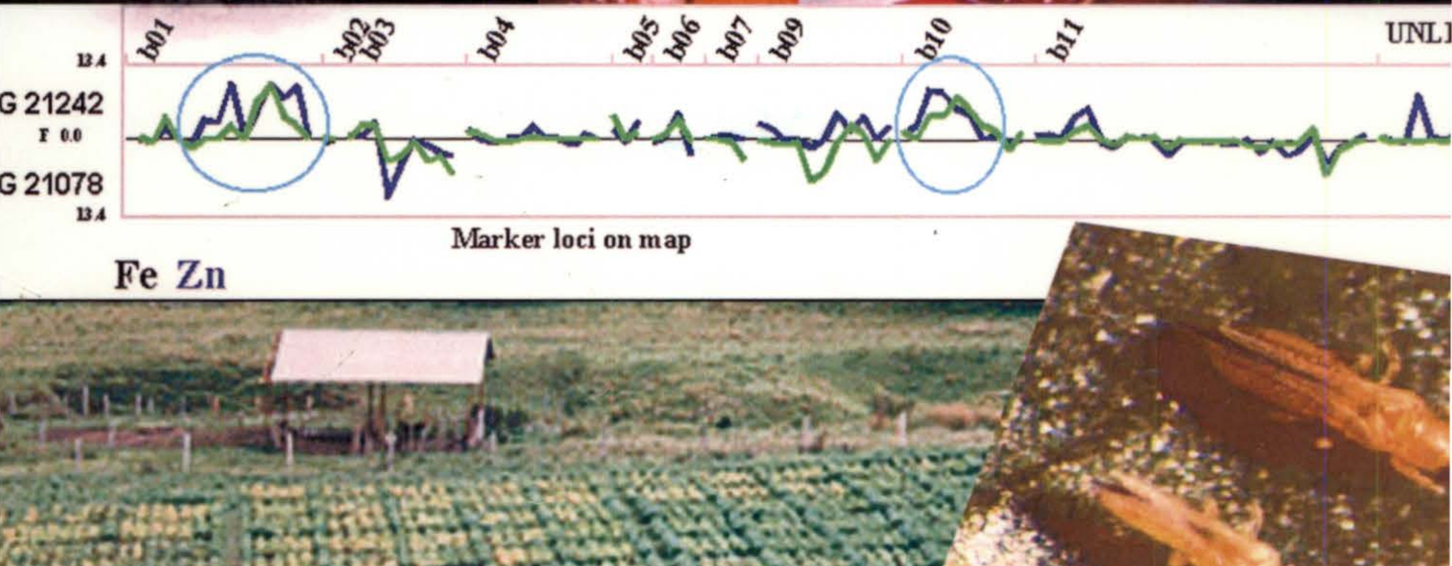
Annual Report 2000

Project IP-1

Bean Improvement for Sustainable Productivity, Input Use Efficiency, and Poverty Alleviation



CIAT
Centro Internacional de Agricultura Tropical
International Center for Tropical Agriculture

ANNUAL REPORT
2000

PROJECT IP-1

Bean Improvement for Sustainable Productivity, Input Use Efficiency, and Poverty Alleviation

Edited by Annie L. Jones

CIAT
Centro Internacional de Agricultura Tropical
International Center for Tropical Agriculture

Table of Contents

IP-1: Project Overview[1]

Title: Bean Improvement for Sustainable Productivity, Input Use Efficiency, and Poverty Alleviation

Objective: To increase bean productivity through improved cultivars and natural resource management practices in partnership with NARS and Regional Networks.

Outputs: High-yielding beans with less dependency on pesticides, fertilizers, and water. Beans with stable yield and high nutritional value that combine abiotic and biotic constraints' resistance.

Gains: Improved varieties grown on 40% of the area in Latin America by year 2003. Productivity stabilized and bean availability secured for poor rural and urban consumers in targeted areas. Pesticide use cut by 40% in targeted areas, thus reducing hazards to environment and health. Public and private researchers have access to beans with multiple resistance. Research capacity strengthened through regional networks.

Milestones:

2000 Lines combining resistance to BGMV, common bacterial blight, and BCMV are distributed in Central America, the Caribbean, and the Andean zone; IPM components and systems for whiteflies, pod borers, and leafminers developed and tested. Phosphorus-efficient and aluminum-tolerant genotypes developed.

2001 Parental materials with improved drought tolerance distributed. Strategy developed for stable angular leaf spot resistance. Molecular markers developed for P efficiency.

2002 Commercial-seeded lines combining resistance to BCMV, BCMNV, BSMV, and bean sterility virus will be available. Nutritional quality traits incorporated into cultivars.

2003 Marker-assisted selection developed for various biotic constraints. Lines with resistance to ALS, drought, and BGMV developed. Specialty types developed in Andean beans.

Users: Small-scale farmers in tropical America and Africa will obtain higher and more stable yields. Poor consumers, especially women and children, will benefit from low-cost protein and micronutrients. The environment and community at large will benefit from reduced pesticide and fertilizer use. Food legume researchers will access an enhanced knowledge base and germplasm.

Collaborators: *Regional networks and institutions*: PROFRIJOL and PROFRIZA (Central and Andean America); PABRA (Africa). *International institutions* such as CATIE and EAP-Zamorano (Central America). Universities and other institutions in Australia, Belgium, Canada, France, Spain, Switzerland, and USA. *Resistance breeding and gene tagging*: Bean/Cowpea CRSP.

CGIAR system linkages: Breeding (70%); Crop Production Systems (10%); Protecting the Environment (10%); Networks (5%); Training (5%).

CIAT project linkages: Germplasm conservation (SB-1), germplasm characterization (SB-2). IP-1 contributes to: improved beans for Africa (IP-2), IPM (PE-1), fertilizer efficiency (PE-2), sustainable hillside systems (PE-5), and participatory research (SN-3). Its impact is assessed in BP-1.

---

[1] For acronyms and abbreviations used, see page 187.

PROJECT WORK BREAKDOWN STRUCTURE

Project IP- 1: Bean Improvement for Sustainable Productivity, Input Use Efficiency, and Poverty Alleviation

Project Purpose

To increase bean productivity through improved cultivars and natural resource management practices in partnership with NARS and Regional Networks.

OUTPUTS	**Improved small-seeded Middle American bean germplasm with less dependence on inputs.**	**Improved large-seeded Andean bean germplasm with less dependence on inputs.**	**Strategies developed for management of diseases and pests in bean-based cropping systems.**	**Improved cultivars and management practices developed and tested in partnership with IP-2 Project (Africa), NARS, and Regional Networks.**
ACTIVITIES	• Developing germplasm tolerant to abiotic stresses of drought and low soil fertility. • Developing germplasm with multiple resistance to diseases. • Developing germplasm with resistance to pests: *Zabrotes, Acanthoscelides, Empoasca, Apion, Thrips palmi,* and bruchids. • Incorporating wider genetic diversity into beans.	• Developing germplasm resistant to diseases. • Developing germplasm resistant to insects. • Incorporating wider genetic diversity into beans.	• Characterizing and monitoring pathogen and insect diversity. • Characterizing disease and insect resistance genes. • Developing IPM components.	• Supporting breeding programs in NARS, Regional Networks, farmers' associations, and CIALs, with germplasm and technical knowledge. • Collaborative projects developed and executed with NARS and Regional Networks. • Supporting NARS and Regional Network researchers on soil and crop management. • Supporting human resource development in NARS and Regional Networks.

LOGICAL FRAMEWORK MATRIX[2]

PROJECT: **Bean Improvement for Sustainable Productivity, Input Use Efficiency, and Poverty Alleviation**
CODE: IP-1
MANAGER: César Cardona
TIME: January 2000- December 2000

Narrative Summary of Outputs	Objectively Verifiable Indicators	Means of Verification	Critical Assumptions
Goal: To obtain a lasting increase in food availability and incomes of the poor through improved bean productivity.	Increased bean production with improved cultivars and natural resource management practices.	National production statistics.	Adoption continues at least at rates comparable to those in the past.
Purpose: To increase bean productivity through improved cultivars and natural resource management practices in partnership with NARS and Regional Networks.	NARS and Regional Networks use improved cultivars and/or management practices on 15% of the area in Latin America by the year 2000.	Reports of NARS and Regional Networks. Publications. CIAT Reports.	Critical mass of bean researchers and operation budgets are maintained. Continued donor support to Regional Networks.
Output: 1. **Improved small-seeded Middle American bean germplasm with less dependence on inputs.**	Improved parents/populations/lines available to NARS and Regional Networks.	Report of NARS and Regional Networks. Annual reports and publications.	Continued donor support to PROFRIJOL and CIAT. Continued input of SS breeder.
Activities: 1.1 Developing germplasm tolerant to abiotic stresses of drought and low soil fertility.	• Parents/populations/lines tolerant to drought/ low soil fertility available.	Report of NARS and Regional Networks. Annual reports and publications.	Continued Plant Nutritionist's input.
1.2 Developing germplasm with multiple resistance to diseases.	• Parents/populations/lines resistant to ALS, ANT, CBB, BCMV, BGMV available.	Report of NARS and Regional Networks. Annual reports and publications.	Continued full SS Pathologist input. Continued Virologist input.
1.3 Developing germplasm with resistance to pests: *Zabrotes*, *Acanthoscelides, Empoasca*, *Apion, Thrips palmi*, and bruchids	• Parents/populations/lines resistant to Mexican bean weevil, leafhopper, and pod weevil are available.	Report of NARS and Regional Networks. Annual reports and publications.	Continued Entomologist's input.
1.4 Incorporating wider genetic diversity into beans.	• QTL analysis completed for at least one population.	Annual reports.	Adequate budget to sustain level of activity.

Continued.

---

[2] For acronyms and abbreviations used, see page 187.

LOGICAL FRAMEWORK MATRIX – continued.

Narrative Summary of Outputs	Objectively Verifiable Indicators	Means of Verification	Critical Assumptions
Output: **2. Improved large-seeded Andean bean germplasm with less dependence on inputs.**	Improved parents/populations/lines available to NARS and Regional Networks.	Report of NARS and Regional Networks. Annual reports and publications.	Continued donor support to the Andean zone, PROFRIJOL and CIAT. Continued input of SS breeder for the Andean zone.
Activities: 2.1 Developing germplasm resistant to diseases.	• Parents/populations/lines resistant to ALS, ANT, CBB, BCMV, and BGMVare available.	Report of NARS and Regional Networks. Annual reports and publications.	Continued full SS Pathologist input. Continued Virologist input.
2.2 Developing germplasm resistant to insects.	• Parents/populations/lines resistant to Mexican bean weevil and leafhopper are available.	Report of NARS and Regional Networks. Annual reports and publications.	Continued Entomologist input.
2.3 Incorporating wider genetic diversity into beans.	• Find QTL derived from wild beans that can be useful in improving cultivated beans.	Molecular analysis.	Continued input of breeder and Pathologist.
Output: **3. Strategies developed for management of diseases and pests in bean-based cropping systems.**	IPM strategies developed. Gene combinations to control insects and pathogens determined.	Report of NARS and Regional Networks. Annual reports and publications.	Continued input of Pathologist, Entomologist, and Virologist. Continued donor support to whitefly IPM project.
Activities: 3.1 Characterizing and monitoring pathogen and insect diversity.	• Variability of pathogens and insects is known. • Spacial distribution of pathotypes/biotypes defined.	Collection of pathogen isolates and insects available.	Continued active collaboration with partners. Core support to collections.
3.2 Characterizing disease and insect resistance genes.	• Genes resistant to specific races of pathogens and biotypes of insects identified. • Strategy for stable resistance to ALS and anthracnose developed.	Reports and publications.	Continued collaboration with ARO.
3.3 Developing IPM components.	• Individual IPM components are available for whitefly control.	Report of NARS and Regional Networks. Annual reports and publications.	Continued participation of members in systemwide initiative on IPM. Continued donor support to whitefly IPM project.

Continued.

LOGICAL FRAMEWORK MATRIX – continued.

Narrative Summary of Outputs	Objectively Verifiable Indicators	Means of Verification	Critical Assumptions
Output: **4. Improved cultivars and management practices developed and tested in partnership with IP-2 Project (Africa), NARS, and Regional Networks.**	Bean productivity increased. Farmers' dependence on inputs reduced. Production costs reduced.	Trials on experiment stations and on-farm. National statistics. Publications.	Continued donor support. Active collaboration with all partners involved, including farmers.
Activities: 4.1 Supporting breeding programs in NARS, Regional Networks, farmers' associations, and CIALs, with germplasm and technical knowledge.	• Improved germplasm and methodologies are incorporated into national and regional breeding programs.	Reports of NARS and Regional Networks. Publications.	Continued interest by partners to use germplasm. Climatic problems permit advance and selection. Support of database programmer.
4.2 Collaborative projects developed and executed with NARS and Regional Networks.	• Projects submitted to donors	Communication from donors to Project Office. Funds received.	Partners are interested. Donors show interest and are committed.
4.3 Supporting NARS and Regional Network researchers on soil and crop management.	• Improved cultivars are tested under different soil fertility conditions.	Document of Operational Plan. NARS Network reports. Publications.	Donor support for Phase VIII of PROFRIJOL. Active participation of collaborators.
4.4 Supporting human resource development in NARS and Regional Networks.	• CIAT scientists participate as partners in regional events	Documents and reports on events. Joint authorship in publications with NARS partners.	Donor support for human resource development.

Research Highlights in 2000

Output 1: Improved small-seeded Middle American bean germplasm with less dependence on inputs

- Multiple stress resistance to abiotic constraints such as drought, aluminum toxicity, and low nutrient supply was confirmed in several genotypes, especially in G 21212, which presents efficient transport and utilization of photosynthates and nutrients toward grainfilling.

- Two bred lines (SEA 5 and CAP 4) and two landraces (G 21212 and G 1977) were very well adapted to drought stress because of their ability to mobilize photosynthates for grain production. Drought resistance equal to or better than that of SEA 5 was obtained in bred lines with superior plant type and acceptable grain color.

- Modest levels of drought resistance were recovered from interspecific crosses with *Phaseolus acutifolius*.

- Lines and landraces tolerant to toxic level of aluminum in soil and tolerant to low nutrient supply were identified.

- Two bred lines and one Mexican landrace were tolerant to waterlogging.

- The selection of the *bgm-1* gene was applied to about 9000 individual plants and the backcross program to improve commercial varieties with intermediate resistance to bean golden yellow mosaic virus (BGYMV) is nearing completion.

- Sources of resistance to bean golden mosaic virus (BGMV), bean common mosaic virus (BCMV), bean severe mosaic virus (BSMV), and cowpea chlorotic mottle virus (CCMV) were identified in parental materials, and in intermediate and advanced common bean breeding lines.

- Resistance to angular leaf spot (ALS) was identified in a number of *P. vulgaris*, *P. polyanthus*, and *P. coccineus* genotypes.

- Potential sources of ALS resistance were identified in interspecific crosses between *P. vulgaris* and *P. polyanthus* or *P. coccineus*.

- 25 bean genotypes with high levels of resistance to *Phaeoisariopsis griseola* races from Africa, Central America, and South America were identified.

- 10 bean genotypes with high levels of resistance to *Macrophomina phaseolina* were identified.

- Breeding for resistance to *Ascochyta* blight has been successful in creating families with superior resistance that will serve to improve both major gene pools and snap bean types.

- New sources of resistance to *Thrips palmi, Empoasca kraemeri, Zabrotes subfasciatus,* and *Acanthoscelides obtectus* were identified.

- The methodology to screen for resistance to thrips was refined.

- New lines possessing disease and insect resistance were selected.

- Incorporation of resistance to leafhopper in Andean bean types was reinitiated.

Output 2: Improved large-seeded Andean bean germplasm with less dependence on inputs

- Genetic improvement efforts to incorporate BCMV resistance in highland common bean cultivars are under way.

- Six genotypes with high levels of resistance to race 651 and 653 were identified.

- Red-mottled beans for the Andean and Caribbean regions were improved for disease resistance by pyramiding sources of resistance to ALS and by using marker-assisted selection to incorporate BGMV-resistance genes. *Empoasca* and bruchid resistances were combined into lines containing virus resistance.

- Cream-mottled beans were improved for yield and quality by crossing with Colombian Cargamanto beans and incorporating BCMV-resistance and bush type architecture.

- A new nursery of Andean genotypes (IBN 2000) was tested for ALS and common bacterial blight (CBB) resistance and distributed to collaborators.

- Higher yielding lines with commercial seed type were obtained from advanced backcross populations derived from crosses between cultivated Andean and wild common beans.

- Triple-cross Andean populations were developed to introgress traits from Mesoamerican climbing beans.

- The inheritance of low-phosphorous tolerance was studied in an Andean population.

- Andean climbing beans of heat-tolerant commercial type were developed and tested.

Output 3: Strategies developed for management of diseases and pests in bean-based cropping systems

- 55 *Phaeoisariopsis griseola* and *Colletotrichum lindemuthianum* isolates were chracterized using host differential interactions.

- 400 isolates of *Xanthomonas campestris* pv. *phaseoli* (XCP) and *X. campestris* pv. *phaseoli* var. *fuscans* (XCPF) have been characterized using repetitive extragenic palindromic polymerase chain reaction (REP-PCR) and DNA restriction fragment length polymorphisms (RFLP) of the 26S ribosomal genes. Results show that XCP is very distinct from XCPF.

- 125 *C. lindemuthianum* isolates were characterized using microsatellites and REP-PCR.

- Polymorphic random amplified microsatellites (RAMS) fragments were cloned to develop locus specific markers.

- 400 *P. griseola* isolates were characterized using RAMS and all isolates were put into Andean and Mesoamerican groups.

- The "Afro-Andean" group is part of the Andean group that represents isolates resulting from point mutations in genes for virulence.

- The presence of BGYMV virus in Colombia was confirmed.

- 150 recombinant inbred lines (RILs) were identified as having high levels of common bacterial blight (CBB) resistance under both field and greenhouse conditions.

- 16 lines were identified that combine Andean and Mesoamerican angular leaf stem (ALS)-resistance genes.

- Inheritance of ALS resistance to Andean and Mesoamerican *P. griseola* races in G 19833 and DOR 364 is different and complex being recessive for one race and dominant for another, depending on the source of resistance.

- Resistance to *Ascochyta* blight was found to be largely under additive gene control in *P. coccineus* although it tended to be recessive in *P. polyanthus*. From two to four genes appeared to control resistance.

- Quantitative trait locus (QTL) mapping of resistance to *Thrips palmi* shows few genes controlling resistance to insect damage and reproductive adaptation under high infestation pressure.

- QTL mapping of ALS and anthracnose disease resistance shows clustering of resistance genes in the bean genome.

- Populations were developed to study the inheritance of ALS resistance.

- Developed reliable sampling methods for *Thrips palmi* on beans and snap beans.

- Established an action threshold for *T. palmi* on snap beans.

- Identified levels of resistance to insecticides in whitefly (*Trialeurodes vaporariorum*) and thrips populations.

- Developed components and successfully tested management strategies for combined populations of whiteflies and thrips affecting snap beans.

Output 4: Improved cultivars and management practices developed and tested in partnership with IP-2 Project (Africa), NARS, and Regional Networks

- Evaluation of red-mottled, and red- and cream-speckled bean genotypes by farmer-led research committees (CIALs) in Colombia has identified broadly adapted bush bean varieties for mid-elevation ecosystems.

- Characterization of on-farm diversity of local common bean varieties in Nicaragua showed greater than expected genetic variability, which will be correlated with agro-morphological variability in the upcoming season.

- The International *Phaseolus* Information System (IPHIS) database was published for the first time with bean pedigrees, and remaining pedigrees are now incorporated into the IPHIS format.

- A project on breeding for aluminum resistance in bean was approved.

- Continuous support was given to breeding programs in the Proyecto Regional de Frijol para Centro América, México y el Caribe (PROFRIJOL), the Andean zone and African networks.

- Seed was distributed to all collaborating partners.

- CIAT scientists participated in the planning of activities of PROFRIJOL, the Andean zone, and Africa networks.

- Individual training of national scientists was provided.

- Joint collaboration and concept notes were prepared.

- Partners are evaluating a set of 49 genotypes for their adaptation to abiotic constraints such as drought, aluminum toxicity, and low nutrient supply.

- Partners are evaluating a set of 19 genotypes for their response to ALS.
- CIAT bean project scientists actively participated in international conferences and meetings that they attended.
- Individual and group training of national and international scientists was provided.
- A marker database was constructed for an RAPD survey of Andean common bean germplasm.
- Colombian research and extension agents identified regional bean production problems.
- The Web Page for IP-1 in English and Spanish was updated and expanded (http://www.ciat.cgiar.org/projects/ip-1/bar_ip1.htm).

Progress Report

Output 1: Improved small-seeded Middle American bean germplasm with less dependence on inputs

Activity 1.1 Developing germplasm tolerant to abiotic stresses of drought and low soil fertility

Highlights:

- Multiple stress resistance to abiotic constraints such as drought, aluminum toxicity, and low nutrient supply was confirmed in several genotypes, especially in G 21212, which presents efficient transport and utilization of photosynthates and nutrients toward grainfilling.
- Two bred lines (SEA 5 and CAP 4) and two landraces (G 21212 and G 1977) were very well adapted to drought stress because of their ability to mobilize photosynthates for grain production. Drought resistance equal to or better than that of SEA 5 was obtained in bred lines with superior plant type and acceptable grain color.
- Modest levels of drought resistance were recovered from interspecific crosses with *Phaseolus acutifolius*.
- Lines and landraces tolerant to toxic level of aluminum in soil and tolerant to low nutrients supply were identified.
- Two bred lines and one Mexican landrace were tolerant to waterlogging.

1.1.1 Evaluation of a set of selected landraces and bred lines for multiple stress resistance

Rationale: In other crops, materials have been identified with resistance to multiple abiotic stresses. In bean there is a long history of studying abiotic stress tolerance, but as individual stresses (drought, phosphorus, nitrogen, aluminum, or generalized low fertility). In 1998, a Multiple Stress Nursery was established that combined materials that had expressed tolerance to different types of physiological stress. The purpose of this nursery was to seek genotypes that express tolerance to multiple stresses, with the expectation that some mechanisms of physiological tolerance could be effective against more than one type of abiotic stress.

Materials and methods: Forty-nine elite materials that had been superior under conditions of low phosphorus, aluminum toxicity, or drought were identified, including landrace germplasm, bred lines, and commercial checks. The nursery was evaluated in Popayán, Santander de Quilichao, and Darien under different edaphic stresses. In Popayán apparently low P and possibly low micronutrients primarily cause the stress, while liming over years has eliminated aluminum toxicity. In Santander de Quilichao there is a combined stress of aluminum toxicity and low P, and occasionally manganese toxicity, depending on the field site and climatic conditions. In Darien the stress is exclusively caused by low P. Evaluations were also carried out in Palmira for drought tolerance. All stressed trials were accompanied by a control treatment with high fertilizer inputs, but at times the background soil fertility was so low that inputs resulted in an intermediate level of stress.

Results: Data from 15 trials are reported here. Table 1 presents data of the best 18 of the 49 materials that were selected for further study.

In the high- and mid-fertility and irrigated treatments, materials that stood out for their responsiveness included Brazilian cultivar Carioca (which is well known for its responsiveness), FEB 192, A774, VAX 1 and VAX 2. AM 38, a Flor de Mayo type for the Mexican highlands, also responded well in Popayán where temperature was more moderate.

In the low fertility trials, some of these same materials continued to perform very well. VAX 1 in particular stood out again, and A 774 and FEB 192 performed acceptably. However, in the low fertility treatment the germplasm accession G 21212 came to the forefront, and was often the best or second best among all materials (e.g., in trials 7, 8, 10 and 12, as well as mid-fertility trial (6). This unique material has been highlighted in past reports for its low-P tolerance (see IP-1 1999 report) and for its QTL with major effects on yield under P stress (see SB-2 1999 report). It has been the object of physiological analysis and appears to have a stress tolerance mechanism for efficient transport of photosynthate to grain.

Two drought trials were carried out, one under moderate stress in 1998 (trial 14) and one under severe stress in 1999 (trial 15). The line SEA 5 that was bred for drought tolerance was excellent under both levels of stress, expressing very good grain-filling traits. BAT 477, long recognized for its tolerance, expressed relatively good yield as expected. Again, materials like A 774 and FEB 192 performed quite acceptably, and under moderate stress the line A 785 stood out. However, under severe stress the accession G 21212 again was outstanding, displaying its trait of excellent grain filling that it also expresses under low P. This suggests that its mechanism of low-P tolerance might also function for tolerance to drought stress, in which case its genes are especially valuable. This topic will be the object of further investigation. Under severe drought, the germplasm accession G 1977 also stood out and displayed vigorous growth, suggesting that it was accessing moisture that other genotypes could not. G 1977 was also selected originally for low-P tolerance, and reasonable performance in trials 2, 3, 4, and 6.

Table 1. Yield (kg ha^{-1}) of selected common bean lines evaluated under multiple stresses.

Genotypes	Trials[a]															Mean
	1 P-98B	2 D-99A	3 Q-99A	4 Q-99B	5 P-98C	6 P-99A	7 D-99B	8 Q-99A	9 Q-99B	10 Q-98B	11 Q-98B	12 P-98C	13 Pa-99B	14 Pa-98B	15 Pa-98b	
A 774	3667	3522	1193	1734	1061	879	532	303	328	339	904	127	2190	1306	705	1252
Carioca	3358	2846	1131	1132	924	1387	497	395	369	416	703	173	2202	1217	446	1146
DICTA 17	2985	2754	839	939	1094	1715	770	296	368	264	589	301	1986	1314	637	1123
FEB 192	3279	3442	1682	1773	421	827	675	235	222	336	886	74	2039	847	725	1164
MAM 38	3579	2949	1012	1244	1460	1280	1074	386	262	155	635	352	1824	1111	564	1192
G 3513	1319	2360	1087	1155	170	950	643	471	180	228	578	216	1238	1038	607	816
BAT 477	2189	2517	867	1342	271	595	548	478	266	323	1110	60	2011	1407	718	980
G 18479	2805	2454	915	965	632	1151	934	319	348	260	594	147	1955	1076	259	987
G 92	3645	2596	1196	1555	811	1595	756	269	404	202	749	231	1891	1278	93	1151
G 19227A	1498	2196	536	495	224	1122	903	606	158	176	345	113	1039	787	280	698
VAX 1	3289	2966	1607	1634	1168	1568	783	389	385	279	690	36	1984	1116	649	1236
G 21212	2542	3003	901	935	1095	1988	1198	505	152	452	736	437	1529	1176	822	1164
A 785	3062	2301	1171	936	1190	1417	870	521	276	306	592	510	2133	1356	334	1131
VAX 2	3812	2579	1085	1675	1403	1232	1123	352	303	254	721	92	1896	1060	523	1207
G 1977	2397	3132	1295	1595	994	1984	710	316	226	446	515	176	1675	1068	801	1155
MAR 1	3626	2884	971	1460	414	298	485	436	480	255	659	107	1864	1164	308	1027
V 8025	2438	2845	691	1248	1182	1379	809	306	179	220	357	387	1675	1142	728	1039
SEA 5	1475	1643	800	629	152	418	631	477	216	442	813	71	2058	1478	820	808
Mean	2629	2401	864	972	697	1098	718	290	230	206	569	139	1605	1009	408	
LSD ($P = 0.05$)	734	677	382	375	360	494	388	234	145	209	446	252	326	292	180	

a. 1 and 2 = high fertility, 3-6 = medium fertility, 7-12 = low fertility, 13 = irrigated check treatment for drought trial, 14 = intermediate drought stress, and 15 = severe drought stress. PxxA = Popayán March, PxxB = Popayán June, PxxC = Popayán October; DxxA = Darien April, DxxB = Darien September; QxxA = Santander de Quilichao April, QxxB = Santander de Quilichao September; and PaxxB = Palmira June.

Conclusions: The multiple stress nursery has been highly useful for identifying materials with multiple stress tolerance, especially G 21212, VAX 1 and A 774. Materials such as A 774 and VAX 1 have also expressed tolerance to flooding in the spring of 2000. These experiences validate the hypothesis that was the basis for establishing the nursery, that multiple stress tolerance is feasible and that common mechanisms might exist for tolerance to several stresses. Lines such as FEB 192, A 774, and VAX 1 also present excellent yield without stress, thus allaying fears that stress tolerance is necessarily associated with low yield potential. Based on the data available, 18 elite entries were selected from among the original 49, and another 18 were added to conform a nursery of 36 entries. This is presently being evaluated under stressed and unstressed conditions.

Contributors: S Beebe, IM Rao, H Terán, JM Osorno, J Ricaurte;
SP Singh (University of Idaho, USA)

1.1.2 Drought resistance

Identification of traits associated with drought resistance

Rationale: A set of 49 genotypes was assembled to evaluate for tolerance to low soil fertility conditions. Several of the genotypes included in this set of materials were known to be good performers under drought conditions. Last year we reported results from a field trial that evaluated genotypic differences in adaptation to moderate drought stress among 49 genotypes. This year we report results obtained from the same 49 genotypes for their adaptation to greater levels of drought stress.

Materials and methods: A field trial was conducted at Palmira in 1999 (June to September) to determine differences in tolerance to high levels of water stress. The field trial included 49 bean genotypes. Details on planting and management of the trial were similar to those reported in the 1997 Bean Project Annual Report, p 33-34. The incidence of *Macrophomina phaseolina* and *Sclerotium rolfsii* was recorded at physiological maturity. A number of plant attributes were measured at mid-podfilling in order to determine genotypic variation in tolerance to water stress. These plant traits included leaf area index, canopy dry weight per plant, shoot nutrient (N, P, K, Ca, and Mg) uptake, shoot ash content, and shoot total nonstructural carbohydrates (TNC). At the time of harvest, grain yield and yield components (number of pods per plant, number of seeds per pod, 100 seed weight) were determined. Seed N, P, ash content, and TNC were also measured.

Results and discussion: During the crop growing season, air temperatures were maximum 32.1 °C and minimum 16.4 °C, while incident solar radiation ranged from 12 to 25 MJ m^{-2} d^{-1}. The total rainfall during the 2 months (July-August) of active crop growth was 38 mm compared to the potential pan evaporation of 318 mm. These results on rainfall and pan evaporation indicated that the crop suffered a high level of water stress during active growth and development.

Under high water stress conditions in the field, the seed yield of 49 genotypes ranged from 15 to 820 kg ha^{-1} (Figure 1). Among the genotypes tested, two land races (G 21212 and G 1977) and two bred lines (SEA-5 and CAP 4) were outstanding in their adaptation to high levels of water stress conditions. These four genotypes were also less affected by the incidence of soil-borne pathogens (*Macrophomina phaseolina* and *Sclerotium rolfsii*) as determined by the percentage of infected plants (Figure 2). Five out of 49 genotypes including MAM 46, A 36, G 3096, Compuesto Chimaltenango, Negro INIFAP, and G 92 showed greater sensitivity to soil-borne pathogens. Several genotypes that yielded well under rainfed conditions were also found to be less affected by the incidence of soil-borne pathogens (Figure 3).

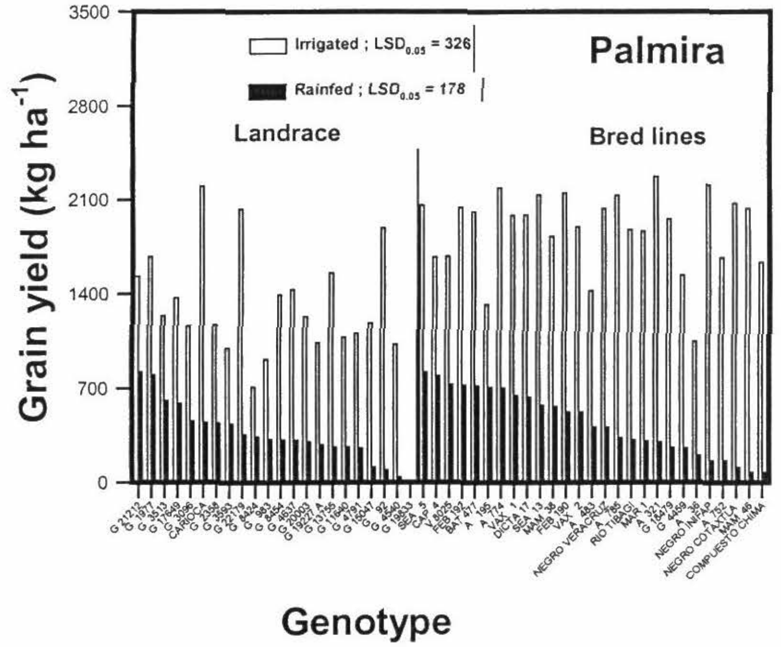


Figure 1. Genotypic variation in adaptation to rainfed and irrigated conditions of 49 common bean genotypes grown in a Mollisol at Palmira, Colombia.

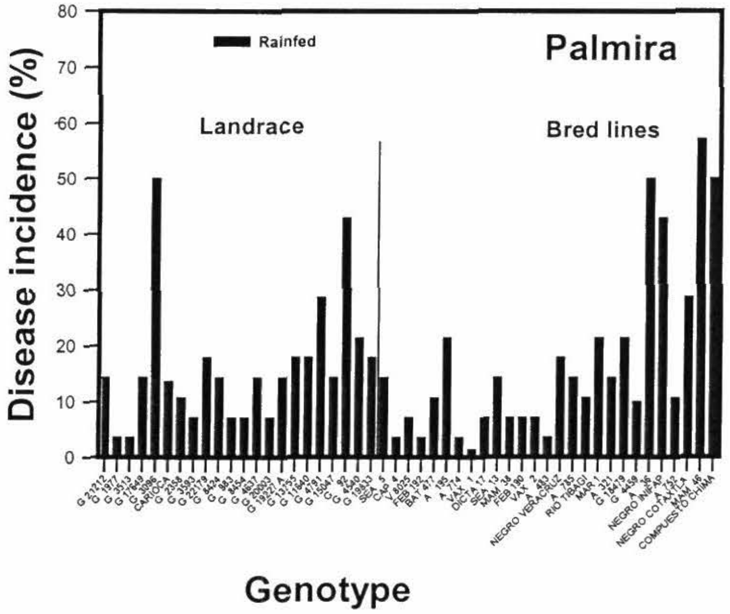


Figure 2. Genotypic variation in incidence of soil-borne pathogens caused by *Macrophomina phaseolina* and *Sclerotium rolfsii* on 49 genotypes of common bean grown in a Mollisol at Palmira.

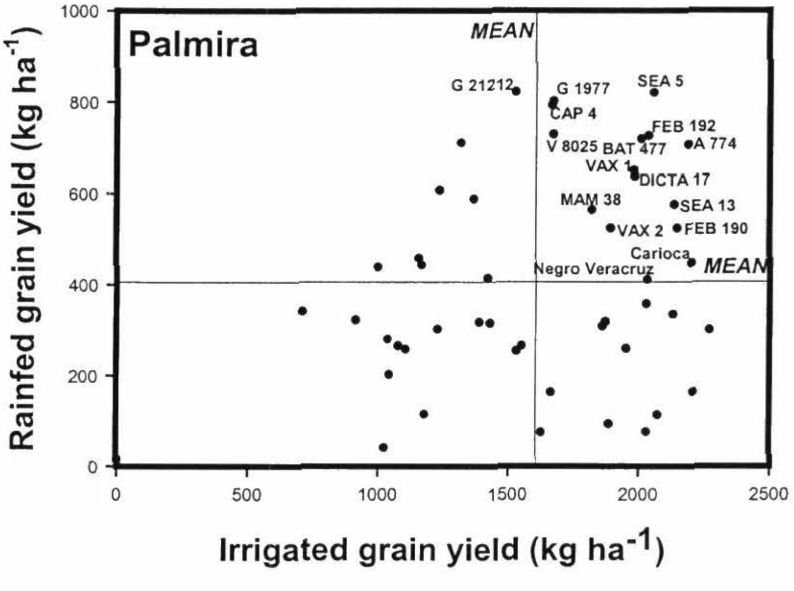


Figure 3. Identification of genotypes that are adapted to rainfed conditions and are less sensitive to soil-borne pathogens in a Mollisol at Palmira. Genotypes that yielded superiorly with drought and were less sensitive to soil-borne pathogens (*Macrophomina phaseolina* and *Sclerotium rolfsii*) were identified in the upper box of the left-hand side.

The relationship between grain yield of rainfed and irrigated treatments indicated that SEA 5 was both adapted to a high level of water stress and responsive to irrigation (Figure 4). SEA-5 was also found to be very well adapted to moderate and severe water stress conditions (1997 and 1998 Bean Project Annual Reports). Among the 49 genotypes tested, G 19833 was the most poorly adapted genotype. This Andean landrace was also the poorest performer at moderate water stress conditions (1998 Bean Project Annual Report). Eighteen of the 49 genotypes were superior in their performance to the most widely planted cultivar, Carioca.

