 86590) and moderately susceptible cultivars, viz., Dh 8 (late leaf spot) and R 8808 (rust) were evaluated in early and late sown experiments, under diseased (UP) and fungicide sprayed (P) conditions during *Kharif*, 1998, for disease severity, productivity (yield/yield components and their losses) and physiological parameters to gain insight into their interrelationships for designing sound breeding strategies.

The results of the analysis of variance for yield/yield components and their losses showed that treatment and genotypic effects were significant for all the parameters (Table 25). All the interaction effects involving genotypes were significant indicating the major role of genotypes than dates of sowing and disease control. The variation among the genotypes in unprotected condition was more compared to that of protected. This can be attributed to the differences among the genotypes for disease resistance (Plates 4 and 6), in addition to the variation in yield potential. Pooled analysis of variance for yield, disease and physiological parameters indicated significant genotypic and interaction effects (dates of sowing × genotype) for all the parameters implying the differential response of genotypes to sowing dates (Table 26a and b). The material and experiments (early and late sowings) were appropriate to investigate the disease and yield interrelations.

Yield and yield loss in relation to resistance

The research in breeding aims at evolving varieties with resistance to diseases and tolerance to yield reduction, besides high yield potential. But often, resistant genotypes have low yield potential and suffer significant yield loss under disease, and differ in yield loss even at the same level of disease. This could be due to complex interrelationships between diseases and yield loss. Crop loss models are eminently suitable to gain insight into these relations and to plan sound strategies in resistance breeding.

Different empirical models were tested for their explanatory value for yield loss in ten genotypes with varying levels of resistance to

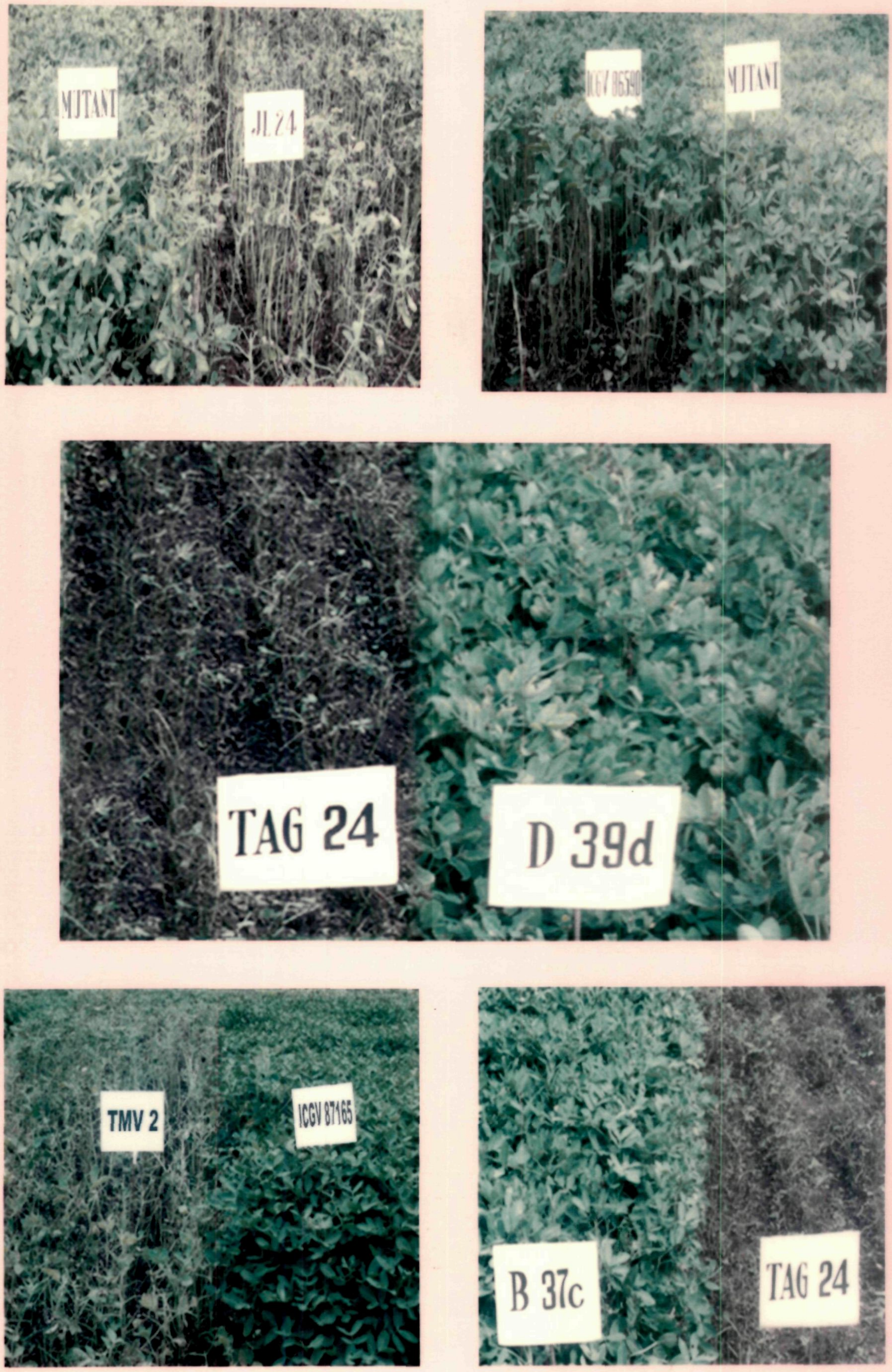


Plate 4: Genotypic differences in disease development at 90 DAS (Field view)

late leaf spot and/or rust (Chandran, 2000). Single point models based on disease did not explain the variation in loss completely, but revealed disease severity at 85 - 95 days after sowing as the critical stage in determining yield loss. This coincides with the pod filling, which was most susceptible stage to late leaf spot and rust (Reddy *et al.*, 2000). Inclusion of physiological traits in stepwise regression models improved the R^2 considerably, revealing their relevance to yield loss.

Based on the results of regression models, disease (disease severity and area under disease progress curve) and physiological (harvest index, reproductive efficiency measures, leaf area index, healthy leaf area duration, vegetative, crop and pod growth rates and partitioning coefficient) parameters were selected to assess their association/effect on yield/yield loss using correlation and path analysis (Tables 27-29) in early and late sown experiments separately and together (pooled analysis).

Strong association and high direct effects of disease parameters in early sown experiment; both disease and physiological parameters in late sown and pooled analysis explained most of the yield and yield loss variation. Therefore, selection for these characters in a breeding program is more realistic in reducing loss due to diseases. Higher disease severity in late sown trial resulted in significance of physiological parameters in effecting yield loss over disease parameters. In the early disease epidemic situation and unstable epidemic rates between growth stages, parameters other than disease are known to become important in determining yield/yield loss (Teng and Johnson, 1988). Yield potential of groundnut genotypes can be expected to vary according to how favorably their physiological growth traits complement the degree of resistance they possess. The physiological conditions determine the resistance reaction to disease at the time of infection and also the yield accumulation behaviour. The physiological characters included in the models deserve consideration in crop improvement programmes, to develop varieties with stability in yield performance.

Performance of genotypes

Disease severity in late sown trial was high compared to early sown trial in almost all the genotypes even at 45 days after sowing (Plate 5b) indicating the early onset of disease due to availability of inoculum from the early sown experiment (Table 30 and Appendix 8). These observations are in agreement with earlier studies (Chevageon, 1953; Lewin *et al.*, 1973; Shokes *et al.*, 1983; Gupta, 1985; Astaputre *et al.*, 1994; Naidu and Chandrika, 1997) showing higher incidence of late leaf spot and rust due to congenial conditions for disease development prevailed in delayed sowings. Late *Kharif* sowing could be utilized for screening germplasm for disease resistance.

All the genotypes had higher yield (pod, kernel, oil and fodder yield) and yield components (shelling out-turn, sound mature kernel per cent, hundred seed mass and oil content) under early sown experiment compared to late sown experiment and were still high in

Determinate **Indeterminate** **Indeterminate** **Determinate**

Plate 5a: Leaf growth differences in susceptible genotypes

Plate 5b: Genotypic differences in disease development at 45 DAS in late sown experiment

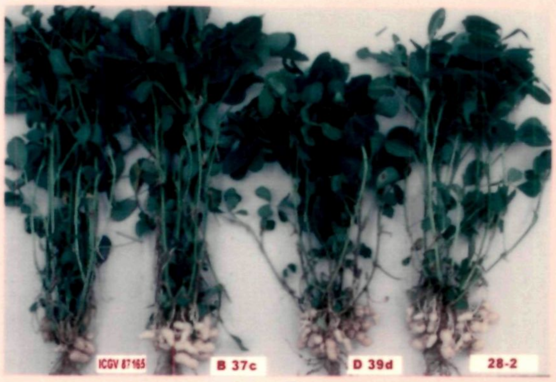
fungicide sprayed condition (Tables 31 and 32, and Appendices 9 - 12). Lower yields in late sown experiment might be due to higher disease severity; shorter growth period and also the unfavorable climatic conditions prevailed during the late sown experiment. Similar results were reported by Nath and Kulkarni (1967), Shokes *et al.* (1983), Astaputre *et al.* (1994), Naidu and Chandrika (1997), and Hazarika *et al.* (2000). Therefore, early sowing gives better yields than late sowing.

The pod yield reduction in early sown experiment ranged from 11.2 to 42.3 per cent. Reduction in kernel (11.8 - 51.6 %) and oil (14.8 - 52.0 %) yield was slightly more. This can be attributed to the reduction in shelling out-turn and oil content due to disease in addition to loss in pod yield. The reduction in fodder yield was in accordance with its relation to disease at later stages. In late sown experiment, mean yields were less and hence yield reduction was more compared to early sown trial. However, the response varied with genotypes. Mutant 28-2 recorded higher yield loss in late sown compared to early sown experiment, which could be due to high incidence of rust at very early stage in late sown experiment. While, B 37c had least yield reduction (pod, kernel and oil yield) in late sown than in early sown experiment. B 37c, a photoperiod sensitive (Naidu, unpublished data) variety performed better under long day conditions prevailed during late sown experiment. Flohr *et al.* (1990) reported that the intervals between flower to resulting peg and pod to mature pod may be increased by long days in photoperiod sensitive varieties.

Yield components viz., shelling out-turn, oil content and hundred seed mass are often emphasized under Indian situation. Shelling out-turn can be increased beyond 70 per cent by genetically manipulating shell thickness, which is a qualitative trait. The oil content of groundnut seed ranges from 35.8 - 54.2 per cent and averages to near 45 per cent. Foliar diseases considerably affect these yield components resulting in poor seed quality. Foliar disease resistant genotype D 39d had high shelling out-turn (75 %) and oil content (48 %) but had low hundred seed mass (36 g) which is preferred by farmers in drill sowing due to lower seed rate requirement and higher pod weight per unit of volume (Table 31). Resistant mutant 28-2 and B 37c with high shelling out-turn and bold kernels could be used as hand pick selection types since, they had higher hundred seed mass than presently used HPS variety JL 24 (Plate 7). Though JL 24 is highly susceptible to foliar diseases, had least reduction in shelling out-turn and oil content due to disease.

Resistant genotypes D 39d and B 37c were superior for pod, kernel and oil yield as they recorded highest values and least reduction due to disease for these productivity parameters (Table 32). They had higher shelling out-turn (70 - 75 %) and oil content (41 - 45 %) leading to more kernel and oil yield in the genotypes besides having high pod growth rate (Plate 6) and per day productivity. Genotypes ICGV 87165 and B 37c had highest fodder yield due to their high vegetative and crop growth rates besides high healthy leaf area duration and per day dry matter accumulation (16 -

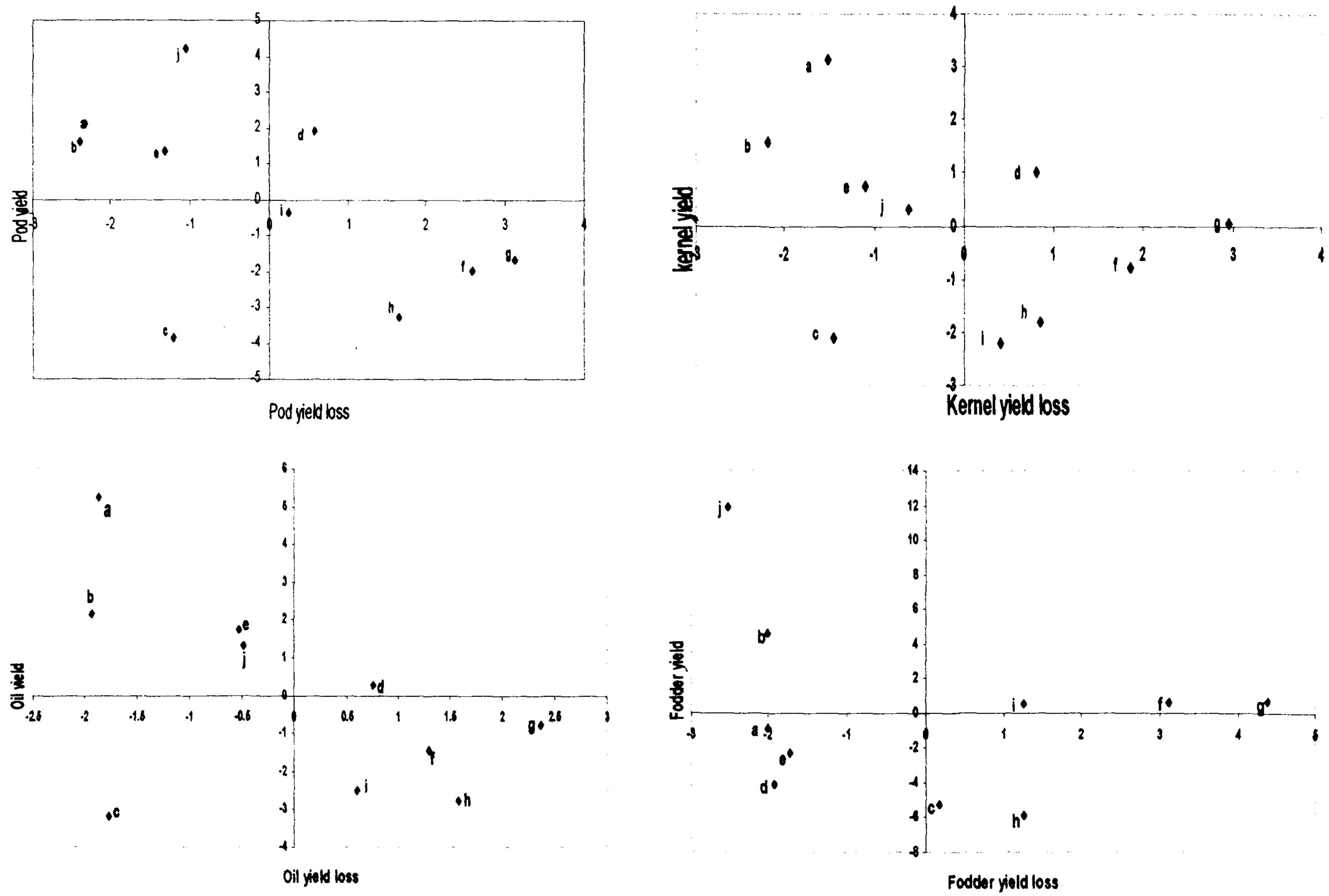
D 39d and its parents



Pod development at 70 DAS in resistant genotypes

Leaf retention and pod bearing at harvest

Plate 6: Disease development and pod bearing in groundnut genotypes



a D 39d b. B 37c c. Dh 8 d. R 8808 e. Mutant (28-2) f. JL 24 g. TMV 2 h. TAG 24 i. ICGV 86590 j ICGV 87165

Figure 11: Genotypic distribution for yield potential and yield loss due to late leaf spot and rust

21 g $m^{-2}d^{-1}$). On the contrary, susceptible cultivars TMV 2, JL 24 and TAG 24 had lower pod, kernel, oil and fodder yield levels and highest reduction due to disease. However, TAG 24 even though highly susceptible to foliar diseases had some tolerance mechanism as it recorded relatively higher yields and per day productivity, and lower reduction due to disease compared to other susceptible cultivars (JL 24 and TMV 2). TAG 24 was early maturing with determinate growth habit and had high partitioning coefficient (Plate 5a). It accumulated nearly 55 - 60 per cent of its pod and kernel yield by 60 days after sowing besides early initiation and accumulation of flowers, escaping the severe disease incidence at peak pod and kernel filling period.

From the breeding point of view, the genotypes having stable productivity across environments with varying levels of disease pressure need to be developed. For that, both high yield potential under normal condition and least reduction in diseased condition are important. Varieties were assessed for these criteria using z-transformed values of yield loss (X-axis) and yield potential (Y-axis) [Figure 11]. The genotypes ICGV 87165, B 37c, D 39d and mutant 28-2 form a separate quadrant with high yield potential and least yield reduction due to disease for pod, kernel and oil yield, while, ICGV 87165 and B 37c were also superior for fodder yield. R 8808 had more pod, kernel and oil yield potential and ICGV 86590, JL 24 and TMV 2 had high fodder yield potential but they suffered heavy loss due to disease.

The yield potential of groundnut is dependent on three factors, the duration of crop growth, the amount of energy intercepted and the distribution of photosynthate between fruits and stems (Williams *et al.*, 1987). The area where there has been some controversy is the interaction between yield potential and disease resistance. Most germplasm identified as resistant to the major foliar diseases had low yield potential based on low partitioning to the fruit (Subrahmanyam *et al*, 1984). Whether these resistances were physiologically associated with low partitioning or not has been the topic of considerable research. Pixley *et al.* (1990 a and b) identified two phenomena involved in resistance - late leaf spot resistance *per se* at the leaf level and low partitioning that caused higher yield by permitting sustained leaf growth and replacement of diseased leaves, providing tolerance to the disease. Partitioning factor and duration of crop growth are the major determinants of differences in yield potential between genotypes (Duncan *et al.*, 1978). Williams *et al.* (1987) observed low dry matter partitioning and late maturity in rust and late leaf spot resistant genotypes. In the present study, late leaf spot and/or rust resistant genotypes, viz., ICGV 87165, B 37c and ICGV 86590 had low partitioning coefficient (42 - 54 %) and late maturity (115 - 120 days). On the contrary, D 39d and mutant 28-2 had desirable combination of late leaf spot and/or rust resistance with early maturity (105-110 days) and high partitioning coefficient (63 %) similar to that of ruling but susceptible cultivars in the Spanish background (Tables 30 and 33). Similarly, Knauft and Gorbet (1990) identified a Virginia breeding line (F 8026) combining both high level of resistance and high rate of partitioning. They also reported that several disease resistant lines partitioning photosynthate to pods at rates similar to that of high yielding cultivar Florunner suggesting that such lines have some true resistance to leaf spot, rather than replacing diseased and lost leaves. Knauft *et al.* (1990) identified rapid early vegetative growth and subsequent high but not absolute partitioning of photosynthate to pods as important characteristics in more stable genotypes. In environments where heavy late leaf spot infections occur, Knauft and Gorbet (1990) have shown that simultaneous selection for resistance and yield can produce lines with moderately high partitioning and foliar disease resistance. Rust (Waliyar *et al.*, 1993) and late leaf spot (Patil *et al.*, 1996) resistant lines with high partitioning have also been reported.

Fatty acid composition and oil quality

As an oilseed, the oil content of kernel and the fatty acid composition of oil determine the quality of groundnuts. Oleic and linoleic acid together constitute about 80 per cent of the fatty acid composition in groundnut oil. Increasing the ratio of oleic to linoleic acid will improve the keeping and nutritional quality. In India, early maturing Spanish bunch varieties cover major area (70 %) but they have poor oil quality with O/L ratio of ~1.0. Various factors, viz., genotype, seasonal variation and foliar diseases affect the fatty acid make up of groundnut oil (Singh *et al.*, 2000). Foliar diseases considerably reduce the oil yield and affect quality also (Dwivedi *et al.*, 1993). There is an urgent need to develop disease resistant Spanish bunch genotypes with high oil recovery and also better oil quality.

Genotypic and interaction effects involving genotype (factor C), viz., AC, BC and ABC were highly significant for fatty acid composition and oil quality parameters and margin of change was also more due to genotypes than date of sowing (factor B) and disease control treatment (factor C) indicating the importance of genotypic effects in determining fatty acid composition and oil quality (Table 35). However, date of sowing had significant effect on linoleic acid, arachidic acid content and O/L ratio. While, disease control treatment affected all the parameters except linoleic and arachidic acid content. Dwivedi *et al.* (1993) also reported significant disease control treatment and genotypic effects for fatty acid composition, and O/L and P/S ratios. They observed increase in linoleic acid content and P/S ratio, and decrease in stearic, oleic and behenic acid content and O/L ratio due to foliar disease control.

Among the genotypes, foliar disease resistant inter-specific derivatives D 39d (Spanish bunch) and ICGV 87165 (Virginia bunch) had highest oleic acid (46 - 48 %) and O/L ratio (1.5 - 1.7) across dates of sowing and disease pressure revealing the improved shelf life and nutritional quality in these cultivars (Table 36 and Appendix 16). D 39d also had higher unsaturated fatty acid content (78.8 %) next to Dh 8 (80.6 %). Taking into consideration all the parameters, D 39d was considered significantly superior over currently cultivated Spanish bunch genotypes for oil quality. Zullo *et al.* (1993) reported higher O/L ratio in five foliar disease resistant lines, besides 46 - 67 % greater oil yield/ha than the control variety Tatu. Similarly, Shokes *et al.* (1997) isolated a high yielding runner cultivar UF 91108, with good oil quality (4.0 O/L ratio) and multiple disease resistance.

Role of source-sink relations in disease development and yield formation

Leaf removal simulating the defoliation effect of foliar diseases and flower removal to unravel the source-sink relationship, may provide greater insight in to the physiological basis of disease-yield relationship. Analysis of variance revealed significant treatment (leaf/flower removal), genotypic and their interaction effects for pod yield and resistance, indicating the differential response of genotypes to artificial leaf/flower removal (Table 37).

Artificial leaf removal even though significantly reduced the lesions on petiole and main stem, its effect on other components was only marginal (Table 38 and 39). Leaf removal reduced remaining green leaf area and increased field disease score values by its direct positive effect on defoliation. The yield reduction due to leaf removal was more in resistant (28-2 and ICGV 87165) than in susceptible genotypes which may be associated with low crop growth rate in mutant (Table 30) and more diversion of photosynthate to new leaf growth in low partitioning genotype, ICGV 87165 (Table 30). Photosynthesis is a major process affected by foliage removal (Boote *et al.*, 1980). Jones *et al.* (1982) reported the reduced carbon dioxide exchange rate after 75 per cent defoliation. Defoliation resulted in reduction in dry weight of stems, pods and seeds (Enyi, 1975), chlorophyll, protein and sugar contents (Ghosh and Biswas, 1995).

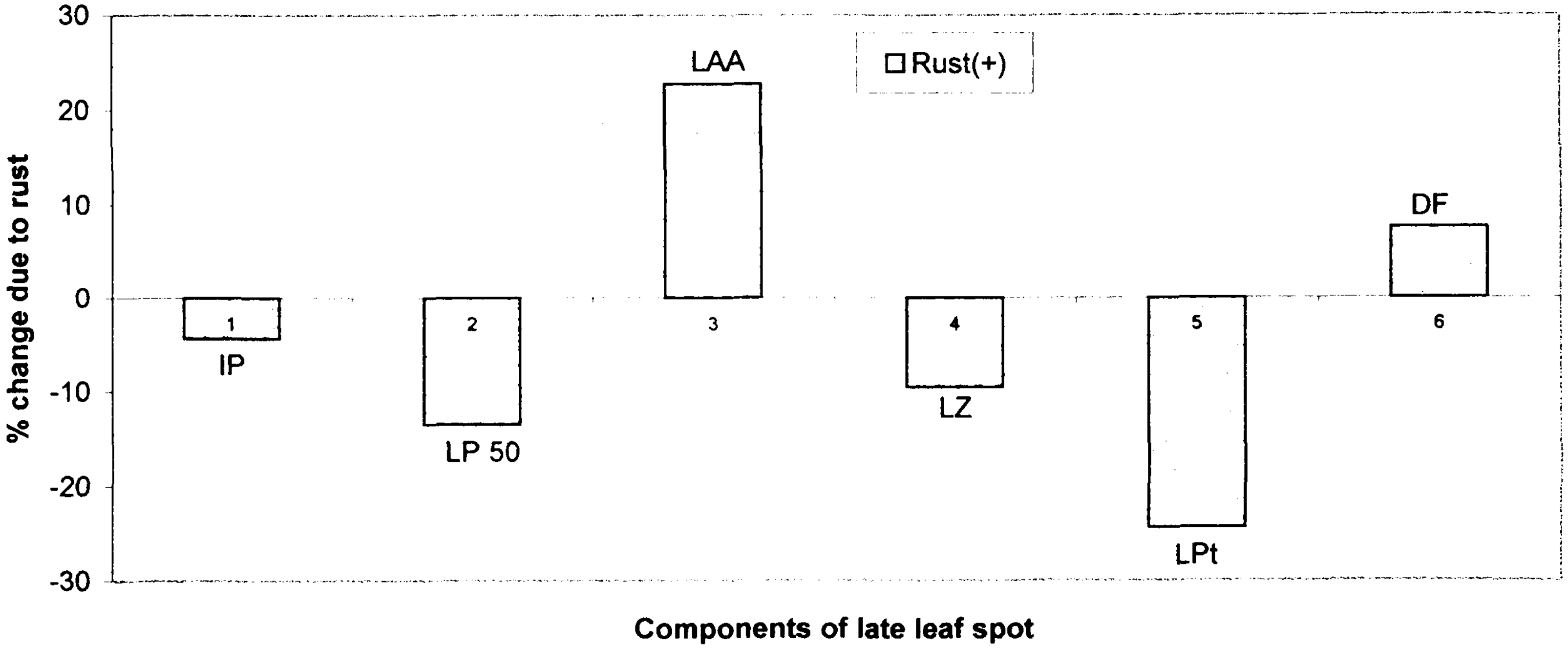
Flower removal significantly enhanced the resistance to late leaf spot and rust but at the cost of nearly 40 per cent pod yield. The effect was more in susceptible (JL 24, Dh 8, TMV 2 and TAG 24) than in resistant genotypes indicating the sink limitation of susceptible genotypes. Leaf senescence is uncoupled from fruit maturation in normal condition, possibly due to sink limitation (Ghosh and Biswas, 1995). They also noticed increased level of chlorophyll, sugar and dry weights of aerial parts in deflorated plants making plants to exhibit resistance reaction. Similarly, bud removal caused low yield, and low disease incidence and late maturity (Miller *et al.*, 1990). Flower removal had more pronounced effect on yield reduction (40 %) than leaf removal (25 %) revealing the importance of sink rather than source limitation in the genotypes. Pennypacker (2000) reported that the expression of quantitative and qualitative disease resistance in alfalfa is affected differentially by changes in carbon assimilation. Quantitative resistance required a greater carbon flux through phenyl propanoid pathway for its expression than qualitative resistance. In the absence of sufficient carbon assimilation and/or carbohydrate reserves, plants with the genes for quantitative resistance may fail to express. Incidentally, the resistance to both the diseases in groundnut is of quantitative type requiring greater energy budget. Many examples of costs of resistance appeared to be due to linkage rather than pleiotropic effects indicating the possibility of producing high yielding resistant lines with both proper breeding designs and large segregating populations (Bergelson, 1994). In spite of cost of energy associated with resistance, as revealed in the present study, it is possible to combine high level of resistance to late leaf spot and rust with high yield in groundnut.

Interactions of late leaf spot and rust

Late leaf spot and rust diseases normally occur together but the incidence and severity of each disease varies with locations and seasons. When two or more pathogens colonize on a single plant, they may interact to produce an outcome that is different from the situation where each disease is present alone. Predominance of one disease interferes with other leading to either biased/underestimation of resistance. The interaction effect is genotype dependent. Hence, there is a need to study these diseases separately and in combination in genotypes with varying levels of resistances. In the present study, the effect of one disease (late leaf spot/rust) on the other was investigated.

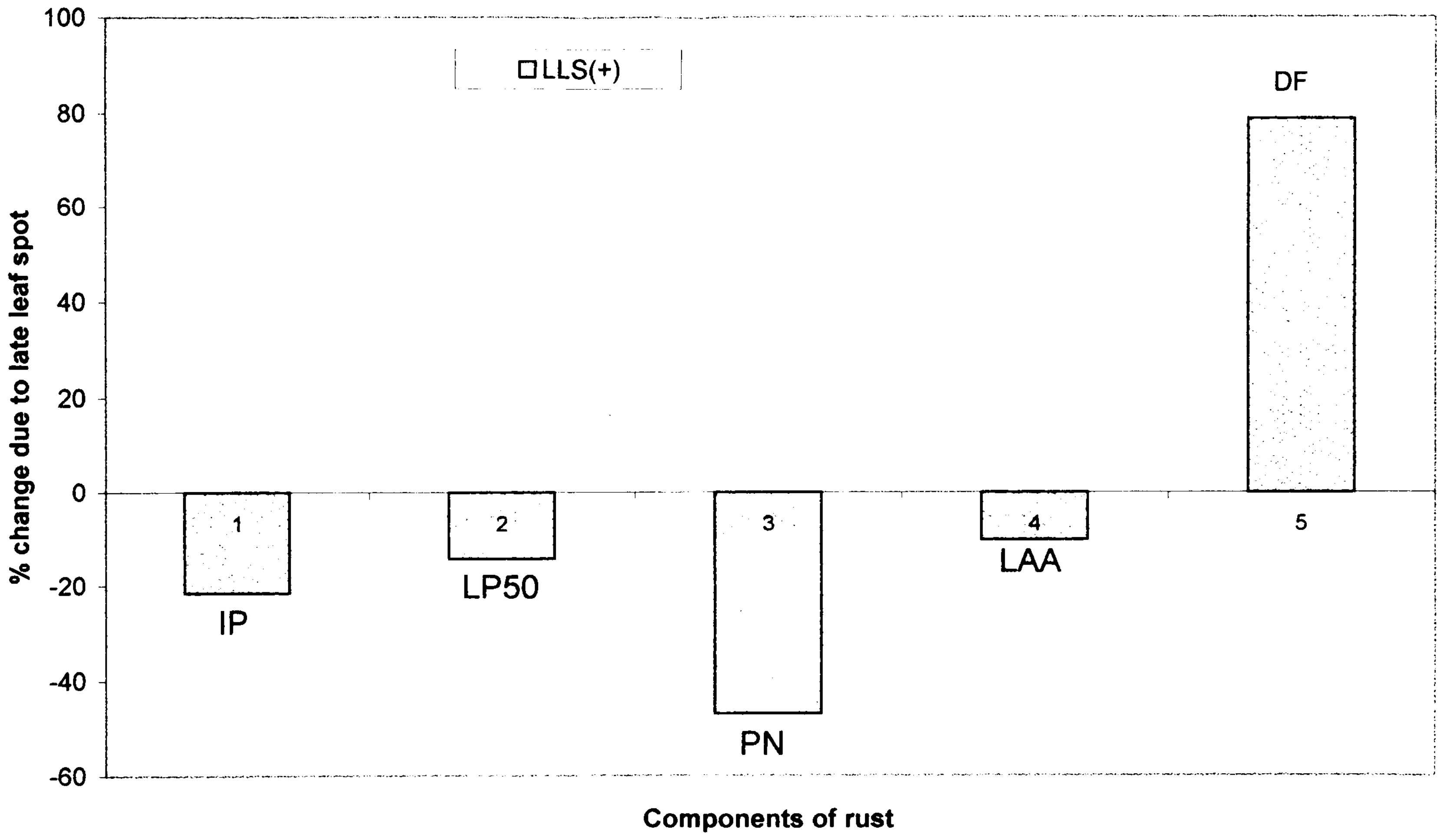
Analysis of variance for components of late leaf spot in relation to rust revealed significant effect of rust on latent period, leaf area affected by late leaf spot, lesion size, lesions on petiole, sporulation score and field disease score of late leaf spot, while, incubation period, lesion number and lesions on mainstem were not affected indicating partial antagonistic effect of rust on late leaf spot at later stages of disease development. Genotypic and interaction effects were significant for most of the late leaf spot components indicating the differential response of genotypes in determining late leaf spot resistance *vis-à-vis* rust (Tables 40 and 42).