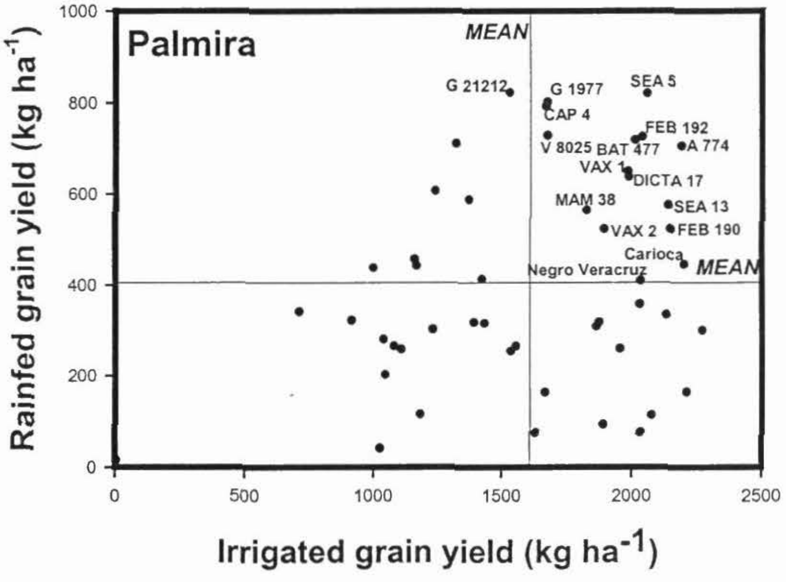


Figure 4. Identification of genotypes that are adapted to rainfed conditions and are responsive to irrigation to a Mollisol at Palmira. Genotypes that yielded superiorly with drought and were also responsive to irrigation were identified in the upper box of the right-hand side.

Measurements of leaf area index indicated that several genotypes had greater leaf area values than the best performers such as SEA 5 and G 21212 under high water stress conditions (Figure 5). This shows that these two genotypes had a better transport system for mobilizing photosynthates to developing grains.

Last year, we reported that the superior performance of SEA 5 in severe drought was related to lower seed P content. We verified this observation with the evaluation of 49 genotypes by measuring seed ash (mineral) content and seed N, P, K, Ca, and Mg content. The relationship between grain yield and seed ash content indicated that the land race G 1977 was outstanding in combining low seed ash content with high grain yield under water stress conditions (Figure 6). The seed ash content of the bred line SEA 5 was intermediate while A 774 was very high. Thus seed ash may not be a very useful indicator of water stress resistance in common bean. Nevertheless, seed P content showed somewhat better negative relationship with grain yield under water stress conditions (Figure 7). Except for the bred lines such as CAP 4 and FEB 192, other superior performers combined high seed yield with lower seed P content. However, several genotypes also showed lower grain yield and lower seed P content. This indicates that seed P content alone may not be adequate as a selection method for water stress.

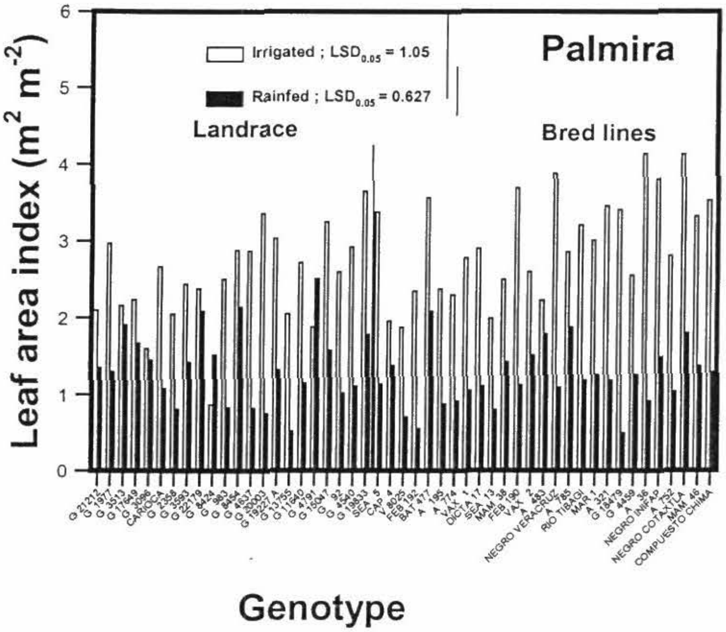


Figure 5. Genotypic variation in leaf area index of 49 genotypes of common bean grown in a Mollisol at Palmira, Colombia.

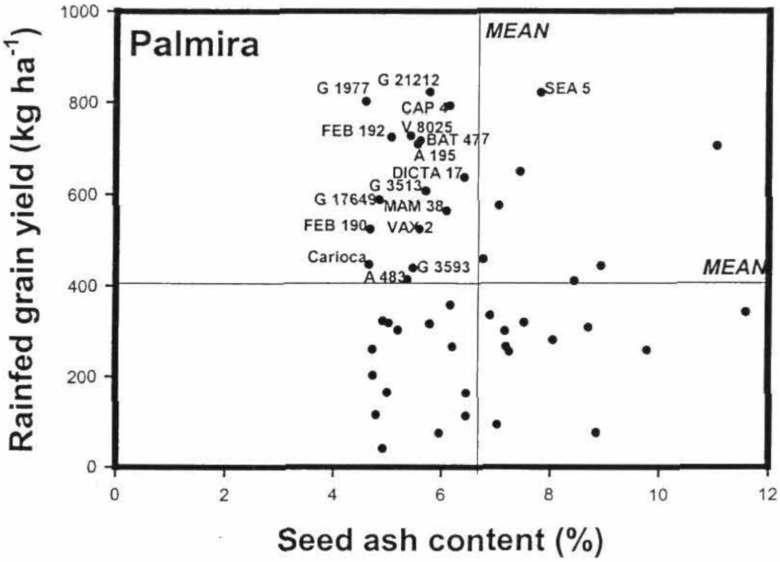


Figure 6. Identification of genotypes that combine superior seed yield with lower ash (mineral) content in seed when grown under rainfed conditions in a Mollisol at Palmira. Genotypes that were superior in grain yield and lower in seed ash were identified in the upper box of the left-hand side.

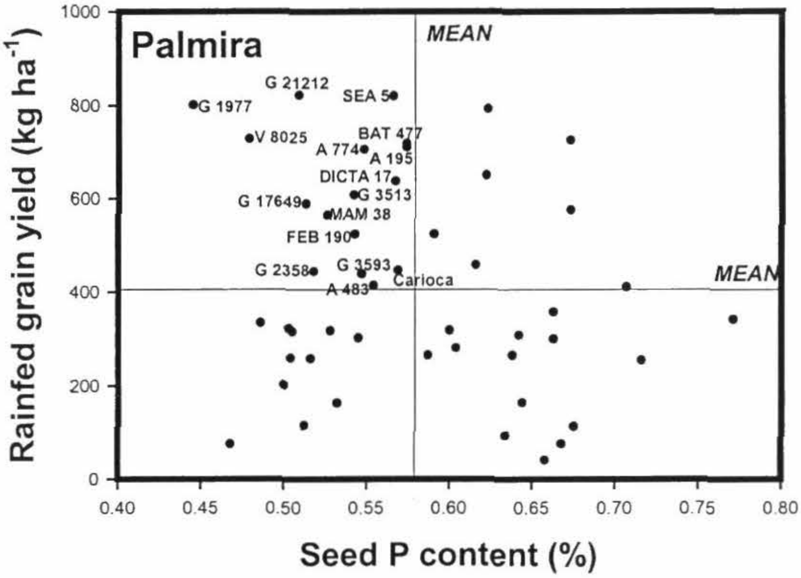


Figure 7. Identification of genotypes that combine superior seed yield with lower P content in seed when grown under rainfed conditions in a Mollisol at Palmira. Genotypes that were superior in grain yield and lower in seed P were identified in the upper box of the left-hand side.

Relationship between seed N and grain yield under water stress conditions indicated that BAT 477 was superior in combining greater seed N content with high seed yield (Figure 8). It is important to note that G 21212 and SEA 5 showed lower levels of seed N. Under rainfed conditions, grain yield was greater and shoot TNC content at mid-podfilling was lower for two landraces (G 21212 and G 1977). This observation indicates that these two land races could mobilize photosynthates better than the other genotypes tested (Figure 9). Two bred lines, SEA 5 and CAP 4 were also moderate in their shoot TNC content. The superior adaptation of these four genotypes to drought was found to be because of their efficient utilization of N and P for grain production (Figure 10) in addition to the mobilization of photosynthates.

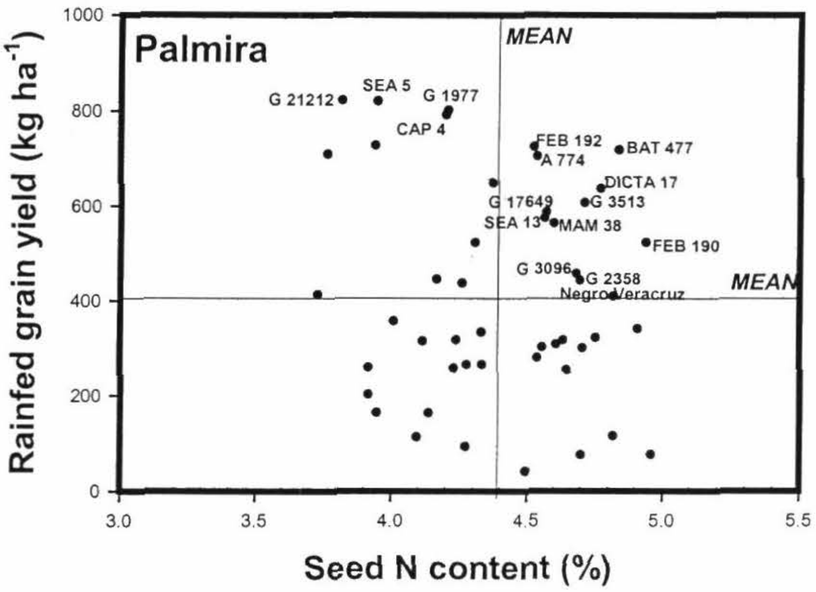


Figure 8. Identification of genotypes that combine superior seed yield with greater N content in seed when grown under rainfed conditions in a Mollisol at Palmira. Genotypes that were superior in grain yield and higher in seed N were identified in the upper box of the right-hand side.

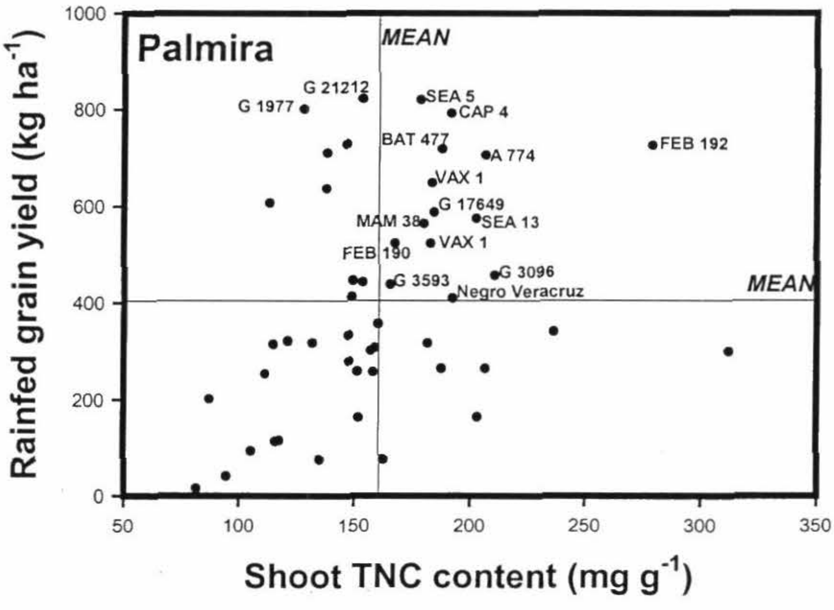


Figure 9. Identification of genotypes that combine superior seed yield with greater amount of total nonstructural carbohydrates (TNC) in the shoot when grown under rainfed conditions in a Mollisol at Palmira. Genotypes that were superior in grain yield and higher in shoot TNC were identified in the upper box of the right-hand side.

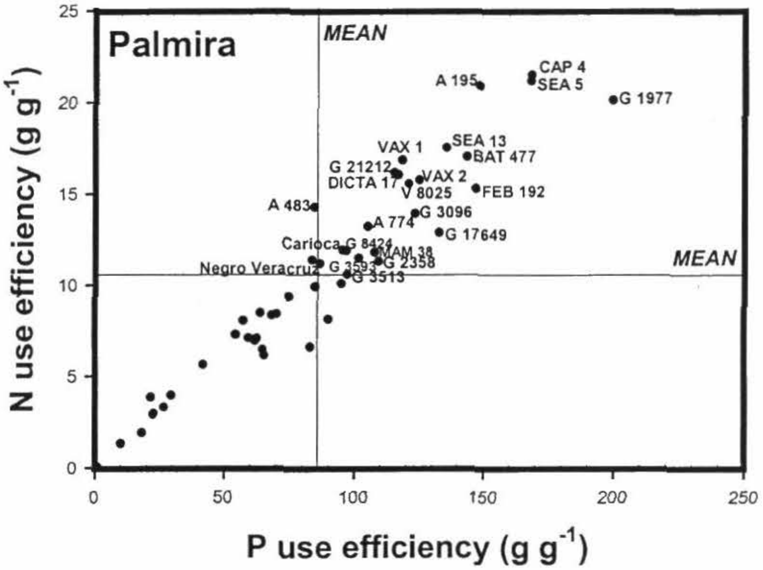


Figure 10. Identification of genotypes that are efficient in the utilization of N and P to produce greater seed yield when grown under rainfed conditions in a Mollisol at Palmira. Genotypes that were superior in both N and P use efficiency were identified in the upper box of the right-hand side.

Correlation coefficients between final grain yield and other plant attributes indicated that leaf area production, shoot biomass production, and shoot nutrient uptake were highly related to seed yield with rainfed conditions (Table 2). Significant positive relationship was also observed between seed yield and shoot TNC content under rainfed conditions. This observation indicates that the superior performers maintained a higher level of photosynthates in the shoot tissue. A negative relationship was observed between seed yield and seed nutrients (N and P) or seed ash content. Although few drought-adapted genotypes showed lower seed P content as observed from another field study that was reported last year; the relationship was not significant. We need to test this relationship using recombinant inbred lines.

Conclusions: This field study indicated that two bred lines (SEA 5 and CAP 4) and two landraces (G 21212 and G 1977) were very well adapted to drought stress. The superior performance of these four genotypes under drought was associated with resistance to soil-borne pathogens combined with their ability to mobilize photosynthates to developing grain and to utilize the acquired N and P more efficiently for grain production. Further work is needed to evaluate the usefulness of seed P as a selection method for identifying bean genotypes adapted to drought.

Table 2. Correlation coefficients (*r*) between final grain yield (kg ha^{-1}) and other plant attributes of 49 genotypes of common bean grown under rainfed conditions in a Mollisol at Palmira, Colombia.

Plant traits	Rainfed[a]	Irrigated[a]
Leaf area index	0.39***	0.18*
Shoot biomass	0.42***	0.44***
Shoot N uptake	0.36***	0.41***
Shoot P uptake	0.38***	0.40***
Shoot K uptake	0.38***	0.39***
Shoot Ca uptake	0.40***	0.29***
Shoot Mg uptake	0.31***	0.29***
Shoot Ca content	0.16	-0.31***
Shoot Mg content	0.02	-0.29***
Shoot TNC[b]	0.23**	0.19*
Shoot ash content	-0.15	-0.14
Seed N content	-0.11	-0.22**
Seed P content	-0.17	-0.07

a. * significant at $P = 0.05$, ** at $P = 0.01$, and *** at $P = 0.001$.
b. TNC = total nonstructural carbohydrate.

Contributors: IM Rao, S Beebe, J Ricaurte, JM Osorno, H Terán, R García, C Jara, G Mahuku

Development and screening of lines for drought resistance

The drought selection project is focussed at present on Middle American types, especially for lowland Central America where the Niño effect has resulted in three consecutive dry years and serious losses in agricultural production. Although drought tolerance presents large genotype x environment (G x E) interaction, results in Palmira tend to correlate better with Central America than with other drought areas, such as highland Mexico. In January, all drought trials were lost because of excessive rainfall that resulted from the Niña effect. In the June planting, drought was much more reliable and the trials received only 60 mm of rainfall until about 62 days after planting, when rainfall resumed. Thus, stress in the June planting was moderately severe. Several trials were evaluated in this period.

Rationale: Several years of drought trials in CIAT had identified promising parental material in both the Mesoamerican and Durango races. Prior breeding had demonstrated that combining these two races could result in superior resistance, as in the case of the check variety, SEA 5.

Materials and methods: A set of 64 lines and checks were planted in a lattice design with three repetitions. These populations had from two to five different drought sources in their pedigrees and thus represented an attempt to recombine genes from several sources and bean races of the Middle American gene pool. In particular, race Durango figured prominently in these crosses. Most lines that were selected for testing have commercial grain color for Central America (red brilliant or black opaque).

Results: Lines that were comparable to the tolerant check (SEA 5) were identified in commercial colors (Table 3). In particular, the line identified as SX 12008-167 presented excellent tolerance and also good plant type, contrary to many other lines derived from race Durango. This represents substantial progress in the development of drought sources for this region, because in the past most sources were of cream or brown color. These new lines have already been incorporated into the crossing program to combine their drought tolerance with the necessary disease resistance, especially resistance to BGMV, which is present in most drought-prone tropical environments.

Table 3. Superior lines for drought tolerance derived from crosses among common bean races.

Line	Code	Color seed	Yield (kg ha^{-1})	Harvest days	100-seed weight (g)
13	SX 12008-180	Black	1479	69	23
12	SX 12008-167	Black	1429	72	17
23	SX 12008-261-2	Cream	1381	69	23
9	SX 12008-35-5	Brown	1364	72	24
2	SX 12293-121	Roxo	1349	63	25
41	SX 12010-40-1	Roxo	1291	73	23
22	SX 12008-261-1	Cream	1278	73	22
19	SX 12008-248-2	Black	1265	72	21
7	SX 12008-35-3	Brown	1248	72	25
8	SX 12008-35-4	Brown	1248	75	23
11	SX 12008-154	Cream mottled	1226	72	23
5	SX 12008-35-1	Brown	1224	77	19
	SEA 5 (tolerant check)	Cream	1189	67	23
	Tio Canela 75 (red check)	Red	1051	72	18
	DOR 390 (black check)	Black	886	79	17
	A 750 (susceptible check)	Purple mottled	115	88	26
	Mean		1063	72	22
	LSD ($P = 0.05$)		264	3	1

Conclusions: In the past, breeding for drought resistance had been managed as an independent project, outside the mainstream breeding program. The lines identified in this trial are much closer to commercial phenotype than lines identified in the past and can be used readily in the mainstream breeding program for Central America and the Caribbean.

Red-seeded lines from the mainstream breeding program

Rationale: Over the past 2 years, a set of red-seeded lines have been developed with resistance to important bean diseases of Central America, especially BGMV and CBB. These had been selected in conditions of medium fertility stress in early generations, but had not been evaluated systematically for drought resistance.

Materials and methods: Eighty-three of these lines were evaluated for drought tolerance in this same planting as the other trials described above, in a lattice design with two repetitions.

Results: A surprising level of tolerance was found in a number of lines, especially in those derived from variety Catrachita (Table 4). These lines were selected under fertility stress and possibly they have acquired a superior root system that is beneficial under drought as well. They have already been shipped to Central America for testing and these data will be shared with colleagues for use in the selection of promising materials.

Conclusions: Several lines presented a surprising level of drought tolerance and could be tested directly in Central America. As in the case of the lines mentioned above, they can be used readily in the mainstream breeding program for Central America.

Table 4. Best bean lines in the Central American red-seeded class under drought stress.

Line	Code	Color seed	Yield (kg ha^{-1})	Harvest days	100-seed weight (g)
33	MR 12439-18	Red	1767	76	23
78	MR 12326-53	Red	1709	74	25
30	MR 12439-105	Red	1702	72	27
71	MR 12326-40	Red	1641	73	21
27	MR 12439-105	Red	1615	73	27
79	MR 12326-53	Red	1612	72	23
51	MR 12438-93	Red	1592	76	25
18	MR 12439-6	Red	1535	72	23
15	MR 12746-48	Red	1521	79	19
72	MR 12326-48	Red	1498	74	21
13	MR 12826-31	Red	1494	75	22
80	MR 12326-53	Red	1485	73	23
	SEA 5 (tolerant check)	Cream	1407	71	24
	Catrachita (red check)	Red	1373	74	24
	Tio Canela 75 (red check)	Red	1044	79	18
	Orgulloso (red check)	Red	672	72	22
	A 750 (susceptible check)	Purple mottled	228	88	26
	Mean		1213	74	22
	LSD ($P = 0.05$)		437	3	2

Lines derived from interspecific crosses

Rationale: The tepary bean (*Phaseolus acutifolius*) is highly resistant to drought. *P. parvifolius* is a close relative of acutifolius. Both *P. acutifolius* and *P. parvifolius* are desert species and can be crossed with *P. vulgaris* using embryo rescue. Interspecific lines were developed in past years to introgress resistance to CBB into common bean, but last year we initiated evaluations for drought tolerance with the same lines.

Materials and methods: A second drought trial contained lines derived from interspecific crosses of *P. vulgaris* with *P. acutifolius*. Several accessions of *P. acutifolius* that had been evaluated as especially resistant were included in the trial. In the present trial, 90 lines and checks were included in a lattice design with three repetitions, representing different amounts of contribution of the three species involved.

Results: Among the accessions of *P. acutifolius*, at least one yielded better than the tolerant *P. vulgaris* check, SEA 5 (Table 5). However, none of the lines presented yields comparable to the *P. vulgaris* check, SEA 5, but two significantly outyielded ICA Pijao, the *P. vulgaris* parent in all crosses and thus a more proper comparison to measure the impact of introgression of drought tolerance genes. Drought tolerance is assumed to be governed by multiple quantitative genes, and thus the introgression of genes from interspecific crosses is an important milestone. However, the gap between the best lines and the best *P. acutifolius* is still wide, indicating that much remains to be done to take advantage of this tolerance. The lines were developed by the congruity backcross system in which the two species are alternated in each generation of backcrossing. This system is thought to favor the genetic recombination among homologous chromosomes and thus the introgression of foreign genetic material. A study of DNA markers (amplified fragment length polymorphism [AFLP]) has confirmed that introgression has been extensive across several lines (see SB-2 report).

Table 5. Yields of *Phaseolus acutifolius* and interspecific lines under drought stress.

Line	Code	Yield (kg ha^{-1})	Harvest days	100-seed weight (g)
41	4V3A1	1014	73	20
16	3V1A1P	921	80	17
	ICA Pijao	675	80	17
	SEA 5 (tolerant check)	1497	67	24
	G 40068 (*P. acutifolius*)	1742	62	13
	G 40159 (*P. acutifolius*)	1684	62	12
	A 750 (susceptible check)	237	88	26
	Mean	769	77	16
	LSD ($P = 0.05$)	246	5	2

Conclusions: The recovery of genes from tepary bean for drought resistance is an important advance, but at present these materials are still inferior to lines derived among common bean races. Much more work is necessary to introgress drought resistance from tepary to common bean.

Yield potential of early maturing lines

Rationale: Another solution to the problem of drought in Central America is the use of early maturing varieties that produce within a limited period of rainfall. Traditional Central American landraces typically are early maturing and are favored for this reason. However, early maturing beans normally have poor yield potential. Thus, improving yield capacity is an important aspect of selecting for earliness.

Materials and methods: A set of 36 lines was yield tested with and without supplemental lighting (18-hr daylength), to verify the photoperiod insensitivity of the lines. Lines were planted in the CIAT station at Santander de Quilichao with high fertility rates to alleviate the soil limitations that normally are present there.

Results: The treatment without supplemental lighting averaged 887 kg ha^{-1}. The bred line, BAT 304, was used as an early maturing check, because it is relatively early compared to other commercial materials (maturing in 70 days in this trial). BAT 304 was in fact the latest material among the lines tested in this trial, and also was the best yielding (1992 kg ha^{-1}). However, two lines in particular (nos. 26 and 19) were noteworthy, not because of their absolute yields, but because their yields almost equaled that of BAT 304 in far less time—59-61 days (Table 6). These lines yielded substantially more than the Central American check varieties, Desarrural and Orgulloso, especially under natural light.

Table 6. Best-yielding, early maturing bean lines under two treatments of daylength.

	Artificial light		Natural light	
	Days to harvest	Yield (kg ha^{-1})	Days to harvest	Yield (kg ha^{-1})
BAT 304	70	1373	70	1992
Line 26[a]	61	1179	62	1851
Line 19[b]	58	888	59	1641
Bola 60 Días	62	1104	64	1483
MCD 2004 (Desarrural)	63	1064	63	1092
Orgulloso	59	490	57	873
Trial average	63	673	61	887
LSD ($P = 0.05$)	8.5	596	4.3	410

a. (Othello x ICA Pijao) x ((A57 x XAN 159) x (BAT 477 x G 17341)).
b. (Chase x PEF 13) x (Early Ray x G 17341).

For reasons that are not understood, the lighted treatment presented lower yields (average = 673 kg ha^{-1}) than the unlighted treatment in general, although the better materials in the unlighted treatment showed the largest yield reductions in this treatment, and the poorest yielders without lights actually presented slightly better yields. Thus, in the lighted treatment, the differences between the best and the worst tended to be narrower. The apparent differential varietal response to lighting suggests that lighting had a real effect on yield, although it had no effect on flowering date for most materials. If this effect were to be confirmed, it would suggest some effects of photoperiod are independent of flowering date, which has been the standard criterion of photoperiod response in bean. Photoperiod response may be affecting photosynthate transport because of feedback inhibition of photosynthesis.

Conclusions: Yield potential of early maturing bean lines was substantially more than check cultivars under natural light and daylength. These materials will be incorporated into the Central American breeding program.

Contributors: IM Rao, S Beebe, H Terán, JM Osorno

1.1.3 Identification of traits associated with aluminum resistance

Rationale: The major soil-fertility related constraints to bean production in the tropics are low availability of P and N, and toxicity of Al and Mn associated with low pH in soil. Toxicity of Al in subsoils is a serious problem and amending subsoils with lime is not only difficult but also prohibitively expensive for resource-poor farmers. Last year, we reported results from a field evaluation of 77 genotypes for resistance to Al-toxic soils and tolerance to low nutrient supply, particularly low P and micronutrients. Based on those results, we selected 49 genotypes for further studies.

Previous research indicated significant genotypic variation in seed yield when grown in Al-toxic soils. These genotypic differences in seed yield could be related to differences in tolerance to Al, acquisition of nutrients, and utilization of nutrients for transport of photoassimilates to developing seeds. Genotypes that are adapted to Al-toxic soils are capable of acquiring essential macro- and micronutrients in a low-pH and high-Al environment.

Field studies were continued at Santander de Quilichao (990 m, Oxisol – Plinthic Kandiudox) to identify Al-resistant genotypes.

Materials and methods: A set of 49 genotypes, including germplasm accessions and bred lines, was evaluated in the field for identification of plant attributes for adaptation to infertile, acid soil conditions. These materials were evaluated in two seasons and the mean values from two trials are reported. Two levels of fertilizer (high and nil) input were applied. Plots with high fertilizer input (HFI) received banded application of P (40 kg ha^{-1}) in the form of triple superphosphate and foliar application (twice) of urea (1 kg ha^{-1}). Plots with no fertilizer input (NFI) received no application of nutrients. Soil characterization data of NFI plots showed toxic levels of exchangeable Al (66% Al saturation) and Mn (8 to 10 ppm) and low availability of Ca (1.4 cmol$_c$ kg^{-1}) and Mg (0.51 cmol$_c$ kg^{-1}) while P availability was more than adequate for plant growth and development. Plots of HFI treatment showed toxic levels of Mn (14 to 21 ppm) with very low levels of exchangeable Al.

A number of plant attributes were measured at mid-podfilling to determine genotypic variation in tolerance to toxic level of Al in soil. These plant traits included leaf area index, and canopy dry weight per plant and shoot nutrient (N, P, K, Ca, and Mg) uptake. At the time of harvest, grain yield and yield components (number of pods per plant, number of seeds per pod, 100-seed weight) were determined. Seed N and P contents were also determined.

Results and discussion: Among the 49 genotypes tested, three landraces (G 19227A, G 21212, and G 3513) and three bred lines (A 785, BAT 477, and SEA 5) were found to be outstanding in their adaptation to Al-toxic soil conditions (Figure 11). With NFI treatment, grain yield ranged from 67 to 606 kg ha^{-1}, while with HFI the range was from 236 to 1682 kg ha^{-1}. Grain yield of A 784 was 33% greater than that of a widely adapted genotype, Carioca, with NFI treatment.

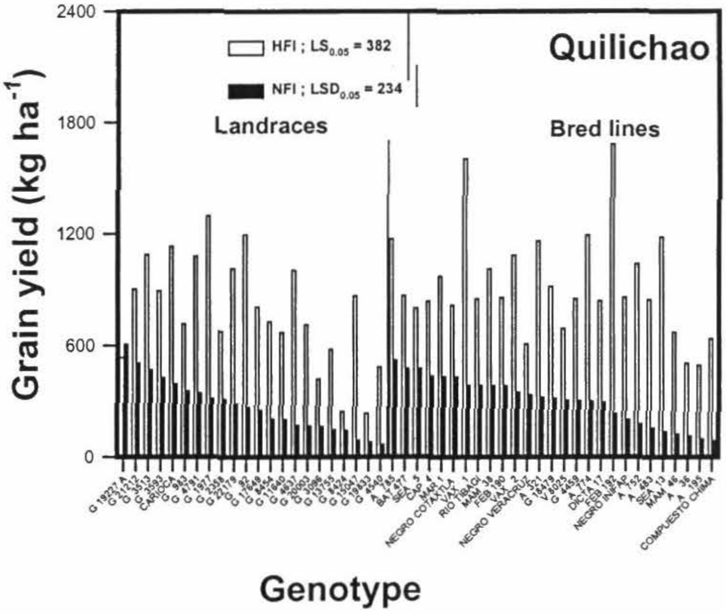


Figure 11. Genotypic variation in adaptation to Al-toxic soil at Santander de Quilichao, Colombia. (NFI = no fertilizer input, HFI = high fertilizer input).

The relationship between grain yield with NFI and that with HFI indicated that A 785 and G 3513 were better adapted to both low and high input of fertilizer (Figure 12).

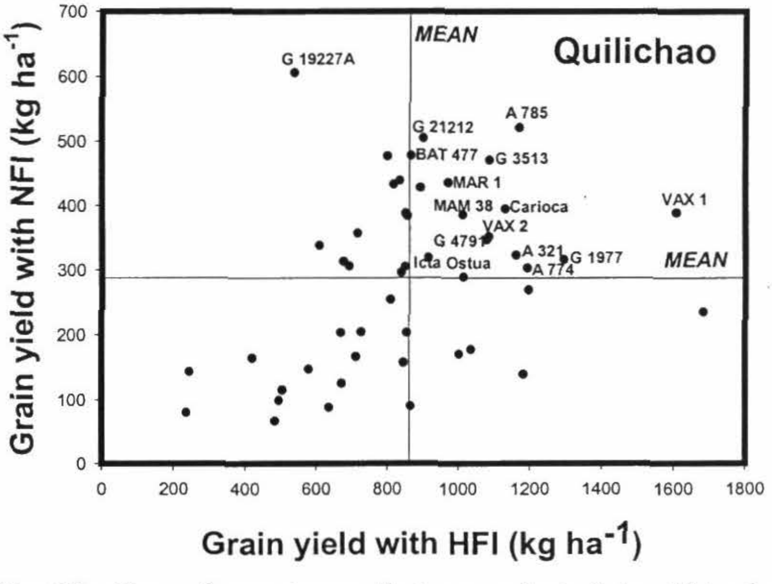


Figure 12. Identification of genotypes that are adapted to Al-toxic soil and are responsive to application of lime and P inputs to an Oxisol at Santander de Quilichao. Genotypes that gave superior yield with no fertilizer inputs (NFI) and were also responsive to application of high fertilizer inputs (HFI) were identified in the upper box of the right-hand side.

With NFI treatment, BAT 477 exhibited greater value of leaf area index at mid-podfilling (Figure 13). This was mainly because of the ability of this genotype to acquire greater amounts of P, Ca, and Mg from soil in the presence of toxic levels of Al (Figures 14 to 17). Shoot Ca content of G 19227A was markedly greater than that of the most of the genotypes tested (Figure 15).

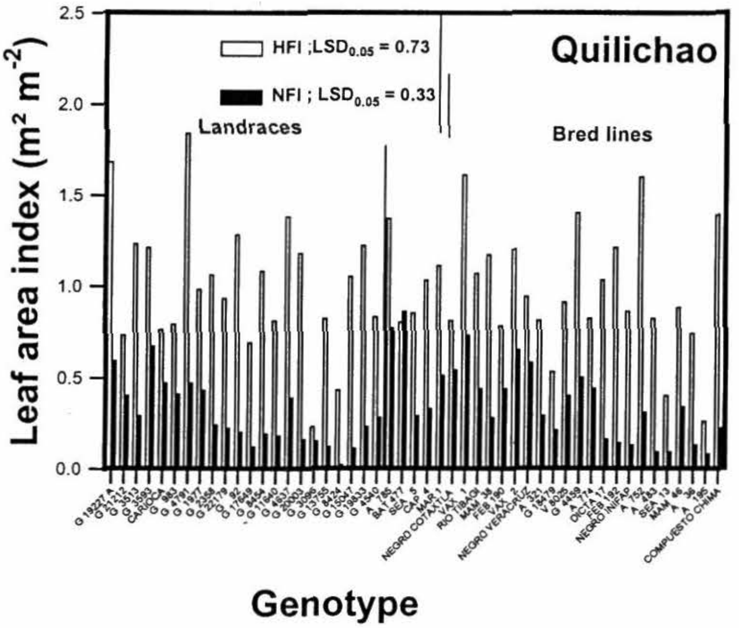


Figure 13. Genotypic variation in leaf area index of 20 genotypes of bean grown in an Oxisol at Santander de Quilichao. NFI= no fertilizer input, HFI= high fertilizer input.

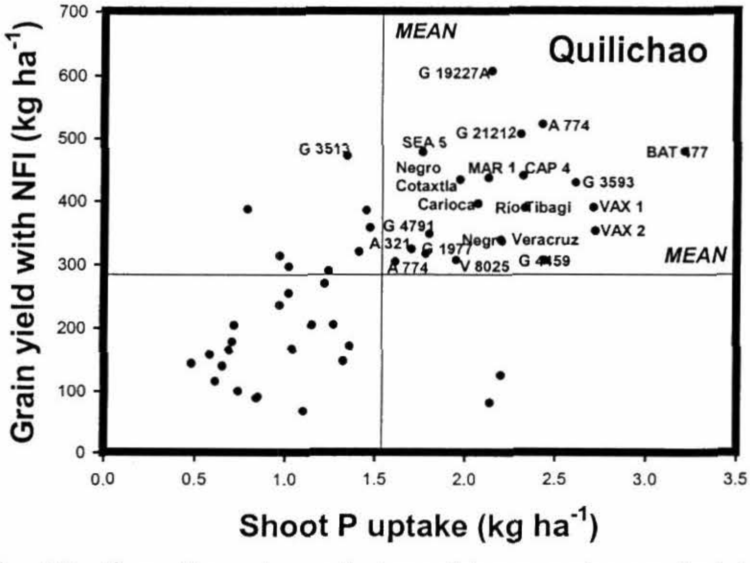


Figure 14. Identification of genotypes that combine superior seed yield with greater P uptake when grown with no fertilizer input (NFI) to an Oxisol at Santander de Quilichao. Genotypes that were superior in grain yield and P uptake were identified in the upper box of the right-hand side.

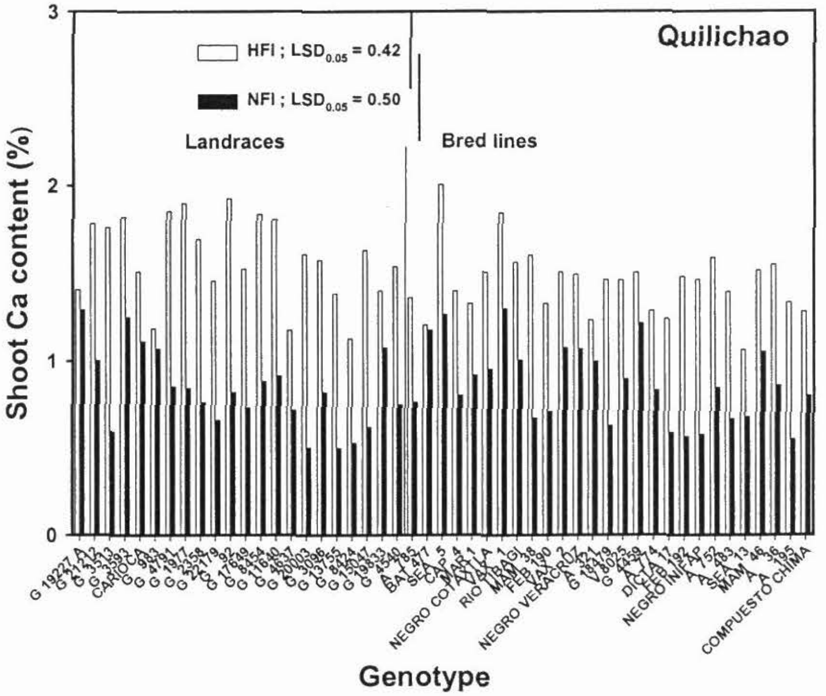


Figure 15. Genotypic differences in shoot Ca content of 49 genotypes of common bean grown under nil (NFI) and high (HFI) fertilizer inputs to an Oxisol at Santander de Quilichao.

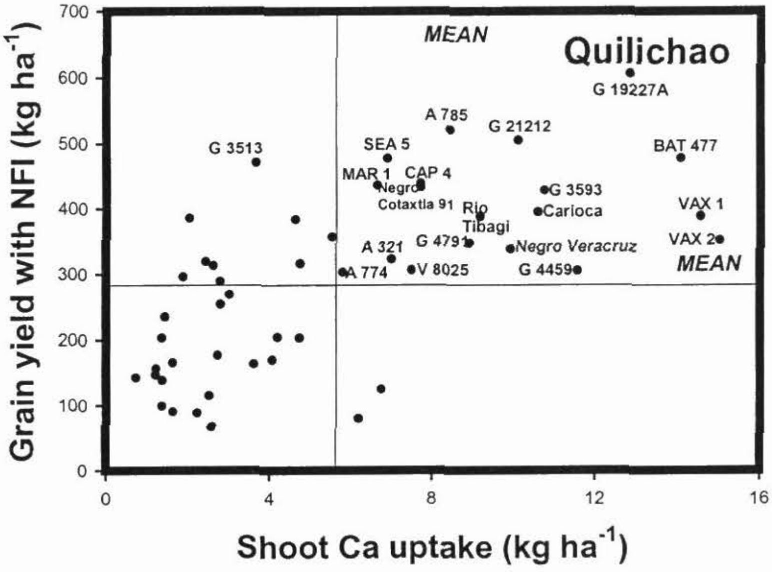


Figure 16. Identification of genotypes that combine superior seed yield with greater Ca uptake when grown with no fertilizer input (NFI) to an Oxisol at Santander de Quilichao. Genotypes that were superior in grain yield and P uptake were identified in the upper box of the right-hand side.

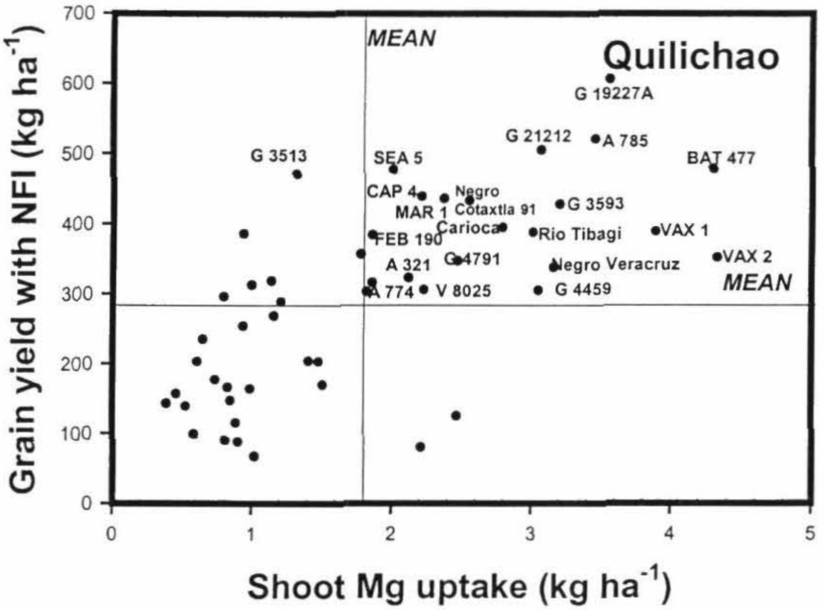


Figure 17. Identification of genotypes that combine superior seed yield with greater Mg uptake when grown with no fertilizer input (NFI) to an Oxisol at Santander de Quilichao. Genotypes that were superior in grain yield and P uptake were identified in the upper box of the right-hand side.

Genotypes that were adapted to Al-toxic soil conditions were also superior in their ability to acquire Ca and Mg from NFI treatment. This observation indicates the importance of Ca and Mg acquisition to seed yield when grown in Al-toxic soil.

Among the three best performers with NFI treatment, BAT 477 and SEA 5 were outstanding in combining greater seed yield with high content of N in seeds (Figure 18). It appears that these two bred lines not only are tolerant to toxic levels of Al in soil, but also are capable of mobilizing a greater proportion of shoot N to developing seeds. Among the land races and bred lines, FEB 190 was outstanding in its high N content in seed with moderate seed yield with NFI treatment. The bred line A 785 and the landrace G 21212 were outstanding in seed yield with NFI treatment, but were low in seed N content.

Correlation coefficients between final grain yield and other plant attributes indicated that leaf area production was highly related to seed yield with NFI treatment (Table 7). Seed yield was also significantly related to shoot nutrient uptake with NFI treatment. Significant negative relationship was observed between seed yield and seed P content indicating that greater P-use efficiency has contributed to superior adaptation to Al-toxic soil conditions.

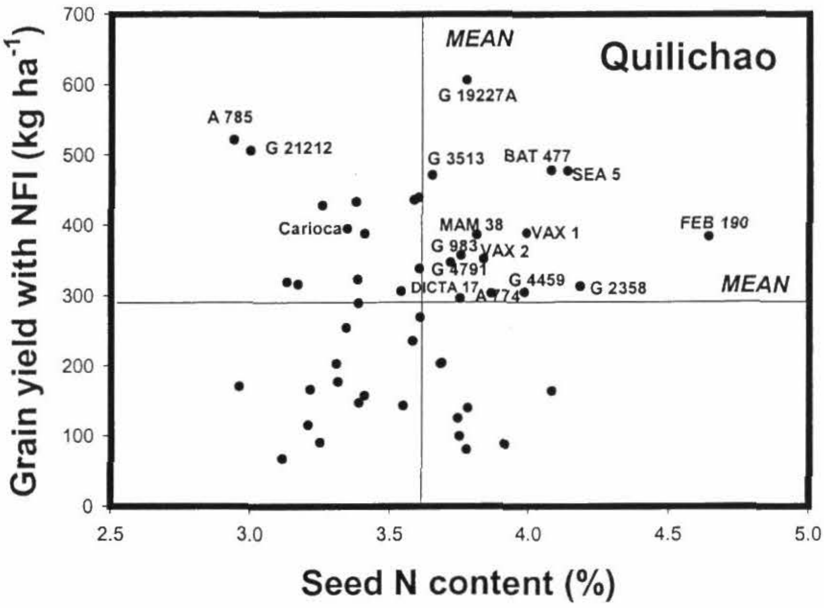


Figure 18. Identification of genotypes that combine superior seed yield with greater N content in seed when grown with no fertilizer input (NFI) to an Oxisol at Santander de Quilichao. Genotypes that were superior in grain yield and seed N were identified in the upper box of the right-hand side.

Table 7. Correlation coefficients (r) between final grain yield (kg ha^{-1}) and other plant attributes at mid-podfilling of 49 genotypes of common bean grown with no fertilizer input (NFI) or high fertilizer input (HFI) to an Oxisol at Santander de Quilichao.

Plant traits	NFI[a]	HFI[a]
Leaf area index	0.71***	0.41***
Shoot biomass	0.73***	0.52***
Shoot N uptake	0.73***	0.46***
Shoot P uptake	0.73***	0.45***
Shoot K uptake	0.73***	0.37***
Shoot Ca uptake	0.69***	0.54***
Shoot Mg uptake	0.73***	0.52***
Shoot Ca content	0.54***	0.31***
Shoot Mg content	0.48***	0.17*
Seed N content	-0.08	-0.16*
Seed P content	-0.32***	-0.35***

a. * = significant at $P = 0.05$, ** at $P = 0.01$, and *** at $P = 0.001$.

Conclusions: Results from this field study in Santander de Quilichao indicate that three bred lines (A 785, BAT 477, and SEA 5), and three germplasm accessions (G 19227A, G 21212, and G 3513) are superior in their resistance to Al. This study also showed that Al resistance can be combined with high seed N content.

Contributors: IM Rao, S Beebe, J Ricaurte, JM Osorno, H Terán, R García

1.1.4 Identification of traits associated with nutrient efficiency

Rationale: Last year, we reported results from a field evaluation of 77 genotypes for tolerance to low nutrient supply, particularly to low phosphorus and micronutrients. Based on those results, we selected 49 genotypes for further studies. Previous research indicated significant genotypic variation in seed yield with no fertilizer input (NFI) to a P-fixing Inceptisol. These genotypic differences in seed yield were associated with differences in acquisition of nutrients and utilization of nutrients for transport of photoassimilates to developing seeds. We also found that some genotypes were capable of combining high seed yield with higher level of N in the seed with NFI treatment.

Field studies were conducted at Popayán (1750 m, Inceptisol – Typic Dystropept) to identify nutrient efficient genotypes.

Materials and methods: The trial at Santander de Quilichao was duplicated at Popayán with the same genotypes and fertilizer inputs. Soil characterization data indicated low P availability (5 ppm) in NFI plots and deficiency of some microelements (Mn, Cu, Zn, and B) in both NFI and HFI treatments. These deficiencies of microelements resulted from heavy applications of lime over several years. The HFI treatment received 60 kg ha^{-1} of P application. Micronutrients were applied by foliar application of Kelatex B, Zn, and Cu at the rate of 2 g L^{-1} of water.

A number of plant attributes were measured at mid-podfilling to determine genotypic variation in tolerance to low nutrient supply in soil. These plant traits included leaf area index, canopy dry weight per plant, shoot nutrient (N, P, K, Ca, and Mg) uptake, and shoot TNC. At the time of harvest, grain yield and yield components (number of pods per plant, number of seeds per pod, 100 seed weight) were determined. Seed N and P contents and seed TNC were also determined.

Results and discussion: Among the 49 genotypes tested, four bred lines (A 785, V 8025, MAM 38, and DICTA 17) and one landrace (G 21212) were tolerant to low nutrient supply, particularly phosphorus and micronutrients (Figure 19). With HFI treatment, grain yield ranged from 152 to 1460 kg ha^{-1}, while with NFI the range was from 22 to 510 kg ha^{-1}. With NFI, grain yield of G 21212 was 2.5-fold greater than that of a widely adapted genotype, Carioca. Relationship between seed yield of NFI and HFI treatments indicated that the bred line A 785 was outstanding with NFI and at the same time highly responsive to application of fertilizer inputs (Figure 20). Acquisition of P by A 785 and G 21212 was only moderate, but seed yield was greater than that of the other genotypes with NFI treatment (Figure 21). Two bred lines, MAM 38 and V 8025, were outstanding in their ability to acquire P from low-P soil.

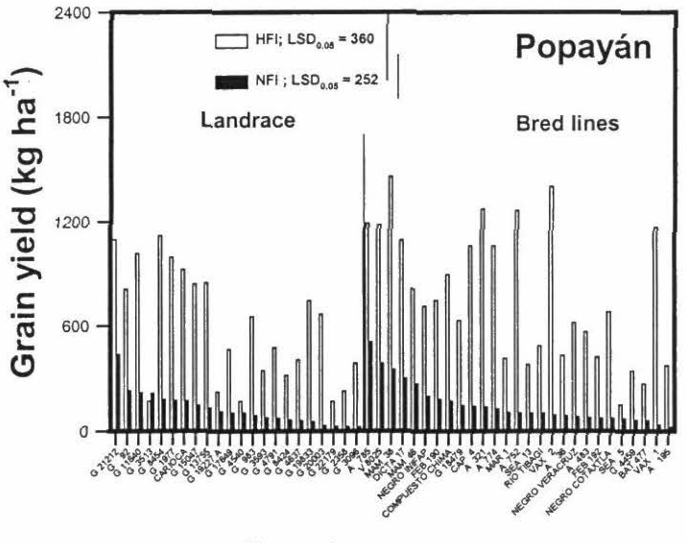


Figure 19. Genotypic variation in adaptation to low nutrient supply in an Inceptisol at Popayán. NFI = no fertilizer input, HFI = high fertilizer input.

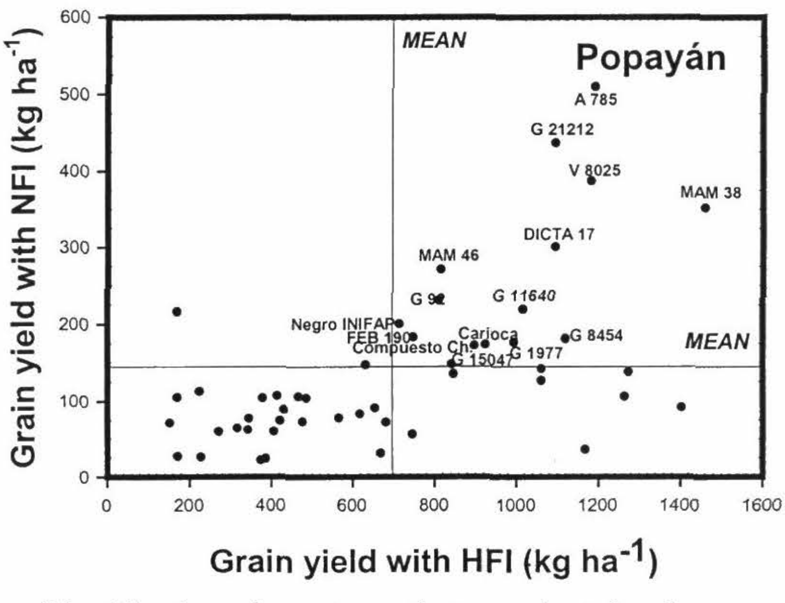


Figure 20. Identification of genotypes that are adapted to low supply of nutrients in soil and are responsive to application of lime and P inputs to an Inceptisol at Popayán. Genotypes that gave superior yield with no inputs and were also responsive to application of inputs were identified in the upper box of the right-hand side.

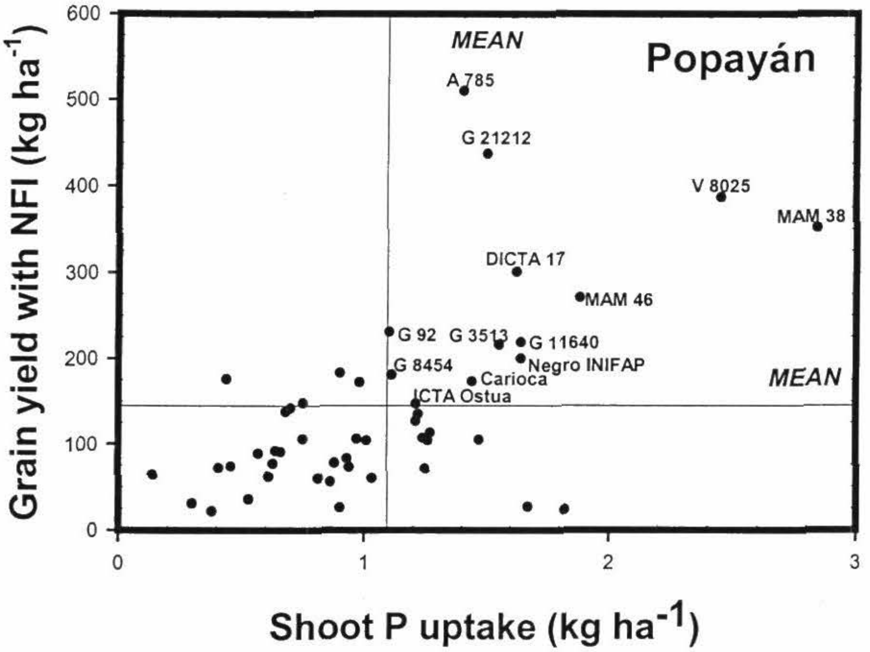


Figure 21. Identification of P-acquiring genotypes from soil with low P supply to an Inceptisol at Popayán. Genotypes that gave superior yield with no fertilizer input (NFI) and were also superior in acquiring P from low P supply in soil were identified in the upper box of the right-hand side.

The relationship between seed yield with NFI and seed P content indicated that the land race G 21212 yielded high with lower seed P content, while the bred line A 785 had moderate seed P-content and greatest seed yield (Figure 22). Moderate level of seed P is a desirable trait for seedling vigor when planted in low-P soils. High seed P-content could sometimes be considered less desirable in terms of nutritional value. Two bred lines, A 785 and BAT 477, combined greater seed yield with high seed N content with NFI treatment (Figure 23).

Genotypes that are efficient in mobilization of photosynthates or TNC can perform better with low P supply in soil (Figure 24). Relationship of grain yield and shoot TNC content with NFI treatment indicated that one bred line (A 785) and one land race (G 21212) were particularly efficient in mobilizing photosynthates to developing seeds. Of these two genotypes, G 21212 showed excellent grain filling under field conditions.

Three genotypes (G 1977, Negro Cotaxtla 91, and A 785 were found to be outstanding in their ability to combine greater N and P use efficiency (Figure 25). Among these three genotypes, G 1977 was particularly outstanding in efficient use of both N and P, both at this site and at Palmira under water stress conditions. One bred line (A 785) and one land race (G 1977) were identified as less P-demanding genotypes per unit seed yield production (Figure 26).

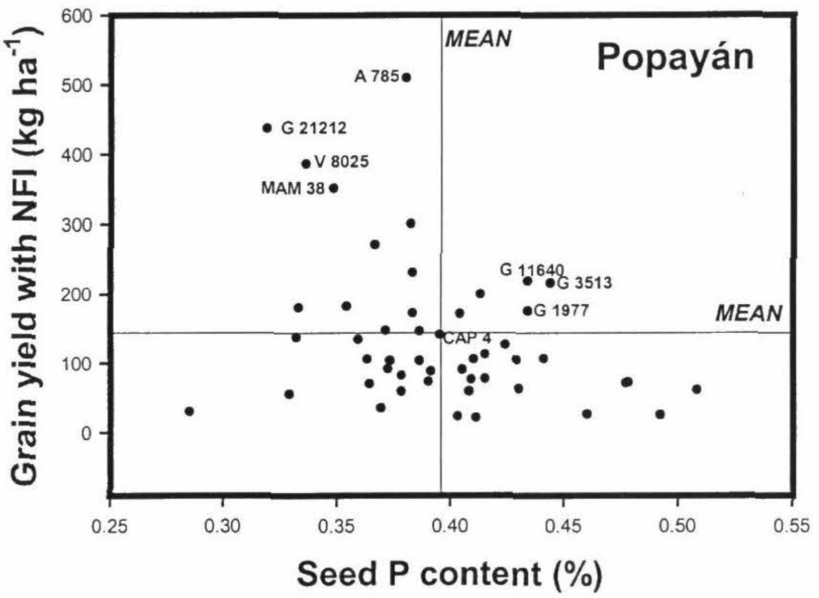


Figure 22. Identification of genotypes that combine superior seed yield with greater P content in seed when grown with no fertilizer input (NFI) in an Inceptisol at Popayán. Genotypes that were high in grain yield and low in seed P were identified in the upper box of the left-hand side.

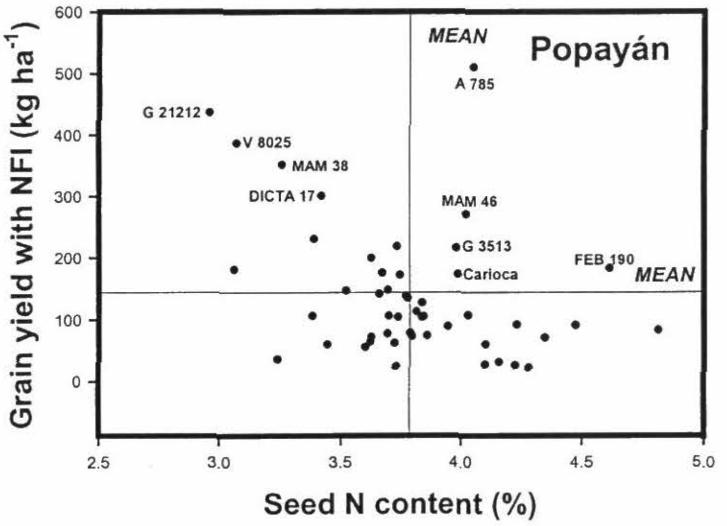


Figure 23. Identification of genotypes that combine superior seed yield with greater N content in seed when grown with no fertilizer input (NFI) in an Inceptisol at Popayán. Genotypes that were superior in grain yield and seed N were identified in the upper box of the right-hand side.

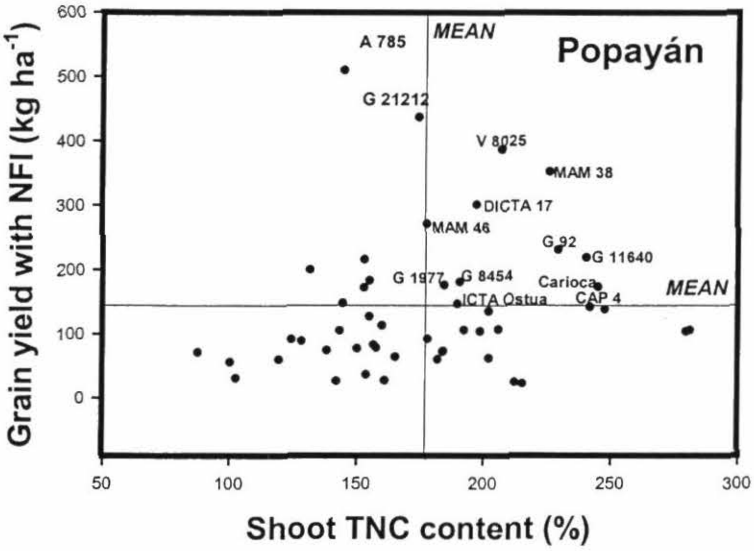


Figure 24. Identification of genotypes that combine superior seed yield with lower amount of total nonstructural carbohydrates (TNC) in the shoot when grown with no fertilizer input (NFI) in an Inceptisol at Popayán. Genotypes that were superior in grain yield and lower in shoot TNC were identified in the upper box of the left-hand side.

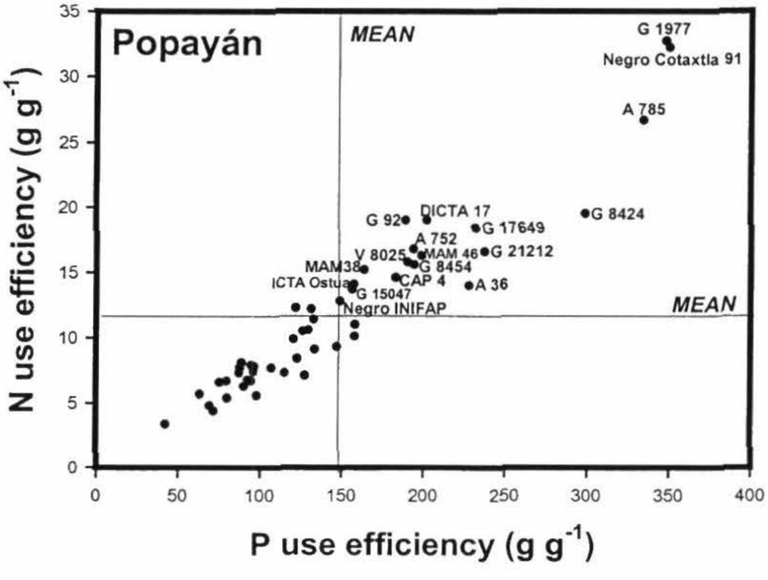


Figure 25. Identification of genotypes that are efficient in the utilization of N and P to produce greater seed yield when grown in low-P soil at Popayán. Genotypes that were efficient in N and P utilization were identified in the upper box of the right-hand side.

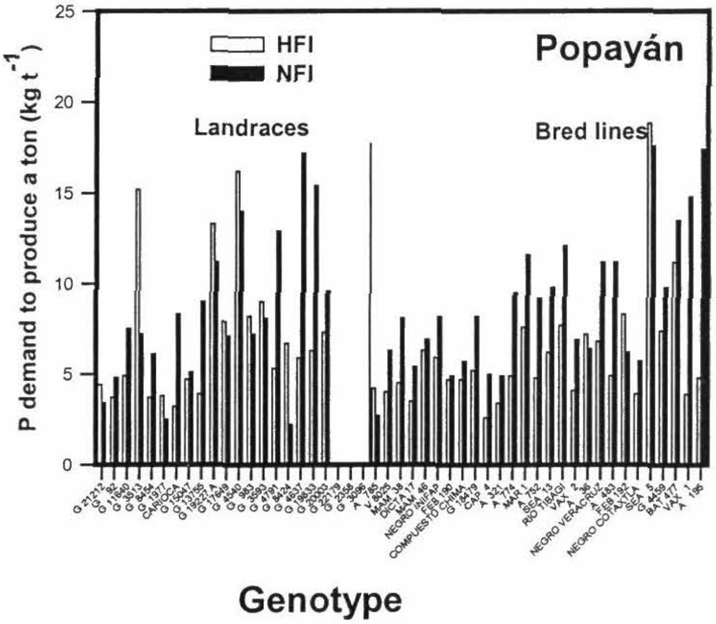


Figure 26. Genotypic differences in P demand to produce a ton of grain yield among 49 genotypes of common bean grown under nil (NFI) and high (HFI) fertilizer inputs to an Inceptisol at Popayán. P demand was defined as kg of shoot P uptake needed to produce one ton of seed yield.

Correlation coefficients between final grain yield and other plant attributes indicated that shoot biomass production, shoot N uptake, and shoot P uptake were highly related to seed yield with NFI treatment (Table 8). Significant negative relationship was observed between seed yield and shoot N and P content, indicating that greater N and P use efficiency has contributed to superior adaptation to low-P soil conditions.

Table 8. Correlation coefficients (*r*) between final grain yield (kg ha^{-1}) and other plant attributes of 49 genotypes of common bean grown under nil (NFI) or high (HFI) fertilizer input to an Inceptisol at Popayán, Colombia.

Plant traits	NFI[a]	HFI[a]
Shoot biomass	0.78***	0.76***
Shoot N uptake	0.72***	0.63***
Shoot P uptake	0.74***	0.62***
Seed N content	- 0.30***	- 0.29***
Seed P content	0.05	- 0.50***
N content in shoot biomass	- 0.47***	- 0.17*
P content in shoot biomass	- 0.19*	- 0.48***
TNC in shoot biomass	0.09	0.23**
Seed TNC content	0.14	- 0.03

a. * = significant at $P = 0.05$, ** at $P = 0.01$, and *** at $P = 0.001$.

Conclusions: This field study indicated that four bred lines (A 785, V 8025, MAM 38, and DICTA 17) and one landrace (G 21212) were tolerant to low nutrient supply, particularly phosphorus and micronutrients. One of the bred lines (MAM 38) was highly responsive to high fertilizer input in terms of seed yield.

Contributors: IM Rao, S Beebe, J Ricaurte, JM Osorno, H Terán, R García

1.1.5 Identification of genotypes with tolerance to waterlogging

Rationale: Climatic fluctuations have become more accentuated in Central America over the last few years. While climatologists still do not agree whether this is a long-term trend, farmers are in fact facing alternating periods of drought and excess water that seem to be more extreme than in the past. Hurricane Mitch was a graphic example of this.

Materials and methods: No trials were consciously planned to study flooding tolerance. However, the Niña effect in the April planting season produced record rainfall in the Santander de Quilichao station and plots were flooded once or twice a week. This led to an unusual level of stress on the plots and marked genotypic differences were observed.

Results: Some populations were lost entirely, but great differences in tolerance to these conditions were observed consistently across studies and fields. The line A 774, a mulatinho type developed for Brazil, presented the best tolerance, followed by the CBB-resistant line, VAX 1. Both lines are used as checks across trials and fields, and thus their superiority was evident and confirmed. Garbancillo Zarco, a Mexican climbing bean, also performed very well. Red-seeded populations presented broad variability, while the commonly used black-seeded parents (DOR 390, A 785, etc) were largely sensitive to flooding.

Conclusions: Flooding tolerance could well be relevant for regions such as Central America if climatic fluctuations become more radical. However, the precise stress in these trials is not clear. Although flooding and poor root aeration was undoubtedly a primary stress, it might have been confounded with nitrogen deficiency and with soil toxicities, especially manganese.

Contributors: S Beebe, H Terán, JM Osorno

1.1.6 Evaluation of symbiotic nitrogen fixation (SNF) in recombinant inbred lines

Rationale: Nitrogen is the most limiting nutrient in bean production after phosphorus. The bred line, BAT 477, was recognized long ago as superior in SNF capacity, including under drought and phosphorus stress. It had been used to develop recombinant inbred lines (RILs) that were evaluated in past years for SNF capacity in the greenhouse, and for yield under P stress and under drought, with the corresponding unstressed treatments. However, an evaluation of SNF capacity in the field had not been carried out.

Materials and methods: *In the past year, another trial with the same* RILs was financed by Agency for International Development (AID) funds with the University of Minnesota. The RILs were planted in small plots in four repetitions at a field site with sandy soil and severe N-deficiency. Data were taken on total N accumulated and the yield on small plots. Nitrogen accumulation in the Minnesota trial was compared to yield in phosphorus and drought stress trials in Colombia.

Results: When data were compiled across yield trials and the SNF trial, lines were identified with multiple stress tolerance (Table 9). One of these (line 98) was particularly outstanding across stress treatments and was incorporated into the breeding program. This once again highlights the potential for obtaining multiple stress tolerance. A broad subset of 30 lines was selected for physiological analysis for a Cuban MSc student. A comprehensive QTL analysis is pending to evaluate QTL for several traits: SNF capacity in the greenhouse with low-P stress, SNF *in the field*, yield under low-P stress, yield under drought, and seed nitrogen content.

Table 9. Total nitrogen as measured in a sandy soil in Minnesota, USA, and yield under drought and phosphorus stresses, of recombinant inbred lines developed from the cross BAT 477 x DOR 364.

Line	Total N (mg N per 4 plants) 4 reps	Yield (kg ha^{-1})			Color
		High P 3 reps	Low P 3 reps	Drought 2 reps	
DOR 364	1543	3331	683	297	
BAT 477	2282	3721	998	383	
SEA 5	-	-	-	648	
G3513	-	3188	990	-	
Carioca	-	3626	901	-	
Line 4	2580	3261	553	1028	Cream brilliant
Line 14	2392	3661	671	703	Brown brilliant
Line 16	2456	3712	549	875	Pink semi-br
Line 25	2544	3527	958	669	Black brilliant
Line 49	2509	3415	851	648	Cream-brown br
Line 61	2712	3899	794	685	Brown brilliant
Line 98	2668	3769	996	724	Black opaque
Mean	2388	3448	723	516	
LSD ($P = 0.05$)		714	318	229	

Conclusion: BAT 477 continues to be an excellent source of multiple stress tolerance. Progenies of BAT 477 demonstrate resistance to multiple stresses including low P, and drought and nitrogen stress, and can make an important contribution to yield stability.

Contributors: S Beebe, H Terán (IP-1); P Graham (University of Minnesota)

Progress towards achieving output milestones:

- **Parents/populations/lines tolerant to drought/low soil fertility available**

We have identified a number of genotypes that are better adapted to drought and low soil fertility conditions. Among these, G 21212, a landrace from Colombia, was outstanding in its adaptation to abiotic stress factors such as drought, low P supply in soil and Al toxicity. In collaboration with partners from national agricultural research systems (NARS) and nongovernmental organizations (NGOs), we are evaluating a set of 49 genotypes including landraces and bred lines. This will allow the breeders from national programs to genetically recombine abiotic with biotic stress adaptation and with commercial grain quality.

Activity 1.2 Developing germplasm with multiple resistance to diseases

Highlights:

- The selection of the *bgm-1* gene was applied to about 9000 individual plants and the backcross program to improve commercial varieties with intermediate resistance to BGYMV is nearing completion.

- Sources of resistance to BGMV, BCMV, BSMV, and CCMV were identified in parental materials, and in intermediate and advanced common bean breeding lines.

- Resistance to ALS was identified in a number of *P. vulgaris*, *P. polyanthus,* and *P. coccineus* genotypes.

- Potential sources of ALS resistance were identified in interspecific crosses between *P. vulgaris* and *P. polyanthus* or *P. coccineus*.

- 25 bean genotypes with high levels of resistance to *Phaeoisariopsis griseola* races from Africa, Central America, and South America were identified.

- 10 bean genotypes with high levels of resistance to *Macrophomina phaseolina* were identified.

- Breeding for resistance to *Ascochyta* blight has been successful in creating families with superior resistance that will serve to improve both major gene pools and snap bean types.

1.2.1 Mainstream breeding F_1, F_2, F_3, including *bgm-1* selection

Rationale: Central America is a priority region for poverty alleviation and for bean production. Therefore, the mainstream breeding program continued to focus on small red and small black beans, largely for Central America, with a smaller effort in Carioca type. Bean golden yellow mosaic virus continues to be an indispensable breeding priority for this region.

Materials and methods: Selection was practiced at four principal sites: Palmira (drought, molecular markers, and seed increase), Santander de Quilichao (poor soil fertility, CBB, and ALS), Popayán (anthracnose), and Darien (adaptation to a mid-altitude site and low P). Selection of the *bgm-1* gene for resistance to BGMV continued, as reported last year, as part of the gamete selection scheme with the purpose of identifying F_1 plants that carry the gene, and on advanced lines. As a complement to the mainstream selection program, certain elite commercial varieties with an intermediate level of resistance to BGMV, but lacking the *bgm-1* gene were selected for introducing this gene and thereby improving their resistance. A source of *bgm-1*, SAM 1, also is highly resistant to CBB.

Results: In 2000, about 60 red-seeded lines were selected across these sites and were shipped to the Escuela Agrícola Panamericana (EAP-Zamorano) for inclusion in regional nurseries in Central America through the PROFRIJOL network. These were the same lines that were evaluated under drought stress in Palmira (Table 4). Compared to previous lines, these represent advances in resistance to CBB and in lesser degree to ALS, in combination with resistance to BGYMV and modest resistance to poor soil and drought. In general, resistance to ALS still needs to be fortified with new sources of resistance. Meanwhile, early generation populations incorporating an increasing contribution of abiotic stress tolerance were selected in F_1 to F_4 generations. About 1200 lines of red and black seed types are being evaluated in Darien (the environment that is most similar to Central American production environments) to develop a set of 150-200 lines for distribution in 2001.

Selection of the *bgm-1* gene for resistance to BGMV was applied to another 9000 F_1 plants. The plan to introduce the *bgm-1* gene by backcrossing into commercial varieties advanced to the F_2BC2 generation. In the F_1BC1, phenotypic selection was also practiced for resistance to CBB, prior to making the BC2. At present, the most advanced lines are in $BC2F_3$ and they are being purified for *bgm-1* and for CBB reaction. Because SAM 1 was not phenotypically distant from the recurrent parents, two cycles of backcrossing are deemed sufficient to recover the phenotype of the recurrent parent.

Conclusions: Marker-assisted selection continues to be an indispensable part of the breeding effort and has served to create lines with multiple disease resistance. It should be extended to other critical disease resistance genes as these are identified and tagged with reliable PCR markers. Resistance to ALS, to regionally important viruses (BSMV and CCMV), and to the abiotic stresses still needs to be strengthened.

Contributors: S Beebe, G Mahuku, H Terán, C Jara, JM Osorno, C Cajiao (IP-1); C Quintero, J Tohme (SB-2)

1.2.2 Bean common mosaic virus (BCMV)

Resistance to viral diseases of common bean in the tropics remains an important breeding activity in the Bean Project because these diseases can severely affect bean production in the main target regions. Bean virology activities seek to identify sources of resistance to emerging bean diseases, such as "amachamiento" (bean sterility), caused by CCMV. Also, effective disease screening methodologies are implemented to select breeding lines possessing resistance to the endemic (BCMV and BGMV) and sporadic (BSMV) viral diseases that limit bean production in the tropics.