Rust disease increased the per cent necrotic area and defoliation and reduced the latent period of late leaf spot (Figure 12), making the plants more sensitive to late leaf spot. Presence of late leafspot pathogen significantly increased defoliation and reduced the pustule number, per cent necrotic area, incubation and latent periods of rust (Figure 13) revealing the antagonistic effect of late leaf spot on rust at early stage of disease development (Tables 41 and 43). The effect was clearly evident in susceptible (JL 24, TMV 2 and TAG 24) and moderately susceptible (R 8808 and Dh 8) genotypes than in resistant genotypes. The effects of rust and late leaf spot on damage were less than additive due to the difference in the mechanisms of damage, i.e., late leaf spot causing damage mainly by defoliation and reduction in healthy leaf area, while rust damage being attributed to different mechanism other than reduction in leaf area (Savary and Zadoks, 1992). Mayee (1986) stated that late leaf spot lessens area for rust to develop and can be a factor in limiting rust epidemic. The reduced germination of rust urediniospores in the presence of late leaf spot may have induced increased resistance to rust by either cross protection or nutrient depletion, imbalance, competition for stomatal openings. High incidence and severity of late leaf spot was found to have antagonistic effect by reducing rust severity (Bulbule and Mayee, 1998). Earnshaw *et al.* (1992) concluded that screening for rust resistance was inconclusive due to interference from late leaf spot. Thus, the study conclusively indicates the need for evaluation for diseases separately to assess true resistance, and together to know the genotypic responses when the diseases occur together.



IP - Incubation period
LP50 - Latent period
LZ - Lesion size
LPt - Lesions on petiole
LAA - Leaf area affected
DF - Defoliation (%)
Rust(+) - Presence of rust

Figure 12: Components of late leaf spot resistance as influenced by rust



IP - Incubation period
LP50 - Latent period
PN - Pustule number
LAA - Leaf area affected
DF - Defoliation (%)
LLS(+) - Presence of late leaf spot

Figure 13: Components of rust resistance as influenced by late leaf spot

Performance of 28-2 and D 39d

Two promising foliar disease resistant genotypes mutant III (28-2) and D 39d (GPBD 4) out-yielded the national check variety JL 24 for pod (20.6 and 16.0 %), kernel (18.1 and 18.0 %), oil (16.8 and 18.0 %) and fodder (16.3 and 19.2 %) yield in multilocation trials of zone 8 (Northern transitional tract of Karnataka) where the incidence of foliar disease is very high. These genotypes are under adoptive trials in farmer's field (Tables 44 and 45).

The mutant 28-2 is resistant to late leaf spot and *Spodoptera* with early maturity besides having desirable pod and kernel features and high yield. National Bureau of Plant Genetic Resources, New Delhi, has registered it as valuable germplasm with INGR number 98003 (Gowda *et al.*, 1998).

Cross derivative D 39d is resistant to late leaf spot and rust, moderately efficient in iron absorption (Motagi *et al.*, 2000c) with early maturity besides desirable pod and kernel features. It recorded high O/L ratio (1.68) and unsaturated fatty acid (78.8 %), oil content (47 %), shelling out-turn (76 %), pod growth rate (23.4), partitioning coefficient (63.10 %) and highest per day productivity. National Bureau of Plant Genetic Resources, New Delhi, has registered it as valuable germplasm with INGR number 01031 (Gowda *et al.*, 2001).

Resistant genotypes, ICGV 86590 and ICGV 87165 had undesirable pod and kernel features (Plate 7), low shelling out-turn and partitioning coefficient besides maturing late (117 - 121 days). On the contrary, foliar disease resistant mutant 28-2 and cross derivative D 39d had desirable pod and kernel features and high partitioning coefficient (Table 51) similar to susceptible but ruling Spanish bunch cultivars (TAG 24 and JL 24) besides higher pod growth rate, shelling out-turn and early maturity (105 - 110 days).

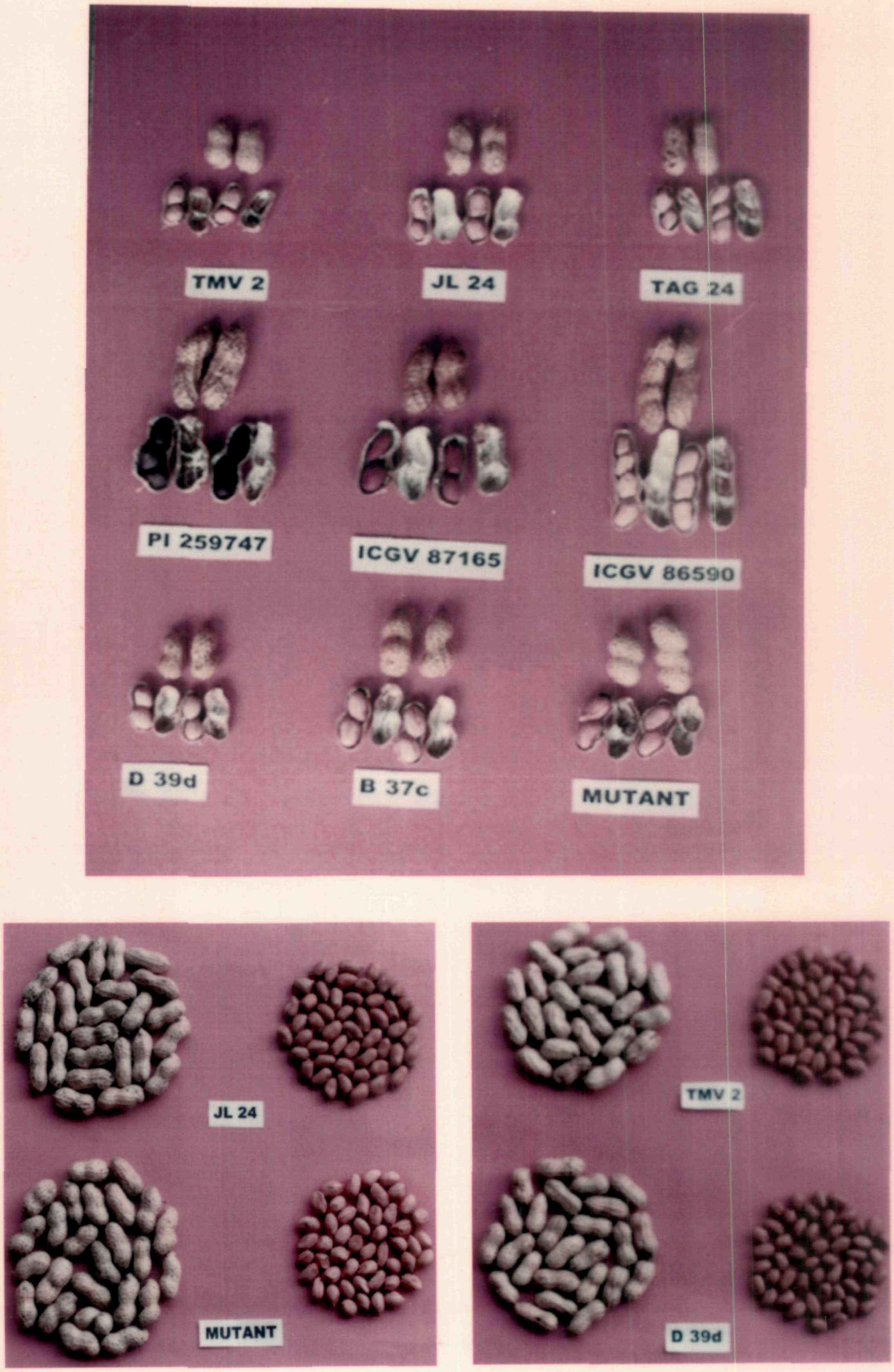


Plate 7: Pod and kernel features in groundnut genotypes

Table 51: Physiological characters, and pod and seed attributes of selected groundnut genotypes

	PGR	PC	DM	SP	HSM	OC	O/L ratio
Resistant genotypes							
D 39d	24.2	63.1	109	76.2	40.6	46.8	1.68
Mutant (28-2)	20.0	63.6	104	70.2	58.7	45.1	0.95
ICGV 86590	21.3	59.8	117	60.0	48.6	42.7	0.96
ICGV 87165	19.0	42.5	121	62.0	57.8	45.3	1.51
Susceptible genotypes							
TAG 24	19.6	63.8	096	69.5	50.2	40.7	1.02
JL 24	19.9	62.8	100	69.7	50.3	42.1	0.97

PGR - Pod growth rate
DM - Days to maturity
HSM - Hundred seed mass (g)
O/L ratio - Oleic acid/Linoleic acid ratio

PC - Partitioning coefficient
SP - Shelling out-turn (%)
OC - Oil content (%)

5.4 Genetics of resistance

Genetic analyses of resistance can help to develop appropriate crossing and selection schemes to increase the efficiency of resistance breeding. Mutants and inter-specific derivatives are important sources of resistance to late leaf spot and or rust. Crosses involving mutants, viz., VL 1 (rust resistant), 28-2, 45 and 110 (late leaf spot resistant) and 45 (S) [susceptible to late leaf spot and rust] and inter-specific derivatives, viz., ICGV 87165, B 37c and D 39d (resistant to late leaf spot and rust) were utilized.

F_1 hybrids involving resistant and susceptible parents to either late leaf spot or rust exhibited intermediate level of susceptibility to late leaf spot/rust, respectively indicating partial dominance nature of the gene(s) conditioning susceptibility (Table 46). These results are in confirmation with Godoy and Moraes (1987) who reported partial dominance of late leaf spot severity. F_2 segregation pattern revealed duplicate complementary recessive genes (9 S : 7 R) controlling late leaf spot resistance in crosses involving resistant (R) and susceptible (S) parents. However, four complementary recessive genes (81 S : 175 R) controlled the late leaf spot resistance in the R x R crosses involving resistant mutants (110 and 28-2) and inter-specific (ICGV 87165, D 39d and B 37c) derivatives revealing two independent duplicate complementary recessive genes for late leaf spot resistance (Table 47). F_3 breeding behaviour confirmed the proposed segregation ratios (Table 48).

Inheritance pattern of late leaf spot resistance in the mutants revealed the duplicate complementary recessive genes controlling the resistance to late leaf spot in VL 1- 45 × VL 1 cross, while, duplicate inhibitory genes in VL 1-45 × DER and VL 1 × DER crosses controlled the resistance indicating the presence of suppressor element of disease resistance in DER parent which was subsequently eliminated by mutation in VL 1 (Motagi *et al.*, 2000b). These results are in agreement with Soriano (1998b) who reported the involvement of two recessive complementary genes. While, Tiwari *et al.* (1984) and Soriano (1988a) suggested the digenic control of late leaf spot resistance similar to duplicate genes. The triploid hybrids of crosses between resistant wild species and susceptible cultivars were susceptible, indicating that resistance was recessive (Sharief *et al.*, 1978).

Hammons (1973), Wynne and Coffelt (1982) concluded that duplicate genes govern several traits in groundnut. This is expected due to the alloteraploid nature of the crop consisting of two genomes, viz., A and B, which are genetically similar (Kochert *et al.*, 1991) and hence more sets of genes controlling the same character would be possible. Involvement of a few recessive factors in determining the disease resistance in intra-Spanish crosses as compared to more factors in inter-sub specific or inter-botanical types of crosses has been reported. Another problem encountered in breeding for foliar disease resistance is the low frequency of disease resistant segregants due to the involvement recessive alleles at 3 or 4 loci determining resistant reaction (Nevill, 1980). Nevill (1982) found that resistance to late leaf spot resulted from multiple recessive genes (five-loci genetic model proposed). While, Vasanthi and Reddy (1997) reported four to five duplicate recessive genes governing the late leaf spot resistance. Three way crosses involving two doses of resistant parents are expected to yield higher frequency of resistant segregants.

Segregation in F_2 generation of the crosses involving the rust susceptible (110 and 28-2) mutants, and resistant inter-specific (ICGV 87165, D 39d and B 37c) derivatives revealed duplicate complementary recessive genes (9 S : 7 R) conferring resistance to rust. Allelic test-cross involving rust resistant mutant and inter specific derivative VL 1 × ICGV 87165 recorded 81 S : 175 R segregation ratio (four complementary recessive genes) indicating independent duplicate complementary recessive genes in mutant and inter-specific source (Table 47).

Resistance to rust in cultivated groundnut is recessive and appears to be governed by only few genes. One gene (Paramasivam *et al.*, 1990) and two gene models (Bromfield and Bailey, 1972; Tiwari *et al.*, 1984) have been proposed, but they are unable to explain the segregation in many crosses (Reddy *et al.*, 1987). Vasanthi and Reddy (1997) reported involvement of 2 - 3 genes acting in duplicate complementary manner in rust resistance. In inter-specific derivatives, rust resistance is governed by partially dominant gene/s (Singh *et al.*, 1984).

Four-locus model was proposed to formulate the genotypic constitution of the parents for late leaf spot and rust resistance based on genetic hypothesis (Table 49). Mutants VL 1 and 45(S) had susceptible reaction to late leaf spot with the genetic constitution $LS_1\ LS_1\ LS_2\ LS_2\ LS_3\ LS_3\ LS_4\ LS_4$ and resistant mutants (28-2, 45 and 110) had $ls_1\ ls_1\ ls_2\ ls_2\ LS_3\ LS_3\ LS_4\ LS_4$ genetic constitution for late leaf spot. While, rust resistant (VL 1) and susceptible mutant [45 (S), 28-2, 45 and 110] had $r_1\ r_1\ r_2\ r_2\ R_3\ R_3\ R_4\ R_4$ and $R_1\ R_1\ R_2\ R_2\ R_3\ R_3\ R_4\ R_4$ genetic constitution for rust, respectively. Late leaf spot and rust resistant inter-specific derivatives (ICGV 87165, D 39d and B 37c) had $LS_1\ LS_1\ LS_2\ LS_2\ ls_3\ ls_3\ ls_4\ ls_4$ and $R_1\ R_1\ R_2\ R_2\ r_3\ r_3\ r_4\ r_4$ genetic constitution for late leaf spot and rust, respectively. These results indicate the independent nature of late leaf spot and rust resistance and independent duplicate recessive genes control late leaf spot/rust resistance in mutational and Inter-specific sources of resistance. It is suggested to use both the sources to diversify the resistance. There is a need to test for allelism between mutational/inter-specific sources of resistance and land races since, the resistant mutants resemble Valencia land races. Inheritance of resistance to rust and late leaf spot was independent and development of cultivars resistance to both the diseases could be possible.

5.5 Isozyme and protein polymorphism for cultivar identification

The rapid pace of production of new crop varieties has pointed out the need of cultivar identification and protection of proprietary rights of both old and newly developed cultivars. To meet this end, electrophoresis of storage and functional proteins has emerged as an efficient, simple and reliable tool supplementing traditionally used morphological parameters (Picket and Jarman, 1994). Seed proteins and isozymes because of their stability and reproducibility have potential to serve as tools for fingerprinting of genotypes. In the present study, 13 genotypes representing different botanical groups were characterized for the isozyme and protein profiles.

Of the four enzymes studied, only glutamate oxaloacetate transaminase was polymorphic. Catalase, peroxidase and super oxide dismutase were monomorphic. The isozyme analysis of glutamate oxaloacetate transaminase indicate that out of four bands, first two bands displayed three banding patterns through their presence/absence, which were specific to the botanical types viz., Spanish bunch (Pattern I with 3rd and 4th bands present), Valencia (Pattern II had 2, 3 and 4th bands) and Virginia bunch (Pattern III with all the four bands). Two polymorphic bands of Rf value 0.338 and 0.385, which were present (Pattern III) in 28-2, B 37c, R 8808, TAG 24, and ICGV 87165 were absent (either of one/both the bands) in other genotypes (Figure 3). Grieshammer and Wynne (1990), and Lacks and Stalker (1993) reported that these two polymorphic bands were absent in Spanish and Valencia botanical types, but present in Virginia types. In the present investigation, three Spanish cultivars (Dh 8, JL 24 and TMV 2) lacked the two polymorphic bands whereas; the Virginia types had those polymorphic bands. In addition to ICGV 87165, a Virginia cultivar, four other genotypes belonging to sub species *fastigiata,* viz., 28-2, B 37c, R 8808 and TAG 24 also possessed these polymorphic bands. Of these, TAG 24 though Spanish bunch in habit, is a cross derivative from two mutants TGE 1 and TGS 2, which were in turn derived from Virginia cultivars, viz., TG 1 and M 13, respectively. The cultivar, R 8808 is a cross derivative of ICGS 11 and Chico. ICGS 11 is a selection from Robut 33-1, which is Virginia bunch. B 37c is a cross derivative of JL 24 × ICGV 87165. ICGV 87165 is a Virginia bunch; mutant 28-2 belongs to sub spp *fastigiata.*

The extent of polymorphism found among the genotypes was not sufficient for varietal identification but the general trend of genetic variability among botanical types of cultivated groundnut shown by pedigree data was reflected by the polymorphic isozyme system of glutamate oxaloacetate transaminase. Thus, the polymorphism in isozymes could be used to assess the genetic diversity of natural plant population for which detailed pedigree data are not available. In groundnut, only three enzymes (glutamate oxaloacetate transaminase, indole dehydrgenase and phosphohexose isomerase) have been reported as polymorphic but all the three could differentiate only the botanical types, hence not useful for cultivar identification (Grieshammer and Wynne, 1990; Lacks and Stalker, 1993). But, the isozymes have potential use as markers to follow the introgression patterns (Lacks and Stalker, 1993), especially in inter-specific hybridization.

Sodium dodicyl sulphate-poly acrylamide gel electrophoresis profiles of seed proteins have been used for differentiating Virginia and Spanish cultivars (Singh *et al.,* 1991 and Lanham *et al.,* 1994). Hartzook *et al.* (1969) obtained highly repeatable clear resolutions showing differences in total seed protein content among the three botanical types (Virginia bunch, Valencia and Spanish bunch) and concluded that poly acrylamide gel electrophoresis of seed proteins could be used as a tool in establishing cultivar identification. In case of Virginia cultivars and four Spanish cultivars 28-2, B 37c R 8808 and TAG 24, which behaved like Virginia for glutamate oxaloacetate transaminase pattern, had two extra bands of Rf value 0.739 and 0.962 (Figure 5). The two cultivars R 8808 and 28-2 can be differentiated from other genotypes as they lacked a band of Rf value 0.567 which was present in all other cultivars. Further, they possessed an extra band of Rf value 0.529 in addition to two bands specific to Virginia cultivars. However, B 37c and TAG 24 behaved like Virginia cultivars for seed protein profiles.

The Glutamate oxaloacetate transaminase isozyme pattern and Sodium dodicyl sulphate-poly acrylamide gel electrophoresis seed protein profile have helped in identification of Spanish and Virginia cultivars. Seed protein profile has got an advantage of five electrophoretic phenotypes compared to the three of glutamate oxaloacetate transaminase. Further, the protein profiles of hypocotyl produced seven electrophoretic phenotypes to classify the genotypes (Figure 4). Bands of Rf vale 0.345, 0.636, 0.691 and 0.945 were polymorphic. But, these polymorphic bands were not useful in differentiating the botanical types. Combining protein profiles of seed and hypocotyl, a total of ten electrophoretic phenotypes have been identified. The genotypes, viz., B 37c, 28-2, R 8808, ICGV 86590, D 39d (S), TAG 24 and TMV 2 could be uniquely identified using these protein profiles. Three classes had two genotypes each. They were viz., D 39d and ICGV 87165; VL 1 and Dh 8; 28-2 (S) and JL 24. However, they could be uniquely identified using glutamate oxaloacetate transaminase isozyme profile. These results indicate that protein profiles of seed and hypocotyl together with glutamate oxaloacetate transaminase isozyme profile have potential in cultivar identification (Figure 6). Gorman *et al.* (1982) suggested the use of multiple enzyme systems for complete cultivar finger printing.

Morphological and molecular markers present an interesting paradox in cultivated groundnut. Despite the huge morphological diversity existing in the crop, the molecular markers such as random amplified polymorphic DNA and random fragment length polymorphism have found no significant DNA variation among its genotypes (Kochert *et al.,* 1991; Halward *et al.,* 1992; Paik-Ro *et al.,* 1992). Similarly, the isozyme and seed protein studies have revealed limited variation among groundnut cultivars (Lu and Pickersgill 1993; Lanham *et al.,* 1994; Stalker *et al.,* 1994). Thus it was concluded that *Arachis hypogaea* might have evolved as the result of a single polyploidization event which occurred relatively recently on an evolutionary time scale (Halward *et al.,* 1991a). However, dramatic shifts in the morphology of plant organs can arise as a result of changes in one/two major genes and a few modifier loci (Hilu, 1983; Doebley and Wendel, 1989).

Isozyme variation in relation to resistance

Traditional groundnut breeding programmes have had limited success in enhancing genetic resistance against diseases due to lack of genetic information and complexity of the genome (Wynne *et al.,* 1991). The resistance to rust and late leafspot is controlled by recessive oligogenes necessitating more generations and large populations to identify resistant segregants. Further, when the diseases occur together, they interfere with each other, leading to difficulties in identification of resistance to a particular disease. Under the circumstances, newly emerging biotechnological tools like molecular marker assisted selection (MAS) can play a crucial role in the success of disease resistance breeding.

Biochemical characterization can help to identify the resistance mechanisms, which may have important implications in rapid screening of germplasm and improving the efficiency of resistance breeding. Oxidative enzymes (peroxidase, catalase and super oxide dismutase) have often been implicated in the resistance to different stresses. Study of these enzymes in hypocotyl tissues of late leafspot resistant mutants (28-2, 45 and 110), inter-specific derivatives (D 39d, B 37c, I 15e and ICGV 86699) and a germplasm line ICG 2271 along with their susceptible variants indicated the presence of an additional band for all the three oxidative enzymes in resistant I 15e as compared to its susceptible counterpart. While, other resistant genotypes had either presence of an additional band or more intense bands for peroxidase as compared to their susceptible counterparts (Figures 7 and 8). The resistant mutant, VL 1-45 and inter-specific derivative, D 39d have shown inducible and constitutive expression, respectively when analyzed for peroxidase in leaf tissues challenged with late leafspot pathogen (Table 50). The present study indicates the potential of utilizing the oxidative enzymes, especially peroxidase, in MAS to improve the efficiency of resistance breeding.

Peroxidase is thought to be important in a variety of plant defense response against pathogens (Hammerschmidt *et al.*, 1982; Anfoka and Buchenauer, 1997; Stout *et al.*, 1999) like hypersensitive response, polymerization of phenolic derivatives in to lignin, formation of papilla and suberization, a process that heals wounds with a layer of phenolic and aliphatic compounds. Furthermore, Peroxidases have been implicated in the cross-linking reactions of cell wall associated proteins such as hydroxyproline-rich or glycine-rich glycoproteins. As a result, cell walls may be strengthened and function as physical barriers against invading pathogens. Daub and Hangarter (1983) reported that exposure of maize to Cercosporin toxin, produces singlet oxygen and super oxide, increased catalase and super oxide dismutase activity through a photosensitized reaction.

Mutant VL 1-45 also possessed high degree of resistance to different abiotic stresses, viz., temperature and moisture. Salim (2000) also reported induction of peroxidase in the mutant under the challenge of these stresses. There seems to be a common mechanism for tolerance to both biotic and abiotic stresses. Mittler and Zilinskas (1992) have reported that, ascorbate peroxidase gene expression is rapidly induced by various stress conditions such as paraquat, abscissic acid, ethylene, and drought and heat shock. As peroxidase is induced under both biotic and abiotic stresses, the role of oxidative burst in both the stress response pathways may be predicted, and hence, the mutants form an ideal source for dissecting the mechanism of stress tolerance.

Future line of work

- There is a need to combine resistance in the background of popular Spanish bunch groundnuts through hybridization with foliar disease resistant mutant, 28-2 and inter-specific derivatives (D 39d and B 37c).
- Mutants and inter-specific derivatives form the important sources of resistance, which could be explored in future breeding program to diversify the resistance.
- There is a need to test the allelic relationship between mutants and *fastigiata* landraces, which have common features.
- Breeders can concentrate on incorporating resistance into TAG 24 which is early maturing and has high partitioning coefficient besides showing tolerance to yield reduction even though highly

susceptible to late leaf spot and rust. This may further minimize losses under disease epidemic condition.

- The biochemical nature of peroxidase representing band of Rf value 0.872 which was polymorphic and present in late leafspot resistant mutants (45 and 110) and germplasm (ICGV 2271) but absent in their susceptible counterparts need to be investigated further. Similarly, the band of Rf value 0.686 was present in I 15e R and absent in its susceptible counterpart. Genetic analysis of this response by using segregating population to find whether there exists any association between these bands and late leafspot resistance should be attempted.
- The constitutive expression of peroxidase in D 39d and its induction in resistant mutants for both biotic and abiotic stresses need to be studied in order to establish their relationship to the stress response.
- The protein and isozyme markers have limited use and restricted to differentiation up to sub-species level only. DNA markers need to be exploited, as these are more polymorphic when compared to protein markers.
- The resistant mutants, cross derivatives have spontaneously yielded susceptible counterparts, which differed only for the resistance parameters. These counterparts form an ideal material for tagging resistance genes through molecular analysis, which can be subsequently used in marker assisted selection.

SUMMARY

VI. SUMMARY

The cultivated groundnut (*Arachis hypogaea* L.) is one of the most important vegetable oilseed crops in the world. Even though. India is a leading producer, the productivity is very low as compared to some of the developed countries. The crop loss due to fungal foliar diseases, viz., late leaf spot and rust is known to be a significant reason for the low productivity. These diseases could be managed through fungicides, but the most effective means of management could be the use of resistant cultivars.

Most of the available resistant germplasm are Valencia landraces or Virginia inter-specific derivatives with many undesirable agronomic features making them unsuitable for direct cultivation. Early maturing Spanish bunch types are most popular among the farmers because of ease in cultivation and harvesting. But, they are highly susceptible to foliar diseases and suffer heavy yield loss, if unprotected. Till today, incorporation of resistance into the Spanish types from the resistant germplasm lines has not been completely successful due to the inherent problems like undesirable linkages and genetic interactions. Induced mutagenesis and extensive hybridization with inter-specific derivatives were sought as an alternative approach to generate material combining desirable agronomic features with disease resistance and high productivity.

The present investigation on assessment of variation in groundnut germplasm for resistance to late leaf spot and rust, diversity in foliar disease resistant mutants, agronomic performance in relation to resistance, and genetic and biochemical analyses of resistance led to the following important conclusions.

Variation in germplasm for resistance

Forty-five groundnut germplasm and fifty-five Trombay genotypes were assessed for reaction to late leafspot and rust in two (*Kharif* and summer, 1998) seasons. Significant seasonal, genotypic and their interaction effects for late leaf spot and rust resistance indicated the need for screening germplasm over seasons.

Components of late leaf spot (lesions on mainstem and petiole) and rust (incubation period and pustule number) in germplasm; incubation period, lesion size and lesions on mainstem of late leaf spot, and incubation and latent periods of rust in the Trombay genotypes had high heritability, genetic advance and coefficient of variation compared to field disease score, defoliation and remaining green leaf area and they had strong association with latter parameters implying the utility of any of these components in assessing genotypes for foliar disease resistance. Remaining green leaf area had strong association with components of late leaf spot and rust and all the components were significantly associated with one other indicating their common genetic control. Association of maturity with components of late leaf spot and rust indicated the late maturity of most of the resistance sources.

All the inter-specific derivatives were resistant to late leaf spot and rust, but were late maturing (except D 39d and B 37c) than ruling cultivars. Most of the advanced breeding lines were rust resistant. Mutants were either resistant to rust or late leaf spot with early maturity. Ruling cultivars were early maturing but highly susceptible to late leaf spot and rust, except ICGV 86590, which was rust resistant but matured late. Late leaf spot and / or rust resistant mutants, landraces and inter-specific derivatives should be exploited to diversify the resistance sources.

Though, most of the Trombay genotypes are highly susceptible to late leaf spot, there was lot of variation in components viz., defoliation, lesion size and lesions on mainstem, which could be exploited in future breeding programs retaining optimum agronomic features.

Diversity in resistant mutants

Eighteen mutants isolated from VL 1 were evaluated for morphological and productivity parameters in relation to late leafspot and/or rust resistance. Diversity analysis grouped the 18 mutants into three clusters. Late leaf spot resistance was strongly associated with rust susceptibility and its strong association was also observed with increased number of primary and secondary branches, hundred seed mass, pod yield and reduced leaflet length and width. In contrast, an opposite trend in interrelationships was evident with rust resistance.

Spontaneously occurring susceptible counterparts were isolated from late leaf spot resistant mutants (28-2, 45 and 110), inter-specific derivatives (D3 9d, B 37c, I 15e and ICGV 86699) and an advanced breeding line (ICG 2271). They constitute valuable resources for gaining insight into the basis and mechanisms of late leaf spot resistance.

Agronomic performance in relation to resistance

A total of ten genotypes comprising of late leaf spot and rust resistant inter-specific derivatives (D 39d and B 37c and ICGV 87165), late leaf spot resistant mutant (28-2), ruling but susceptible cultivars (JL 24, TMV 2 and TAG 24), rust resistant cultivar (ICGV 86590) and moderately susceptible cultivars, viz., Dh 8 (late leaf spot) and R 8808 (rust) were evaluated in early and late sown experiments, under diseased (UP) and fungicide sprayed (P) conditions during *Kharif*, 1998, for disease, productivity and physiological parameters to gain insight into their interrelationships for designing sound breeding strategies.

Analysis of variance for yield, disease and physiological parameters indicated significant genotypic and interaction effects (dates of sowing × genotype) for all the parameters implying the differential response of genotypes to sowing dates.

Disease severity in late sown experiment was higher compared to early sown experiment in almost all the genotypes, even at 45 days after sowing, severity was more indicating the early incidence of disease. Late *Kharif* sowing may be utilized for screening germplasm for disease resistance. All the genotypes had higher yield and lower yield reduction under early sown experiment compared to late sown experiment suggesting that early sowing is better to get higher yields. However, the response varied with genotypes.

Based on regression analyses, disease (disease severity at different stages and area under disease progress curve) and physiological (leaf area index, harvest index, healthy leaf area duration, reproductive efficiency measures, partitioning coefficient and growth rates) parameters were selected to assess their association/effect on yield/yield loss. Strong association and high direct effects of disease parameters in early sown experiment; both disease and physiological parameters in late sown and pooled analysis explained most of the yield and yield loss variation.

D 39d had high shelling out-turn (75 %) and oil content (47 %) but had low hundred seed mass (36 g). Mutant 28-2 and B 37c had high shelling out-turn and bold kernels can be used as hand pick selection (HPS) types. JL 24 even though, highly susceptible to foliar diseases had least reduction in shelling out-turn and oil content.

Genotypes TAG 24, JL 24, TMV 2 and D 39d accumulated nearly 70-85 per cent of their pod and kernel yield by the end of 75 days after sowing. However, TAG 24 was significantly early by accumulating 55-60 per cent of its pod and kernel yield by 60 days after sowing. On the contrary, B37c, ICGV 87165 and Dh 8 accumulated nearly 20 per cent of their pod and kernel yield during later part of growth period. This contrasting response was evidenced by very early initiation and accumulation of flowers in TAG 24 and very late in ICGV 87165 and Dh 8. Resistant genotypes, viz., ICGV 87165, B 37c and ICGV 86590 had low partitioning coefficient (45-55 %) and late maturity (115-120 days). On the contrary, D 39d and mutant 28-2 had desirable combination of late leaf spot and/or rust resistance with early maturity (105-110 days) and high partitioning coefficient (65 %).