Rationale: The BCMV is the most widely distributed pathogen of common bean in the world. Thus genetic resistance continues to be incorporated in all breeding lines developed by CIAT in collaboration with national agricultural research institutes (NARIs), as the main prerequisite for germplasm development.

Materials and methods: The screening methodology implemented at CIAT for BCMV targets segregating populations in order to select homozygous BCMV-resistant lines in the F_3 generation (dominant monogenic resistance) or in subsequent generations (dominant/recessive genes). Hence, 1200 entries from segregating populations were screened this year for their reaction to BCMV. Also, 960 lines from multiple crosses were evaluated this year for their resistance to this virus. Incorporating BCMV resistance in red-seeded Central American cultivars has been a difficult task because of genetic linkage problems between genes determining BCMV-susceptibility and the red seed-coat color. This year, we evaluated 83 Central American, red-seeded materials for their reaction to BCMV.

Results: These evaluations showed that 91% of the materials possessed monogenic dominant resistance to BCMV, 5% were susceptible to the virus, and 4% were segregating for this trait (R/S). This proportion of BCMV-resistant lines would be a major achievement for other bean-producing regions of Latin America. However, this type of resistance is not adequate for those Central American countries, such as El Salvador, where the commercial red-seeded varieties are preferred (varieties with monogenic dominant resistance to BCMV have a darker red seed-coat color, which reduces their commercial value). Also, a different viral disease (BSMV) selectively attacks these genotypes.

Conclusions: The strategy proposed to counteract this problem was the gradual replacement of bean genotypes possessing monogenic dominant resistance by genotypes protected against BCMV by the recessive *bc 3* gene. This gene is not selectively attacked by BSMV and does not have a linkage problem related to seed color and BCMV susceptibility. However, 44 potential *bc 3* donor parents evaluated under field conditions in El Salvador last year succumbed to BGMV. This experience clearly points out the need to breed for multiple disease resistance, in this case to BGMV, BCMV, and BSMV simultaneously. This approach was followed this year with 96 advanced materials possessing multiple disease resistance to different pathogens, including bacterial blight and viral diseases. Of the 96 lines screened, 28% showed multiple resistance to the biotic factors mentioned.

Contributors: FJ Morales, M Castaño, CJ Alvarez

1.2.3 Bean severe mosaic virus (BSMV)

Rationale: Bean severe mosaic is a generic name given to a complex disease of common beans caused by different strains of cowpea severe mosaic virus (CPSMV) in Latin America. The problem is more "severe" in bean cultivars possessing monogenic dominant resistance to BCMV because of hypersensitive reactions between the pathogen and the dominant *I* gene. Also, the disease is more prevalent in Central America, where the chrysomelid vectors of the causal viruses are common in bean plantings. In bean cultivars possessing recessive resistance to BCMV, the disease is not as severe, and some genotypes only show mild mosaic symptoms.

Materials and methods: We have finished the evaluation of a Bean Core Collection of 1218 accessions for their reaction to CPSMV. These evaluations were conducted under controlled conditions by standard mechanical inoculation methods.

Results: About 88% of the accessions evaluated reacted with CPSMV, thus indicating that those genotypes were devoid of the dominant *I* gene; whereas 10% of the accessions inoculated reacted with mosaic and necrosis (bean severe syndrome), demonstrating the presence of the dominant *I* gene in these genotypes. About 2% of the accessions evaluated reacted with top necrosis, a reaction that is conditioned by yet another dominant gene previously characterized at CIAT (Morales and Singh 1997[1]) as *Anv*, apparently epistatic to the dominant *I* gene.

Conclusions: No immune genotypes were detected in these evaluations, but many of the accessions that reacted with mild mosaic could be used as potential sources of resistance or tolerance to CPSMV. Nevertheless, it is important to replace the dominant *I* gene with the recessive *bc 3* gene for resistance to BCMV/BCMNV in the breeding project for the improvement of Central American common bean cultivars.

Contributors: FJ Morales, M Castaño, CJ Alvarez

1.2.4 Bean "sterility" (amachamiento)

Rationale: "Amachamiento" is a syndrome associated with a marked yield reduction of bean plantings in Costa Rica and Nicaragua. The etiology of this syndrome was elucidated in 1998, as a viral disease caused by the chrysomelid-transmitted CCMV, often found associated with BCMV in local bean cultivars. The CCMV was known to attack beans in the lowlands of Central America and the Caribbean, where it caused the disease previously known as "bean yellow stipple". At higher altitudes, where this virus is now located, the characteristic yellowing disappears, to be replaced by foliar distortion. However, the main effect of the virus continues to be the significant yield reduction it causes both in the lowland and mid-altitude bean production areas.

Materials and methods: A yield loss experiment was conducted under controlled conditions over a 2-year period, with eight selected bean cultivars manually inoculated in six replications. The line DOR 364 is a BGYMV-resistant cultivar widely adopted in Central America. We also evaluated three genotypes of the Durango race of common beans, previously shown to have field resistance to a variety of different bean viruses.

Results: The red-seeded landrace "Sacapobres" suffered an average 52% yield loss, whereas the improved "Talamanca" cultivar showed an average yield loss of 34% under the experiment glasshouse conditions of the study. The DOR 364 is a BGYMV-resistant line (cultivar) widely adopted in Central America. We tested this line for its reaction to CCMV, and observed an average yield reduction of 45% in five replications. We also

---

[1] Morales FJ, Singh SP. 1997. Inheritance of the mosaic and necroses reactions induced by bean severe mosaic common viruses in *Phaseolus vulgaris* L. Euphytica 93:223-226.

evaluated three genotypes of the Durango race of common beans, previously shown to have field resistance to a variety of different bean viruses. Under the test conditions selected, Pinto 114 suffered average yield reduction of 6.6%, Great Northern 123 of 37%, and Red Mexican 35 of 52.4%. Another source of resistance to bean viruses, belonging to the Nueva Granada (Andean) race, cultivar "Red Kloud", showed the highest level of resistance in these tests, with an average yield loss of 0% and a range between 0% and 25%.

Conclusions: Possibly the significant yield loss of "Sacapobres" could be further aggravated by its susceptibility to BCMV under field conditions. We will test this possibility next year. In field visits made to the affected Brunca region of southern Costa Rica, it was evident that "Talamanca" had excellent vegetative growth, but very few, if any, pods per plant. The "amachamiento" symptoms on this cultivar are expressed mainly as a mild mottle, so possibly the cultivar is also showing symptoms of poor adaptation to that region. Talamanca is a black-seeded genotype developed in Colombia. However, it was tested for adaptation in the region of Perez Zeledón, not far from the affected areas visited in Costa Rica, which were located at a higher altitude. Whereas it was apparent that yield under the artificial test conditions of this study was significantly influenced by the varying environmental conditions found during the year, the averages given here reflect the expected level of resistance to CCMV in each of the common bean genotypes tested. Thus, and in anticipation of further germplasm screening work, we recommend the genotypes Porrillo Sintético and Red Kloud for crop improvement purposes in the presence of CCMV.

Contributors: FJ Morales, M Castaño, CJ Alvarez

1.2.5 Bean golden yellow mosaic virus (BGYMV)

Rationale: This virus is one of the most devastating problems of common bean in the lowlands and mid-altitude valleys of Central America.

Materials and methods: This year, 83 selected red-seeded advanced lines bred for Central America were evaluated for their reaction to BGYMV under controlled conditions, following a standard mechanical inoculation methodology.

Results: Of the 83 lines, 21 (about 25%) showed a high level of virus resistance, 37 (44%) were moderately resistant, and the remaining lines (31%) were susceptible to BGYMV.

Conclusions: The high proportion of virus-resistant lines (>50%) reflects the use of BGYMV-resistant parents in their crosses, namely DOR 482, ICA Pijao, DOR 364, MD-30-75, Red MEX 35, and Tio Canela (DOR 364, 367, 391, 483).

Contributors: FJ Morales, M Castaño, CJ Alvarez

Summary: Table 10 shows the reaction of the selected 83 red-seeded lines to four different viral diseases prevalent in Central America. As can be concluded from these results, most of the red-seeded genotypes possess monogenic dominant resistance to BCMV, which renders these materials susceptible to BSMV, and creates genetic linkage problems that hinder the selection of commercial red-seeded grain types. An effort must be made to rapidly change the breeding strategy to replace the dominant *I* gene with the recessive *bc 3* gene.

Table 10. Reaction[a] of 83 selected red-seeded lines to four different viral diseases[b] prevalent in Central America.

Entry	Code	Identification	BCMV	BGMV	BSMV	CCMV
1	MN12917-26	ICA Pijao x (XAN 252 x MAR 1) x (DOR 482 x J117)	R(I)	S	S	I
2	MN12917-22	ICA Pijao x (XAN 252 x MAR 1) x (DOR 482 x J117)	R(I)	S	S	I
3	MN12917-22	ICA Pijao x (XAN 252 x MAR 1) x (DOR 482 x J117)	R(I)	R	S	I
4	MN12917-22	ICA Pijao x (XAN 252 x MAR 1) x (DOR 482 x J117)	R(I)	R	S	I
5	MN12917-22	ICA Pijao x (XAN 252 x MAR 1) x (DOR 482 x J117)	R(I)	S	S	I
6	MN12917-4	ICA Pijao x (XAN 252 x MAR 1) x (DOR 482 x J117)	R(I)	S	S	I
7	MR12826-8	VAX3 x MD30-75 x DOR 364 x MAR 1 x BELD x XAN 309	R(I)	S	S	I
8	MR12826-8	VAX3 x MD30-75 x DOR 364 x MAR 1 x BELD x XAN 309	R(I)	S	S	I
9	MR12826-8	VAX3 x MD30-75 x DOR 364 x MAR 1 x BELD x XAN 309	R(I)	S	S	I
10	MR12826-8	VAX3 x MD30-75 x DOR 364 x MAR 1 x BELD x XAN 309	R(I)	S	S	I
11	MR12826-8	VAX3 x MD30-75 x DOR 364 x MAR 1 x BELD x XAN 309	R(I)	R	S	I
12	MR12826-8	VAX3 x MD30-75 x DOR 364 x MAR 1 x BELD x XAN 309	R(I)	S	S	I
13	MR12826-31	VAX3 x MD30-75 x DOR 364 x MAR 1 x BELD x XAN 309	R(I)	R	S	I
14	MR12826-32	VAX3 x MD30-75 x DOR 364 x MAR 1 x BELD x XAN 309	R(I)	S	S	I
15	MR12746-48	MD30-75 x PVPA 9576 x XAN 310 x CATRACH x MAR 1	R(I)	R	S	I
16	MR12747-10	MD30-75 x PVPA 9576 x XAN 310 x CATRACH x MAR 1	R(I)	S	S	S
17	MR12910-15	XAN 252 x MAR 1 x DOR 482 x J 117	R(I)	S	S	I
18	MR12439-6	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	S	S	I
19	MR12439-31	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
20	MR12439-31	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
21	MR12439-31	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
22	MR12439-31	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
23	MR12439-31	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
24	MR12439-31	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
25	MR12439-31	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
26	MR12439-105	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
27	MR12439-105	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
28	MR12439-105	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
29	MR12439-105	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
30	MR12439-105	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
31	MR12439-18	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
32	MR12439-18	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
33	MR12439-18	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
34	MR12439-18	Catrachita x XAN 309 x Orgullo x Tio Canela	R(I)	R	S	I
35	MR12437-3	MD30-75 x PVPA 9576 x XAN 310	R(I)	R	S	I
36	MR12437-3	MD30-75 x PVPA 9576 x XAN 310	R(I)	R	S	I
37	MR12437-3	MD30-75 x PVPA 9576 x XAN 310	R(I)	R	S	I
38	MR12437-2	MD30-75 x PVPA 9576 x XAN 310	R(I)	R	S	I
39	MR12437-2	Orgullo x Tio Canela x XAN 309 x G 17341 x DCelaya	R(I)	R	S	S
40	MR12437-2	Ogrullo x Tio Canela x XAN 309 x G 17341 x DCelaya	R(I)	R	S	S
41	MR12437-135	Orgullo x Tio Canela x XAN 309 x G 17341 x DCelaya	R(I)	S	S	S
42	MR12437-135	Orgullo x Tio Canela x XAN 309 x G 17341 x DCelaya	R(I)	S	S	I
43	MR12437-135	Orgullo x Tio Canela x XAN 309 x G 17341 x DCelaya	R(I)	R	S	I
44	MR12437-135	Orgullo x Tio Canela x XAN 309 x G 17341 x DCelaya	S	S	M	I
45	MR12437-168	Orgullo x Tio Canela x XAN 309 x G 17341 x DCelaya	R(I)	S	S	I
46	MR12438-76	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	S	S	I
47	MR12438-81	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	R	V	I
48	MR12438-93	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	R	S	I

Continued.

Table 10. Continued.

Entry	Code	Identification	BCMV	BGMV	BSMV	CCMV
49	MR12438-93	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	R	S	I
50	MR12438-93	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	R	S	I
51	MR12438-93	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	R	S	I
52	MR12438-93	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	S	S	I
53	MR12438-97	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	S	S	I
54	MR12438-97	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	V	S	S	I
55	MR12438-97	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	S	S	I
56	MR12438-97	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	S	S	S
57	MR12438-27	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	S	S	I
58	MR12438-78	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	S	S	I
59	MR12438-78	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	R	S	I
60	MR12438-46	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	S	R	M	I
61	MR12438-46	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	S	R	M	I
62	MR12438-46	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	V	R	S	I
63	MR12438-96	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	S	V	I
64	MR12438-96	RMEX 35 x Rojo Seda x Tio Canela x XAN 309 x Orgullo	R(I)	S	V	I
65	MR12440-22	Rojo Seda x Tio Canela x XAN 309 x G 17341 x G 1345	R(I)	R	S	I
66	MR12440-22	Rojo Seda x Tio Canela x XAN 309 x G 17341 x G 1345	R(I)	R	S	I
67	MR12440-22	Rojo Seda x Tio Canela x XAN 309 x G 17341 x G 1345	R(I)	R	S	I
68	MR12440-22	Rojo Seda x Tio Canela x XAN 309 x G 17341 x G 1345	R(I)	S	S	I
69	MR12326-40	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	I
70	MR12326-40	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	R	S	I
71	MR12326-40	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	R	S	I
72	MR12326-48	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	I
73	MR12326-1	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	R	S	I
74	MR12326-1	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	I
75	MR12326-7	XAN 309 x Orgullo x Tio Canela x XAN 309	S	S	M	I
76	MR12326-53	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	R
77	MR12326-53	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	V	I
78	MR12326-53	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	I
79	MR12326-53	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	I
80	MR12326-53	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	I
81	MR12326-53	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	R
82	MR12326-13	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	I
83	MR12326-14	XAN 309 x Orgullo x Tio Canela x XAN 309	R(I)	S	S	I

a. R = resistant, M = medium susceptibility, I = *I* gene, V = segregating, and S = susceptible.

b. Bean common mosaic virus (BCMV), bean golden yellow mosaic virus (BGYMV), bean severe mosaic virus (BSMV), and cowpea chlorotic mottle virus (CCMV).

1.2.6 Identifying genotypes with resistance to angular leaf spot

Rationale: Because of the high variability that is exhibited by most pathogens, identification of sources of resistance to major diseases is a continuous activity. Understanding the mechanisms underlying disease resistance is essential for developing appropriate breeding strategies. This year, we screened materials from the germplasm bank to look for sources of ALS resistance in the small-red type of bean that are grown widely in Central America. In addition, we screened the primary and secondary gene pools for possible sources of ALS resistance and interspecific crosses derived from crossing *P. vulgaris* with *P. polyanthus* and/or *P. coccineus*.

Materials and methods: 117 bean germplasm representing small-red materials that were identified as having resistance to local *P. griseola* isolates in Santander de Quilichao in 1999 were screened again in Darien, using other races found in this area. In a separate experiment, 233 small reds that were not evaluated in 1999 were evaluated this year in

Santander de Quilichao. In both locations, these materials were inoculated with a mixture of the widest genetic diversity of the pathogen, locally isolated from the same area (Tables 11 and 12). Evaluations for disease severity were assessed four times, starting 2 weeks after inoculation, using a CIAT 1 – 9 scale, where 1 represents no visible symptoms and 9 represents severe symptoms and disease expression (van Schoonhoven and Pastor-Corrales 1987[2]). Plants that had a rating of 3 or less were considered resistant, 4-6 were intermediate, and a rating greater than 6 were considered susceptible.

Table 11. Virulence phenotype of *Phaeoisariopsis griseola* isolates used for inoculation of potential sources of resistance in Darien, Colombia.

Isolate	Race	Differential cultivars[a]											
		A	B	C	D	E	F	G	H	I	J	K	L
PG 81 COL	5-47	a		c				g	h	i	j		l
PG 261 COL	31-47	a	b	c	d	e		g	h	i	j		l
PG 270 COL	63-0	a	b	c	d	e	f						
PG 289-1 COL	47-0	a	b	c	d		f						

a. Andean differential cultivars: A = Timoteo, B = G 11796, C = Bolón Bayo, D = Montcalm, E = Amendoin, and F = G 5686. Mesoamerican differential cultivars: G = PAN 72, H = G 2858, I = Flor de Mayo, J = MEX 54, K = Bat 332, and L = Cornell 49242.

Table 12. Virulence phenotype of *Phaeoisariopsis griseola* isolates used for inoculation of potential sources of resistance in Santander de Quilichao, Colombia.

Isolate	Race	Differential cultivars[a]											
		A	B	C	D	E	F	G	H	I	J	K	L
PG 3 COL	63-0	a	b	c	d	e	f						
PG 61 COL	31-63	a		c	d			g	h	i	j	k	l
PG 65 COL	1-55	a						g	h	i		k	l
PG 32 COL	31-55	a	b	c	d	e		g	h	i		k	l
PG 1 COL	7-55	a	b	c				g	h	i		k	l

a. Andean differential cultvars: A = Timoteo, B = G 11796, C = Bolón Bayo, D = Montcalm, E = Amendoin, and F = G 5686. Mesoamerican differential cultivars: G = PAN 72, H = G 2858, I = Flor de Mayo, J = MEX 54, K = BAT 332, and L = Cornell 49242.

---

[2] van Schoonhoven A, Pastor-Corrales MA. 1987. Standard system for the evaluation of bean germplasm. CIAT, Cali, Colombia. 53 p.

Ninety-six sources of ALS resistance that include bred and germplasm materials were evaluated under field conditions with a mixture of races (Tables 13 and 14) that are encountered in Darien and Santander de Quilichao. These materials had been identified as having good levels of ALS resistance in previous screenings.

Table 13. Bean genotypes resistant to *Phaeoisariopsis griseola* in Darien and/or Santander de Quilichao, Colombia (R = resistant, I = intermediate, and S = susceptible).

Genotype identification	Disease rating	
	Darien	Santander de Quilichao
A 223	R	R
A 384	R	R
AFR 645	R	R
AFR 702	R	R
AFR 703	R	R
AND 1056	R	R
AND 277	R	R
APN 47	R	R
BRU 13	R	R
CAL 143	R	R
CAL 173	R	R
CNF 5558	R	R
G 10474	R	R
G 10736	R	R
G 10909	R	R
G 14301	R	R
G 18970	R	R
G 22257	R	R
G 04333	R	R
G 05698	R	R
G 15396	R	R
G 20523	R	R
G 20743	R	R
G 22255	R	R
G 22267	R	R
A 247	S	R
G 5207	S	I
G 5377	S	I
G 10865	S	R
G 22447	S	R
G 00811	S	R
G 01805	R	S
G 01845	S	I
G 01916	S	R
G 02647	S	R
G 09462	I	S
G 18451	S	R
G 20748	S	R
ICTA Texel	S	I
Jacinto	S	S
NIC 147	S	I
NIC 159	S	I
RWR 222	S	R

Table 14. Response of 96 bean genotypes to inoculation with an angular leaf spot race, 63-47, from Malawi under greenhouse conditions.

Entry	Disease response[a]	Entry	Disease response[a]	Entry	Disease response[a]
A 233	R	G 18970	I	ZAA 91	I
G 18451	R	G 18842	I	G 14301	I
G 11405	R	AFR 188	I	G 8152	I
G 04333	R	AND 277	I	G 14508	I
G 01845	R	NAB 69	I	G 916	I
G 10909	R	NIC 147	I	A 240	I
MAR 3	R	RAB 354	I	CNF 5558	I
RWR 222	R	G 09462	I	G 9282	I
G 10613	R	MAR 1	I	G 22267	S
G 19833	R	G 02647	I	G 6727	S
CAL 173	R	G 4691	I	AND 1056	S
G 22447	R	G 18224	I	CAL 143	S
G 19115	R	A 82	I	G 15396	S
G 01805	R	G 20818	I	CAL 123	S
G 05653	R	G 20523	I	A 384	S
G 05698	R	G 20743	I	Jacinto	S
AFR 735	R	A 339	I	A 247	S
AFR 702	R	AFR 703	I	G 09603	S
G 5207	R	A 791	I	G 20748	S
G 10474	R	A 216	I	BRB 191	S
G 10736	R	G 03991	I	A 785	S
BAT 496	R	G 20939	I	ICA Tex	S
G 01916	R	DE CELA	I	G 11104	S
A 222	R	G 00811	I	G 5377	S
BAT 1458	I	G 04032	I	G 22301	S
NIC 159	I	BRB 190	I	EMP 365	S
G 22255	I	APN 47	I	G 20525	S
G 2923	I	BRU 13	I	Gordo	S
AND 829	I	RIZ 97	I	EMP 364	S
				G 4724	S

a. R = resistant, I = intermediate, and S = susceptible.

The same 96 sources of resistance were also evaluated under greenhouse conditions using race 63-47 from Africa. The objective was to identify ALS-resistant materials with a broad activity that could also be used to manage this disease in Africa.

Sixteen wild and weedy *P. vulgaris* materials that were identified as resistant under field conditions in Darien and Santander de Quilichao during the 1999 season were screened under greenhouse conditions using race 63-63, the most virulent and aggressive identified to date. In addition, 37 lines from the Costa Rican national breeding program were screened using race 63-63 under greenhouse conditions.

Results and discussion: Of the 177 small-red genotypes selected in Sander de Quilichao during 1999, only one (G 5608) was resistant in Darien, while 17 that had a resistant or intermediate phenotype in Santander de Quilichao (1999 data) were susceptible in Darien. Of the genotypes that were resistant or intermediate in both locations none had a resistant or intermediate reaction to race 63-63 under greenhouse conditions (Table 15, Figure 27). These results show that the small-red type of beans has very little resistance to *P. griseola*. Therefore, resistance has to be introgressed from other genotypes outside this type of bean.

Table 15. Potential sources of angular leaf spot in small-red beans to inoculation with *Phaeoisariopsis griseola* in Darien and Santander de Quilichao, Colombia

Genotype	Disease rating[a]	
	Darien	Quilichao
G 7004	2	4
G 2094	3	6
G 7005	3	5
G 7874	3	7
G 5608	2	3
G 15804	4	2
G 5622	7	2
G 4075	8	2
G 7185	8	2
G 14512	6	3
G 1925	7	3
G 2059	7	3
G 2746	7	3
G 2757	7	3
G 3697	7	3
G 6430	7	3
G 7185	7	3
G 2168	8	3

a. Disease rating on a score of 1-9, where 1 = no visible symptoms and 9 = severe symptoms and disease expression.

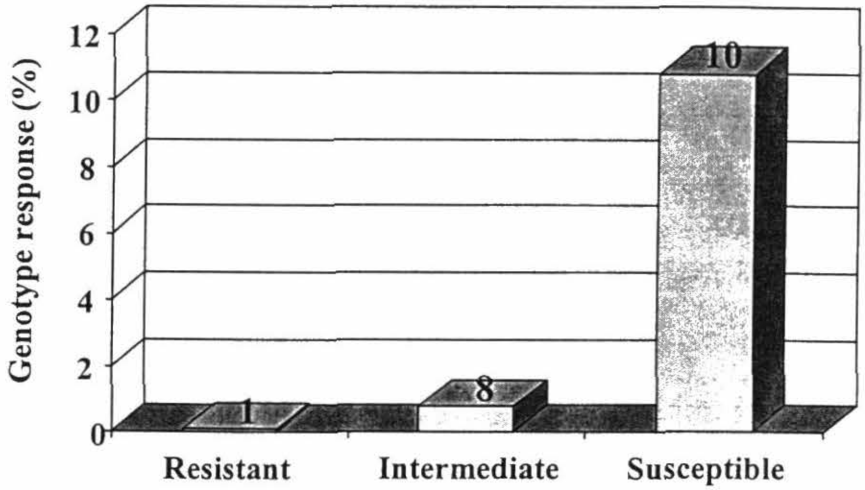


Figure 27. Response of 117 small-red type of common bean to inoculation with *Phaeoisariopsis griseola* under field conditions at Darien and Santander de Quilichao, Colombia.

Similarly, of the 233 small-red genotypes evaluated in Santander de Quilichao, only six were resistant, while 277 were either susceptible or had an intermediate reaction (Figure 28). These materials (six) will be evaluated in the greenhouse using the most virulent race (63-63) from Central America. However, previous results have shown that very little resistance to ALS exists within the small-red genotypes. Small reds are very important for Central America; therefore, efforts should be made to introgress ALS resistance from other materials that have been identified as having high levels of ALS resistance.

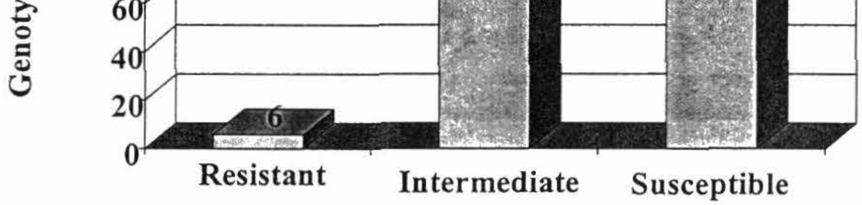


Figure 28. Response of 233 accessions of small-red type of beans to inoculation with *Phaeoisariopsis griseola* under field conditions at Santander de Quilichao, Colombia.

Of the 96 materials previously identified as having some ALS resistance, 25 (12 bred lines and 13 germplasm material) were resistant to the diversity found in both Santander de Quilichao and Darien (Figure 29, Table 13). However, most of the materials that were resistant in Santander de Quilichao were susceptible in Darien, showing the differences in the race structure and composition of *P. griseola*. These results show that simultaneous evaluation of potential sources of resistance in these two areas results in better selection of ALS resistance. Because of the differences in the environmental conditions in Santander de Quilichao and Darien, the race composition is different and using both sites ensures that potential sources of ALS resistance are exposed to the greatest diversity that exists in the pathogen.

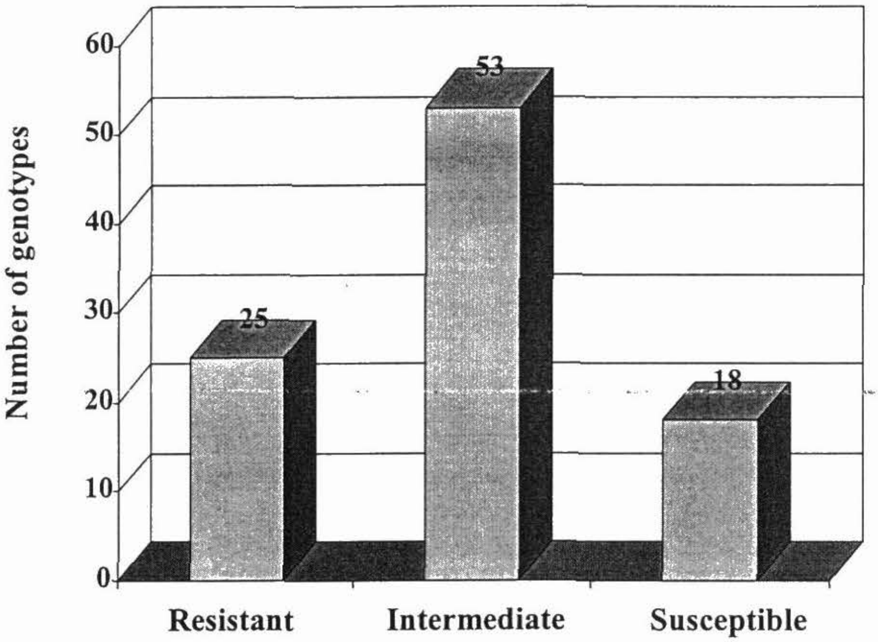


Figure 29. Response of 96 bean materials to inoculation with *Phaeoisariopsis griseola* under field conditions at Darien and Santander de Quilichao, Colombia.

When the same 96 materials were evaluated under greenhouse conditions with race 63-47 from Africa, 25 genotypes were identified as resistant (Table 14). These materials constitute an import source of ALS resistance for African bean researchers.

Of the 16 wild and weedy materials that had been identified as having resistance following field evaluations, only four (G 23435C, G 23477, G 23478, and G 23479) showed high levels of resistance to race 63-63 (Table 16). Two of these materials are from Guatemala and the other is from Mexico. This is very interesting because most of the high levels of resistance found in *P. vulgaris* are materials that originated from the highlands of Mexico and Guatemala. Future evaluations for ALS resistance should focus on germplasm from these areas.

Table 16. Response of wild and weedy *Phaseolus vulgaris* to inoculation with race 63-63 of *Phaeoisariopsis griseola* under greenhouse conditions.

Accession	Origin	Disease rating (race 63-63)[a]
G 10001	Mexico	S
G 10001A	Mexico	S
G 10002A	Mexico	I
G 10005	Mexico	I
G 11031	Mexico	I
G 12866A	Mexico	S
G 12882A	Mexico	S
G122866	Mexico	I
G 12028	Mexico	S
G 23416	Costa Rica	S
G 23434C	Guatemala	R
G 23435A	Guatemala	I
G 23465	Mexico	I
G 23477	Guatemala	R
G 23478	Guatemala	R
G 23479	Mexico	R

a. Disease rating on a score of 1-9, where 1 = no visible symptoms and 9 = severe symptoms and disease expression.

Of the 37 lines from the Costa Rican national program, only two materials, UCR-59 and CFR-31, were resistant to race ALS 63-63 (Table 17). Most of these materials were highly susceptible.

Conclusion: Sources of ALS resistance have been identified in *P. vulgaris* and wild and weedy *P. vulgaris*. This group constitutes a very interesting source of ALS resistance and is a first step towards durable ALS resistance. However, the activity spectrum of these genes needs to be established. They must be sufficiently characterized to identify the ones with the broadest activity as well as gene combinations to pyramid. In addition, this information will allow for proper deployment of these resistance genes in ways that will prolong their durability. Inheritance studies for some of these materials have been initiated as well as transferring the identified genes into well-adapted, market-class type beans.

Table 17. Reaction of bean lines from the Costa Rican national program evaluated for reaction to race 63-63 of *Phaeoisariopsis griseola* under greenhouse conditions.

Entry	Disease rating[a]	Entry	Disease rating[a]
UCR-56	S	CFR-25	S
UCR-58	S	CFR-26	S
UCR-59	R	CFR-27	S
UCR-60	S	CFR-28	S
UCR-61	S	CFR-29	I
CFR-11	S	CFR-30	S
CFR-12	S	CFR-31	R
CFR-13	S	CFR-32	S
CFR-14	S	CFR-33	I
CFR-15	S	CFR-34	S
CFR-16	S	CFR-35	S
CFR-17	S	CFR-36	S
CFR-18	S	CFR-37	S
CFR-19	I	CFR-38	S
CFR-20	I	CFR-39	S
CFR-21	S	CFR-40	S
CFR-22	S	CFR-41	S
CFR-23	S	CFR-42	S
CFR-24	S		

a. Disease rating: R = resistant, I = intermediate, and S = susceptible.

Contributors: G Mahuku, C Jara

1.2.7 Screening of the secondary gene pool and interspecific crosses for sources of angular leaf spot resistance

Rationale: Because of the highly variable nature of bean fugal pathogens, beans that are resistant in one location are more likely to be susceptible in another location in the same or different year. This resistance is not durable and the exercise of looking for sources of resistance is therefore a continuous activity. Because some traits are expressed at inadequate levels within the primary gene pool, last year we evaluated 100 genotypes of *P. polyanthus* and *P. coccineus* and found high levels of resistance to ALS in the secondary *Phaseolus* gene pool. With the hypothesis that long-lasting and durable ALS resistance will be found in the secondary and/or tertiary *Phaseolus* gene pools, we screened the *P. polyanthus* and *P. coccineus* Core Collection for resistance to ALS and anthracnose under field conditions. In addition, we screened 1012 interspecific crosses between *P. vulgaris* and *P. polyanthus* and *P. coccineus*, in order to identify lines carrying ALS resistance.

Materials and methods: Materials comprising the Core Collection of *P. polyanthus* and *P. coccineus* (162) were inoculated separately with Andean and Mesoamerican races of *P. griseola* and *Colletotrichum lindemuthianum*. In a separate experiment, 481 interspecific crosses were screened in Darien using local races of *P. griseola*. Crosses were between *P. vulgaris* and *P. coccineus* and *P. polyanthus* (ICA Pijao x G 335172; ICA Pijao x G 35171; ICA Pijao x G 35877; ICA Pijao x G 33720; ICA Pijao x DGD 2119). During the second semester, 534 interspecific crosses that involved wider *P. vulgaris* / *P. polyanthus* or *P. coccineus* crosses were evaluated in Darien. All materials were inoculated, with a mixture of *P. griseola* races found in Darien, four times starting 25 days after planting and every 10 days thereafter. Evaluations for disease severity were assessed four times, starting 2 weeks after inoculation, using a CIAT 1 – 9 scale, where 1 represents no visible symptoms and 9 = severe symptoms and disease expression. Plants that had a rating of 3 or less were considered resistant, 4-6 were intermediate, and a rating greater than 6 were considered susceptible.

Results and discussion: High levels of resistance to ALS were observed among the *P. polyanthus and P. coccineus* Core Collections. Andean races of *P. griseola* and *C. lindemuthianum* did not infect any of these materials (Figures 30 and 31). However, Mesoamerican races of *C. lindemuthianum* infected only one genotype, while 11 had an intermediate reaction with a Mesoamerican race of *P. griseola* (Figures 32 and 33). When these materials were evaluated in the greenhouse with race 3841, only two had intermediate reaction, while the rest of the materials were resistant (Figure 34). These results show that the secondary *Phaseolus* gene pool has high levels of resistance to both anthracnose and ALS of common bean and these are potential sources of durable resistance.

When we screened 481 interspecific crosses that had been generated as part of the BGMV improvement program for resistance to ALS, we found low levels of resistance. Only 3.3% of the materials (16) had resistance to mixtures of *P. griseola* races found in Darien (Figure 35). These low levels of resistance were possibly because of the narrow base of the parental materials used in the crosses. In addition, these populations had gone through several cycles of screening for common bean phenotype and possibly the resistance to ALS that was in the original parents might have been lost.

We therefore pulled out 531 interspecific crosses from the germplasm bank that included populations from F_2 to F_9. Only 93 of these materials were resistant to *P. griseola* in Darien (Figure 36). However, most of these materials were segregating and individual selections were made for resistance to ALS.

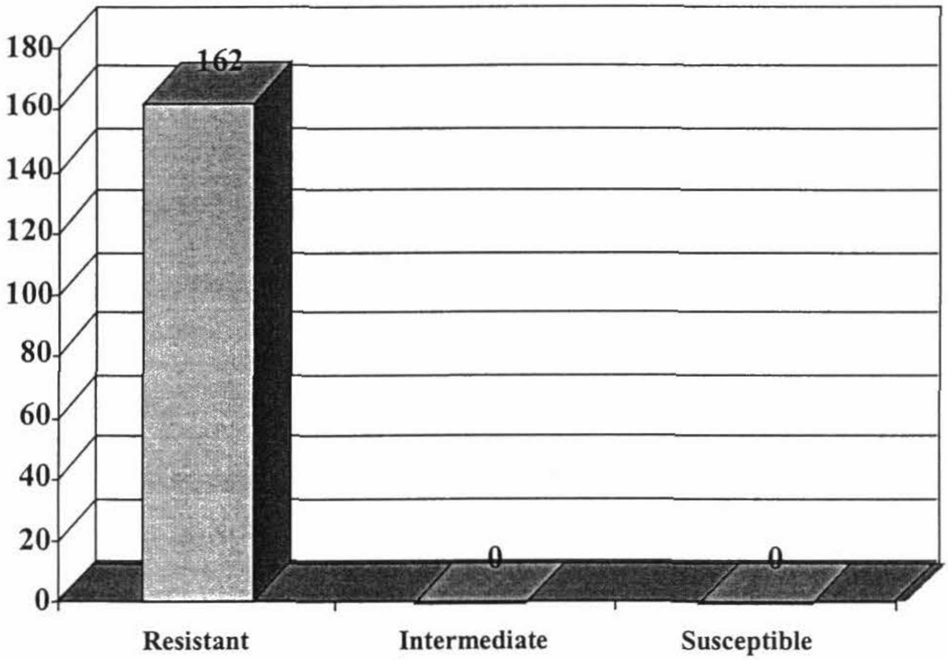


Figure 30. Field evaluation of *Phaseolus coccineus* and *P. polyanthus* using Andean races of *Phaeoisariopsis griseola*.