Resistant genotypes D 39d and B 37c were superior for pod, kernel and oil yield, and ICGV 87165 and B 37c for fodder yield by recording highest values and least reduction due to disease. On the contrary, susceptible cultivars TMV 2, JL 24 and TAG 24 had lower yield levels and highest reduction due to disease. TAG 24 though highly susceptible to foliar diseases had some tolerance mechanism. Genotypes D 39d, B 37c, mutant 28-2 and R 8808 had higher per day pod, kernel and oil productivity, while B 37c and ICGV 87165 had higher fodder production in both diseased and protected conditions. D 39d and mutant 28-2 recorded higher per day fodder yield under diseased condition. TAG 24 exhibited superiority over other susceptible genotypes (JL 24 and TMV 2) for pod and kernel yield under diseased condition.

Two promising foliar disease resistant genotypes, mutant III (28-2) and D 39d (GPBD 4) out yielded the national check variety JL 24 for pod (20.6 and 16.0 %), kernel (18.1 and 18.0 %), oil (16.8 and 18.0 %) and fodder (16.3 and 19.2 %) yield in multilocation trials of zone 8 (Northern transitional tract of Karnataka) where the incidence of foliar disease is very high. They have been registered as valuable germplasm by NBPGR, New Delhi with INGR numbers 98003 and 01031, respectively.

Fatty acid composition and oil quality

Genotypic and interaction effects involving genotype were highly significant for fatty acid composition and oil quality parameters indicating the importance of genotypic effects in determining fatty acid composition and oil quality. However, date of sowing had significant effect on linoleic acid, arachidic acid content and O/L ratio. Foliar disease resistant inter-specific derivatives D 39d (Spanish bunch) and ICGV 87165 (Virginia bunch) had highest oleic acid (46-48 %) and O/L ratio (1.5-1.7) revealing the improved shelf life and nutritional quality in these cultivars. Genotype, D 39d also had higher unsaturated fatty acid content (78.8 %) next to Dh 8 (80.6 %) indicating its superiority over currently cultivated Spanish bunch genotypes for oil quality.

Role of source-sink relations in disease development and yield formation

Leaf removal simulating the defoliation effect of foliar diseases and flower removal to unravel the source-sink relationship, may provide greater insight in to the physiological basis of disease-yield relationship. Artificial leaf removal significantly reduced the lesions on petiole and mainstem. The yield reduction due to leaf removal was more in resistant (28-2 and ICGV 87165) than in susceptible genotypes. Flower removal significantly enhanced the resistance to late leaf spot and rust but at the cost of pod yield. The effect was more in susceptible (JL 24, Dh 8, TMV 2 and TAG 24) than in resistant genotypes indicating the sink limitation of susceptible genotypes. Flower removal had more pronounced effect on yield reduction (40 %) than leaf removal (25 %) revealing the importance of sink rather than source limitation in the genotypes.

Interactions of late leaf spot and rust

Analysis of variance for components of late leaf spot in relation to rust indicated the partial antagonistic effect of rust on late leaf spot at later stages of disease development. Presence of late leafspot pathogen significantly increased defoliation and reduced the pustule number, per cent necrotic area, incubation and latent periods of rust revealing the antagonistic effect of late leaf spot on rust at early stage of disease development. The effect was clearly evident in susceptible (JL 24, TMV 2 and TAG 24) and moderately susceptible (R 8808 and Dh 8) genotypes than in resistant genotypes.

Genetics of resistance

Crosses involving mutants, viz., VL 1 (rust), 28-2, 45 and 110 (late leaf spot) and 45 (S) [susceptible to both diseases] and inter-specific derivatives, viz., ICGV 87165, B 37c and D 39d (resistant to both diseases) were utilized. F_1 hybrids involving resistant and susceptible parents to either late leaf spot or rust exhibited intermediate level of susceptibility to late leaf spot/rust, respectively indicating partial dominance nature of the gene(s) conditioning susceptibility. F_2 segregation revealed duplicate complementary recessive genes (9 S : 7 R) controlling late leaf spot resistance in crosses involving resistant (R) and susceptible (S) parents. However, four complementary recessive genes (81 S : 175 R) control the late leaf spot resistance in R x R crosses involving mutants (110 and 28-2) and inter-specific (ICGV 87165, D 39d and B 37c) derivatives revealed two independent duplicate complementary recessive genes controlling late leaf spot resistance in mutational and inter-specific sources.

Segregation in F_2 generation of the crosses involving the rust susceptible (110 and 28-2) mutants, and resistant inter-specific (ICGV 87165, D 39d and B 37c) derivatives revealed duplicate complementary recessive genes (9 S : 7 R) conferring resistance to rust. Allelic test cross, VL 1 X ICGV 87165 exhibited 81 S : 175 R segregation ratio (four complementary recessive genes) indicating two independent duplicate complementary recessive genes in mutant and inter-specific source. Four-locus model was proposed to formulate the genotypic constitution of the parents for late leaf spot and rust resistance based on genetic hypotheses.

Isozyme and protein polymorphism

Thirteen genotypes were evaluated for protein and isozyme polymorphism for their use in fingerprinting these genotypes. The hypocotyl protein profile had seven and seed protein profile had five electrophoretic phenotypes. All Spanish cultivars had a particular electrophoretic phenotype of seed protein and the Virginia cultivars had a different electrophoretic phenotype possessing two bands (Rf value 0.739 and 0.962) more than Spanish cultivars. The two Spanish bunch genotypes, viz., R 8808 and 28-2 were similar to Virginia cultivars with respect to these two bands but lacked a major band (Rf value 0.567) and possessed a unique minor band (Rf value 0.529).

Among four isozymes viz., peroxidase (POX), catalase (CAT), super oxide dismutase (SOD) and glutamate oxaloacetate transaminase (GOT) analyzed, variation was present only for GOT. Spanish cultivars had two bands; Valencia had three bands, where as Virginia types had four bands. The Spanish bunch genotypes, viz., 28-2, R 8808 and TAG 24 also behaved like Virginia cultivars in terms of GOT isozyme patterns. However, when protein profiles of seed and hypocotyl were used together to classify the genotypes, a total of ten phenotypic classes were obtained and seven of thirteen genotypes could be uniquely distinguished. The other three groups comprised of two genotypes each (D 39d and ICGV 87165; VL 1 and Dh 8; and 28-2 (S) and JL 24) were also uniquely distinguished by considering GOT profile in combination with seed and hypocotyl protein profiles.

Polymorphism in oxidative enzymes viz., POX, CAT and SOD in late leafspot resistant mutants, inter-specific derivatives and advanced breeding lines when compared to their susceptible counterparts revealed the presence of an additional band for all the three oxidative enzymes in resistant I 15e as compared to its susceptible counterpart and possibility of utilizing these enzymes, especially POX, in marker assisted selection to improve the efficiency of resistance breeding. The resistant mutant VL 1-45 and inter-specific derivative D 39d showed inducible and constitutive expression for POX, respectively in leaf tissue challenged with the late leaf spot pathogen.

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*Only CAB Abstract has been seen

APPENDICES

Appendix 1: Weekly meteorological data collected at University of Agricultural Sciences, Dharwad during early and late sown experiments of rainy season, 199

Week	Early sown experiment					Late sown experiment				
	Temperature (°C)		Humidity (%)	Rainfall (mm)	No. of Rainy Days	Temperature (°C)		Humidity (%)	Rainfall (mm)	No. of Rainy Days
	Max.	Min				Max.	Min			
I	25.4	21.5	90.7	052.2	07	28.9	21.1	80.0	021.5	03
II	25.8	21.5	89.4	026.2	05	26.9	20.7	79.1	006.8	03
III	27.9	21.9	79.6	009.6	02	26.6	21.3	90.9	015.9	05
IV	29.4	21.2	70.3	004.8	02	27.6	21.2	80.1	001.0	01
V	28.9	21.1	80.0	021.5	03	29.2	21.7	78.1	025.4	04
VI	26.9	20.7	79.1	006.8	03	27.8	21.1	84.7	004.9	04
VII	26.6	21.3	90.1	015.9	05	28.9	21.5	81.6	002.0	01
VIII	27.6	21.2	80.1	001.0	01	27.4	21.2	83.1	010.0	03
IX	29.2	21.7	78.1	025.4	04	29.1	20.5	75.3	000.0	00
X	27.8	21.1	84.7	004.9	04	27.5	20.7	87.4	202.4	06
XI	28.9	21.5	81.6	002.0	01	29.1	21.2	75.4	007.2	01
XII	27.4	21.2	83.1	010.0	03	27.6	21.3	84.0	070.3	04
XIII	29.1	20.5	75.3	000.0	00	27.4	19.5	79.7	012.0	01
XIV	27.5	20.7	87.4	202.4	06	30.1	19.6	66.9	008.0	01
XV	29.1	21.2	75.4	007.2	01	29.7	19.1	69.1	000.0	00
XVI	27.6	21.3	84.0	070.3	04	29.4	19.9	70.6	038.6	03
XVII	27.4	19.5	79.7	012.0	01	29.4	16.8	70.9	000.0	00
XVIII	30.1	19.6	66.9	008.0	01	29.6	16.5	66.6	001.6	01
Mean/Total	29.5	22.4	86.9	472.2	52	30.2	21.8	83.6	426.0	40

Appendix 2: Path analysis indicating the effects of selected disease/physiological parameters on yield variables in early sown experiment

	DS 3	DS 5	DS 6	AUDPC	REM 5	HAD		DS 3	DS 5	DS 6	AUDPC	REM5	HAD
DS 3							**AUDPC**						
PY	-0.187	-0.885	0.010	0.058	0.213	-0.342	PY	-0.185	-0.905	0.010	-0.059	0.231	-0.366
KY	-2.605 ^{III}	-0.201	-5.921	8.567	0.040	-0.970	KY	-2.575	-0.206	-6.022	-8.664 ^{I}	0.043	-1.036
OY	-2.383 ^{III}	0.242	-4.369	6.164	-0.064	-0.789	OY	-2.356	0.248	-4.444	-6.234 ^{I}	-0.070	-0.843
FY	-0.764 ^{IV}	-1.394	-0.742	1.059	0.072	-0.664	FY	0.755	-1.425	-0.755	-1.071 ^{II}	0.078	-0.710
DS 5							**REM 5**						
PY	-0.182	-0.910 ^{I}	0.010	0.059	0.229	-0.369	PY	-0.073	-0.382	0.004	0.025	0.545 ^{II}	-0.185
KY	-2.535	-0.207	-6.038	8.619	0.043	-1.045	KY	-1.016	-0.087	-2.165	3.669	0.103	-0.524
OY	-2.319	-0.249	-4.455	6.202	-0.069	-0.849	OY	-0.929	0.105	-1.598	2.640	0.164	-0.426
FY	0.743	-1.433 ^{I}	-0.757	1.066	0.078	-0.715	FY	0.298	-0.602	-0.271	0.454	0.185	-0.359
DS 6							**HAD**						
PY	-0.183	-0.905	-0.010	0.059	0.195	-0.360	PY	0.153	0.799	-0.009	-0.051	-0.240	0.420 ^{III}
KY	-2.543	-0.206	-6.065 ^{II}	8.602	0.037	-1.019	KY	2.125	0.181	5.198	-7.551	-0.045	1.189
OY	-2.326	0.248	-4.475 ^{II}	6.190	-0.059	-0.829	OY	1.944	-0.219	3.836	-5.433	0.072	0.967
FY	0.746	-1.426	-0.760	1.064	0.066	-0.698	FY	-0.625	1.259	0.652	-0.934	-0.082	0.814 ^{III}

Note: underlined values are direct effects
DS 3, 5 and 6 - Disease severity at 65, 85 and 95 days after sowing
REM - Reproductive efficiency measure

PY, KY, OY and FY - Pod, kernel, oil and fodder yield
AUDPC - Area under disease progress curve
HAD - Healthy leaf area duration

Appendix 3: Path analysis indicating the effects of selected disease/physiological parameters on yield variables in late sown experiment

	DS 5	DS 6	HAD	VGR	CGR	PGR		DS 5	DS 6	HAD	VGR	CGR	PGR
DS 5							**VGR**						
PY	-1.711^{II}	-1.920	-0.815	0.703	-0.115	-0.254	PY	-0.040	1.159	0.829	1.157^{III}	0.142	0.055
KY	-1.658^{III}	-2.053	-1.213	1.037	-0.535	-0.098	KY	-1.007	1.239	1.235	1.707^{II}	0.661	0.021
OY	-1.368^{III}	-1.603	-1.041	1.113	-0.906	-0.050	OY	-0.881	0.968	1.060	1.832^{I}	1.119	0.011
FY	-0.615^{I}	-0.472	-0.145	-0.059	-0.318	0.228	FY	-0.374	0.285	0.147	0.097	0.393	-0.049
DS 6							**CGR**						
PY	1636	-2.008^{I}	-0.768	0.668	-0.104	-0.193	PY	-1.255	1.334	0.852	-1.048	0.156	0.852
KY	1.586	-2.146^{I}	-1.143	0.985	-0.484	-0.074	KY	-1.216	1.426	1.268	-1.547	0.729	1.268
OY	1.309	-1.676^{II}	-0.981	1.057	-0.821	0.038	OY	-1.004	1.114	1.088	-1.660	1.235^{IV}	1.088
FY	0.588	-0.494^{II}	-0.136	-0.056	-0.288	0.174	FY	-0.451	0.328	0.151	0.088	0.433^{IV}	0.151
HAD							**PGR**						
PY	-1.483	1.640	0.940^{IV}	-1.020	0.142	0.178	PY	-0.891	0.795	0.343	-0.130	0.082	0.488
KY	-1.437	1.753	1.400^{IV}	-1.506	0.660	0.069	KY	-0.863	0.850	0.511	-0.192	0.381	0.188
OY	-1.186	1.369	1.202	-1.616	1.119	0.035	OY	-0.712	0.664	0.439	-0.206	0.645	0.096
FY	-0.533	0.403	0.167	0.086	0.392	-0.160	FY	-0.320	0.195	0.061	0.011	0.226	0.439^{III}

Note: underlined values are direct effects

PY, KY, OY and FY - Pod, kernel, oil and fodder yield
HAD - Healthy leaf area duration
CGR - Crop growth rate

DS 5 and 6 - Disease severity at 85 and 95 days after sowing
VGR - Vegetative growth rate
PGR - Pod growth rate

Appendix 4: Path analysis indicating the effects of selected disease/physiological parameters on yield (pooled analysis)

	DS 6	REM 2	HAD	PGR	VGR	CGR		DS 6	REM 2	HAD	VGR	CGR	PGR
DS 6							**VGR**						
PY	-0.479	0.073	-2.698	-5.485	-11.114	17.148	PY	0.247	-0.046	2.605	21.558^{II}	-23.339	00.437
KY	-4.896^{IV}	-0.742	-0.361	-4.423	-10.940	13.743	KY	2.524	0.469	0.348	21.219^{I}	-18.705	00.352
OY	-5.384^{IV}	-0.978	0.350	-3.331	-09.602	10.475	OY	2.776	0.618	-0.338	18.624^{I}	-14.257	00.265
FY	-0.037	0.265	-0.696	1.503	03.403	-04.663	FY	0.019	-0.167	0.672	06.600^{II}	06.346	-00.120
REM 2							**CGR**						
PY	-0.148	-0.236	-1.204	-4.322	-04.220	08.732	PY	0.319	-0.080	2.900	19.570	25.709^{I}	04.973
KY	-1.516	-2.396	-0.161	-3.485	-04.154	06.998	KY	3.266	0.814	0.388	19.263	20.605^{II}	04.010
OY	-1.667	-3.157	-0.156	-2.624	-03.646	05.334	OY	3.591	1.072	-0.377	16.907	15.705^{II}	03.020
FY	-0.011	-0.856^{IV}	-0.311	1.184	01.292	-02.374	FY	0.025	-0.291	0.748	-05.991	06.991^{I}	-01.363
HAD							**PGR**						
PY	0.418	-0.092	3.088^{IV}	4.923	18.181	-24.144	PY	0.241	-0.094	1.393	00.862	-11.710	10.919^{III}
KY	4.278	0.934	0.413	3.970	17.895	-19.351	KY	2.460	0.948	0.186	00.849	-09.386	08.804^{III}
OY	4.704	1.231	0.401	2.990	15.707	-14.749	OY	2.705	1.250	-0.181	00.745	-07.154	06.630^{III}
FY	0.032	-0.333	0.797	-1.349	-05.566	06.565	FY	0.019	-0.339	0.359	-00.264	03.184	02.992^{III}