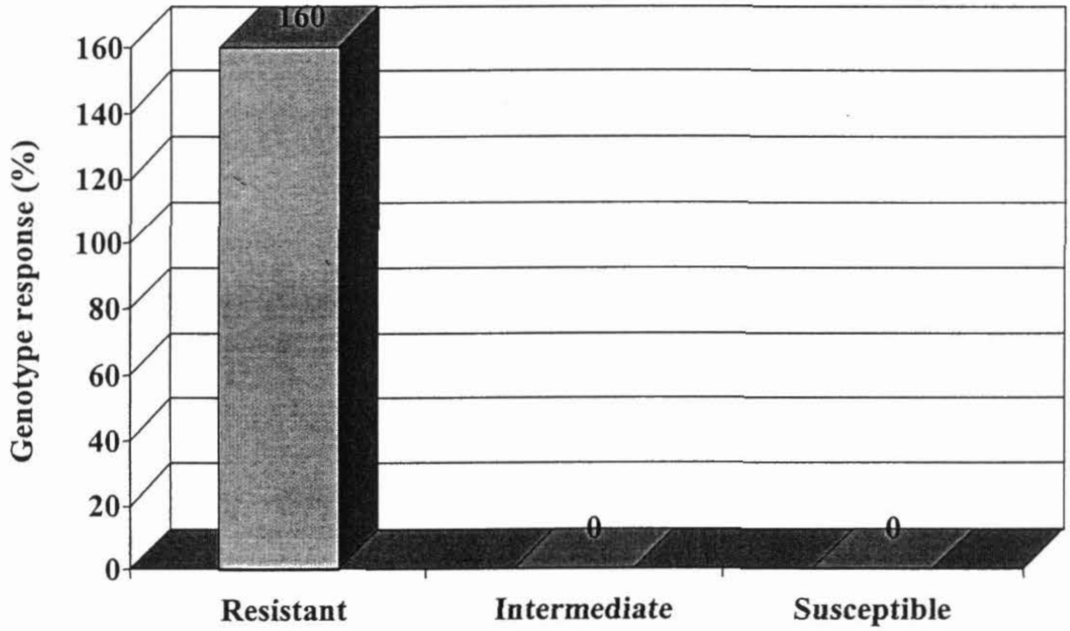


Figure 31. Field evaluation of *Phaseolus coccineus* and *P. polyanthus* using Andean races of *Colletotrichum lindemuthianum*.

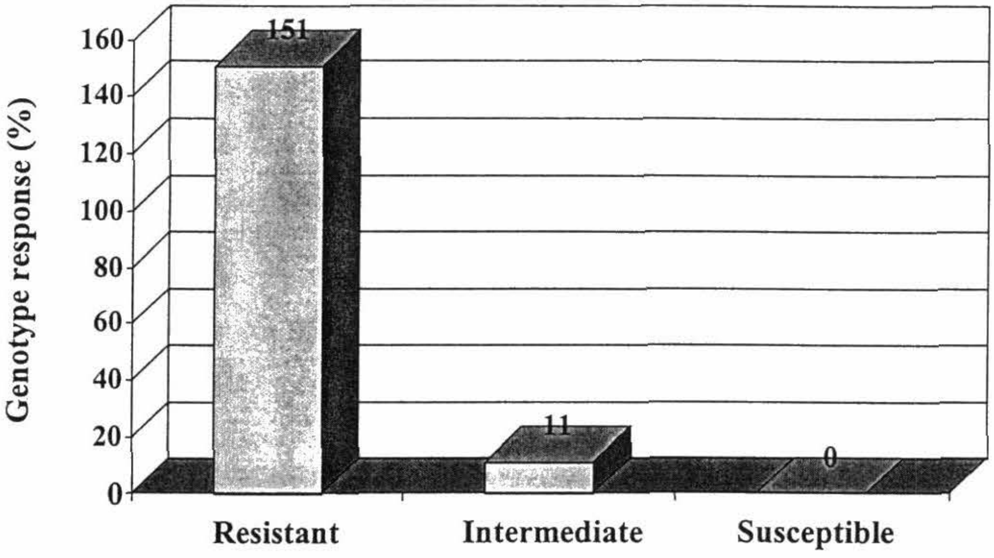


Figure 32. Field evaluation of *Phaseolus coccineus* and *P. polyanthus* using Mesoamerican races of *Colletotrichum lindemuthianum*.

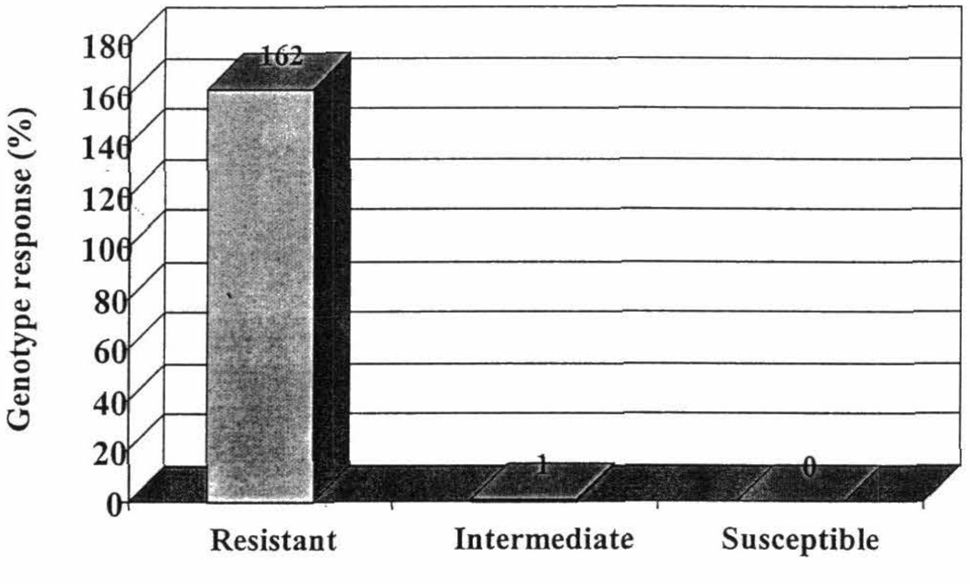


Figure 33. Field evaluation of *Phaseolus coccineus* and *P. polyanthus* using Mesoamerican races of *Phaeoisariopsis griseola*.

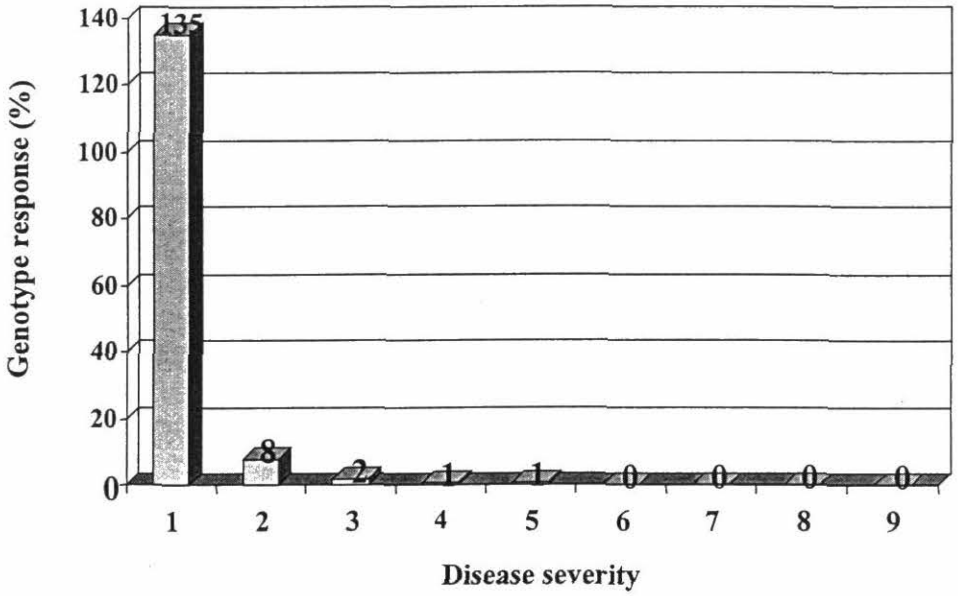


Figure 34. Response of *Phaseolus coccineus* and *P. polyanthus* to inoculation with race 3841 of *Colletotrichum lindemuthianum* under greenhouse conditions using a CIAT 1 – 9 scale, where 1 represents no visible symptoms and 9 = severe symptoms and disease expression.

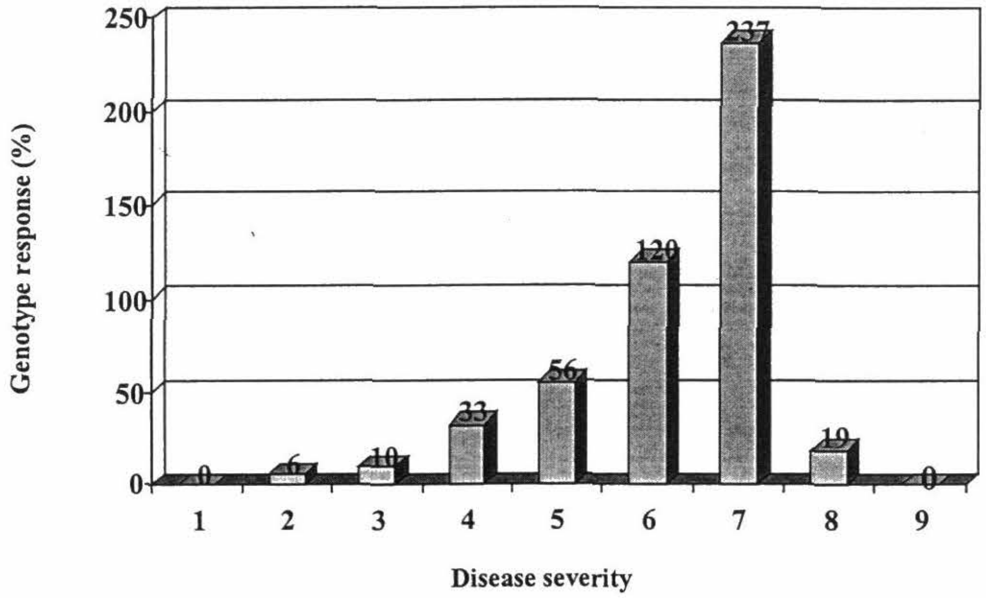


Figure 35. Response of 481 lines derived from interspecific crosses of *Phaseolus vulgaris* and *P. polyanthus* or *P. coccineus*, following field inoculations with mixtures of *Phaeoisariopsis griseola* races using a CIAT 1 – 9 scale, where 1 represents no visible symptoms and 9 = severe symptoms and disease expression.

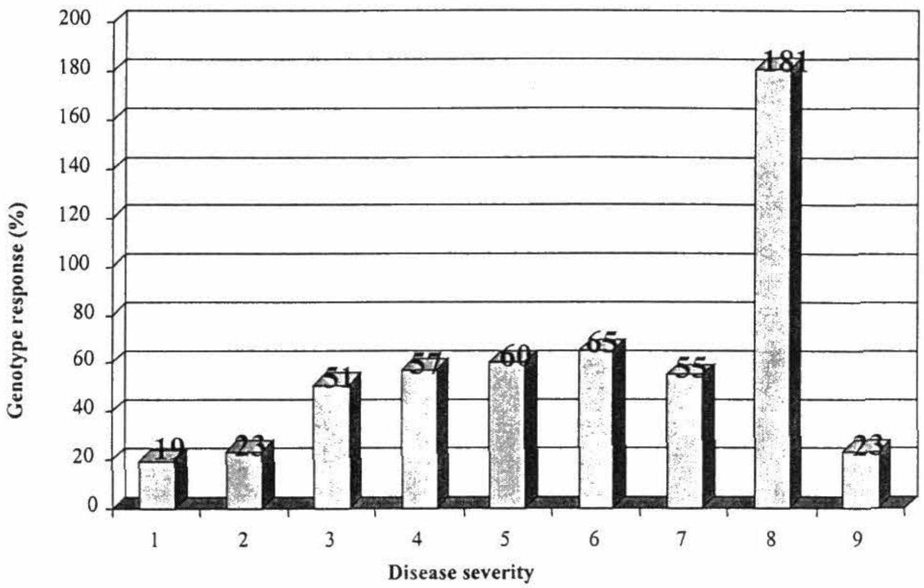


Figure 36. Response of 531 lines derived from interspecific crosses of *Phaseolus vulgaris* and *P. polyanthus* or *P. coccineus*, following field inoculations with mixtures of *Phaeoisariopsis griseola* races using a CIAT 1 – 9 scale, where 1 represents no visible symptoms and 9 = severe symptoms and disease expression.

Conclusion: High levels of resistance to anthracnose and ALS were observed in the secondary *Phaseolus* gene pool. Durable resistance to these diseases potentially might be found within these materials. The interspecific materials identified with ALS resistance form an interesting group of potential sources of ALS resistance. These materials will be screened under greenhouse conditions using isolates of a diverse origin to identify the most promising lines with wide resistance gene activity.

Contributors: G Mahuku, C Jara, C Cajiao, S Beebe

1.2.8 Developing sources of angular leaf spot resistance through breeding

Rationale: Angular leaf spot is considered the most important foliar pathogen of bean in Africa and Brazil, and has become increasingly important in Central America. The development of agronomically acceptable lines that can serve as sources of resistance is an urgent need of breeding programs for these regions.

Materials and methods: Populations were created with several sources of resistance. Several sources are derived from the Andean gene pool. These populations were inoculated under field conditions and have been selected for resistance in Santander de Quilichao for several generations.

In addition to previously identified sources, with the pathologist, germplasm accessions were identified that maintain resistance to the highly virulent race 63-63 that has been identified in Central America. Many of these are climbing beans from Central America of race Guatemala. These were crossed with other sources (e.g., with G 4691, a Colombian accession with CH phaseolin) and the F_1 in turn was crossed with adapted commercial varieties.

Results: From three superior populations, 79 lines were selected with high resistance under field conditions and with good plant type and adaptation to medium fertility levels. These are largely of Carioca type, but include some black-seeded lines, and are pending an evaluation with races of the ALS pathogen that correspond to other production areas.

Many of the newer populations with climbing bean sources were lost because of flooding in Santander de Quilichao in the first season. However, it appears that these new sources will not produce agronomically useful progeny in the short run and will require two to several cycles of crossing and selection to recover their resistance.

Conclusions: Breeding for ALS resistance was successful in the Santander de Quilichao environment, but the selected lines must now be confronted with races from other regions. It is known that some races, such as the 63-63 race from Honduras, are able to overcome many of the sources that were used in the past and that were apparently resistant in Santander de Quilichao.

Contributors: S Beebe, G Mahuku, H Terán, C Jara, JM Osorno, C Cajiao (IP-1);
C Quintero, J Tohme (SB-2)

1.2.9 Identifying genotypes with resistance to *Macrophomina phaseolina*

Rationale: Field studies showed that bean genotypes that are tolerant or resistant to *Macrophomina phaseolina* yield and perform well under drought conditions. Greenhouse evaluations followed by field experiments showed that, indeed, the genotypes that are resistant to *Macrophomina* have high levels of tolerance to drought and vice versa. This study was carried out to take advantage of, and screen, parents used to develop recombinant inbred lines (RILs) for response to *M. phaseolina*. It was hoped that parents would be contrasting for *M. phaseolina* response and the RILs derived from these parents would be used to tag genes for resistance to *Macrophomina* for subsequent use in developing adapted genotypes. In addition, 49 genotypes that were selected from iron and tannin studies were screened under greenhouse conditions for their response to *M. phaseolina*.

Materials and methods: Sixteen genotypes that were used to develop RILs were screened under greenhouse conditions for their reaction to *Macrophomina* resistance. The following is a list of the parents in their respective combinations: (G 19833 x DOR 364; MAR 1 x VAX 6; BAT 477 x DOR 364; G 21212 x BAT 881; G 3513 x DOR 364; G 19227A x DOR 364; and DOR 476 x SEL 1309).
In a separate experiment, 49 genotypes previously selected for evaluations of tannin content were screened for resistance to *M. phaseolina* under greenhouse conditions. These materials were inoculated with *M. phaseolina sclerotia* at a concentration of

1.5 g kg^{-1} of soil. The inoculum was put in the top 4 cm of the pot after planting. Incidence and severity of *M. phaseolina* was evaluated starting 12 days after planting until the plants were 20 days old.

Results and discussion: All the parental materials of RILs were either susceptible or resistant to *M. phaseolina* (Table 18). Therefore, we could not take advantage of the existing RILs to characterize and tag genes for resistance to *M. phaseolina*.

Table 18. Response of 16 genotypes used to create recombinant inbred lines for inoculation with *Macrophomina phaseolina* (*Mp*) under greenhouse conditions.

Genotypes	*Mp*	Total plants	% incidence	Disease response[a]
G 21212	8	12	67	S
BAT 881	12	12	100	S
G 3513	3	12	25	R
DOR 364	1	12	8	R
G 19227 A	1	12	8	R
G 19833	3	12	25	R
BAT 477	1	12	8	R
MAR 1	9	12	75	S
VAX 6	11	12	92	S
DOR 476	0	12	0	R
SEQ 7	4	12	33	R
AFR 475	3	12	25	R
CARIOCA	7	12	58	S
A 70	12	12	100	S
SEA 5	2	12	17	R
San Cristobal 83	10	12	83	S

a. R = resistant and S = susceptible.

Of the 49 genotypes screened in this study, 10 had high levels of resistance *to M. phaseolina* (Table 19). The most resistant genotypes were G 5841, G 6891, G 7945, G 13778, and G 4790. When we increased the inoculum load to 3g kg^{-1} of soil, these genotypes had no symptoms, showing that they are highly resistant and probably dominant genes control the resistance. Because of seed shortage, only G 5481, G 13778, and G 4790 were evaluated under drought conditions. These materials had very low incidences of *M. phaseolina* under field drought conditions. These materials will be screened for response to drought conditions during the coming season.

Table 19. Response of bean germplasm to inoculation with *Macrophomina phaseolina* under greenhouse conditions.

Entry	Disease severity rating[a]	Incidence	Entry	Disease severity rating	Incidence
G 4756	S	88	G 6981	R	0
G 16664	R	13	G 18264	I	63
G 17913	R	13	G 4258	S	88
G 5481	R	0	G 17166	S	100
G 3815	I	50	G 2494	R	38
G 7945	R	0	G 23804	S	75
G 16157	S	88	G 20592	I	38
G 13778	R	0	G 12403	S	88
G 6639	R	25	G 12037	S	100
G 22365	I	50	G 2906	S	88
G 18244	I	75	G 22805	I	75
G 4495	I	63	G 2276	S	100
G 4790	R	0	G 12171	S	100
G 58	S	75	G 14778	S	75
G 5285	S	100	G 2769	I	63
G 5758	I	63	G 19515	S	100
G 9384	S	75	G 22291	S	75
G 3821	S	100	G 995	S	75
G 16072	S	100	G 23773	S	100
G 13177	S	88	G 12169	S	88
G 19497	S	100	G 1083	S	100
G 11957	S	100	SEA 5	R	13
G 1400	S	75	BAT 332	I	50
G 11640	S	88	A 70	S	100
G 23283	S	100	BAT 477	S	100

a. R = resistant, I = intermediate, and S = susceptible.

Conclusions: These results are preliminary, but promising. The materials identified will be part of the drought trial next season and their response to drought will be assessed then. A rapid greenhouse technique for screening large volumes of bean genotypes for response to *M. phaseolina* has been developed. More genotypes should be passed through this test, to identify genotypes with resistance to *M. phaseolina* and drought tolerance. We need to start making crosses using contrasting parents with tolerance or resistance to multiple factors for subsequent developing of molecular markers.

Contributors: G Mahuku, C Jara, G Castellanos, IM Rao, S Beebe

1.2.10 Developing breeding lines resistant to *Ascochyta* blight

Rationale: *Ascochyta* is a highly destructive disease of bean in the rainy, higher altitude regions of the Andean zone and Africa. In these areas, *Ascochyta* severely limits the potential use of bean, especially of bush types that are exposed to splashing of inoculum from soil. These are regions that do not produce large volumes of bean, but they are especially poverty stricken regions, and resistance to *Ascochyta* would afford an important crop option to farmers there. Further, in the Andean zone, snap beans are especially susceptible to *Ascochyta*, and an *Ascochyta* attack can trigger a vicious cycle of pesticide abuse.

Materials and methods: In previous years we reported on the progress in implementation of resistance from interspecific crosses. Additionally, a bred variety from Guatemala, ICTA-Hunapú, has proved to be an excellent source. Crosses were created among sources and between sources of resistance and commercial types in several grain classes: Mesoamerican small black-seeded, some Andean grains such as Calima type and Cargamanto, and snap beans. Populations and families were planted in the Popayán station and inoculated three times with isolates obtained locally.

Results: Families derived from crosses among sources produced progenies that were superior to the resistant common bean check, ICTA Hunapú (Table 20). In crosses to susceptible cultivars, observations of F_3 progeny rows suggest that selection was successful in recovering resistance, implying that heritability is acceptably high to permit progress in selection. Families are being purified for subsequent testing and confirmation of resistance. Populations were also sent to Guatemala and promising families will be shared with the national program of Rwanda for selection of locally adapted lines.

Conclusion: For the first time, a level of resistance to *Ascochyta* is available that can permit genetic gain against this disease. Heritability of resistance also appears to be acceptably high. This resistance can make an important contribution in certain high altitude regions of the Andes and Africa.

This research was carried out with the support of the Belgian government.

Table 20. Populations and selected families derived from simple crosses that include the best interspecific selections for resistance to *Ascochyta*, evaluated under inoculated field conditions, 1999B – 2000A, Popayán, Colombia.

Identification	F_2 families 1998B	F_2 plants evaluated 1999A	F_3 families selected 1999B	F_4 bulks selected 2000A	*Ascochyta* mean 2000 A
ASC 73 x ASC 77	11	234	0	0	-
ASC 73 x ICTA Hunapú	5	235	12	5	5.0
ASC 74 x ASC 77	10	250	11	2	4.5
ASC 74 x ICTA Hunapú	19	420	15	8	4.7
ASC 75 x ASC 77	4	160	17	2	5.5
ASC 75 x ICTA Hunapú	19	475	48	13	5.3
Total	68	1774	103	30	-
G 35182					2.7
ICTA Hunapú					5.8
G 17723					9.0

Contributors: S Beebe, G Mahuku, C Cajiao

Progress towards achieving output milestones:

- Sources of resistance to the major viral diseases of common bean in Middle America were identified in all cases, and are currently being combined in advanced breeding lines.

- Bean genotypes (25) with high levels of resistance to Andean and Mesoamerican isolates of *Phaeoisariopsis griseola* from Africa, Central America, and South America were identified. These can be used as parents in developing germplasm with multiple resistance to diseases.

- High levels of resistance to ALS and anthracnose were identified in the wild and weedy *Phaseolus vulgaris* materials as well as secondary *Phaseolus* gene pool.

- Of 77 red-seeded lines distributed to Central America, all were resistant to BCMV, 49 were resistant to BGMV, 32 were resistant to CBB, and 20 were resistant to all three diseases.

Activity 1.3 Developing germplasm with resistance to pests: *Zabrotes*, *Acanthoscelides*, *Empoasca*, *Apion*, *Thrips palmi*, and bruchids

Highlights:

- New sources of resistance to *Thrips palmi, Empoasca kraemeri, Zabrotes subfasciatus,* and *Acanthoscelides obtectus* were identified.
- The methodology to screen for resistance to thrips was refined.
- New lines possessing disease and insect resistance were selected.
- Incorporation of resistance to leafhopper in Andean bean types was reinitiated.

1.3.1 Screening for sources of resistance to major insect pests

Rationale: Identification of sources of resistance to major insect pests is a continuous activity. Understanding of the mechanisms responsible for resistance to insects is essential for the development of appropriate breeding strategies. Apart from bruchids and leafhopper, major emphasis in 2000 was given to the study of resistance to *Thrips palmi.*

Materials and methods: Genotypes are screened under high insect pressure. For bruchids, nurseries are tested in the laboratory using 3-5 replications of 50 seeds per genotype infested with seven pairs of *Z. subfasciatus* or two eggs per seed in the case of *A. obtectus*. Genotypes are classified for resistance according to values for percentage adult emergence and days to adult emergence. Leafhopper and thrips nurseries are planted in the field with 3-4 replications per genotype under high natural infestation levels. Resistance is based on visual damage scores, reproductive adaptation scores, and in some cases, insect counts.

Results and discussion: ***Thrips palmi.*** This insect is a new pest of beans and many other crops in Latin America. Beans and snap beans are two of its most important host plants. Studies on *T. palmi* included refinement of methodologies to screen for resistance, development of sampling methods, measurement of yield losses and insecticide resistance levels, and preliminary work on management strategies (see Activity 3.3). In 2000, more than 500 genotypes were tested for resistance in replicated nurseries at CIAT and Pradera, a nearby site with high natural infestation (up to 40 adults per leaflet). Materials were rated for visual damage scores using a 1-9 scale (described in the 1999 Annual Report) and reproductive adaptation scores (the ability to set and fill pods under insect pressure) A few genotypes selected in 1999 were reconfirmed for resistance in 2000. These are Brunca, DOR 714, EMP 486, BAT 477, BH 160, FEB 115, among others. As shown in Figure 37, several received damage scores of 6 or less, coupled with reproductive adaptation scores of less than 5. There was a good correlation ($r = 0.71$; $P < 0.001$) between damage scores and reproductive adaptation scores. Five resistant genotypes and a susceptible check were chosen to initiate studies on mechanisms of resistance in collaboration with the Eidgenössische Technische Hochschule-Zentrum (ETHZ) Institute in Switzerland (Andrea Frei's PhD Thesis).

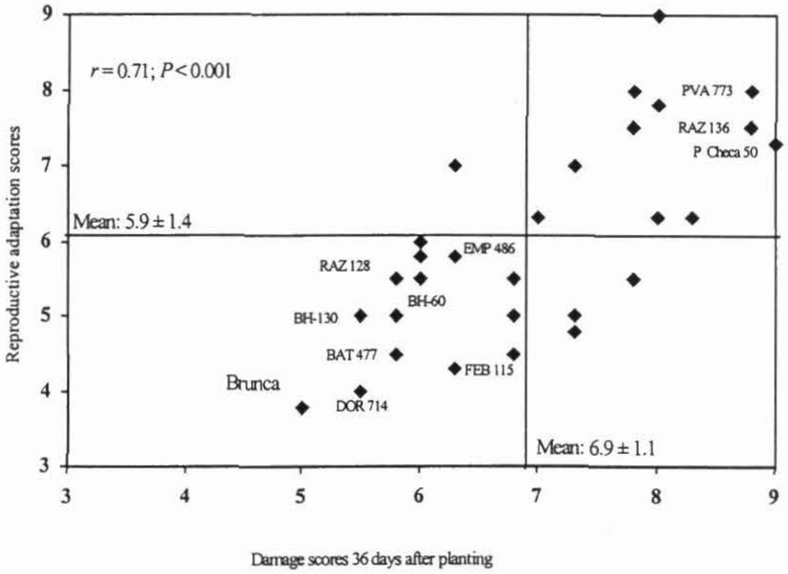


Figure 37. Relationship between damage and reproductive adaptation scores in bean genotypes screened for resistance to the melon thrips, *Thrips palmi*.

Other materials tested for resistance to *T. palmi* included 93 genotypes from the "Vipadogen" and "Potential Parents" nurseries of the Bean Project. Infestation levels in this nursery were high (7.3 adults per leaflet). Damage scores averaged 7.1 ± 1.4 (range: 2.0-8.9); reproductive adaptation scores averaged 7.3 ± 1.3 (range: 4-9). There was a good correlation ($r = 0.72$; $P < 0.05$) between damage and reproductive adaptation scores. As a result of these evaluations, 43 materials were selected for reconfirmation of resistance levels in 2000B. Table 21 shows best genotypes.

Table 21. Response of selected bean genotypes to *Thrips palmi* attack under high natural infestation levels. Means of three replications per genotype.

Genotype	Source (nursery)	Visual damage scores[a]	Reproductive adaptation scores[b]
A 729	Potential parents	2	4
A 730	Potential parents	3	5
Xamego	Potential parents	4	5
A 734	Potential parents	4	6
A 788	Potential parents	5	6
A 725	Potential parents	5	5
A 724	Potential parents	5	6
A 727	Potential parents	5	6
XAN 285	Potential parents	5	6
V 8025	Potential parents	6	6
VAX 3	Vipadogen	6	6
A 722	Potential parents	6	6
A 728	Potential parents	6	6
VAX 5	Vipadogen	6	7
BAT 41	Susceptible check	9	9

a. On a 1-9 scale, where 1 = no damage, 3 = initial damage to leaf ribs, 5 = obvious damage to leaf ribs, leaf deformation, 7 = heavy damage along leaf ribs, heavy leaf deformation, silvery appearance of the foliage, stunting of the plant, and 9 = severe damage, all leaves deformed, buds are killed, defoliation.

b. On a 1-9 scale, where 1 = good pod formation, 9 = no pods are formed.

As reported in 1999, further studies on resistance to *T. palmi* were conducted using RILS derived from a cross between BAT 881 and G 21212 (a source of low-P tolerance). In a replicated reconfirmation nursery planted at Pradera, under a high level of infestation (7.2 adults per leaflet) 139 RILs and parents showed an array of responses. These fit a distribution skewed towards susceptibility for both visual damage scores and reproductive adaptation scores (Figure 38), with 19% of the lines being rated resistant for damage.

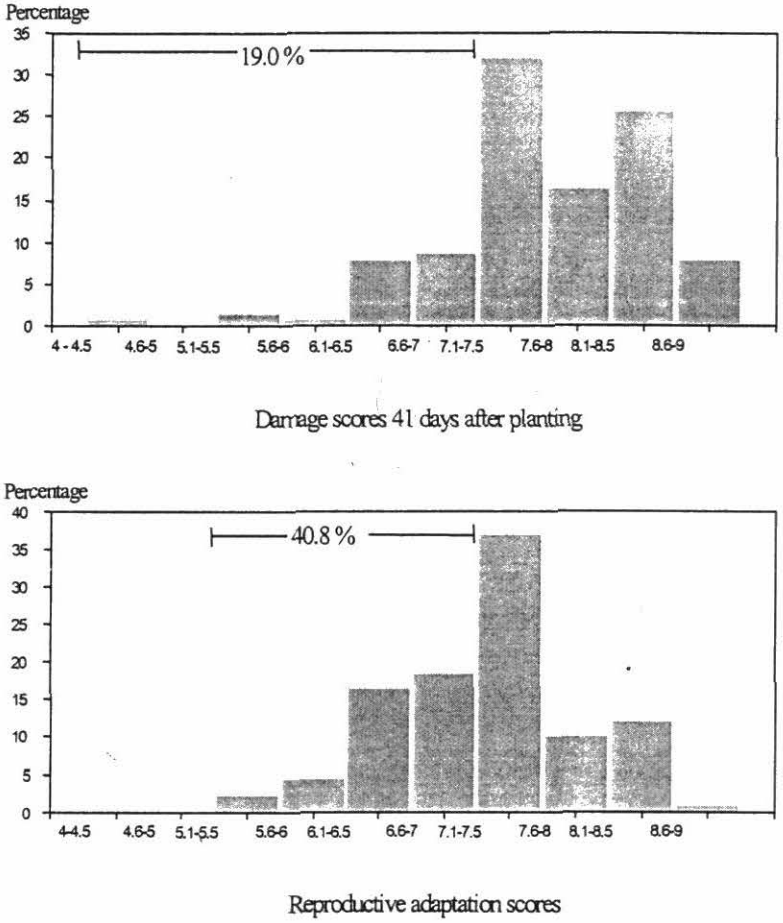


Figure 38. Population distribution for damage and reproductive adaptation scores among 139 recombinant inbred lines derived from the BAT 881 x G 21212 cross-tested for resistance to the melon thrips, *Thrips palmi*.

As in other nurseries, the correlation between damage and reproductive adaptation scores ($r = 0.81$; $P < 0.001$) was high. The rank correlation coefficient between this and the preliminary evaluation conducted in 1999 was high and significant ($r = 0.763$; $P < 0.001$) suggesting that genetic differences tend to show consistency across seasons and infestation levels. Table 22 shows some of the selected genotypes.

The QTL mapping and heritability study of resistance to *Thrips palmi* in common bean is reported in Activity 3.2, section 3.2.7.

Table 22. Levels of resistance to *Thrips palmi* in selected recombinant inbred lines derived from the cross BAT 881 x G 21212. Means of three replications.

Genotype	Damage scores in a 1 (best) to 9 (worst) scale	Reproductive adaptation scores in a 1 (best) to 9 (worst) scale
BH 21134-60-1-1-M-M-M	4.3	5.3
BH 21134-103-1-1-M-M-M	5.3	5.7
BH 21134-144-1-1-M-M-M	5.3	6.0
BH 21134-104-1-1-M-M-M	5.7	6.0
BH 21134-128-1-1-M-M-M	6.0	5.7
BH 21134-46-1-1-M-M-M	6.0	6.0
BH 21134-94-1-1-M-M-M	6.0	6.3
BAT 881	7.6	7.3
G 21212	8.2	7.6
PVA 773 (commercial check)	8.8	8.4

Contributors: C Cardona, JM Bueno, A Frei, MW Blair

Results and discussion: Leafhopper. In 2000, 1087 new germplasm bank accessions were screened for resistance to the leafhopper. Ninety-three accessions were selected for further reconfirmation. To reinitiate the incorporation of resistance to leafhopper in Andean bean types, all EMP lines of this type developed in previous years were evaluated again in 2000. Under high infestation levels (7.1 nymphs per leaf), 16 EMP lines were selected as potential parents for breeding purposes (Figure 39).

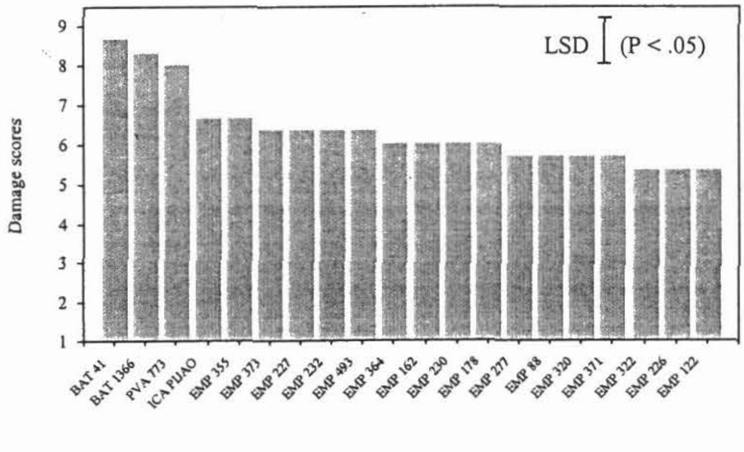


Figure 39. Levels of resistance to the leafhopper (*Empoasca kraemeri*) in selected, Andean-type EMP lines.

Contributors: C Cardona, JM Bueno

Results and discussion: Bruchids. The process of identification of sources of resistance to bruchids continued in 2000 with the evaluation of 61 wild *Phaseolus vulgaris* accessions. None of these was resistant to either *Z. subfasciatus* or *A. obtectus*. The *P. acutifolius* accessions G 40202 and G 40244 were resistant to *Z. subfasciatus* while G 40188 was intermediate. No sources of resistance to *A. obtectus* were found among 35 *P. acutifolius* evaluated. In contrast, high levels of resistance to *A. obtectus* were detected in 25 of 143 *P. lunatus* accessions studied.

In preparation for the second phase of the collaborative project with the University of Gent, a comprehensive study on comparative resistance to bruchids in three *Phaseolus* species was undertaken. As shown in Figure 40, high levels of resistance to *A. obtectus* are common in *P. lunatus* while the occurrence of resistance in *P. vulgaris* and *P. acutifolius* is limited to a handful of genotypes.

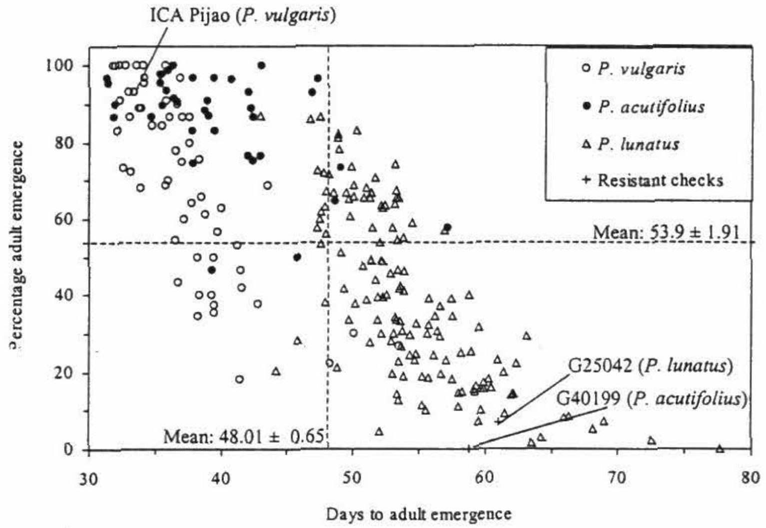


Figure 40. The relationship between days to adult emergence and percentage of adult emergence in accessions of three *Phaseolus* species tested for resistance to the bean weevil, *Acanthoscelides obtectus*. "ICA Pijao" is a commercial susceptible variety. G25042 and G 40199 are resistant checks.

In the case of *Z. subfasciatus*, resistance occurs in a few wild *P. vulgaris* accessions and in a handful of *P. acutifolius* accessions (Figure 41). No resistance to *Z. subfasciatus* has ever been found *in P. lunatus*. Understanding of the mechanisms underlying differential resistance to bruchid species will be attempted within Phase 2 of the Gent Project.

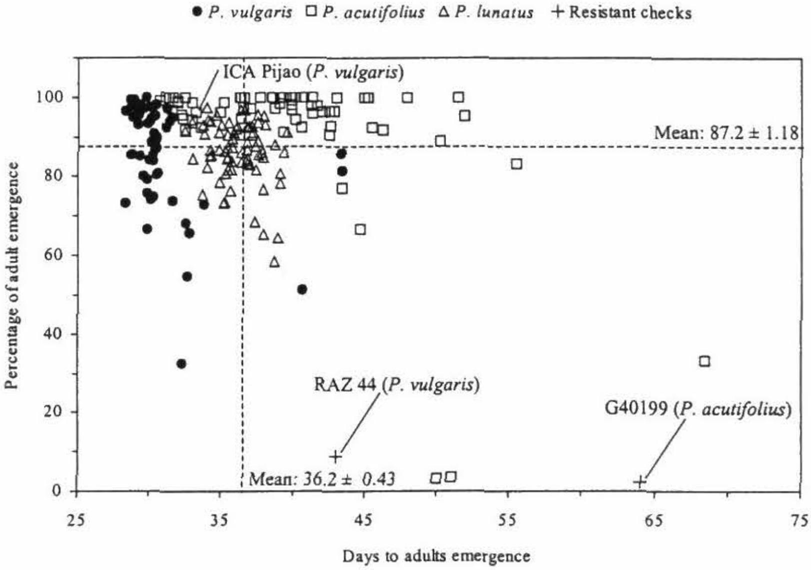


Figure 41. The relationship between days to adult emergence and percentage of adult emergence in accessions of three *Phaseolus* species tested for resistance to the Mexican bean weevil, *Zabrotes subfasciatus*. "ICA Pijao" is a commercial susceptible variety. RAZ 44 and G 40199 are resistant checks.

Contributors: C Cardona, JF Valor

1.3.2 Developing germplasm resistant to insects

Leafhopper: To support breeding efforts within the Project, we evaluated several nurseries developed for adaptation to Andean zone and Mesoamerican conditions. A nursery of 100 F_7 lines combining resistances to BGMV and leafhopper was evaluated under average insect pressure of 6.5 nymphs per leaf. Selections were made for leafhopper resistance, seed types, and agronomic performance. Twenty-four lines were selected for further reconfirmation.

Simultaneously, five F_2 populations were tested for resistance to leafhoppers. Populations EMP 496 x PVA 773 and EMP 250 x PVA 773, were selected. The F_3 populations are being yield-tested at present.

Red lines for Central America and Carioca-type lines for Brazil that combine resistance to leafhopper, BGMV, and CBB were yield-tested in 2000. The best, some of which are shown in Table 23, were coded EMP.

Table 23. Damage scores and yield performance of best Carioca and red lines combining resistances to leafhopper, bean golden mosaic virus, and cassava bacterial blight that were selected for resistance to leafhoppers in 2000. Means of three replications.

Line	Cross[a]	Seed type or color	Damage scores[b]	Yield ($kg\ ha^{-1}$) Protected	Yield ($kg\ ha^{-1}$) Unprotected	Susceptibility index
EMP 584	RM 11493	Carioca	6.3	2531	1076	0.94
EMP 587	RM 11493	Carioca	6.0	2088	1088	0.88
EMP 588	RM 11492	Red	4.1	1662	1037	0.86
EMP 589	RM 11492	Red	5.3	1612	984	0.84
EMP 598	RM 11492	Red	5.8	1700	830	0.97
ICA Pijao	Tolerant check	Black	7.1	2067	831	1.03
Bat 41	Susceptible check	Red	9.0	981	141	1.71

a. RM 11492 = EMP 473 x ((FEB 200 x XAN 252) F_1 x ((OAC 88-1 x G 5686)F_1 x (A 429 x G 2333)F_1)F_1)F_1/- and RM 11493 = EMP 443 x (FEB 188 x XAN 252)F_1 x ((OAC 88-1 x ABA 36)F_1 x (A429 x K2)F_1)F_1)F_1/-.

b. Damage scores on a 1 (best) to 9 (worst) scale.

White-, black-, and cream-seeded new EMP lines (Table 24) were developed in collaboration with the University of Guelph in Canada. These materials were selected for combined resistance to *Empoasca kraemeri* and *E. fabae*.

Table 24. Damage scores and yield performance of best lines combining resistances to *Empoasca kraemeri* and *E. fabae* selected in 2000. Means of three replications.

Line	Cross	Seed color	Damage scores[a]	Yield ($kg\ ha^{-1}$) Protected	Yield ($kg\ ha^{-1}$) Unprotected	Susceptibility index
EMP 547	93-1 x EMP 423-1	White	5.9	1460	862	0.94
EMP 548	EMP 423 x EMP 419-18	White	6.4	1552	759	0.93
EMP 549	EMP 423 x EMP 419-28	White	6.6	1533	876	0.90
EMP 550	Laser x EMP 423-6	White	7.2	1209	599	0.90
EMP 558	Laser x EMP 419-18	White	6.0	1665	705	0.90
EMP 573	2B5 x EMP 423-19	Black	6.3	1626	790	0.85
EMP 580	2B5 x EMP 423-16	Black	6.3	1349	877	0.94
EMP 571	EMP 423 x EMP 419-6	Cream	5.2	1602	665	0.94
ICA Pijao	Tolerant check	Black	7.3	1544	783	0.99
Bat 41	Susceptible check	Red	9.0	1060	197	1.74

a. Damage scores on a 1 (best) to 9 (worst) scale.

Contributors: C Cardona, JM Bueno

***Z. subfasciatus*:** Backcrossed lines to obtain *Zabrotes*-resistant ICA Pijao lines were tested for resistance to the insect and for yield performance. Some of the lines (Table 25) showed a very high level of resistance and yielded as well as the susceptible recurrent parent. These lines are now available as parents for the incorporation of multiple resistances into Mesoamerican black-seeded cultivars.

Table 25. Levels of resistance to *Zabrotes subfasciatus* and yield performance of five best BC3F$_9$ lines derived from backcrosses to "ICA Pijao".

Line	Days to adult emergence	Percentage of adult emergence	Rating	Days to flower	Yield (kg ha^{-1})
RAZ 154	44.7	5.4	Resistant	41	1507
RAZ 159	47.4	6.3	Resistant	42	1568
RAZ 162	48.3	1.9	Resistant	42	1573
RAZ 163	49.5	2.3	Resistant	43	1781
RAZ 165	46.3	10.4	Resistant	42	1624
G 12882[a]	47.0	7.0	Resistant	51	164
ICA Pijao[b]	30.5	94.7	Susceptible	42	1548

a. Donor (Arcelin-1) parent.
b. Recurrent parent.

Contributors: C Cardona, JM Bueno, JF Valor

As reported in 1999, a highlight of the work with *Z. subfasciatus* is the incorporation of arcelin selection criteria into the mainstream-breeding program. Eighteen multiple crosses were developed combining sources of resistance to *Z. subfasciatus*, BGMV, and fungal diseases with Mesoamerican parents. In 2000, we monitored the presence of arcelin in the F$_1$ seed of these progenies (Table 26) using a nondestructive serological test. Plants positive for arcelin will be planted in the field and screened for other traits within the marker-assisted selection (MAS) approach adopted by the Bean Project.

Table 26. Selection for arcelin in F_1 seeds from crosses for molecular-assisted selection of beans with various useful traits.

Cross	Seeds evaluated (no.)	Seeds selected (no.)
ICTA Ostua x (A 785 x ((RAZ 44 x SEL 1360)F_1 x (A 429 x XAN 309)F_1)F_1)F_1	100	46
((DOR 390 x (DOR 390 x SAM 3)F_1)F_1 x (A 785 x ((RAZ 44 x SEL 1360)F_1 x (A 429 x XAN 309)F_1)F_1	100	52
DOR 390 x (Raven x ((RAZ 44 x SEL 1360)F_1 x (A 429 x XAN 309)F_1)F_1)F_1	99	40
A 801 x (Compuesto Chimaltenango 2 x ((A 429 x XAN 309) F_1 x (RAZ 44 x Royal red) F_1) F_1	26	10
Tio Canela 75 x (DICTA 17 x ((A 429 x XAN 309) F_1 x (RAZ 44 x Royal red) F_1) F_1	135	60
Chingo x (DICTA 17 x ((A 429 x XAN 309) F_1 x (RAZ 44 x Royal red) F_1) F_1	131	63
Rojo de seda x (DICTA 17 x ((A 429 x XAN 309) F_1 x (RAZ 44 x Royal red) F_1) F_1	59	33
A 801 x (Apore x ((RAZ 44 x SEL 1360) F_1 x (A 429 x XAN 309) F_1)F_1)F_1	81	41
(IPA 7 x (Tio Canela 75 x SAM 3) F_1) F_1 x (DOR 500 x ((RAZ 44 x Royal red) F_1 x (Catrachita x Wilkinson 2) F_1)F_1)F_1	212	106
Tio Canela 75 x (Tio Canela 75 x ((RAZ 44 x SEL 1360) F_1 x (A 429 x XAN 309) F_1)F_1)F_1	34	20
DOR 364 x (Tio Canela 75 x ((RAZ 44 x SEL 1360) F_1 x (A 429 x XAN 309) F_1) F_1) F_1	51	19
9825-49-3/F_6 x (Tio Canela 75 x ((RAZ 44 x SEL 1360) F_1 x (A 429 x XAN 309) F_1)F_1)F_1	62	31
9825-46-1/F_6 x (Tio Canela 75 x ((RAZ 44 x SEL 1360) F_1 x (A 429 x XAN 309) F_1)F_1)F_1	49	18
9824-56-2/F_7 x (Tio Canela 75 x ((RAZ 44 x SEL 1360) F_1 x (A 429 x XAN 309) F_1)F_1)F_1	46	26
9824-47-1/F_7 x (Tio Canela 75 x ((RAZ 44 x SEL 1360) F_1 x (A 429 X XAN 309) F_1)F_1)F_1	60	32
Chingo x (Tio Canela 75 x ((RAZ 44 x SEL 1360) F_1 x (A 429 x XAN 309) F_1)F_1)F_1	41	26
Rojo de seda x (Tio Canela 75 x ((RAZ 44 x SEL 1360) F_1 x (A 429 x XAN 309) F_1)F_1)F_1	32	21
A 801 x (FEB 212 x ((RAZ 44 x A 429 F_1 x (Catrachita x Wilkinson 2) F_1)F_1)F_1	150	79
Total	1468	723

Contributors: C Cardona, S Beebe, JF Valor, H Terán

1.3.3 Pyramiding *Empoasca* resistance in red-mottled beans

Rationale: Leafhoppers are one of the most serious pests of Andean beans grown in low to mid-elevation areas. Andean beans have traditionally had less *Empoasca* resistance than Mesoamerican beans. The purpose of this research was to transfer the *Empoasca* resistance found in some Mesoamerican genotypes into red-mottled Andean beans.

Materials and methods: Multiple, triple, double, and simple crosses were made between *Empoasca*-resistant lines and susceptible commercial types. The resistant lines included the red-mottled genotypes (EMP 122, EMP 277, EMP 320, EMP 322, and EMP 364) and the Carioca genotypes (EMP 250 and EMP 496). The susceptible lines included large-seeded commercial types for South America (Colombia, Ecuador, and Bolivia), such as PVA 773 and CAL 143. Susceptible lines also included small-seeded types for the Caribbean (Haiti and the Dominican Republic), such as BGMV-resistant lines from the University of Puerto Rico, UPR 9945-138 and 226, and the standard commercial variety, PC 50.

Results and discussion: The crosses with EMP 250 and EMP 496 produced the progeny with the best levels of resistance. The simple crosses with only one Andean parent produced smaller seeded progeny than the triple crosses with two Andean parents. The red-mottled and Carioca seed types combined well to produce progeny with good red-mottled seed types. Some of the progeny of the triple crosses had better seed quality than the current red-mottled EMP lines. Other triple crosses were used to combine Arcelin-based bruchid resistance with the *Empoasca* resistance present in the current red-mottled lines. Many of the double cross progenies that had only one EMP-line parent were eliminated in initial *Empoasca* trials. Similarly, most of the multiple crosses that used a final parent that was *Empoasca*-susceptible produced progeny that were also susceptible.

Conclusions and future plans: It appears necessary to pyramid *Empoasca*-resistant parents to obtain progeny that is resistant. In future multiple crosses we will use final parents that are *Empoasca* resistant in the hopes of obtaining better progeny. The inheritance of quantitative trait loci for leafhopper resistance will be analyzed using the RILs developed by single seed descent from the simple crosses EMP 496 x PVA 773 and EMP 250 x CAL 143. In the future, we hope to develop molecular markers for the selection of *Empoasca* resistance in common beans.

Contributors: MW Blair, C Cardona, JM Bueno

1.3.4 Resistance to *Zabrotes*

Rationale: *Zabrotes* (or the Mexican bean weevil) is one of the most important storage pests of bean. Unusual seed storage proteins called arcelin are derived from wild bean, and confer resistance. In previous reports we have described the selection of arcelin in complex crosses with sources of agronomic traits.

Materials and methods: Complex crosses segregating for arcelin and the *bgm-1* gene were created 2 years ago. The F_1 plans of these crosses were selected first for arcelin with electrophoretic gels and then for the *bgm-1* gene with the SCAR marker. Thus, two important resistance genes were selected by indirect methods to create populations with both genes.

Results and conclusions: Progeny families were selected that are now in the F_3 generation and soon will be selected for anthracnose resistance in Popayán. At that stage they will be selected as individual plant selections for progeny testing. Conclusions are pending.

1.3.5 Resistance to *Apion godmani*

Rationale: *Apion godmani*, the bean pod weevil, is normally controlled in Central America with the use of extremely dangerous pesticides, although resistant varieties DICTA 113 and 122 are reportedly reducing the use of pesticides in Honduras. However, at present there is no longer an active breeding program for resistance to this pest. Because the pest does not exist in Colombia, selection cannot be practiced here either. An alternative strategy is to improve the DICTA varieties by backcrossing other traits into them, thereby maintaining their level of *Apion* resistance.

Materials and methods: The two DICTA varieties are derived from BGMV-resistant cultivar DOR 364 and present an intermediate reaction to BGMV. To fortify the value of these varieties, they were included in the *bgm-1* backcross program. The introduction of *bgm-1* will make these varieties more viable and attractive for farmers who face BGMV as well as *Apion*.

Results and conclusions: The backcross program with the DICTA lines is in the F_1BC2 phase. Conclusions are pending.

Contributors: S Beebe, C Cardona, H Terán, JM Osorno, (IP-1);
C Quintero, J Tohme (SB-2)

Progress towards achieving output milestones:

- Studies on insect resistance and development of parental lines with multiple disease and insect resistance contribute to the mainstream breeding efforts of the project.
- Insect resistance to thrips (never studied before on dry beans) can be a key component in the formulation of management strategies for this important pest of the crop.

Activity 1.4 Incorporating wider genetic diversity into beans

1.4.1 Wild quantative trait loci pursued in population of DOR 390 and G 19892

Rationale: Wild relatives of several crops were investigated as sources of QTL for complex traits, including yield. Wild *P. vulgaris* has been demonstrated to have much broader genetic variability than cultivated bean and feasibly could serve as a source of useful variability for broadening the base of the cultivated bean.

Materials and methods: Several populations involving wild bean were explored using the advanced backcross or backcross selfing method, whereby a large number of lines are generated by backcrossing a wild x cultivated hybrid twice to the cultivated parent. Marker and QTL analyses were initiated in the advanced backcross population of DOR 390 and G 19892. DOR 390 is a widely used Mesoamerican, small, black-seeded cultivar resistant to BGYMV, and G19892 is a wild bean from Argentina that presents Andean DNA patterns. Thus this cross represents a combination of wide genetic diversity within *P. vulgaris*, essentially bridging the two major gene pools. One hundred and thirty eight markers were applied to the population, including 25 SSRs, 111 RAPDs, and two SCARs.

Field trials were established in Santander de Quilichao under moderate fertility stress in the fall of 1999. Subsequently a second trial was planted in Palmira in January 2000 with normal (high) fertility levels. In the first trial, a population of 99 lines was planted in a 10 x 10 lattice, but it was observed that the advanced backcross method had resulted in very few lines with introgression for any given wild bean DNA segment, thus prejudicing the statistical test. Therefore, an additional 35 lines were included in a satellite yield test in the Palmira station and in the DNA analysis.

Results: Among the markers utilized, 17 SSRs, 27 RAPDs, and one SCAR could be mapped to the CIAT mapping population based on DOR 364 x G 19833. These mapped markers were calculated to cover about 692 cM or about 32% of the total genome length. The remaining 93 markers undoubtedly have covered another sizable portion of the genome, but it not yet possible to say how much, or if significant segments of the genome remain unsampled.

In the field, no line presented a statistically significant yield advantage over DOR 390. In the QTL analysis, many significant effects of introgressed DNA were detected by a Student's *t*-test on yield, seed size, and flowering date. However, most of the effects of introgressed DNA were negative, resulting in lower yield or smaller seed size. Indeed, results of negative QTL for yield were relatively consistent across the two sites, although more negative effects were detected in the Santander de Quilichao trial. It appears that the alleles from the wild bean were especially deleterious at the lower fertility level; wild beans have been noted to be sensitive to fertility stress. Only one positive yield QTL from the wild bean was detected in the yield trial that was carried out in Palmira, but it was not confirmed in Santander de Quilichao. This QTL was marked by the RAPD AI1405S, and was mapped to the linkage group B07. In Palmira, this marker was associated with a yield advantage of 175.7 kg ha^{-1} in lines that carried the marker. It must be stressed that this QTL has still to be confirmed. Lines with the marker are being planted together with DOR 390 to verify if they continue to express any yield advantage. The negative QTL of the wild bean are also being mapped to determine other regions of the genome with important yield effects. The coverage of the map must also be saturated as soon as more microsatellites are available.

Conclusions: As expected, more negative than positive effects proceeded from the wild bean. Unfortunately, no positive yield QTL have yet been confirmed.

Contributors: S Beebe, H Terán, JM Osorno, HF Buendía (IP-1);
MW Blair, F Pedraza, J Tohme (SB-2)

Progress towards achieving output milestones:

- This activity would have contributed toward the milestone of developing improved lines with resistance to diseases, specifically to BGMV, because the improved lines with better yield QTL would carry this resistance derived from the recurrent parent. Given that reliable QTL remain to be identified, little substantial progress can be reported as of yet.

99635

Output 2: Improved large-seeded Andean bean germplasm with less dependence on inputs

Activity 2.1 Developing germplasm resistant to diseases

Highlights:

- Genetic improvement efforts to incorporate BCMV resistance in highland common bean cultivars are under way.
- Six genotypes with high levels of resistance to race 651 and 653 were identified.
- Red-mottled beans for the Andean and Caribbean regions were improved for disease resistance by pyramiding sources of resistance to ALS and by using marker-assisted selection to incorporate BGMV-resistance genes. *Empoasca* and bruchid resistances were combined into lines containing virus resistance.
- Cream-mottled beans were improved for yield and quality by crossing with Colombian Cargamanto beans and incorporating BCMV-resistance and bush type architecture.
- A new nursery of Andean genotypes (IBN 2000) was tested for ALS and CBB resistance and distributed to collaborators.

2.1.1 Breeding for resistance to bean common mosaic virus

Rationale: Bean common mosaic virus resistance has been a *sine qua non* requirement for most breeding lines generated by the CIAT Bean Project in collaboration with NARIs. The relatively low incidence of BCMV in the Andean highlands observed in the past somehow relegated this task to second place in past years. However, the increasing frequency of the El Niño phenomenon has created suitable climatic conditions (warming) in the Andean highlands for the aphid vectors of this virus. Consequently, BCMV epidemics have occurred in the Andean highlands, and particularly in the region of Rionegro, Antioquia, Colombia, where the predominant, high-value cultivar "Cargamanto" has suffered severe BCMV attacks in past years. A project coordinated by Ms. Gloria Esperanza Santana of the Corporación Colombiana de Investigación Agropecuaria (CORPOICA)-Rionegro, with the collaboration of CIAT, is trying to introduce resistance to BCMV in this climbing, common bean cultivar.

Materials and methods: 50 different genotypes including climbing cultivars, germplasm bank accessions, "Cargamanto" varieties, breeding lines, and some sources of BCMV resistance, were screened for their reaction to a strain of bean common mosaic necrosis virus (BCMNV), which also helps identify bean genotypes with resistance to BCMV. Farmers in the region currently grow nine cultivars and three improved cultivars (ICA Viboral, ICA-Llanogrande, and Frijolica L.S. 3.3).

Results: Eight breeding lines from Cargamanto x G 17668 crosses made at CIAT were resistant to BCMV. The remaining materials were either segregating or susceptible to BCMV. Nine germplasm bank accessions maintained by CORPOICA were also susceptible to BCMV. Of three CIAT breeding lines selected for their resistance to anthracnose, another prevalent disease of climbing beans in Rionegro, only one was resistant to BCMV. Another set of nine bush beans possessing anthracnose resistance was also evaluated and shown to include two genotypes that were homozygous resistant. Finally, three lines selected as sources of the BCMV-resistance recessive gene *bc 3* were confirmed as resistant to this virus and thus are potential sources of virus resistance to improve Cargamanto for this character, without the undesirable genetic linkage problems associated with the dominant *I* gene.

Conclusions: Crosses with parental materials possessing the recessive *bc 3* gene must be initiated in order to preserve the commercial red color of the characteristic Cargamanto grain type. Other sources of the *I* gene from the Andean gene pool have also been recommended to avoid the linkage problems associated with the incorporation of monogenic dominant resistance, but this hypothesis has not been thoroughly tested.

Contributors: FJ Morales, M Castaño, CJ Alvarez

2.1.2 Identifying genotypes with resistance to anthracnose

Rationale: Identification of resistance to major diseases is a continuous activity. Anthracnose is a major limitation of production in the highlands of Colombia, especially in the Rionegro area of Antioquia. Last year, we reported on a project to identify sources of anthracnose resistance to race 651 and 653. This study is a follow up to last year's evaluations and includes a wide genetic base of bean germplasm.

Materials and methods: In collaboration with CORPOICA Rionegro, we screened 40 bean lines for their reaction to anthracnose races 651 and 653. Ten plants of each genotype were evaluated in each of the two repetitions. Inoculum production, inoculations, and evaluations were done according to standard protocols.

Results and discussion: The genotypes G 4, LAS 129, LAS 435, SUG 130, SEQ 1035 and PR 93201473 were resistant to both race 653 and 651 (Table 27). These genotypes form a highly interesting group of materials that can either be deployed or used as sources of anthracnose resistance in breeding programs. Some genotypes (e.g., G 6, G 8, LAS 331, ICA Llanogrande, BRB 204, and FOT 54) had a resistant reaction with one race and an intermediate reaction with the other. Given that the inoculum concentration is usually high under controlled conditions, these genotypes might serve as good sources of resistance under field conditions, where inoculum loads are generally low.

Conclusion: Six genotypes (G 4, LAS 129, LAS 435, SUG 130, SEQ 1035, and PR 93201473) with high levels of resistance to race 653 and 651 were identified in this study. These can be used as parents in crosses, but they first must be evaluated under field conditions, to get a feeling of the activity of the resistance genes.

Table 27. Reaction of 36 advanced bean lines to race 651 and 653 of *Colletotrichum lindemuthianum*.

Entry	Disease rating[a]		Entry	Disease rating[a]	
	Race 653	Race 651		Race 653	Race 651
G 1	R	S	CC21148-218-3	S	S
G 3	I	I	CC21148R218-4	S	S
G 4	R	R	CC21148-218-5	S	S
G 5	I	I	CC211482-18-6	S	S
G 6	R	I	CC21148 R-5-1	S	S
G 7	R	S	CC21148-R-59-1	S	S
G 8	R	I	CC21148-67-3	S	S
G 9	R	S	BRB 151	R	S
G 11	S	S	BRB 203	R	S
LAS 106	I	I	BRB 204	I	R
LAS 129	R	R	SEQ 1035	R	R
LAS 331	I	R	SEQ 1040	S	R
LAS 384	R	S	FOT 28	R	S
LAS 435	R	R	FOT 29	R	S
LAS120	S	S	FOT 54	I	R
AND 1084	I	I	FOT 59	R	S
ICA Llanogrande	R	I	SUG 130	R	R
CC21148-4-1	S	S	SUG 143	R	S
FOT 49	I	R	PR 93201473	R	R
G 17668	S	S	PR 93201474	R	R

a. R = resistant, I = intermediate, and S = susceptible.

Contributors: G Mahuku, C Jara, G Castellanos; GE Santana (CORPOICA)

2.1.3 Pyramiding angular leaf spot resistance into Calima-type, red-mottled beans

Rationale: Angular leaf spot is a serious disease in humid low-and mid-elevation bean production areas. A fungal pathogen, *Phaeoisariopsis griseola*, which is well known for its pathogenic variability, is the cause of the disease. Resistance is often location-specific depending on the races prevalent in a given area. The disease reaction exhibited by leaves and pods from the same genotype can be different, suggesting that separate genes can control resistance in these organs. Therefore pyramiding various sources of resistance is important when trying to develop new varieties that will be field resistant to the widest array of races in many bean-growing regions. The objective of this research was to compare advanced lines, which were developed from multiple crosses that pyramid ALS-resistant parents together, for their level of field resistance to the disease.

Materials and methods: In Darien in 2000A, 834 Andean genotypes, representing the red-mottled, cream-mottled, large-red, and yellow-seeded bean classes, were grown in single 3-m row plots. The genotypes consisted mostly of $F_{5:6}$ lines from multiple crosses made in 1996-97, which were advanced through a gamete selection program over the course of 4 years. A smaller number of earlier generation F_3 bulks was also tested. The crop was fertilized with 100 kg ha^{-1} of superphosphate, but was not protected with fungicides. A natural epidemic of ALS occurred in the second half of the growing season. The lines were evaluated for ALS resistance at 40 days after planting with the standard 1-9 scale for CIAT evaluations.

Results and discussion: The average level of resistance found in the advanced lines from a given pedigree was correlated with (1) whether the final parent was ALS resistant, and (2) how many parents in the multiple cross pedigree were ALS resistant (Table 28). The average ALS scores for the pedigrees ranged from 1.94 to 7.00. The most outstanding pedigrees included the parents AND 277, AND 279, Cornell 49-242, G 5686, and MAR 3, which are all well-known sources of ALS resistance. The genotypes CAL 143 and PVA 800A also appeared to be proportioning resistance to some of the crosses. Crosses with no resistant parents such as PVA 773 x (A 483 x G 6416) were highly susceptible. The advanced lines performed well compared to the susceptible red-mottled checks A 36, A 483, AFR 619, AND 1005, CAL 96, and ICA Tundama. The best red-mottled checks were AFR 612, AND 277, AND 279, POA 12, and PVA 800A.

Conclusions and future plans: Good levels of resistance to the prevalent ALS isolates existed in the red-mottled seed class parents and progeny we tested in Darien. The popularity of AFR 612 in Cauca may be partly because of its good ALS resistance. Several other parents were also successful in other parts of the world where ALS is a problem, so we are hopeful that the material developed here will be useful in other regions. POA 12 is being included in new crosses. The advanced lines from this trial were evaluated for commercial seed type by a farmer-led participatory research committee (a CIAL) from Restrepo, Valle that will be testing the lines for performance in their fields in 2000B. The parents of these populations were included in crosses made to study the inheritance of ALS resistance.

Contributor: MW Blair

Table 28. The angular leaf spot (ALS) scores of red-mottled advanced $F_{5:6}$ lines from different crosses of multiple ALS-resistant parents (indicated in bold).

Pedigree	No. lines	Ave. ALS
(DRK 138 x Pompadour J)F_1 x (**PVA 800A** x ((DOR 708 x G 1344)F_1 x (A 429 x A 193)F_1)F_1)F_1/	33	NA
ICA Quimbaya x A 483	18	NA
(MAM 48 x AFR 612)F_1 x (PI 150414 x **PVA 800A**)F_1/	1	NA
(San Cristobal 83 x ICA Quimbaya)F_1 x (**PVA 800A** x **AND 277**)F_1/	14	NA
PVA 800A x (Paragachi x ((MAM 49 X Bola 60 Dias)F_1 x (**PVA 800A** x Bayo MEX)F_1)F_1)F_1/-	23	NA
Paragachi x (Paragachi x((MAM 49 x Bola 60 Dias)F_1 x (**PVA 800A** x Bayo MEX)F_1)F_1)F_1/-	1	NA
ARA 18 x (I 414 x ((**PVA 800A** x Bayo MEX)F_1 x (CAP 4 x Wilkinson 2)F_1)F_1)F_1/-	1	NA
AND 1005 x ((Catrachita x Bola 60 Dias)F_1 x (MAM 13 x Montcalm)F_1)F_1/	33	4.24
A797 x ((**JaloEEP558** x (Indeterminate Jamaica Red x Wilkinson 2)F_1)F_1/	4	3.50
AND 279 x ((MAM 38 x CAL 143)F_1 x (**PVA 800A** x **AND 277**)F_1)F_1/	139	2.50
(**AND 279** x **PVA 800**A)F_1 x ((**Cornell 49-242** x **G 5686**)F_1 x (Montcalm x **CAL 143**)F_1)F_1/	18	1.94
(Cardinal x **PVA 800**A)F_1 x ((Catrachita x PVA 773)F_1 x (**PVA 800A** x **AND 277**)F_1)F_1/	6	2.00
PVA 773 x ((MAM 48 x AFR 612)F_1 x (PI 150414 x **PVA 800A**)F_1)F_1/	96	2.86
(PVA 773 x ICA Tundama)F_1 x (**PVA 800A** x ((XAN 309 x A 193)F_1 x (**MAR 3** x G 5653)F_1)F_1)F_1/	109	2.51
(**PVA 800A** x **AND 277**)F_1 x (**PVA 800A** x ((XAN 309 x A 193)F_1 x (**MAR 3** x G 5653)F_1)F_1)F_1/	2	2.00
PVA 800A x ((San Cristobal 83 x ICA Quimbaya)F_1 x (**PVA 800A** x **AND 277**)F_1)F_1/	61	2.15
I414 x ((**PVA 800A** x G 5896) x (CAP 4 x Wilkinson 2))	12	4.42
PVA 1441 x ((MAM 49 x Bola 60 Dias) x (**PVA 800A** x G 5896))	4	4.50
PVA 773 x (A 483 x G 6416)	6	7.00
PVA7 73 x ((AND 1005 x (Catrachita x Bola 60 Dias)) x (MAM 13 x G 6416))	4	3.75
(**PVA 800A** x PVA 1441) x ((MAM 49 x Bola 60 Dias) x (**PVA 800A** x G 5896))	8	3.13
Total	594	3.32

2.1.4 Marker-assisted selection of bean golden mosaic virus-resistant red-mottled beans

Rationale: Bean golden mosaic virus is the most serious viral disease of beans in lowland tropical Latin America. A bipartite geminivirus, which is transmitted by the whitefly, *Bemisia tabaci*, causes the disease. Red-mottled beans are one of the few Andean types that are grown in low- and mid-altitude areas of the region where the vector and virus are present. The virus is a well-established endemic problem in red-mottled beans grown in the Caribbean (Haiti and the Dominican Republic) and has the potential to be a serious threat to some production areas in South America (Colombia, Ecuador, and especially lowland Bolivia). Other diseases that often occur when BGMV is present are CBB, rust, and ALS. The whitefly vector often occurs in conjunction with heavy infestations of leafhoppers. Therefore, it is important to pyramid genes for resistance to all these pests and pathogens together with BGMV resistance into the same genotypes. The objective of this work was to deploy BGMV resistance genes into new red-mottled genotypes through MAS of advanced lines in later generations. Because BGMV cannot be field-screened at CIAT and the virus is difficult to inoculate artificially, MAS is a good substitute for phenotypic selection.

Materials and methods: Two molecular markers were used to select for BGMV resistance in red-mottled beans. The SCAR marker, DOR 21, is closely linked to the major recessive resistance gene, *bgm-1*, while a second SCAR marker, W012, is associated with a QTL for BGMV resistance found on chromosome B04. A third SCAR marker, SU 91, was used to select for a major QTL for CBB resistance in a subset of the segregating lines.

Results and discussion: In the first set of trials, BGMV resistance was incorporated into advanced, red-mottled breeding lines through gamete and pedigree selection. Of 334 single plant selections made in the F_6 generation, 40 of the resulting $F_{6:7}$ lines were positive for the *bgm-1* marker. The positive lines were derived from two crosses,
(1) PVA 773 x ((PVA 800A x DOR 482)F_1 x (Belmineb RMR-3 x Montcalm)F_1)F_1, where the source of BGMV resistance was DOR 482, and (2) Calima x (MAM 48 x A 483)F_1)F_1 x (PVA 800A x ((EMP 376 x A 193)F_1 x (NW 63 x A 429), where A 429 was the source of BGMV resistance. The new advanced lines were used in crosses with larger-seeded, determinate red-mottled beans. Several red-mottled lines from the University of Puerto Rico, with resistance derived from DOR 482, were also used as donor parents. In addition, the segregating F_1 plants from the multiple cross, PVA 800A x ((A 429 x XAN 309) x (RAZ 44 x Royal Red)), were screened for the presence of arcelin and the *bgm-1* marker before being crossed to a group of Andean genotypes. These included AFR 619, Calima, CAL 96, CAL 143, CIAS 95, JB 178, PC 50, Quimbaya, Saladín 97, and Velasco Largo (Table 29). Twenty-two cross combinations were made, resulting in a total of 552 selected F_1 plants. The progeny of these crosses are being advanced to homozygosity when they will be screened again to make sure they contain the arcelin and *bgm-1* genes.

Table 29. Crosses with bean golden mosaic virus-positive plants from a multiple cross F_1 of PVA 800A x ((A 429 x XAN 309) x (RAZ 44 x Royal Red)).

Final parent	Color	Cross	Gametes	Final parent	Color	Cross	Gametes
AFR 619	6M,G	3	54	JB178	7M,M	1	23
Calima	6M,G	1	9	PC50	7M,P	5	94
CAL 96	6M,G	2	52	Quimbaya	7,G	1	15
CAL 143	6M,G	3	94	Saladín 97	7M,P	1	122
CIAS 95	7M,M	1	20	Velasco Largo	5,G	3	58

In the second set of trials, a single backcross was used to transfer the *bgm-1* gene and CBB QTL into a Pompadour variety (PC 50 or G 18264 from the Dominican Republic). SAM 1, a line derived from the cross DOR 476 x SEL 1309 and positive for all three SCAR markers, was the donor parent for these crosses. Twenty-one individual plants were selected in the BC_1F_1 generation and advanced two generations by pedigree selection. Eight $BC_2F_{2:3}$ progeny per family were grown in the greenhouse for MAS. DNA was extracted from a balanced bulk of plant tissues from each family member and genotyped for each of the SCARs. Although eight families were positive for *bgm-1*, four for the CBB QTL, and one for both markers, none of the families contained all the genes in a phenotype resembling the recurrent parent PC 50 (Table 30). However, several families were phenotypically very similar to PC 50 and contained a single resistance gene. Therefore, families that were complementary for the markers that they contained were crossed to produce PC 50 like segregants with more than one resistance gene.