Note: underlined values are direct effects

PY, KY, OY and FY - Pod, kernel, oil and fodder yield
REM - Reproductive efficiency measure
CGR - Crop growth rate
DS 6 - Disease severity at 95 days after sowing
HAD - Healthy leaf area duration
PGR - Pod growth rate
VGR - Vegetative growth rate

Appendix 5: Path analysis indicating the effects of selected disease/physiological parameters on yield-loss variables in early sown experiment

	DS 3	DS 5	DS 6	AUDPC	REM 3	REM 5		DS 3	DS 5	DS 6	AUDPC	REM 3	REM 5
DS 3							**AUDPC**						
PYL	0.049	0.807	-0.317	1.254	-0.317	-0.224	PYL	-0.048	0.825	-0.322	-1.269^{I}	-0.297	-0.243
KYL	1.383^{II}	0.633	3.845	-4.795	-0.144	-0.138	KYL	1.368	0.648	3.911	-4.849^{I}	-0.135	-0.140
OYL	2.000^{III}	0.576	4.709	-6.289	-0.120	0.014	OYL	1.978	0.589	4.790	-6.361^{I}	-0.112	0.015
FYL	0.452	2.382	4.434	-6.857	-0.081	-0.191	FYL	0.446	2.435	4.510	-6.935^{I}	-0.076	-0.208
DS 5							**REM 3**						
PYL	-0.047	0.829^{II}	-0.323	1.262	-0.292	-0.241	PYL	-0.027	0.419	-0.146	0.652	-0.577^{III}	-0.410
KYL	1.346	0.651^{IV}	3.921	-4.824	-0.132	-0.149	KYL	0.759	0.329	1.773	-2.493	-0.262	-0.253
OYL	1.946	0.592^{IV}	4.802	-6.328	-0.110	0.015	OYL	1.098	0.299	2.172	-3.270	-0.218	0.025
FYL	0.439	2.448^{III}	4.522	-6.899	-0.074	-0.206	FYL	0.248	1.237	2.045	-3.565	-0.147	-0.350
DS 6							**REM 5**						
PYL	-0.047	0.825	0.325	1.260	-0.260	-0.205	PYL	-0.019	0.348	-0.116	0.537	-0.412	-0.575^{IV}
KYL	1.350	0.645	3.939^{II}	-4.815	-0.118	-0.126	KYL	0.539	0.274	1.406	-2.053	-0.187	-0.354
OYL	1.953	0.590	4.824^{II}	-6.315	-0.098	0.013	OYL	0.780	0.249	1.722	-2.694	-0.156	-0.036
FYL	0.441	2.437	4.542^{II}	-6.885	-0.066	-0.175	FYL	0.176	1.029	1.622	-2.937	-0.105	-0.490

Note: underlined values are direct effects
PYL, KYL, OYL and FYL - Pod, kernel, oil and fodder yield-loss
AUDPC - Area under disease progress curve

DS 3 and 5 - Disease severity at 65 and 85 days after sowing
REM - Reproductive efficiency measure

Appendix 6: Path analysis indicating the effects of selected disease/physiological parameters on yield-loss variables in late sown experiment

	DS 5	DS 6	HAD	VGR	CGR	PGR
DS 5						
PYL	2.983^{II}	2.920	1.809	-1.586	0.702	0.185
KYL	3.558^{I}	2.858	2.343	-1.465	0.379	0.187
OYLL	3.369^{I}	2.148	1.921	-1.609	1.011	-0.038
FYL	1.273^{III}	2.074	-0.510	-0.601	1.630	-0.592
DS 6						
PYL	-2.853	3.054^{I}	1.705	-1.507	0.636	0.141
KYL	-3.403	2.983^{II}	2.209	-1.392	0.343	0.143
OYL	-3.222	2.246^{II}	1.811	-1.529	0.916	-0.029
FYL	-1.218	2.169^{II}	-0.480	-0.571	1.477	-0.451
HAD						
PYL	2.585	-2.499	-2.087^{III}	2.303	-0.867	-0.130
KYL	3.083	-2.437	-2.704^{III}	2.127	-0.468	-0.132
OYL	2.2919	-1.834	-2.217^{III}	2.336	-1.248	0.027
FYL	1.104	-1.772	-0.588	0.873	-2.013	0.416

	DS 5	DS 6	HAD	VGR	CGR	PGR
VGR						
PYL	1.813	-1.763	-1.841	-2.611	-0.867	-0.040
KYL	2.162	-1.722	-2.385	-2.411	-0.468	-0.041
OYL	2.047	-1.296	-1.956	-2.648	-1.248	0.008
FYL	0.774	-1.252	0.519	-0.990^{IV}	-2.014	0.128
CGR						
PYL	2.188	-2.029	-1.891	2.367	-0.957^{IV}	-0.186
KYL	2.610	-1.982	-2.449	2.186	-0.517^{IV}	-0.188
OYL	2.470	-1.92	-2.008	2.401	-1.378^{IV}	0.038
FYL	0.934	-1.441	0.533	0.897	-2.222^{I}	0.595
PGR						
PYL	1.553	-1.209	-0.763	0.294	-0.500	-0.356
KYL	1.852	-1.181	-0.988	0.272	-0.270	-0.360
OYL	1.753	-0.889	-0.810	0.298	-0.720	-0.073
FYL	0.663	-0.859	0.215	0.111	-1.161	-1.138

Note: underlined values are direct effects
DS 5 and 6 - Disease severity at 85 and 95 days after sowing
PGR - Pod growth rate

PYL, KYL, OYL and FYL - Pod, kernel, oil and fodder yield-loss
VGR - Vegetative growth rate; CGR - Crop growth rate

Appendix 7: Path analysis indicating the effect of selected disease/physiological parameters on yield-loss variables (Pooled analysis)

	DS 5	DS 6	HAD	PGR	VGR	CGR		DS 5	DS 6	HAD	VGR	CGR	PGR
DS 5							**VGR**						
PYL	0.552	3.528	3.784	12.428	25.788	-36.928	PYL	-0.306	-1.797	-3.437	-46.515^{II}	44.270	-00.795
KYL	1.529	4.325	3.373	9.676	21.182	-29.124	KYL	-0.848	-2.203	-3.065	-38.208^{II}	34.914	-00.619
OYLL	3.366	5.834	2.005	9.929	23.822	-30.164	OYL	-1.866	-2.971	-1.822	-42.969^{I}	36.161	-00.635
FYL	2.316^{IV}	1.294	-0.477	4.134	9.377	-12.208	FYL	-1.284	-0.659	0.433	-16.915^{I}	14.636	-00.265
DS 6							**CGR**						
PYL	0.559	3.485	3.561	9.992	23.981	-32.669	PYL	-0.418	-2.335	-3.826	-42.231	-48.761^{I}	-09.053
KYL	1.548	4.273^{IV}	3.715	7.779	19.698	-25.765	KYL	-1.158	-2.863	-3.411	-34.688	-38.456^{I}	-07.048
OYL	3.408	5.763	1.887	7.983	22.153	-26.686	OYL	-2.549	-3.861	-2.028	-39.011	-39.830^{II}	-07.232
FYL	2.344	1.278	-0.449	3.324	8.720	-10.800	FYL	-1.754	-0.856	0.482	-15.357	-16.120^{II}	-03.011
HAD							**PGR**						
PYL	-0.512	-4.076	-0.476^{IV}	-8.967	-39.229	45.772	PYL	-0.345	-1.751	-1.838	-01.860	22.194	-19.889^{I}
KYL	-1.419	-3.634	-3.634	-6.981	-32.223	36.099	KYL	-0.955	-2.147	-1.638	-01.528	17.504	-15.484^{I}
OYL	-3.125	-2.160	-2.160	-7.164	-36.238	37.389	OYL	-2.104	-2.895	-0.974	-01.719	18.129	-15.889^{I}
FYL	-2.150	-0.514	-0.514	-2.983	-14.265	15.132	FYL	-1.447	-0.642	0.232	-00.676	07.337	-06.616^{I}

Note: underlined values are direct effects
PYL, KYL, OYL and FYL - Pod, kernel, oil and fodder yield-loss
HAD - Healthy leaf area duration
CGR - Crop growth rate

DS 5 and 6 - Disease severity at 85 and 95 days after sowing
VGR - Vegetative growth rate
PGR - Pod growth rate

Appendix 8: Mean performance of groundnut genotypes for disease and physiological parameters in early and late sown experiments

Genotype	DS 3		DS 5		DS 6		AUDPC		REM 3		REM 5		HAD		VGR		CGR		PGR		PC	
	E	L	E	L	E	L	E	L	E	L	E	L	E	L	E	L	E	L	E	L	E	L
D 39d	10.1^{a}	27.8^{a}	31.1^{a}	47.2^{a}	37.8^{a}	54.7^{ab}	0836.5^{a}	1562.1^{a}	35.2^{d}	30.1^{c}	28.2^{cd}	20.6^{e}	228.0^{c}	192.8^{c}	13.2^{c}	15.2^{c}	37.4^{b}	39.4^{c}	24.2^{a}	24.2^{ab}	64.7^{ab}	61.4^{b}
B 37c	15.3^{b}	32.5^{t}	32.7^{ab}	50.3^{bc}	42.9^{b}	58.2^{c}	1068.1^{b}	1816.4^{c}	25.5^{f}	19.0^{e}	21.8^{e}	14.2^{g}	250.4^{b}	237.1^{b}	19.3^{b}	18.7^{b}	43.8^{a}	40.8^{b}	24.0^{a}	22.1^{ab}	54.8^{c}	54.2^{c}
Dh 8	44.0^{g}	66.0^{i}	70.3^{f}	76.6^{f}	73.7^{e}	85.5^{e}	2593.0^{h}	3337.5^{h}	47.0^{a}	44.1^{a}	36.6^{b}	26.6^{b}	137.8^{g}	110.2^{g}	10.5^{d}	12.1^{e}	29.0^{e}	32.3^{g}	18.5^{cd}	18.2^{fd}	63.8^{b}	60.1^{bc}
R 8808	38.8^{e}	48.0^{c}	56.8^{d}	58.7^{d}	67.3^{d}	67.6^{d}	2118.6^{e}	2535.4^{e}	33.9^{d}	23.7^{d}	25.4^{d}	15.3^{g}	187.4^{d}	147.4^{e}	10.2^{d}	13.9^{cd}	31.2^{c}	34.0^{d}	21.0^{b}	20.9^{b}	67.3^{a}	60.1^{bc}
Mutant (28-2)	21.7^{c}	40.4^{c}	39.1^{c}	51.7^{bc}	47.1^{c}	55.4^{ab}	1330.6^{d}	2096.0^{d}	31.7^{de}	29.9^{c}	25.6^{d}	21.3^{e}	188.5^{d}	169.0^{d}	09.7^{d}	14.4^{cd}	28.8^{e}	34.2^{d}	19.1^{cd}	20.8^{bc}	66.3^{ab}	60.8^{bc}
JL 24	43.9^{g}	63.0^{e}	70.3^{f}	76.8^{f}	75.6^{f}	98.8^{g}	2291.3^{f}	2532.0^{e}	39.0^{c}	30.1^{c}	30.0^{c}	24.3^{c}	167.8^{e}	128.5^{f}	11.1^{cd}	12.4^{e}	31.0^{cd}	32.2^{e}	19.9^{c}	19.8^{bc}	64.2^{b}	61.5^{b}
TMV 2	48.0^{h}	66.0^{i}	77.4^{g}	80.1^{g}	83.8^{g}	99.8^{g}	2408.7^{g}	2722.2^{f}	40.5^{b}	28.6^{c}	28.9^{c}	15.5^{g}	184.4^{d}	130.7^{f}	13.1^{c}	11.0^{ef}	32.8^{c}	31.2^{e}	19.7^{cd}	19.3^{c}	63.1^{b}	61.9^{b}
TAG 24	42.2^{f}	84.2^{g}	85.5^{h}	94.4^{h}	92.6^{h}	99.5^{g}	2779.6^{i}	3029.2^{g}	38.1^{c}	32.6^{b}	28.1^{c}	18.1^{f}	106.7^{h}	084.3^{h}	11.2^{cd}	10.8^{g}	30.8^{cd}	30.5^{ef}	19.6^{cd}	19.5^{c}	63.6^{b}	63.9^{a}
ICGV 86590	38.8^{e}	63.0^{e}	67.8^{e}	71.3^{e}	73.2^{e}	88.0^{f}	2418.3^{g}	3001.4^{g}	40.9^{c}	34.1^{b}	43.8^{a}	30.4^{a}	157.3^{f}	156.0^{e}	11.4^{cd}	17.7^{b}	30.2^{cd}	40.7^{b}	19.5^{cd}	23.0^{ab}	63.1^{b}	56.5^{d}
ICGV 87165	28.4^{d}	32.1^{t}	33.4^{ab}	49.4^{b}	43.2^{b}	53.4^{a}	1147.6^{c}	1675.9^{b}	39.5^{c}	29.4^{c}	27.1^{cd}	22.6^{d}	266.7^{a}	258.0^{a}	24.4^{a}	27.0^{a}	43.7^{a}	45.6^{a}	19.3^{cd}	18.6^{cd}	44.2^{d}	40.8^{f}
Mean	32.9	52.3	56.4	65.7	63.7	76.1	1979.6	2350.4	36.9	30.2	29.3	20.9	187.5	161.4	14.0	15.7	34.1	36.3	20.1	20.6	61.6	58.1
C.D.(5%)	01.4	02.0	01.6	01.4	01.2	01.6	024.9	084.0	02.1	02.1	02.2	01.2	09.0	011.1	02.2	01.0	01.2	01.0	01.3	01.2	01.7	01.1
C.V.(%)	02.5	02.2	01.6	01.2	01.1	01.2	00.7	02.1	03.3	04.0	03.9	03.5	03.7	004.0	02.1	03.0	02.9	01.6	03.7	02.1	03.2	02.8

Figure with same superscript (s) do not differ significantly at 5 percent level of probability

E - Early sown experiment

L - Late sown experiment

UP - Unprotected condition

P- Protected condition

AUDPC - Area under disease progress curve

PGR - Pod growth rate

REM - Reproductive efficiency measure

HAD - Healthy leaf area duration

VGR - Vegetative growth rate

CGR - Crop growth rate

PC - Partitioning coefficient

DS 3, 5 and 6 - Disease severity at 65, 85 and 95 days after sowing

Appendix 9: Yield components as influenced by foliar diseases in groundnut genotypes in early sown experiment

Genotype	Shelling outturn (%)			Sound mature kernel %			Hundred seed mass (g)			Oil content (%)		
	UP	P	% R	UP	P	% R	UP	P	% R	UP	P	% R
D 39d	78.83^{a}	79.01^{a}	00.4^{a}	87.16^{a}	94.44^{ab}	07.7^{a}	37.60^{d}	40.70^{d}	07.6^{a}	47.96^{a}	48.49^{a}	01.1^{a}
B 37c	71.78^{b}	76.51^{a}	06.2^{de}	84.01^{ab}	95.42^{ab}	12.0^{b}	56.97^{a}	62.20^{a}	08.4^{a}	43.13^{b}	44.99^{c}	04.1^{bc}
Dh 8	64.71^{c}	68.06^{b}	04.9^{d}	82.20^{ab}	89.29^{c}	08.0^{a}	27.50^{f}	34.40^{e}	20.0^{d}	40.58^{c}	42.72^{e}	05.0^{bc}
R 8808	68.66^{bc}	69.84^{b}	01.7^{ab}	84.04^{ab}	96.36^{ab}	12.8^{bc}	43.90^{c}	49.97^{bc}	12.1^{b}	40.86^{c}	44.50^{cd}	08.2^{e}
Mutant (28-2)	69.13^{bc}	69.61^{b}	00.7^{a}	87.29^{ab}	93.08^{ab}	06.2^{ab}	54.07^{a}	60.93^{a}	11.4^{b}	40.87^{c}	46.61^{b}	03.7^{b}
JL 24	67.56^{bc}	69.80^{b}	03.2^{c}	84.91^{ab}	95.72^{ab}	11.3^{b}	41.63^{c}	52.30^{bc}	20.3^{d}	43.71^{b}	43.97^{cd}	00.6^{a}
TMV 2	66.28^{bc}	70.29^{b}	05.7^{de}	81.07^{ab}	97.18^{a}	16.6^{d}	33.91^{de}	47.70^{bc}	29.0^{e}	39.83^{cd}	40.38^{f}	01.3^{a}
TAG 24	66.68^{bc}	70.37^{b}	05.2^{de}	82.69^{ab}	96.27^{ab}	14.1^{bc}	36.60^{de}	53.20^{b}	31.2^{f}	38.27^{cd}	42.69^{e}	10.4^{f}
ICGV 86590	57.00^{d}	59.78^{c}	04.7^{d}	81.95^{ab}	90.87^{c}	09.5^{ab}	37.40^{d}	52.67^{b}	28.7^{e}	39.93^{cd}	45.16^{c}	11.6^{f}
ICGV 87165	59.43^{d}	62.22^{c}	04.8^{d}	85.30^{ab}	93.56^{ab}	08.8^{ab}	49.62^{b}	59.76^{a}	17.0^{c}	43.54^{b}	46.54^{b}	06.4^{d}
Mean	67.00	69.57	03.8	84.06	94.22	10.70	41.92	51.39	18.4	41.62	44.92	05.30
C.D. (5%)	03.63	02.75	01.11	03.70	03.19	01.78	03.24	04.69	01.85	02.04	00.97	01.19
C.V. (%)	03.15	02.30	14.28	02.57	01.97	09.70	04.51	05.32	05.81	02.36	01.03	13.24

Figure with same superscript (s) do not differ significantly at 5 percent level of probability

UP - Unprotected condition P- Protected condition

% R - Percent reduction over protected condition

Appendix 10: Yield components as influenced by foliar diseases in groundnut genotypes in late sown experiment

Genotype	Shelling outturn (%)			Sound mature kernel %			Hundred seed mass (g)			Oil content (%)		
	UP	P	% R	UP	P	% R	UP	P	% R	UP	P	% R
D 39d	71.88^{a}	77.45^{a}	07.2^{c}	85.90^{a}	94.95^{ab}	09.5^{a}	35.40^{d}	40.56^{f}	12.7^{a}	42.67^{a}	45.04^{a}	05.3^{ab}
B 37c	69.96^{ab}	70.94^{b}	01.4^{a}	84.16^{ab}	94.98^{ab}	11.4^{ab}	52.16^{a}	59.38^{a}	12.2^{a}	38.81^{c}	42.43^{b}	08.5^{c}
Dh 8	64.57^{bc}	70.00^{bc}	07.8^{e}	81.63^{ab}	93.36^{ab}	12.6^{a-c}	29.56^{e}	34.39^{g}	14.0^{a}	36.95^{c-e}	38.20^{d}	03.3^{a}
R 8808	65.49^{bc}	69.99^{bc}	06.4^{cd}	81.70^{ab}	94.84^{ab}	13.9^{bc}	41.52^{c}	52.11^{c}	20.3^{bc}	34.46^{f}	36.70^{e}	06.1^{bc}
Mutant (28-2)	67.14^{b}	70.88^{bc}	05.3^{cd}	85.91^{a}	98.57^{a}	12.8^{ab}	44.39^{b}	56.49^{ab}	21.4^{bc}	35.34^{f}	43.51^{ab}	18.8^{d}
JL 24	67.83^{ab}	69.53^{bc}	02.4^{ab}	84.65^{ab}	95.71^{ab}	11.6^{ab}	39.20^{c}	48.30^{d}	18.8^{b}	38.48^{cd}	40.13^{c}	04.1^{ab}
TMV 2	65.56^{bc}	68.17^{bc}	03.8^{a-c}	81.41^{ab}	95.08^{ab}	14.4^{bc}	33.30^{d}	45.20^{de}	26.3^{e}	38.84^{c}	41.18^{c}	05.7^{b}
TAG 24	61.97^{d}	68.55^{bc}	09.6^{f}	83.17^{ab}	96.09^{ab}	13.5^{bc}	33.70^{d}	47.30^{d}	28.7^{f}	31.94^{g}	38.80^{d}	17.7^{d}
ICGV 86590	56.18^{f}	60.36^{d}	06.9^{e}	76.05^{c}	90.92^{ab}	16.4^{d}	33.80^{d}	44.50^{de}	24.1^{d}	37.28^{c-e}	40.21^{c}	07.3^{bc}
ICGV 87165	59.11^{e}	61.80^{d}	04.4^{bc}	81.45^{ab}	91.69^{ab}	11.2^{ab}	45.10^{b}	55.80^{ab}	19.2^{b}	40.53^{b}	44.09^{ab}	08.1^{c}
Mean	64.97	68.77	05.50	82.60	94.62	12.80	38.82	48.40	19.80	37.53	41.03	08.50
C.D. (5%)	02.47	02.67	01.37	04.11	03.94	01.77	03.50	03.31	01.96	01.20	01.13	01.50
C.V. (%)	02.22	02.26	14.46	02.90	02.43	08.07	05.25	03.98	05.78	01.87	01.60	10.30

Figure with same superscript (s) do not differ significantly at 5 percent level of probability
UP - Unprotected condition P - Protected condition
% R - Percent reduction over protected condition

Appendix 11: Productivity as influenced by foliar diseases in groundnut genotypes in early sown experiment

Genotype	Pod yield (q ha^{-1})			Kernel yield (q ha^{-1})			Oil yield (q ha^{-1})			Fodder yield (t ha^{-1})		
	UP	P	% R	UP	P	% R	UP	P	% R	UP	P	% R
D 39d	39.73^{a}	45.74^{ab}	13.1^{ab}	30.79^{a}	36.58^{a}	15.8^{ab}	14.93^{a}	17.54^{a}	14.8^{a}	14.03^{c}	15.71^{c}	10.6^{a}
B 37c	39.24^{a}	47.09^{ab}	16.6^{ab}	28.20^{ab}	36.03^{a}	21.8^{b}	12.17^{ab}	16.20^{ab}	24.9^{b}	18.14^{b}	20.34^{b}	10.8^{a}
Dh 8	29.11^{bc}	38.36^{bc}	24.1^{cd}	22.09^{ab}	26.04^{bc}	15.4^{ab}	08.94^{ab}	11.07^{ab}	17.6^{a}	07.30^{g}	09.62^{e}	27.3^{b}
R 8808	32.61^{b}	45.65^{ab}	23.7^{c}	22.39^{ab}	31.81^{ab}	29.6^{c}	09.15^{ab}	14.16^{ab}	35.4^{c}	09.87^{ef}	10.98^{e}	10.1^{a}
Mutant (28-2)	38.30^{a}	43.06^{ab}	11.2^{a}	26.48^{ab}	29.99$^{a\text{-}c}$	11.8^{a}	11.81^{ab}	13.98^{ab}	15.5^{a}	11.84^{d}	13.04^{d}	09.2^{a}
JL 24	23.88^{c}	39.98^{bc}	40.4^{f}	16.11^{c}	27.90$^{a\text{-}c}$	42.3^{d}	07.04^{ab}	12.27^{ab}	42.6^{cd}	08.51^{ef}	17.5^{c}	51.5^{d}
TMV 2	23.53^{c}	40.73^{bc}	42.3^{f}	15.57^{c}	32.25^{ab}	51.6^{e}	06.20^{ab}	13.03^{ab}	52.0^{e}	06.80^{g}	17.75^{c}	61.7^{e}
TAG 24	25.12^{bc}	37.24^{bc}	32.6^{e}	16.79^{c}	25.54^{bc}	27.4^{c}	06.43^{ab}	10.91^{ab}	38.1^{cd}	06.31^{g}	09.86^{e}	36.0^{c}
ICGV 86590	30.61^{b}	42.44$^{a\text{-}c}$	28.0^{cd}	17.49^{c}	25.39^{bc}	31.2^{c}	07.05^{ab}	11.47^{ab}	38.7^{cd}	10.32^{e}	17.04^{c}	39.5^{c}
ICGV 87165	41.22^{a}	49.50^{a}	15.9^{ab}	25.54^{ab}	30.80^{ab}	20.4^{ab}	10.66^{ab}	14.33^{ab}	25.6^{b}	24.28^{a}	27.33^{a}	11.2^{a}
Mean	32.34	42.98	24.8	22.04	30.23	26.70	09.43	13.50	30.50	11.74	15.92	26.8
C.D. (5%)	05.17	04.64	03.9	04.96	04.99	05.34	04.96	04.99	05.71	01.39	01.26	04.0
C.V. (%)	06.32	06.29	09.1	11.64	09.62	13.12	10.90	09.45	13.04	06.88	04.63	08.7

Figure with same superscript (s) do not differ significantly at 5 percent level of probability

UP - Unprotected condition P- Protected condition

% R - Percent reduction over protected condition

Appendix 12: Productivity as influenced by foliar diseases in groundnut genotypes in late sown experiment

Genotype	Pod yield (q ha^{-1})			Kernel yield (q ha^{-1})			Oil yield (q ha^{-1})			Fodder yield (t ha^{-1})		
	UP	P	% R	UP	P	% R	UP	P	% R	UP	P	% R
D 39d	37.66^{a}	42.25^{ab}	10.9^{b}	27.05^{a}	32.72^{a}	17.3^{b}	11.54^{a}	14.74^{a}	21.6^{b}	10.08^{b}	12.74^{cd}	20.9^{b}
B 37c	36.87^{a}	39.47^{ab}	06.6^{a}	26.62^{a}	27.15^{ab}	01.9^{a}	10.33^{b}	11.52^{bc}	10.4^{a}	05.28^{e}	19.27^{b}	20.7^{b}
Dh 8	28.79^{c}	32.70^{d}	12.0^{b}	18.61^{bc}	22.90^{cd}	18.7^{b}	06.99^{cd}	08.74^{de}	20.1^{b}	06.66^{cd}	09.79^{e}	32.0^{d}
R 8808	28.35^{c}	41.82^{ab}	32.3^{d}	18.53^{bc}	29.28^{ab}	36.7^{e}	06.38^{de}	10.74^{cd}	40.6^{e}	08.38^{bc}	10.80^{e}	22.4^{bc}
Mutant (28-2)	33.00^{ab}	42.77^{a}	23.8^{c}	21.78^{b}	30.07^{ab}	27.4^{cd}	07.69^{cd}	13.08^{b}	41.0^{e}	09.69^{b}	12.43^{d}	25.9^{bc}
JL 24	22.72^{d}	36.46^{bc}	37.7^{e}	15.41^{de}	26.22^{c}	39.0^{e}	05.93^{e}	10.11^{cd}	41.6^{e}	07.60^{cd}	13.88^{cd}	45.3^{e}
TMV 2	21.72^{d}	36.58^{bc}	41.9^{f}	13.68^{de}	25.03^{cd}	45.3^{f}	05.32^{ef}	10.31^{cd}	48.4^{f}	06.82^{cd}	13.92^{cd}	51.0^{f}
TAG 24	23.97^{d}	35.55^{bc}	35.4^{e}	14.83^{de}	24.51^{cd}	39.5^{e}	04.74^{ef}	09.51^{de}	50.2^{f}	04.82^{e}	08.18^{f}	37.2^{de}
ICGV 86590	29.18^{c}	38.60^{a-c}	24.4^{c}	16.37^{d}	23.19^{cd}	29.4^{cd}	06.10^{de}	09.36^{de}	34.8^{d}	09.10^{bc}	14.33^{c}	33.7^{de}
ICGV 87165	34.73^{ab}	44.53^{a}	22.1^{c}	20.52^{bc}	27.54^{ab}	25.5^{c}	08.32^{c}	12.14^{bc}	31.5^{c}	23.19^{a}	26.84^{a}	13.6^{a}
Mean	29.65	39.07	24.70	19.34	26.76	28.10	07.34	11.02	34.00	10.16	14.22	30.30
C.D. (5%)	03.48	03.30	02.45	02.03	03.04	02.99	00.80	01.17	02.89	01.14	01.40	03.50
C.V. (%)	05.79	04.92	06.84	06.12	06.62	06.81	06.39	06.16	04.95	06.56	05.75	06.80

Figure with same superscript (s) do not differ significantly at 5 percent level of probability
UP - Unprotected condition P- Protected condition
% R - Percent reduction over protected condition

Appendix 13: Per day productivity (g m^{-2} d^{-1}) of groundnut genotypes across disease pressure and dates of sowing

Genotype	Pod yield				Kernel yield				Oil yield				Fodder yield			
	Early sown		Late sown		Early sown		Late sown		Early sown		Late sown		Early sown		Late sown	
	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P
D 39d	3.65	4.16	3.56	3.91	2.83	3.32	2.55	3.03	1.37	1.60	1.09	1.37	12.87	14.28	09.51	11.88
B 37c	3.47	4.10	3.35	3.52	2.50	3.13	2.42	2.42	1.08	1.41	0.94	1.03	16.05	17.69	13.89	17.21
Dh 8	2.91	3.80	2.94	3.27	2.21	2.58	1.90	2.29	0.89	1.10	0.71	0.87	07.30	09.53	06.79	09.79
R 8808	3.26	4.52	2.89	4.18	2.24	3.15	1.89	2.93	0.92	1.40	0.65	1.07	09.87	10.87	08.55	10.80
Mutant (28-2)	3.76	4.06	3.30	4.19	2.60	2.83	2.18	2.95	1.16	1.32	0.77	1.28	11.61	12.30	09.69	12.19
JL 24	2.39	3.96	2.32	3.64	1.61	2.76	1.57	2.62	0.70	1.22	0.61	1.11	08.51	17.33	07.76	13.88
TMV 2	2.35	4.03	2.22	3.66	1.56	3.19	1.40	2.50	0.62	1.29	0.54	1.03	06.80	17.57	06.96	13.92
TAG 24	2.64	3.76	2.66	3.86	1.77	2.58	1.65	2.66	0.68	1.10	0.53	1.03	06.64	09.96	05.36	08.90
ICGV 86590	2.66	3.59	2.61	3.35	1.52	2.15	1.46	2.01	0.61	0.97	0.55	0.81	08.97	14.44	08.13	12.46
ICGV 87165	3.44	4.07	2.94	3.71	2.13	2.52	1.74	2.29	0.89	1.20	0.71	1.00	20.23	22.40	19.65	22.37
Mean	3.07	4.00	2.88	3.72	2.09	2.81	1.88	2.55	0.90	1.26	0.71	1.05	11.14	14.82	09.88	13.56

UP - Unprotected condition P - Protected condition

Appendix 14: **Pod and kernel accumulation (%) pattern of groundnut genotypes across disease pressure and dates of sowing**