Table 30. $BC_1F_{2:3}$ families positive for bean golden mosaic virus resistance markers in PC 50 (G 18264).

Selection[a]	bgm-1 (DOR21)	CBB (SU91)
- 2W	+	+
- 4W	-	+
- 5W	+	-
- 6W	-	+
- 7W	+	-
-11W	+	+
-22W	+	-
-24W	+	-
-29W	+	-
-37W	+	-

a. Pedigree of selections = G 18264 x (G 18264 x SAM 1).

Conclusions and future plans: Here we show the application of MAS to determine which advanced $F_{6:7}$ lines carry a gene of interest. MAS has also been successfully applied to selection of segregating F_1 plants from multiple crosses in early generations. Once we have incorporated the *bgm-1* gene widely into red-mottled germplasm, we plan to use the W012 SCAR more intensively in MAS of BGMV resistance. We also plan to pyramid BGMV resistance into red-mottled populations with *Empoasca* resistance and arcelin-based resistance to bruchids (see Output 2.2). Although the emphasis has been on bush beans we also plan to add BGMV resistance to red-mottled climbing beans, which might be grown in the Caribbean.

Contributors: MW Blair, S Beebe

2.1.5 Development and yield-testing of bean common mosaic virus-resistant, Cargamanto-type, cream-mottled, bush and climbing beans

Rationale: Cream-mottled beans are popular in many areas of the world, including southern Africa, southern Europe, and the Middle East. The class includes both Cranberry and Sugar beans. In Colombia, a special type of cream-mottled beans known as Cargamanto is grown. These are larger than the other cream-mottled seed types and are renowned for their flavor and cooking characteristics. Most Cargamanto varieties are aggressive type IV climbing beans adapted to altitudes above 2000 m in the departments of Antioquia and Nariño. The objective of this study was to use a Cargamanto variety to improve the seed types of cream-mottled bush beans and to incorporate BCMV resistance into both bush and climbing Cargamanto-type beans.

Materials and methods: Triple crosses were made between BCMV resistant (*I* + *bc3* genes) Cranberry bush beans and Cargamanto-type climbing bean selections. The Cargamanto lines (SEL 1383, SEL 1384, SEL 1386, SEL 1389, and SEL 1390) were derived from a simple cross between the commercial Cargamanto variety, ICA Viboral (G 5702), and Cran 28, which is a source of *I* gene for BCMV resistance that is not associated with dark-red seed mottling. These advanced lines were crossed to the F_1s of eight simple crosses between BCMV resistant lines, BRB 151 and BRB 203, which contain the *bc3* gene, with the Cranberry lines, FOT 28, FOT 54, and SUG 30. The F_1 plants were individually harvested and their progeny planted in Darien. Single F_2 plant selections from this generation were divided into three groups: (1) late type IIIs, which were planted in Nariño, (2) early type IIIs, which were planted in Antioquia, and (3) bush beans, which were planted in Darien. In the $F_{2:3}$ generation, the bush bean selections were planted in a replicated yield trial in Palmira.

Results and discussion: One hundred and twenty nine type III selections (67 early and 62 late) were sent to Nariño and Antioquia. Most of these were not adapted to the higher elevations at these locations and only 20 lines were selected for a second planting. Meanwhile, 311 selections were made among the bush beans in Darien. These were taken to a replicated trial during the next season to determine if they would adapt to the higher temperatures in Palmira compared to Darien. A large number of superior genotypes were identified among the $F_{2:3}$ selections, many of which surpassed the 12 cream-mottled check varieties grown in the experiment (Table 31). Most importantly, many of the new genotypes yielded as well as the best check variety, COS 16, and had the large, round seed size and shape of Cargamanto beans. This is the grain quality that commands a premium price in the marketplace.

Conclusions and future plans: The selections made during this season will be tested for the presence of several diagnostic molecular markers for BCMV resistance. These results will be confirmed with viral inoculation if needed. The climbing bean lines selected at the University of Nariño and CORPOICA-La Selva (Antioquia) will be grown for the second time this year. The bush bean lines will be offered to collaborators in Colombia, Bolivia, and Iran for testing in these environments. The new lines compare favorably to the Cranberry lines developed at CIAT for adaptation to mid-elevation areas and warm growing environments such as Palmira. One of these lines, COS 16, was released as a variety in Bolivia. Bolivian farmer and producer associations hope to find Cargamanto beans that will be acceptable in the Colombian market. We plan to test the Cargamanto-derived lines in Bolivia and Colombia at low and mid elevation growing areas to see if they perform as well as COS 16. We hope that some of the new Cargamanto bush lines may provide high yield and excellent grain quality for Latin American producers and consumers of the cream-mottled seed class.

Table 31. Yield of Cargamanto-type bush beans compared to Cranberry and Sugar check varieties in a replicated trial in Palmira, 2000A.

	Size	Yield per plant (no. of pods per plant)	Yield per hectare (kg)
Best line	Small (12)	17.0	2877
	Medium (203)	25.0	3773
	Large (96)	19.5	2592
Best 10 lines	Small (12)	11.1	1529
	Medium (203)	20.6	2851
	Large (96)	17.5	2309
Checks	BRB 151	14.0	2151
	BRB 203	12.0	1893
	COS 16	18.3	2577
	FOT 28	11.3	1536
	FOT 54	12.8	1993
	SEQ 1027	14.2	1846
	SEQ 1040	12.3	1642
	SUG 46	12.3	1706
	SUG 47	10.0	1564
	SUG 130	10.2	1774
	SUG 131	10.5	1188
	SUG 137	14.0	1969
CV		34.1	38.6

Contributors: MW Blair, S Beebe

2.1.6 Crosses for anthracnose-resistant climbing and bush type popping beans (ñuñas)

Rationale: Ñuñas or popping beans are a special class of common bean whose seed will burst open and expand to double their size when toasted, fried, or microwaved. They are a traditional crop of the Andean highlands of South America. Almost all varieties of ñuñas are climbing beans, which have a good yield potential, but require a long growing season. As a result of the extended time that ñuñas are in the field, they are exposed to a range of diseases, such as anthracnose, *Ascochyta*, halo blight, and rust. The objective of this research is to improve popping beans for disease resistance, adaptation to a wider range of environments, and early-maturity. We also hope to create bush-type popping beans.

Materials and methods: Fifty-eight genotypes from Peru, the CIAT germplasm bank, and the Core Collection were evaluated for popping ability in hot oil and in the microwave. The percentage of seeds that popped and the time to pop were measured (Table 32). In addition, the popping ability was rated on a 0-5 scale where 0 = no popping, 1 = seed coat splits and less than 10% expansion, 2 = up to 30% expansion, 3 = up to 50% expansion, 4 = up to 75% expansion, and 5 = 100% expansion. The best popping beans were selected and crossed to non-popping beans that were sources of BCMV and anthracnose resistance, early maturity, and bush bean architecture. We gave extra weight to crosses with popping beans that had type III (bush) growth habit because we wanted to develop bush-type ñuñas.

Results and discussion: Nine popping beans (six climbing and three bush types) were selected and crossed to the anthracnose resistance source (G 2333) and to three bush type non-popping beans (AFR 612, CAL 96, and CAL 143). The bush-type popping beans were G 11785, a small, round white-seeded genotype, G 23604, a large-seeded, black-speckled genotype, and G 23614, a brown-and-white-mottled genotype. Among the climbing bean popping beans were red- (G 12572), brown- (G 12621 and G 12623) and gray- (G 23691) seeded genotypes. The F_1s of simple crosses between bush-type popping bean and non-popping beans were double crossed amongst each other and backcrossed to the non-popping bean parent. Segregants from the white-seeded parent may be the most readily acceptable. Other combinations are being made among growth habits, seed colors, and popping ability.

Conclusions and future plans: How ñuñas pop is not well understood. We will be studying the inheritance of popping ability and developing markers to help expedite the transfer of the trait from ñuñas into bush types. Triple crosses will be made to incorporate anthracnose and BCMV resistance simultaneously into bush- and climbing-type popping beans. A wider range of anthracnose resistance sources will be used in the future. We will also use crosses to Gloriabamba, a Mesoamerican climbing bean variety released in Peru. With these crosses we hope to create new varieties of ñuñas that will increase the availability of this product. Increased supply might stimulate exports and marketing of popping beans from Peru. This project will work with the Peruvian Institute for Grain Legumes - IPEL (Instituto Peruano de Leguminosas de Grano) and the National University of Cajamarca to develop, test, and promote new popping beans.

Contributor: MW Blair

Table 32. Popping beans examined for popping ability in hot oil and in the microwave.

Genotype	Seeds popped (of 6)		Time to pop (minutes)		Popping scale (0-5)[a]	
	Microwave	Hot oil	Microwave	Hot oil	Microwave	Hot oil
Ñuña Pava	6	6	1.02	0.53	5	2
Ñuña Jabona	6	5	1.04	0.45	5	1
Mani Bola 12582	6	6	0.57	0.51	5	2
Ñuña Limona	5	6	1.12	0.50	4	1
Mani Palida	6	6	1.33	1.25	4	5
Huevo de Huanchaco	5	6	0.43	0.50	1	3
Ñuña Mani Roja	6	6	1.14	0.35	5	4
Ñuña Parcoyana	5	6	0.45	0.35	5	5
Ñuña Poroto Blanco	4	5	0.45	0.29	4	3
Ñuña Conejita	4	6	1.38	1.05	5	3
Ñuña Paloma	5	6	0.45	0.32	4	3
Ñuña Azul o Negra	6	6	1.13	1.00	1	0
Ñuña Poroto Canario	5	6	1.05	0.35	5	3
Ñuña Ploma	6	6	0.42	0.28	5	4
Ñuña Angel Poroto	4	6	0.40	0.30	4	4
G 11785	6	6	1.13	0.33	5	5
G 11786	6	6	1.00	0.39	5	3
G 11808	4	6	1.00	0.44	5	3
G 12572	6	6	0.58	0.39	5	5
G 12575	6	6	0.55	0.51	4	3
G 12588	6	6	1.17	0.54	4	5
G 12589	3	6	1.03	0.39	1	2
G 12621	6	6	0.50	0.39	5	5
G 12623	6	6	0.54	0.40	5	4
G 12627	3	5	0.48	0.42	3	4
G 12628	6	6	1.20	0.40	4	3
G 23603	1	5	1.19	0.32	0	4
G 23604	3	4	0.55	0.15	1	2
G 23604A	5	5	1.08	0.29	3	2
G 23605	2	6	0.53	0.41	5	5
G 23610	2	4	0.46	0.38	0	2
G 23612	4	3	1.40	0.32	2	3
G 23614	5	6	1.00	0.52	5	5
G 23643	5	4	0.54	0.33	3	2
G 23688	5	5	1.16	0.49	2	1
G 23691	6	6	1.05	0.45	5	4
G 23695	6	6	0.37	0.27	1	2
G 23697A	3	6	0.36	0.36	0	3
G 23701	4	6	0.58	0.43	4	3
G 23703	5	5	1.40	0.42	2	2
G 23704	4	6	0.40	0.32	0	2
G 23705	5	6	1.01	0.40	2	2
G 23706	5	6	1.02	0.39	5	4
G 23707	6	6	0.41	0.27	4	4
G 23710	6	6	0.55	0.40	2	3
G 23711C	4	6	0.50	0.39	1	3
G 23714	3	4	0.53	0.41	1	1
G 23716	5	5	0.54	0.48	1	2
G 23717	5	6	0.50	0.41	2	2
G 23719	6	6	1.26	0.43	5	3
G 23746	4	6	1.00	0.40	5	5
G 23754	6	6	0.48	0.32	4	2
G 23766A	6	6	0.46	0.34	5	4
G 23766B	5	5	0.45	0.35	1	1
G 23767	3	5	1.02	0.36	5	3
G 23767A	6	6	0.45	0.41	5	5
G 23874	3	6	0.58	0.31	0	1

a. where 0 = no popping, 1 = seed coat splits and less than 10% expansion, 2 = up to 30% expansion, 3 = up to 50% expansion, 4 = up to 75% expansion, and 5 = 100% expansion.

Activity 2.2 Developing germplasm resistant to insects

2.2.1 Pyramiding *Empoasca* resistance in red-mottled beans

See Activity 1.3, Section 1.3.3.

Activity 2.3 Incorporating wider genetic diversity into beans

Highlights:

- Higher yielding lines with commercial seed type were obtained from advanced backcross populations derived from crosses between cultivated Andean and wild common beans.
- Triple-cross Andean populations were developed to introgress traits from Mesoamerican climbing beans.
- The inheritance of low-phosphorous tolerance was studied in an Andean population.
- Andean climbing beans of heat-tolerant commercial type were developed and tested.

2.3.1 Analysis of Andean advanced backcross populations for yield traits derived from wild *P. vulgaris*

Rationale: The genetic diversity of cultivated *P. vulgaris* is thought to be narrower than that of wild common bean because of a genetic bottleneck that occurred during domestication. Yield-increasing alleles may still reside untapped in the wild accessions that could be exploited to improve cultivated beans. The advanced backcross method has been shown to be useful for incorporating wild germplasm into cultivar breeding programs for tomato and rice. Although wild beans have been used before to transfer resistance to diseases and insects, as in the noted case of the Arcelin gene that provides resistance to bruchids, the studies presented here are among the first to attempt to obtain a higher yield potential from wild beans. The objective of this research was to conduct a molecular analysis of two advanced backcross populations to find QTL derived from wild beans that can be useful in the improvement of cultivated beans.

Materials and methods: Four Andean advanced backcross populations were planted over eight seasons. The populations were derived from two backcrosses of wild beans to a Colombian large red-seeded "Radical" type, commercial variety, ICA Cerinza. The wild donor parents were G 24390 (from Mexico), G 24404 (Colombia), G 10022 (Mexico), and G 23585 (Peru). Each population consisted of 95 selected lines. Some of the populations also had from 62 to 215 additional lines. The selected lines were yield-tested in three locations for each of the G 24390 and G 24404 populations; and in one

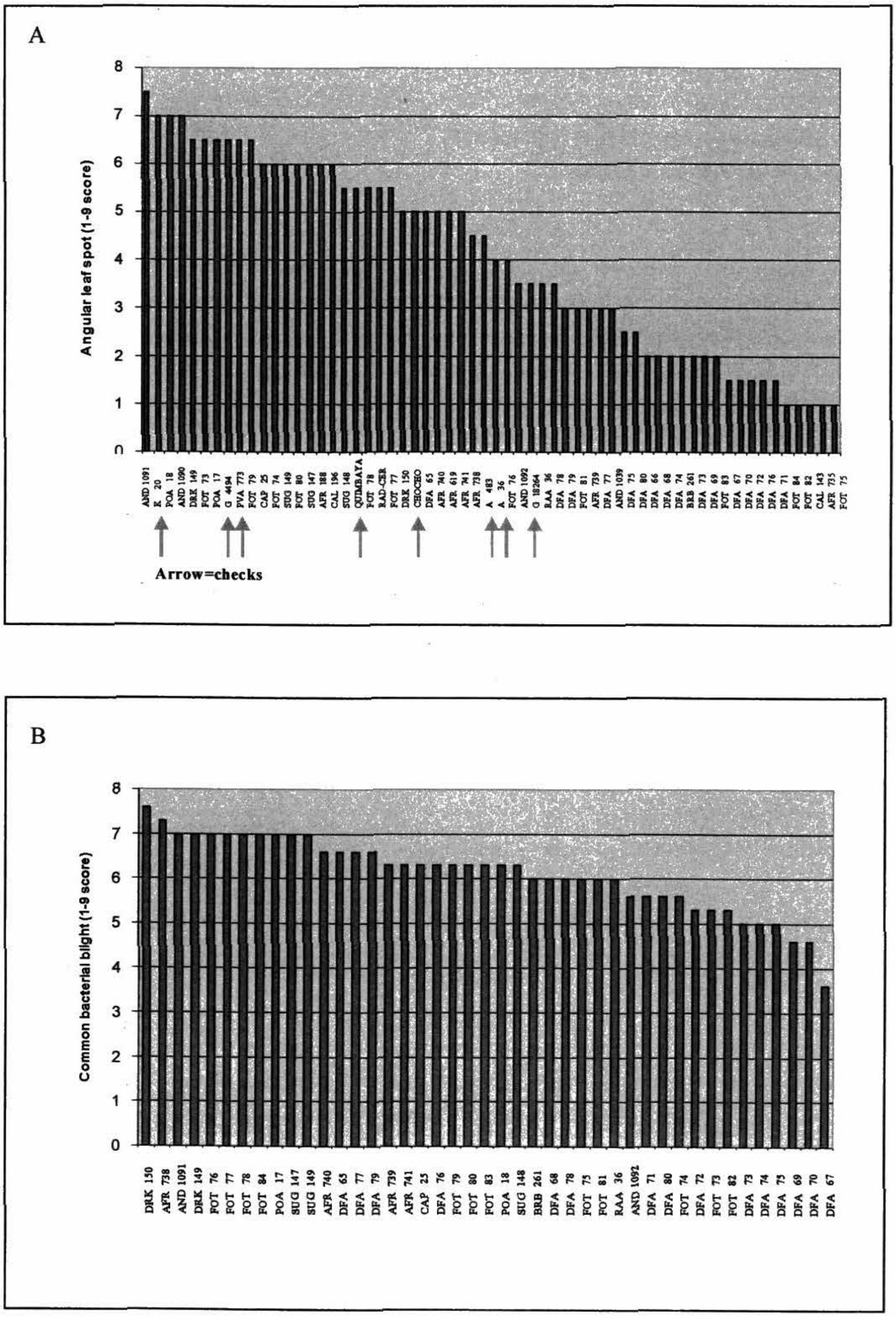


Figure 42. Disease reactions (1-9 scale) of genotypes from the IBN 2000 nursery with (A) Andean isolates of angular leaf spot in Darien 1999B, and (B) common bacterial blight in Palmira 2000A.

Progress towards achieving output milestones:

- **Lines combining resistance to BGMV, CBB, and BCMV distributed to the Caribbean and Andean Zone**

Red-mottled beans are a popular seed class in the Caribbean, Andean region, and Africa. We have developed multiple-disease resistant, red-mottled genotypes with a range of seed size and red color tones that contain combinations of resistance genes for BGMV, BCMV, and ALS. Marker-assisted selection was implemented to facilitate the breeding of BGMV resistance and will be used in the future for other diseases and insect pests. Work will continue on transferring the high level of resistance to CBB found in the VAX lines to red-mottled beans. *Empoasca* and bruchid resistances are being incorporated into the seed class as well. The red-mottled beans are being used to improve other Andean seed classes important to the region.

Activity 2.2 Developing germplasm resistant to insects

2.2.1 Pyramiding *Empoasca* resistance in red-mottled beans

See Activity 1.3, Section 1.3.3.

Activity 2.3 Incorporating wider genetic diversity into beans

Highlights:

- Higher yielding lines with commercial seed type were obtained from advanced backcross populations derived from crosses between cultivated Andean and wild common beans.
- Triple-cross Andean populations were developed to introgress traits from Mesoamerican climbing beans.
- The inheritance of low-phosphorous tolerance was studied in an Andean population.
- Andean climbing beans of heat-tolerant commercial type were developed and tested.

2.3.1 Analysis of Andean advanced backcross populations for yield traits derived from wild *P. vulgaris*

Rationale: The genetic diversity of cultivated *P. vulgaris* is thought to be narrower than that of wild common bean because of a genetic bottleneck that occurred during domestication. Yield-increasing alleles may still reside untapped in the wild accessions that could be exploited to improve cultivated beans. The advanced backcross method has been shown to be useful for incorporating wild germplasm into cultivar breeding programs for tomato and rice. Although wild beans have been used before to transfer resistance to diseases and insects, as in the noted case of the Arcelin gene that provides resistance to bruchids, the studies presented here are among the first to attempt to obtain a higher yield potential from wild beans. The objective of this research was to conduct a molecular analysis of two advanced backcross populations to find QTL derived from wild beans that can be useful in the improvement of cultivated beans.

Materials and methods: Four Andean advanced backcross populations were planted over eight seasons. The populations were derived from two backcrosses of wild beans to a Colombian large red-seeded "Radical" type, commercial variety, ICA Cerinza. The wild donor parents were G 24390 (from Mexico), G 24404 (Colombia), G 10022 (Mexico), and G 23585 (Peru). Each population consisted of 95 selected lines. Some of the populations also had from 62 to 215 additional lines. The selected lines were yield-tested in three locations for each of the G 24390 and G 24404 populations; and in one location for the G 10022 and G 23585 populations. The field sites included Isabela (Puerto Rico), Palmira (Valle, Colombia), Popayán (Cauca, Colombia), and Darien (Valle, Colombia). Three repetitions in a lattice design were used for each of the experiments, except in Puerto Rico where an RCBD with two repetitions was used. The check varieties were AFR 612, Rosada, or Quimbaya, depending on the environment. Two of the populations were genotyped with molecular markers and analyzed for QTL as described in the SB-2 Annual Report.

Results and discussion: In all four advanced backcross populations some progeny significantly out-yielded Cerinza (Table 33), which had an average yield across the eight environments of 1162 kg ha^{-1}. Meanwhile, the yield increase of the best line over the recurrent parent averaged 61.7% (or 407 kg ha^{-1}) across the eight experiments. The yield of the best line even surpassed the local check in four of the eight environments. In each experiment, Cerinza yielded more than the average yield of all $BC_2F_{3:5}$ progeny of the population, indicating that the progeny still contained negative factors from the wild that depress yield compared to the recurrent parent.

Table 33. Yield data (kg ha^{-1}) for four Andean advanced backcross populations derived from Cerinza as recurrent parent and four wild beans, G 24390, G 24404, G 10022, and G 23585 as donor parents.

	G 24390			G 24404			G 10022	G 23585
	Popayán 1998B	Puerto Rico 1999A	Palmira 1999B	Popayán 1998B	Popayán 1999A	Darien 1999B	Palmira 1999B	Darien 2000A
Best line	1374	2067	592	1139	509	2114	1840	2917
Average 10 best	1190	1864	542	1086	439	1759	1698	2513
Cerinza	915	1680	434	759	146	1747	1367	2250
Local check	1172	2347	703	1258	340	1905	2216	2719
Variety used	AFR 612	Rosada	Quimbaya	AFR 612	AFR 612	AFR 612	Quimbaya	AFR 612
Average $BC_2F_{3:5}$	845	1407	377	813	236	1333	1300	1904
Number of reps	3	2	3	3	2	3	3	3
CV	33.2	31.7	32.7	33.9	47.9	30.51	15.8	23.3
LSD ($P = 0.05$)	337	905	186	418	158	563	332	654
Increase/ Cerinza	459	387	158	380	363	367	473	667
Increase (%)	50.2	23.0	36.4	50.1	248.6	21.0	34.6	29.6

Quantitative trait loci analysis supports the observation that some introgressions from the wild parent have a detrimental effect on yield. Significant QTL for yield were found in both the Cerinza x G 24390 and Cerinza x G 24404 populations. However, most of the QTL associated with the wild alleles were negative, in effect positive QTL whose source was Cerinza. This indicates that a large number of the alleles were still transmitted from the wild parent that had negative effects on yield and that remained to be eliminated from the progeny. Positive QTL were found for the two populations analyzed for markers when grown in Popayán. This field site at 2100 m was closer to the ideal growing environment for the Cerinza variety and therefore a more appropriate testing site for advanced backcross progeny derived from Cerinza. In Popayán, the positive QTL had phenotypic effects that ranged from 99 to 225 kg ha^{-1} increased yield and these significant QTL explained from 7% to 22% of the variance for yield in these seasons. This suggests that MAS of QTLs could be successful at transferring these yield genes into other commercial seed-types.

Future plans: Two of the populations are being analyzed in collaboration with CORPOICA in Nariño. These studies will be definitive because they are being conducted in regions where ICA-Cerinza is a popular commercial variety among farmers. The QTL identified in this study are being introgressed into other Andean seed types through crosses between the F_1 plants of the first backcross of G 24390 x Cerinza and commercial varieties. These include varieties such as CAL 96, a red-mottled variety released in Uganda and Malawi, ICA Quimbaya, a red kidney variety released in Colombia, and PC 50, a Pompadour variety released in the Dominican Republic. The QTL analysis of some of these populations is described in more detail in the SB-2 Annual Report. We will compare the location of QTL found for the Andean populations. We will also analyze the QTL controlling seed size, days to flowering, and days to harvest to determine if these are associated with the yield QTL identified here.

Contributors: MW Blair, S Beebe, A Hoyos, G Iriarte

2.3.2 Use of triple-cross Andean populations for the introgression of traits from the Mesoamerican climbing beans

Rationale: Populations developed from Andean by Mesoamerican bush bean gene pools frequently have been unproductive in terms of developing new bean varieties. The reason for the poor phenotypes of inter-gene pool hybrids may be the complex epistatic interactions that occur in progeny derived from such wide crosses. Backcrossing has been used to overcome this problem and to introgress specific traits from one gene pool to the other. We were interested in trying a different approach by making inter-gene pool crosses between Andean bush and Mesoamerican climbing beans and triple crosses between their hybrid and another Andean bush bean parent. We hoped to answer the following questions. Is one backcross to the Andean bush habit enough when incorporating genes from Mesoamerican climbing beans? Can the heterosis that has often been seen in crosses between Andean bush by Mesoamerican climbing beans be fixed to produce a yield advantage in Andean bush bean varieties?

Materials and methods: Fifteen simple crosses and 100 triple crosses were made. The Mesoamerican climbing bean parents were chosen based on their resistance to ALS, anthracnose, bean fly, or low phosphorous. The Andean bush beans used as parents in the simple cross provided resistances to BCMV and drought. The final parents in the triple crosses were also Andean bush beans from various commercial seed classes. These included red-mottled (AFR 619, AFR 699, BRB 198, CAL 96, CAL 143, G 13910, Paragachi, POA 12), large red (DRK 57, Montcalm), purple-speckled (G 15430), and cream-mottled (SUG 131, SUG 137) beans. Triple-cross F_1 plants were bulk harvested in Darien in 1999B. In the following season, both simple- and triple-cross F_2 populations were grown in Darien both under trellises and in field rows and in Palmira under trellises. Single plant selections were made for both bush and climbing growth habits.

Results and discussion: In total, 2310 selections (1662 bush and 648 climbing beans) were made in the simple- and triple-cross populations. Across both environments, 57% of the selections out of the simple crosses were climbing beans, while only 24% of the selections out of the triple crosses were climbing beans (Table 34). More climbing bean selections were made for the triple crosses in Palmira than in Darien. This difference may have been because of the interaction of the climbing bean phenotype with temperature and fertility, which are higher in Palmira, along with the trellising for support. Indeed many of the climbing bean selection were determinate, but reached a height of 2 meters in Palmira. Meanwhile, in Darien, the triple crosses planted under trellises produced few (11%) climbing bean selections.

Table 34. Single plant selections (SPS) from simple and triple crosses involving Mesoamerican climbing beans and Andean bush beans.

Location / population	Bush SPS	Climbing SPS	Climbing (%)
Palmira - trellis:			
Simple crosses	27	86	76
Triple crosses	136	324	70
Darien:			
Simple crosses	97	78	44
Triple crosses	1402	160	11
Across environments:			
Simple crosses	124	164	57
Triple crosses	1538	484	24
Total	1662	648	-

Conclusions and future plans: The F_3 families from the climbing and bush bean selections with the best seed type and plant architecture will be advanced in either Darien or Palmira. Heat-tolerant Andean climbing beans will be selected in Palmira. Yielding ability of the bush bean selections will be measured. The selected families will be screened with disease inoculation to confirm the introgression of resistance genes from the Mesoamerican parents.

Contributors: MW Blair, S Beebe

2.3.3 Inheritance of low phosphorous tolerance in the Andean recombinant inbred line population AND 696 x G 19833

Rationale: Of the soils in Latin America, 82% suffer from phosphorous deficiency, which is widespread in East Africa as well. Studies at CIAT have identified several sources of tolerance to low-P conditions. These genotypes can take up or use phosphorous more efficiently. This study aimed to confirm that G 19833 is a source of tolerance to low-P stress and to compare the inheritance of tolerance in the AND 696 x G 19833 population of RILs to that in other Mesoamerican and inter-gene pool populations. We were also interested in comparing the phosphorous efficiency of segregants from this population with determinate versus indeterminate growth habit.

Materials and methods: The population was planted in Darien (Valle, Colombia) in March 2000 in a 9 x 9 lattice design with three repetitions under high- and low-P conditions. The Darien field site has very low natural levels of phosphorous in the soil (< 8 ppm). The low-P treatment in the experiment received 30 kg ha^{-1} while the high-P treatment received 300 kg ha^{-1} of superphosphate fertilizer. Seventy-seven RILs were planted plus four check varieties, G 19833, G 4017 (Carioca), and G 16140. Data were collected on growth habit, days to flowering, days to harvest, and yield per plant and per plot.

Results and discussion: The yields in the high-P treatment were 136% higher on the average than were those in the low-P treatment. Among the RILs, some were both responsive to P fertilization and adapted to low-P conditions (Figure 43). The correlation between yield in high- and low-P environments was $r = 0.584$. Among the check varieties, G 4017 was the highest yielding in both fertilizer treatments; G 16140 was the most efficient under low phosphorous. G 19833 was low yielding in high P and moderate yielding in low P. Of the 77 RILs tested in this trial, 56 had a determinate growth habit and 21 were indeterminate (Figure 44). In the low-P treatment, the average yield of indeterminate lines was higher than that of the determinate lines. The peak in the distribution of yields among the determinate RILs was higher than for the indeterminate lines. Meanwhile, in the high-P treatment, the average yield of the indeterminate lines was lower than that of the determinate lines. In the high-P treatment, the population distribution for yield of both the determinate and indeterminate lines was bimodal suggesting that a single gene was determining adaptation. Many of the RILs that were indeterminate were late and unadapted like the G 19833 parent. Even though G 19833 and the late RILs produced a large amount of biomass, their photoperiod sensitivity did not allow these genotypes to reach their full yield potential.

Conclusions and future plans: On low-P soils, the yield potential of the indeterminate genotypes in the population was higher than that of determinate genotypes. However, on high-P soils the indeterminate genotypes do not appear to provide a yield advantage and indeterminacy may be associated with a lack of reproductive adaptation associated with the G 19833 source of tolerance.

Contributors: MW Blair, S Beebe, A Hoyos

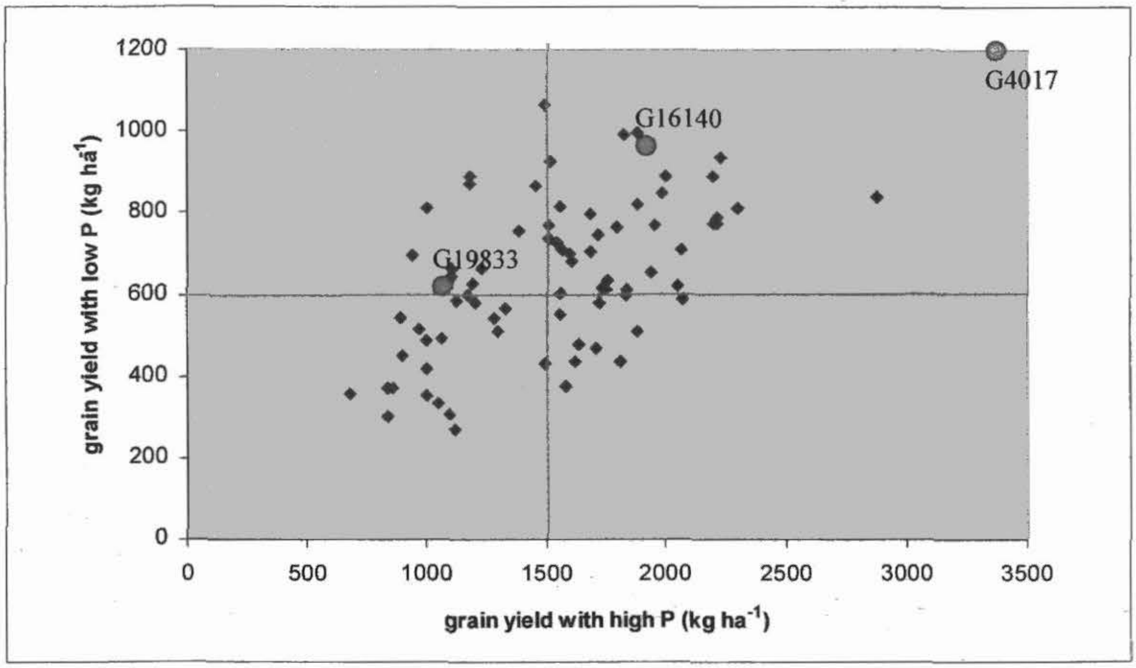


Figure 43. Regression of grain yield under low- and high-phosphorous treatment for recombinant inbred lines from the AND 696 x G 19833 population.

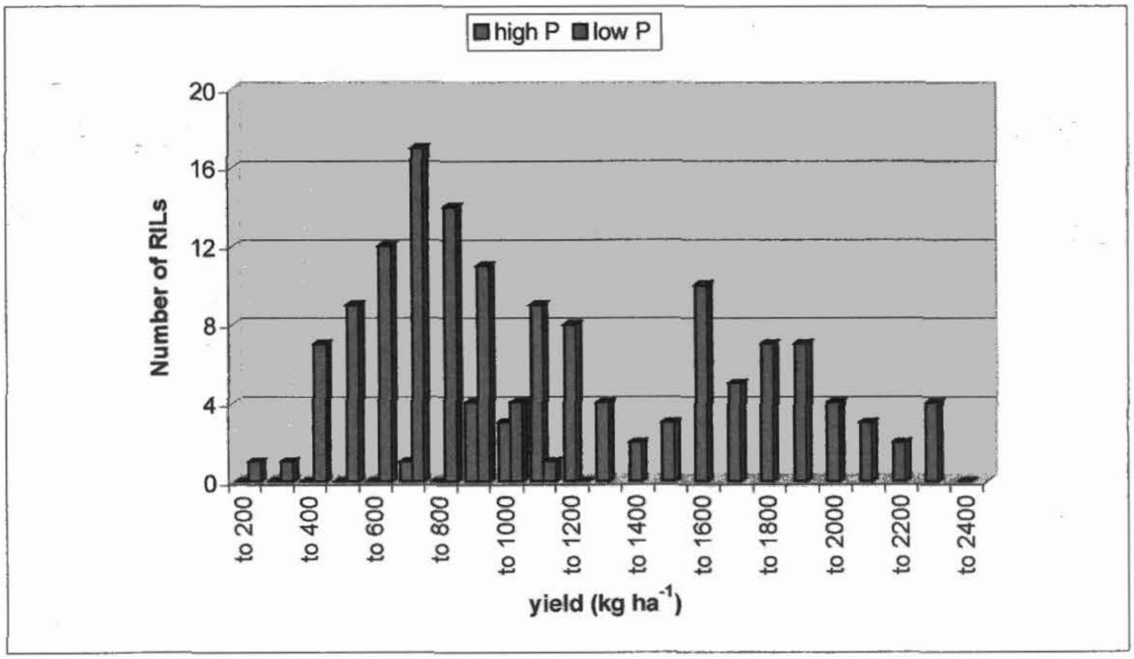


Figure 44. Population distribution of grain yield under high- and low-phosphorous treatment for recombinant inbred lines from the AND 696 x G 19833 population.

2.3.4 Development of mid-elevation, commercial-type, Andean climbing beans

Rationale: The most outstanding characteristic of climbing beans is their high yield potential compared to more commonly grown bush beans. Climbing beans have been an important component of traditional societies in Central America and the Andes for centuries. More recently, climbing beans have become important in certain areas of Africa. The principal limitation to the expansion of climbing bean technology into new areas has been the lack of new varieties. Most currently available climbing beans come from high-altitude areas of Central and South America and do not grow well in lower elevations or hotter climates. An urgent need exists for climbing bean varieties that are adapted to lower elevations (800 to 1800 m) and resistant to the diseases encountered there. Currently, very few climbing bean varieties are available with the red-mottled or red kidney seed types, which are preferred in many areas of the Caribbean, Africa, and South America. Therefore, an additional challenge for breeders is to develop climbing bean varieties that produce grain with the proper color and size. The objective of this research is to hybridize, develop, and test mid-altitude adapted, commercial-type, Andean climbing beans.

Materials and methods: In 1999B, we initiated screening for climbing beans with adaptation to Palmira (1000 m). We planted four sets of germplasm, including 61 accessions from the Core Collection, 92 accessions from Mexico, 182 accessions from Rwanda, and 50 bulk selections made from Andean climber x Andean bush crosses. Single plant selections were made from the most promising bulks. In the second season in 2000A we repeated some of the germplasm and also planted out F_2 seed from 15 simples crosses between Mesoamerican climbers and Andean bush beans, as well as from 24 triple crosses between Andean bush x (Mesoamerican climber x Andean bush beans). The climbing beans were all planted at a low density of 10 plants per meter of linear row with 1.2 m between rows and the vines were supported on bamboo and wire trellises at about 2.0 m aboveground.