Genotype		Pod accumulation pattern (%)								Kernel accumulation pattern (%)							
		60 DAS		60-75 DAS		75-90 DAS		90 DAS -DOH		60 DAS		60-75 DAS		75-90 DAS		90s DAS -DOH	
		UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P
D 39d	E	29.5	34.3	37.7	34.4	24.7	28.7	08.3	02.7	19.6	20.0	38.8	49.2	35.0	25.8	06.6	05.0
	L	37.6	37.9	43.5	51.6	06.5	07.3	12.5	03.3	21.0	22.5	59.8	54.3	17.5	13.1	01.6	10.1
B 37c	E	13.9	20.9	39.7	35.0	16.9	13.9	29.5	30.3	07.2	07.7	36.2	33.0	21.9	27.9	34.7	31.4
	L	13.6	13.7	48.1	66.2	27.3	04.2	11.0	15.8	04.3	05.5	48.4	51.6	32.9	29.1	14.4	13.8
Dh 8	E	28.4	24.3	13.9	37.1	34.7	24.6	23.0	14.0	13.2	17.3	29.1	45.1	42.4	22.3	15.3	15.4
	L	36.6	39.4	39.0	40.8	15.9	05.7	08.3	14.0	31.0	34.8	55.7	40.5	10.2	16.5	03.1	09.6
R 8808	E	39.5	36.8	37.7	30.1	15.9	28.6	06.8	04.6	24.6	23.3	53.7	38.7	16.1	30.6	05.7	07.4
	L	45.3	38.6	41.2	41.6	07.7	07.3	05.8	12.5	22.8	21.8	48.7	49.2	16.9	18.2	11.5	10.8
Mutant	E	28.2	32.0	47.6	35.6	15.2	12.1	13.5	20.3	21.3	21.4	45.2	43.1	23.7	19.9	09.9	15.6
(28-2)	L	49.0	44.0	23.6	34.2	26.4	09.0	01.0	12.7	27.7	27.0	41.1	37.2	27.4	21.9	03.8	14.0
JL 24	E	44.8	44.6	40.8	41.8	08.7	07.4	05.6	06.3	36.3	32.7	50.5	51.6	06.4	08.8	06.8	06.9
	L	56.2	52.5	32.6	37.0	06.2	04.7	05.0	05.8	39.2	33.0	45.5	49.8	08.4	11.3	06.9	05.9
TMV 2	E	36.1	42.3	45.0	40.0	16.4	08.7	02.6	08.9	35.2	28.7	51.1	44.5	11.3	19.4	02.5	07.4
	L	54.9	51.7	27.4	32.7	11.3	06.7	06.4	08.9	43.5	40.0	35.7	35.5	15.3	15.4	05.6	09.1
TAG 24	E	65.1	63.3	26.8	07.5	05.9	20.2	02.1	09.0	65.5	54.3	22.3	20.5	09.0	16.4	03.2	08.8
	L	70.8	55.4	22.8	34.9	02.3	05.4	04.1	04.3	56.7	45.9	26.4	40.9	12.1	06.4	04.8	06.8
ICGV	E	23.9	17.9	44.6	47.3	26.4	22.6	05.2	12.3	14.0	13.5	47.0	44.4	31.4	28.3	07.7	13.8
86590	L	41.5	44.6	43.6	53.5	02.0	01.2	12.8	00.7	21.4	21.3	42.7	46.8	28.0	36.5	07.9	03.0
ICGV	E	08.5	07.3	41.2	50.8	18.9	10.9	31.5	30.9	03.4	04.1	40.1	49.1	24.4	19.3	32.1	27.5
87165	L	06.2	07.7	44.5	34.5	41.5	50.8	07.9	07.0	02.8	05.0	38.2	25.2	52.5	60.7	06.5	09.2
Mean	E	32.0	32.3	37.2	35.8	18.3	17.9	12.6	13.8	24.2	22.3	41.2	41.9	22.1	22.0	12.6	13.8
	L	41.1	38.8	36.7	42.7	14.6	10.4	07.7	08.4	27.1	25.7	44.2	43.1	22.1	22.9	06.6	09.2

E - Early sown experiment
DAS - Days after sowing

L - Late sown experiment
DOH - Date of harvest

UP - Unprotected condition

P- Protected condition

Appendix 15: Flowering behaviour/pattern in groundnut genotypes in early and late sown experiments

Genotype	DIF		DFF		D 25FA		D 50FA		D 75FA		TFC	
	E	L	E	L	E	L	E	L	E	L	E	L
D 39d	27.7^{b}	25.7^{c}	30.3^{bc}	29.0^{ab}	06.9^{ab}	06.5^{ab}	13.3^{ab}	11.8^{ab}	19.2^{ab}	15.8^{ab}	69.4^{bc}	091.5^{ab}
B 37c	28.3^{bc}	26.0^{c}	31.0^{bc}	28.7^{ab}	07.9^{b}	07.1^{b}	13.2^{ab}	12.9^{ab}	23.2^{cd}	18.5^{c}	82.1^{a}	110.0^{a}
Dh 8	30.7^{cd}	28.7^{d}	34.3^{e}	30.7^{ab}	07.5^{ab}	07.9^{c}	15.1^{ab}	15.0^{c}	25.0^{cd}	18.0^{c}	55.4^{cd}	053.4^{cd}
R 8808	28.3^{bc}	25.0^{b}	30.7^{bc}	28.7^{ab}	08.4^{bc}	07.0^{b}	14.4^{ab}	12.1^{ab}	19.8^{ab}	17.8^{c}	69.1^{b}	097.1^{ab}
Mutant (28-2)	30.0^{cd}	26.0^{c}	33.0^{d}	29.0^{ab}	06.5^{ab}	06.5^{ab}	13.4^{ab}	12.5^{ab}	21.2^{ab}	21.5^{d}	59.9^{bc}	064.3^{cd}
JL 24	29.0^{bc}	25.0^{b}	31.0^{bc}	28.0^{ab}	07.0^{ab}	06.8^{ab}	12.5^{ab}	12.0^{ab}	19.4^{ab}	14.0^{a}	50.8^{cd}	057.1^{cd}
TMV 2	28.3^{bc}	26.0^{c}	30.0^{b}	27.7^{ab}	06.5^{ab}	06.2^{ab}	12.4^{ab}	10.1^{a}	20.8^{ab}	13.8^{a}	50.8^{cd}	067.6^{cd}
TAG 24	24.3^{a}	22.3^{a}	28.3^{a}	27.0^{a}	05.5^{a}	05.8^{a}	11.3^{a}	10.7^{ab}	19.0^{a}	15.0^{ab}	55.1^{cd}	059.3^{cd}
ICGV 86590	29.0^{bc}	25.0^{b}	30.7^{b}	27.7^{ab}	11.5^{d}	11.2^{d}	19.9^{c}	20.8^{d}	22.0^{ab}	22.0^{d}	55.0^{cd}	066.3^{cd}
ICGV 87165	30.7^{cd}	28.3^{d}	33.3^{d}	35.0^{ab}	14.7^{c}	15.0^{c}	23.4^{d}	24.4^{e}	27.6^{e}	32.2^{e}	65.0^{b}	073.5^{c}
Mean	28.6	25.8	31.3	29.1	08.2	08.0	14.9	14.2	21.7	18.9	60.2	073.0
C.D. (5%)	1.00	0.61	0.85	1.38	1.16	0.61	1.95	2.23	2.03	1.83	8.16	14.07
C.V. (%)	2.10	1.40	1.70	2.90	8.50	4.60	7.90	9.4	5.70	5.90	8.20	11.60

Figure with same superscript (s) do not differ significantly at 5 percent level of probability

E - Early experiment
L - Late sown experiment
DIF - Days to initiation of flowering
DFF - Days to fifty percent flowering
TFC - Total flower count
D 25, 50 and 75 FA - Days taken for 25, 50 and 75 flower accumulation

Appendix 16: Mean performance of groundnut genotypes for fatty-acid composition in different disease pressure and dates of sowing

Genotype		Palmitic acid (16:0)		Stearic Acid (18:0		Oleic acid (18:1)		Linoleic acid (18:2)		Arachidic acid (20:0)		Ecosenic acid (20:1		Behenic acid (22:0		Lignoceric acid (24:0)		USF		SF		O/L Ratio		P/S Ratio	
		UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P	UP	P
D 39d	E	10.6	10.5	2.5	2.2	49.5	49.2	27.8	28.2	1.5	1.4	1.5	1.5	4.9	5.0	2.0	2.1	78.7	78.9	21.3	21.1	1.78	1.76	1.30	1.34
	L	10.7	10.4	2.4	2.5	48.0	47.5	29.5	29.9	1.5	1.6	1.4	1.5	4.8	4.9	1.9	1.9	78.8	78.8	21.2	21.2	1.63	1.55	1.40	1.42
B 37c	E	12.1	11.7	2.4	2.8	43.8	42.8	32.8	32.8	1.3	1.6	1.3	1.2	4.4	5.0	2.0	2.2	77.8	76.8	22.2	23.2	1.36	1.31	1.44	1.41
	L	12.1	11.3	2.1	2.4	42.1	43.8	34.1	33.5	1.4	1.4	1.4	1.3	4.9	4.3	2.1	2.0	77.6	78.6	22.4	21.4	1.23	1.31	1.53	1.57
Dh 8	E	11.3	10.2	2.0	1.7	44.9	48.3	33.2	32.1	1.2	1.0	1.4	1.4	4.2	3.5	2.0	1.9	79.4	81.8	20.6	18.3	1.36	1.50	1.62	1.76
	L	11.1	10.4	2.2	2.0	45.3	45.4	33.6	34.6	1.2	1.2	1.2	1.3	3.8	3.5	1.8	1.7	80.1	81.2	20.0	18.8	1.35	1.32	168	1.85
R 8808	E	12.3	12.1	1.6	1.7	36.2	36.3	40.2	41.2	1.0	1.1	1.6	1.4	4.8	4.3	2.4	2.1	78.0	78.8	22.0	21.2	0.90	0.88	1.84	1.94
	L	12.5	12.3	1.7	1.9	36.1	37.5	40.1	39.5	1.1	1.1	1.6	1.5	4.9	4.5	2.2	1.9	77.7	78.5	22.2	21.6	0.90	0.93	1.81	1.83
Mutant (28-2)	E	13.2	12.6	2.5	2.7	36.6	38.0	38.5	38.3	1.4	1.4	1.1	1.0	5.0	4.2	1.9	1.7	76.2	77.3	23.8	22.6	0.96	0.99	1.62	1.70
	L	12.7	12.8	2.0	2.5	36.0	37.3	39.3	39.1	1.4	1.4	1.2	1.0	5.8	4.3	1.9	1.7	76.4	77.4	23.7	22.6	0.92	0.96	1.67	1.73
JL 24	E	13.0	12.6	3.0	2.8	36.6	37.6	38.2	39.1	1.6	1.4	1.0	0.9	5.0	4.2	1.7	1.5	75.8	77.6	24.0	22.4	0.96	0.96	1.58	1.75
	L	12.6	12.5	3.0	2.6	37.2	38.0	38.4	39.0	1.6	1.4	1.0	1.0	4.9	4.3	1.6	1.5	76.5	78.0	23.6	22.1	0.97	0.98	1.63	1.77
TMV 2	E	13.0	12.1	3.5	4.1	37.3	38.9	35.3	35.3	1.9	1.9	1.1	0.9	6.2	5.3	1.8	1.5	73.7	75.3	26.5	24.9	1.06	1.10	1.35	1.42
	L	12.7	12.1	4.5	3.5	36.4	38.1	35.4	35.7	2.3	1.8	0.9	0.9	6.4	6.2	1.5	1.6	72.7	74.7	27.4	25.2	1.03	1.07	1.30	1.42
TAG 24	E	13.3	12.3	3.1	3.5	36.9	39.7	37.9	37.2	1.6	1.6	1.0	0.8	4.7	3.6	1.6	1.3	75.8	77.7	24.2	22.3	0.97	1.07	1.57	1.67
	L	13.1	11.9	3.3	3.4	36.5	38.9	37.7	36.9	1.7	1.6	1.0	0.8	5.3	5.3	1.6	1.4	75.2	76.6	25.6	23.5	0.97	1.06	1.52	1.58
ICGV 86590	E	12.2	12.0	1.9	2.1	36.6	36.5	39.6	40.7	1.2	1.2	1.4	1.4	5.3	4.5	2.0	1.8	77.5	78.5	22.5	21.5	0.93	0.90	1.76	1.90
	L	12.4	12.6	2.1	1.9	37.3	38.2	39.0	37.0	1.2	1.3	1.4	1.5	4.9	5.3	1.9	2.3	77.6	76.6	22.4	23.3	0.96	1.04	1.74	1.60
ICGV 87165	E	11.1	11.1	2.5	2.5	47.1	46.3	30.3	30.9	1.5	1.4	1.2	1.2	4.7	4.7	1.9	2.0	78.5	78.4	21.5	21.6	1.56	1.50	1.41	1.44
	L	10.6	10.7	2.8	2.5	46.5	45.7	30.4	31.6	1.6	1.5	1.3	1.3	4.9	4.9	2.0	2.0	78.1	78.6	21.8	21.5	1.53	1.45	1.39	1.47
Mean	E	12.2	11.7	2.5	2.6	40.5	41.3	35.4	35.6	1.4	1.4	1.2	1.2	4.9	4.4	1.9	1.8	77.0	78.1	22.8	21.9	1.18	1.20	1.55	1.63
	L	12.1	11.7	2.6	2.5	40.0	40.1	35.7	35.7	1.5	1.4	1.2	1.2	5.1	4.7	1.8	1.8	77.1	77.9	23.0	22.1	1.15	1.17	1.57	1.62
C.D.(5%)	E	0.5	0.4	0.3	0.4	1.8	1.5	1.4	1.1	0.2	0.1	0.1	0.1	0.3	0.2	0.1	0.1	0.5	0.4	0.3	0.4	0.1	0.1	0.1	0.1
	L	0.4	0.7	0.6	0.6	2.0	2.3	1.1	2.6	0.1	0.2	0.2	0.2	1.0	1.4	0.2	0.3	0.8	1.1	0.8	1.1	0.1	0.1	0.1	0.2
C.V. (%)	E	1.8	1.7	5.2	6.7	2.2	1.7	1.9	1.5	5.6	4.5	5.3	4.3	2.9	1.7	3.6	2.8	0.4	0.3	0.7	1.1	4.3	3.4	1.9	1.7
	L	1.4	3.0	10.9	11.1	2.4	2.7	1.4	3.5	4.6	5.4	8.4	7.0	9.0	13.8	3.9	6.7	0.6	0.8	1.9	3.0	3.4	5.9	2.1	6.3

E - Early sown experiment L - Late sown experiment UP - Unprotected condition P - Protected condition

GENETIC ANALYSES OF RESISTANCE TO LATE LEAF SPOT AND RUST *VIS-À-VIS* PRODUCTIVITY IN GROUNDNUT (*Arachis hypogaea* L.)

B. N. MOTAGI

ABSTRACT

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Evaluation of 100-groundnut germplasm revealed inter-specific derivatives and mutants as the most potential source of resistance to late leaf spot (LLS) and rust. Components of resistance were more reliable than field disease scores in assessing resistance in germplasm. Though resistance was strongly associated with late maturity, mutants and second cycle inter-specific derivatives combined resistance and early maturity.

Resistant mutants isolated from VL 1 were grouped in to three distinct clusters. Late leaf spot resistant mutants were susceptible to rust and had more branches; higher seed mass and pod yield and reduced leaf size. An opposite trend was evident with rust resistant mutants indicating their pleiotrophic nature.

Evaluation of 10 selected genotypes revealed significant variation for yield loss. Besides resistance parameters, physiological attributes viz., growth rates and partitioning contributed to reduction in yield loss. Late sowing was ideal for disease screening. An inter-specific derivative (D 39d) and a mutant (28-2) combined resistance with high yield and early maturity and they were superior to cultivated varieties. D 39d was also superior in oil quality.

Physiological analyses of yield loss variation indicated predominant role for sink than source in determining the yield potential of genotypes. Significant interaction between LLS and rust revealed a need for evaluation of genetic material both under natural, where they occur together, as well as individual disease conditions.

Two sets of duplicate-complementary recessive genes independently determined resistance to LLS and rust in inter-specific derivatives and mutants.

A combination of isozyme (Glutamate Oxaloacetate Transaminase) and protein (seed and hypocotyl) profiles could be used uniquely to fingerprint selected genotypes. Polymorphism for peroxidase in resistant and susceptible variants indicated its potential for marker-assisted selection. Peroxidase activity also revealed inducible and constitutive nature of LLS resistance in mutants and inter-specific derivatives, respectively.