Results and discussion: The accessions from the Core Collection adapted to the Palmira site were almost entirely Mesoamerican genotypes and therefore were related to the accessions tested from Mexico. The Rwandan accessions were highly diverse in terms of seed color and their climbing ability and probably represent natural hybridizations between climbing and bush beans from both Andean and Mesoamerican gene pools. The best red-seeded types from Rwanda and Mexico were included in a larger trial the following season. Single plant selections were made in the $F_{5:7}$ generation of Andean climber x Andean bush populations based on the best seed types in the bulk. The F_7 lines were then tested in the second season to confirm their adaptation to mid-elevation regions and increase seed. Of the selections, 27 were red-mottled, 13 were large red, and 32 were cream-mottled, all with average seed sizes around 50 g per 100 seed. Figure 45 shows the yield of these genotypes. The new Andean climbing bean lines yielded much better than unadapted highland climbers such as ICA Viboral and LAS 399 (Andeans) and G 2337 (Mesoamerican). The yield advantage of the adapted climbing beans over bush beans, such as Kirundo, AND 930, Rojo 70, MAM 39, DRK 49, and SUG 92, was evident. This is even more significant because these were the bush bean parents of the advanced lines. Some of the new Andean climbing beans yielded as well as the Mesoamerican climbing beans, G 2333, G 685, and Magdalena 3, which are all standard varieties throughout climbing-bean growing areas of Africa.

Conclusions and future plans: We are hybridizing best accessions from Mexico, Rwanda, and the Core Collection with single plant selections from Andean populations with tolerance to higher temperatures. We are also beginning to pyramid in the resistance and tolerance factors (ALS, BCMV, BGMV, CBB, bean fly, bruchid, *Empoasca*, and low fertility) that will be necessary for successful production of climbing beans at mid-elevation, bean-producing areas. New lines developed from these crosses will be included in an international climbing bean nursery to test the best advanced lines and accessions at a range of elevations. We hope to test early generation climbing bean populations in participatory plant breeding projects and on-farm trials.

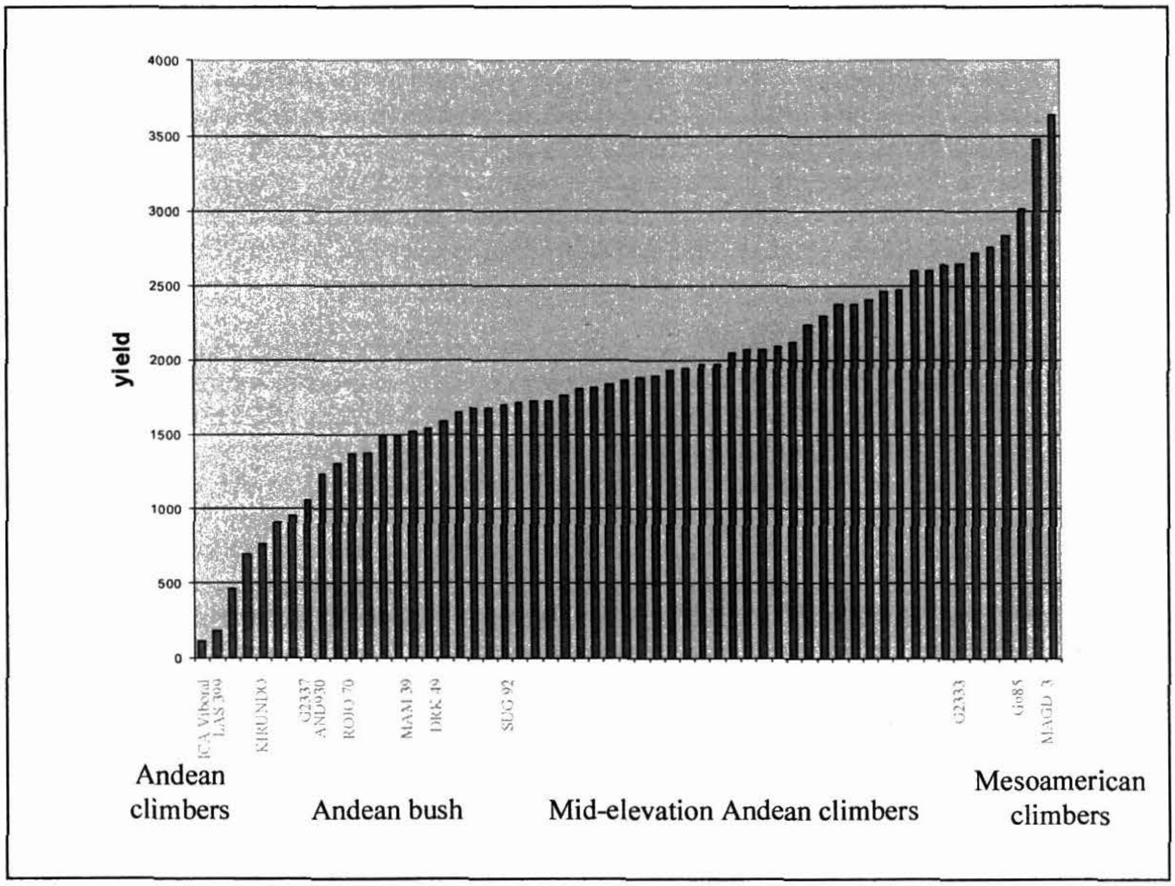


Figure 45. The yield (kg ha^{-1}) of mid-elevation, heat-tolerant, Andean climbers compared to Andean bush beans, Mesoamerican climbing beans, and unadapted Andean climbing beans.

Contributors: MW Blair, A Hoyos, C Cajiao

Progress towards achieving output milestones:

- **Phosphorous efficient genotypes developed**

The inheritance of low-phosphorous tolerance from G 19833 was studied in an Andean background. Interactions with determinate growth habit will be studied further.

019636

Output 3. Strategies developed for management of diseases and pests in bean-based cropping systems

Activity 3.1 Characterizing and monitoring pathogen and insect diversity

Highlights:

- 55 *Phaeoisariopsis griseola* and *Colletotrichum lindemuthianum* isolates were characterized using host differential interactions.

- 400 isolates of *Xanthomonas campestris* pv. *phaseoli* (XCP) and *X. campestris* pv. *phaseoli* var. *fuscans* (XCPF) have been characterized using repetitive extragenic palindromic polymerase chain reaction (REP-PCR) and RFLP of the 26S ribosomal genes. Results show that XCP is very distinct from XCPF.

- 125 *C. lindemuthianum* isolates were characterized using microsatellites and REP-PCR.

- Polymorphic RAMS fragments were cloned to develop locus specific markers.

- 400 *P. griseola* isolates were characterized using RAMS and all isolates were put into Andean and Mesoamerican groups.

- The "Afro-Andean" group is part of the Andean group that represents isolates resulting from point mutations in genes for virulence.

- The presence of BGYMV virus in Colombia was confirmed.

3.1.1 Characterizing pathogen diversity

Rationale: Genetic diversity and pathogen population structure information is useful in identifying sources of disease resistance and deployment of the resistance genes in ways that prolong their durability. The breakdown of resistance has been attributed to the change in the population structure. Understanding the amount of genetic diversity that exists within populations helps us predict the rate at which a resistant variety will break down, understand factors that contribute to the breakdown of resistance, and predict how long a resistant variety will last before being overcome by new pathotypes. Therefore, monitoring the pathogen for emergence of new and more virulent (aggressive) races should be a continuous activity in a disease management program.

***Phaeoisariopsis griseola* (PG):** Thirty-five *P. griseola* isolates were characterized on a set of 12 host differential cultivars. Six of the isolates were from Bolivia, one from Colombia, two from El Salvador, seven from Haiti, three from Malawi, 11 from Nicaragua, and five from Tanzania (Table 35). Twenty-one races were defined. However, all these have been described before. This brings the total of isolates characterized using virulence markers to 446.

Table 35. Virulence phenotypes of 35 *Phaeoisariopsis griseola* isolates characterized during 2000.

	Isolate[a]	Differential cultivars[b]												Race
		A	B	C	D	E	F	G	H	I	J	K	L	
1	Pg 307 COL		b	c	d	e	f							62-0
2	Pg 5 TZA	a	b	c	d	e	f						l	63-32
3	Pg 6 TZA	a	b	c	d		f	g	h	i		k		47-23
4	Pg 9 TZA	a	b	c	d	e	f	g					l	63-0
5	Pg 10 TZA	a	b	c				g	h	i			l	7-39
6	Pg 611TZA			c	d									12-0
7	Pg 32 BOL	a	b	c	d	e	f	g	h	i		k		63-23
8	Pg 33 BOL	a	b	c	d	e	f	g	h	i		k		63-23
9	Pg 34 BOL	a	b	c				g	h	i		k		7-23
10	Pg 35 BOL	a	b	c		e		g	h	i		k		23-23
11	Pg 36 BOL	a	b	c	d	e	f	g	h	i		k		63-23
12	Pg 38 BOL	a	b	c	d			g	h	i		k		31-23
13	Pg 33 MWI	a	b	c	d			g	h	i			l	31-39
14	Pg 34 MWI	a	b	c	d			g	h	i			l	31-39
15	Pg 35 MWI	a	b	c	d			g	h	i			l	31-39
16	Pg 19 ELS	a	b	c				g	h		J	k		7-27
17	Pg 20 ELS	a	b	c	d	e	f	g	h		J	k		63-27
18	Pg 11 NIC	a	b	c	d	e		g	h	i		k	l	31-55
19	Pg 12 NIC	a	b	c	d	e	f	g	h		J	k		63-27
20	Pg 13 NIC	a	b	c	d	e	f	g	h	i	J	k		63-31
21	Pg 14 NIC	a	b	c	d	e	f	g	h		J	k		63-27
22	Pg 15 NIC	a	b	c		e		g	h		J	k		23-27
23	Pg 16 NIC	a	b	c	d	e		g	h			k	l	31-51
24	Pg 17 NIC	a	b	c	d	e	f	g	h	i	J	k		63-31
25	Pg 18 NIC	a	b	c		e		g	h		j	k		23-27
26	Pg 19 NIC	a	b	c	d	e	f	g	h		j	k		63-27
27	Pg 20 NIC	a	b	c	d	e	f	g	h		j	k	l	63-59
28	Pg 21 NIC	a	b	c	d	e		g	h	i	j	k	l	31-63
29	Pg 1 HTI	a	b	c	d	e		g	h	i			l	31-39
30	Pg 2 HTI	a	b	c	d	e	f	g	h	i			l	63-39
31	Pg 3 HTI	a	b	c	d	e		g	h	i			l	31-39
32	Pg 4 HTI	a	b	c	d	e	f	g	h	i			l	63-39
33	Pg 5 HTI	a	b	c	d	e		g	h	i			l	31-39
34	Pg 6 HTI	a	b	c	d	e		g	h	i				31-7
35	Pg 7 HTI	a	b	c	d	e		g	h	i				31-7

a. Pathogen identification: the last three letters represent the country of origin. HTI = Haiti, NIC = Nicaragua, COL = Colombia, BOL = Bolivia, TZA = Tanzania, and MWI = Malawi.

b. Andean differential cultivars: A = Timoteo, B = G 11796, C = Bolón Bayo, D = Montcalm, E = Amendoim, F = G 5686. Mesoamerican differential cultivars: G = PAN 72, H = G 2858, I = Flor de Mayo, J = MEX 54, K = BAT 332, L = Cornell 49242.

***Colletotrichum lindemuthianum* (CL):** Twenty isolates collected from Ecuador were characterized using host differential interactions. Seven races were identified among the 20 isolates (Table 36). An interesting observation was the incidence of simple races, race 0 (six isolates), race 1, race 4, race 6, and race 7. Only race 256 was the most complex. These results show that the *C. lindemuthianum* population pathogen structure in Ecuador is predominantly Andean and composed of relatively simple races. Introgressing resistance genes found in the differential cultivars Cornell 49242, MEX 222, PI 207262, Tu, AB 136, and G 2333 will be sufficient to manage anthracnose in this country.

Table 36. Virulence phenotype of 20 *Colletotrichum lindemuthianum* isolates collected from Ecuador.

Isolate	Differential cultivars[a]												Race
	A	B	C	D	E	F	G	H	I	J	K	L	
	1	2	4	6	18	32	64	128	256	512	1024	2048	
CL 163		b	c										6
CL 164													0
CL165		b	c										6
CL166		b	c										6
CL167	a	b	c		e								23
CL168			c										4
CL169	a	b	c										7
CL170		b	c										6
CL171		b	c										6
CL172													0
CL173													0
CL174													0
CL175													0
CL176	a												1
CL177													0
CL178			c										4
CL179									i				256
CL180	a												1
CL181	a												1
CL182													0

a. Differential cultivars: A = Michelite, B = Michigan Dark Red Kidney, C = Perry Marrow, D = Cornell 49242, E = Widusa, F = Kaboon, G = MEX 222, H = PI 207262, I = To, J = Tu, K = AB 136, and L = G 2333. The binary value used to designate race of the isolate is given underneath the letters.

Contributors: G Mahuku, C Jara, G Castellanos, J Cuasquer (IP-1);
R Buruchara (IP-2)

3.1.2 Molecular characterization of *Xanthomonas campestris* pv. *phaseoli*, causal agent of common bacterial blight

Rationale: A clear understanding of the genetic variation that exists in pathogen populations is essential not only in formulating appropriate management strategies, but also in understanding the origin and maintenance of genetic variation and the emergence of new pathogen variants and/or races. Common bacterial blight is a major disease of common bean in temperate and tropical countries, and yield losses can be as high as 60%. Two phytogenetically distinct *Xanthomonas*, XCP and XCPF, cause the disease. Variation in pathogenicity occurs among XCP isolates. This variation is mainly quantitative and differential interactions between host and isolate are not clearly exhibited. Controversy surrounds the existence of genetic diversity within XCP, with some researchers reporting the existence of host differential interactions in common bean, while others have disputed this report. This study is aimed at using molecular techniques to elucidate the amount of genetic diversity that exists within and between XCP and XCPF. This information will be used to select strains to screen a range of *Phaseolus* genotypes and establish if host differential interaction occurs within CBB.

Materials and methods: DNA was extracted from 450 CBB pathogens and amplified using three enterobacterial repetitive intergenic consensus (ERIC) REP-PCR primers, REP-PCR sequences, and BOX elements (BOX PCR). In addition, restriction fragment length polymorphisms (RFLPs) of the 26S ribosomal gene were obtained using conserved primers and digestion with restriction endonucleases. We also made bacterial isolations and pathogenicity tests for 20 samples: seven from Malawi, one from Colombia, one from Puerto Rico, one from Honduras, three from Nicaragua, and seven from Iran. These isolates were pathogenic on BAT 41, the susceptible check.

Results and discussion: Preliminary analysis of the results has shown that XCP and XCPF are distinct at the molecular level and should be separated into different groups (Figure 46). However, very little genetic diversity exists for the 26S ribosomal gene. Only three restriction enzymes (*RSA* 1, *MBO* 1, and *HAE* III) showed polymorphisms that separated XCP from XCPF and showed no within-group polymorphisms. Figure 47 shows profiles generated after digestion with RSA 1. The REP-PCR revealed greater genetic diversity that was correlated to geographical origin of the isolates. We are analyzing all the molecular data and generating molecular genetic groups to use for host differential analysis.

Conclusions: Preliminary analysis has shown that XCP and XCPF are distinct. However, more information will be obtained following completion of this study.

Contributors: G Mahuku, C Jara

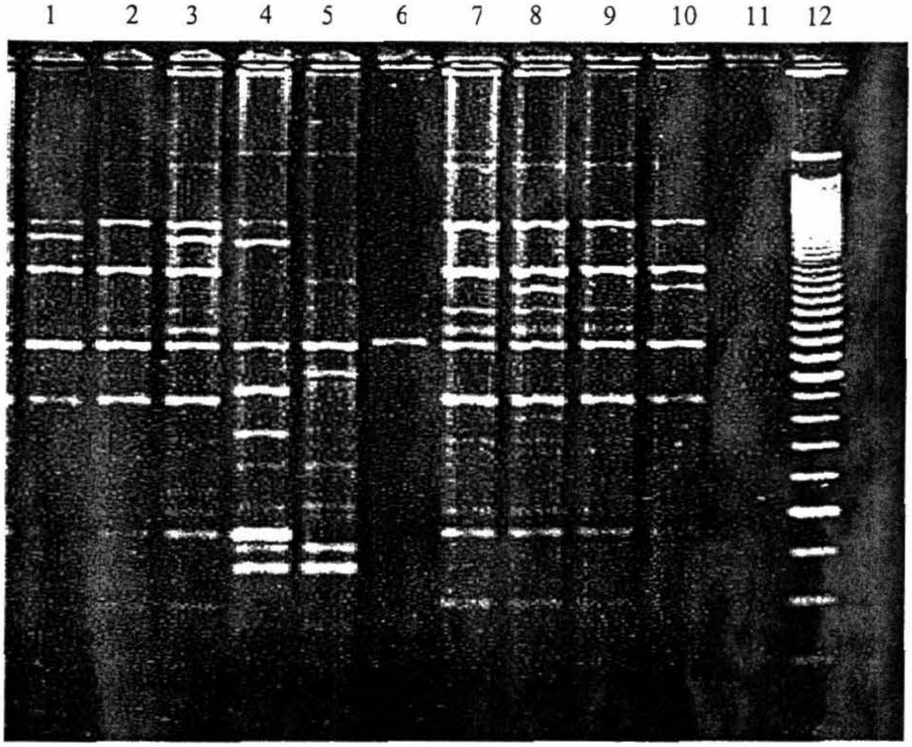


Figure 46. Enterobacterial repetitive intergenic consensus (ERIC) – polymerase chain reaction (PCR) profiles for some *Xanthomonas campestris* pv. *phaseoli* (XCP) and XCP var. *fuscans* (XCPF) strains. Lanes 1, 2, 3, 6, 7, 8, 9, and 10 are XCP, while lanes 4 and 5 are XCPF strains. Lane 11 is negative control and lane 12 is the 100 bp DNA ladder.

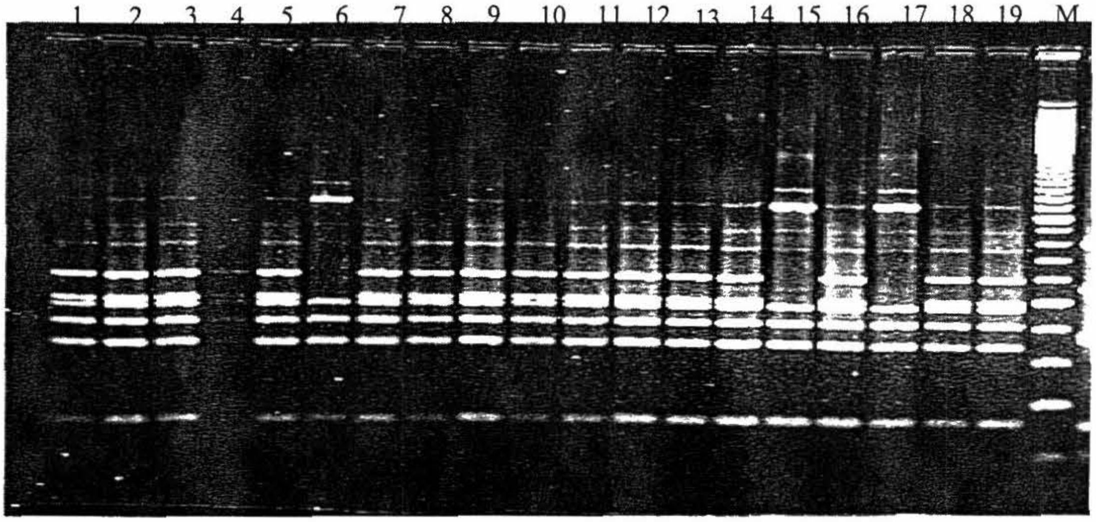


Figure 47. Profiles generated by digesting the amplified 26S ribosomal gene with the restriction enzyme *RSA*1. Lanes 6, 15, and 17 are *Xanthomonas campestris* pv. *fuscans*, while the other lanes are *Xanthomonas campestris* pv. *phaseoli*. Lane M is the 100 bp DNA molecular marker.

3.1.3 Molecular and virulence characterization of *Colletotrichum lindemuthianum*, causal agent of anthracnose of common bean

Rationale: Anthracnose of bean, caused by *C. lindemuthianum,* is an important disease in the highlands of Africa and Latin America. Yield losses from this pathogen can be as high as 90%. It has been shown to exist in many different forms (races), and the major reason for the continued susceptibility of bean to anthracnose is pathogen variation. By analyzing the structure of pathogen populations and the ways in which populations respond to experimental, agricultural, and natural constraints, the mechanisms by which pathogen population change can be understood. This understanding can provide the basis for formulating disease support systems that lead to effective disease management. This project seeks to develop molecular markers (microsatellites) for genetic characterization and differentiation of *C. lindemuthianum* races.

Materials and methods: To check if the isolates maintained their virulence during long periods of storage, 12 isolates from different countries and representing different races were tested in the greenhouse on a set of host differential genotypes. From our collection of 1050 isolates, 125 *C. lindemuthianum* isolates were selected and DNA extracted from them. The isolates were selected to represent the greatest genetic diversity possible (i.e., the most widely distributed and frequently occurring *C. lindemuthianum* race from different geographical origin). We took into account the geographical origin of the isolates and the race designation based on host differential interaction on 12 bean genotypes.

Molecular characterization of the isolates was done using RAMS and REP-PCR primers, ERIC-PCR, REP-PCR sequences, and BOX-PCR, originally developed for amplifying conserved repetitive sequences in the bacterial genome.

Results and discussion: Evaluation of the 12 isolates on a set of host differentials showed that the isolates had maintained their virulence despite long periods of storage (Table 37). Initial race designations were in agreement with our current test characterization, showing that the storage conditions did not influence the virulence of the pathogen.

Preliminary results obtained from characterization of isolates using RAMS have shown high levels of polymorphism among and within *C. lindemuthianum* races (Figure 48). No clear correlation between race designation and molecular phenotype were apparent (Figure 49). However, we are in the process of correlating individual RAMS bands for each of the RAMS primers used in this study in order to identify race-discriminating bands.

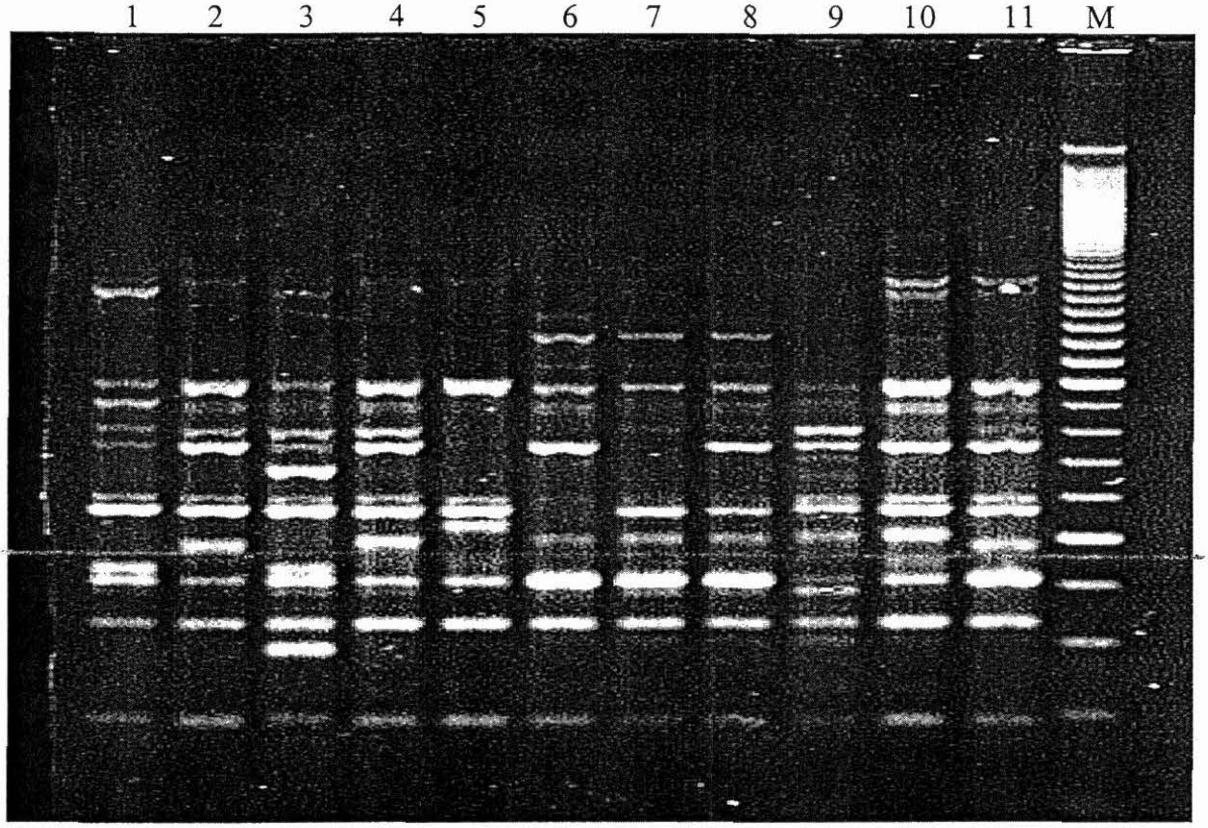
Table 37. Virulence phenotype and race designation of 12 *Colletotrichum lindemuthianum* isolates evaluated on 12 differential varieties 7 years after storage.

Isolates[a]	Differential varieties[b]												Race
	A	B	C	D	E	F	G	H	I	J	K	L	
CL11CRI*	a	.	.	d	.	.	g	h	i	j	k	.	1993
CL11CRI	a	.	.	d	.	.	g	h	i	j	k	.	1993
CL82CRI*	a	.	.	d	.	.	g	h	i	.	.	.	457
CL82CRI	a	.	.	d	.	.	g	h	i	.	.	.	457
CL41CRI*	a	.	.	d	e	.	g	h	i	.	k	.	1497
CL41CRI	a	.	.	d	e	.	g	h	i	.	k	.	1497
CL7CRI*	a	b	c	.	.	.	.	.	.	.	.	.	7
CL7CRI	a	b	c	.	.	.	.	.	.	.	.	.	7
CL96BRA*	a	b	c	.	e	.	.	.	.	.	.	.	23
CL96BRA	a	b	c	.	e	.	.	.	.	.	.	.	23
CL114CRI*	a	.	.	.	.	.	.	h	.	.	k	.	1153
CL114CRI	a	.	.	.	.	.	.	h	.	.	k	.	1153
CL93CR*	a	.	.	d	.	.	.	.	i	.	.	.	1033
CL93CR	a	.	.	d	.	.	.	.	i	.	.	.	1033
CL5CRI*	a	.	.	d	.	.	.	.	.	j	.	.	521
CL5CRI	a	.	.	d	.	.	.	.	.	j	.	.	521
CL154CRi*	a	.	.	d	.	.	.	h	.	.	.	.	137
CL154CR	a	.	.	d	.	.	.	h	.	.	.	.	137
CL72CRI*	a	.	.	d	e	.	.	h	i	.	k	l	3481
CL72CRI	a	.	.	d	e	.	.	h	i	.	k	l	3481
CL106CRI*	a	.	.	.	.	.	.	.	.	.	k	.	1025
CL106CRI	a	.	.	.	.	.	.	.	.	.	k	.	1025
CL90CRI*	a	.	.	d	.	.	g	.	.	.	.	.	73
CL90CRI	a	.	.	d	.	.	g	.	.	.	.	.	73

a. * First evaluation of *C. lindemuthianum* isolates evaluated previously by the Bean Pathology section.

b. Anthracnose differential cultivars: A = Michelite, B = Michigan Dark Red Kidney, C = Perry Marrow, D = Cornell 49242, E = Widusa, F = Kaboon, G = MEX 222, H = PI 207262, I = To, J = Tu, K = AB 136, and L = G 02333.

We have started cloning polymorphic and race-discriminating bands for subsequent sequencing and development of locus-specific microsatellite markers for *C. lindemuthianum* that can be used for population genetic studies and to elucidate the mechanisms leading to the high genetic diversity and distribution observed in this fungus. The wide genetic polymorphism among *C. lindemuthianum* races revealed by microsatellite markers shows the great potential of this type of marker for population genetic studies of this fungus.



1 = 202COL, 2 = 17COL, 3 = 31GTM } R = 1545
4 = 14COL, 5 = 250COL, 6 = 40PER } R = 9
7 = 28ECU, 8 = 150ECU } R = 4
9 = 2COL → R = 7
10 = → R = 385
11 = → R = 15

Figure 48. Profiles generated by microsatellite primers (GT)n for different races of *Colletotrichum lindemuthianum*. Lanes 1, 2, and 3 represents race 1545, lanes 4–6 = race 9, lanes 7 and 8 = race 4, lane 9 = race 7, lane 10 = race 385, and lane 11 = race 15. Lane M represents the 100 bp DNA molecular marker.

Contributors: JJ Riascos, G Mahuku

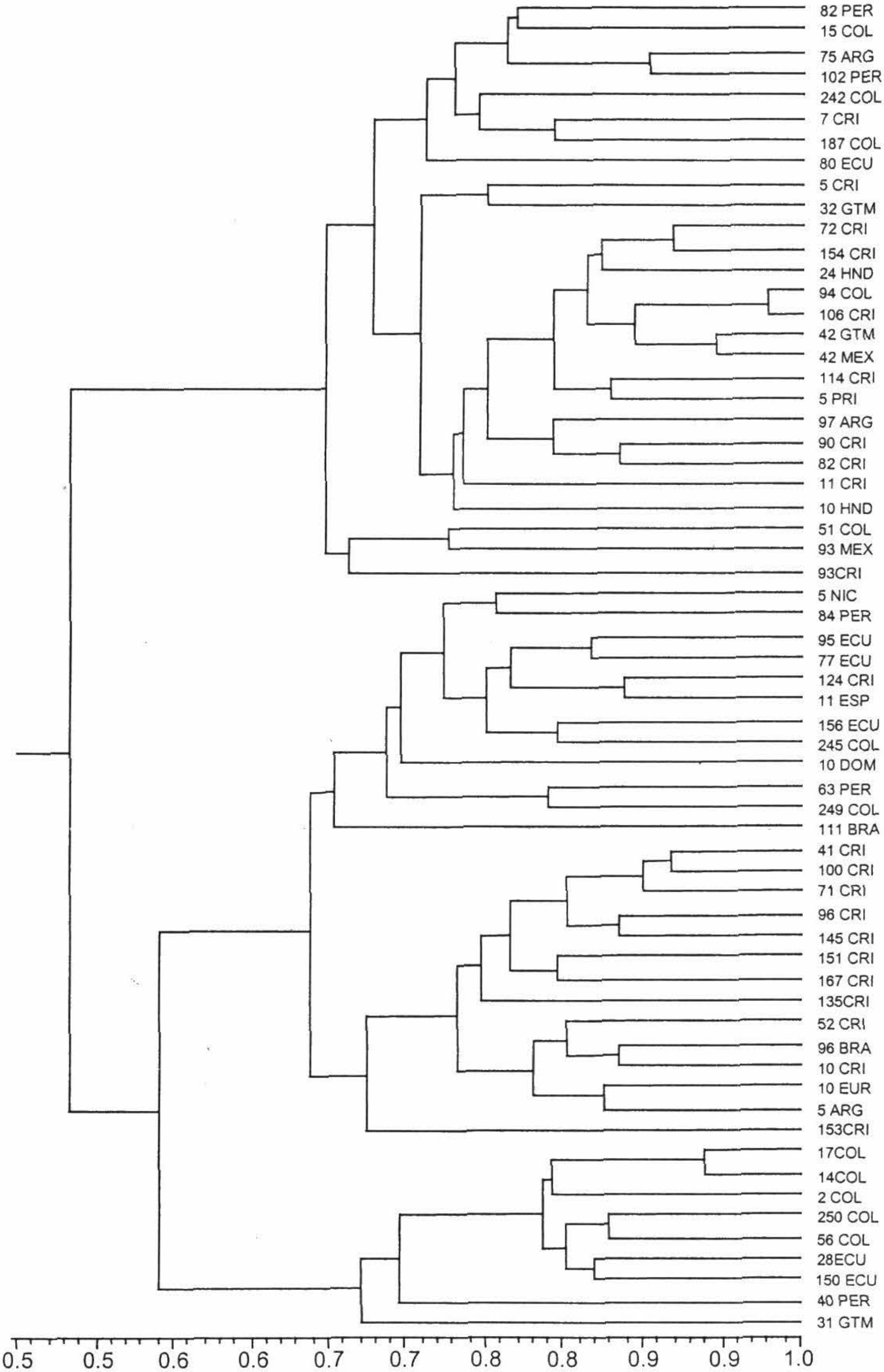


Figure 49. Dendrogram of *Colletotrichum lindemuthianum* isolates based on unweighted pair-group distance method of averaging (UPGMA) analysis of random amplified microsatellite data using numerical taxonomy system (NTSYS) program Version 1.8.

3.1.4 Molecular characterization of the angular leaf spot pathogen, *Phaeoisariopsis griseola*

Rationale: Two major groups of the ALS pathogen, *P. griseola,* were described using virulence and molecular markers. Isolates belonging to the Andean group were shown to infect and colonize bean varieties belonging to the Andean gene pool, while Mesoamerican isolates have a broader virulence spectrum, although preferring Mesoamerican beans. Recently, a group of typical Andean isolates, designated "Afro-Andean", which are able to infect one or two Mesoamerican differential cultivars, have been identified and only from Africa. This study was conducted to elucidate the relationship between the Afro-Andean, Andean, and Mesoamerican PG groups, and to establish if the Afro-Andean group represented a new group of isolates within *P. griseola.*

Materials and methods: *P. griseola* isolates were divided into three groups: Andean, Mesoamerican, and Afro-Andean, based on differential interaction on 12 bean cultivars. The molecular profiles of these isolates were assessed using RAPD, RAMS, and restriction digestion of the amplified ribosomal intergenic spacer region (IGS-RFLP). Analysis of molecular variance (AMOVA) and cluster and multiple correspondence analysis were used to determine the relationship existing between *P. griseola* groups. In addition, statistical support for phenogram branching in qualitative analyses was obtained using bootstrapped analysis.

Results and discussion: Polymorphic and easily scorable banding patterns were obtained using RAMS, RAPDs, and IGS-RFLP. Figure 50 shows comparative banding patterns obtained using the RAMS primer (CA)n for some *P. griseola* isolates.

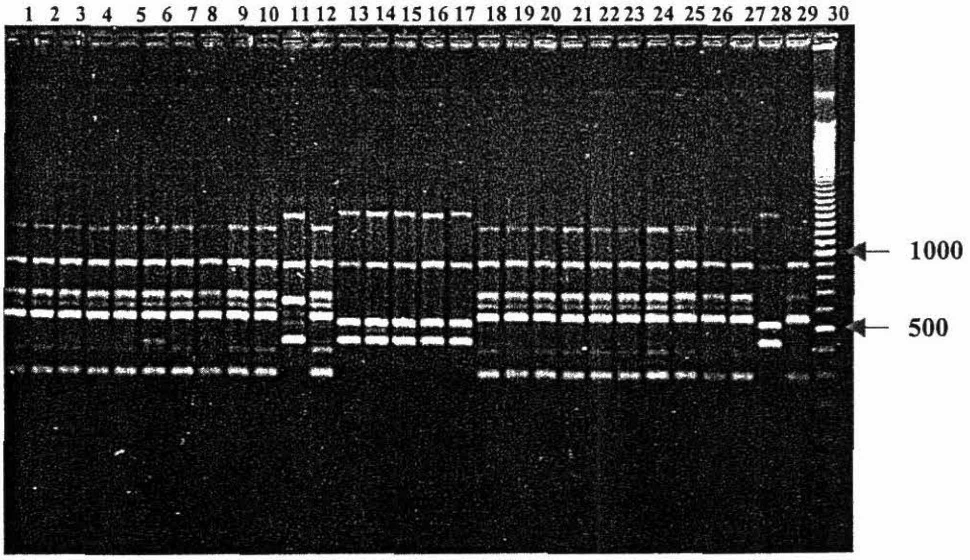


Figure 50. Band profiles generated for *Phaeoisariopsis griseola* isolates using RAMS primer (CA)n. The isolates in lanes 1-10, 12, 18-27, and 29 belong to the Andean group, while isolates in lanes 11, 13-17, and 28 are Mesoamerican. Lane 30 represents the 100 bp molecular DNA step marker.

Figure 51 shows the size of IGS products and the profiles obtained following digestion with the restriction enzyme *RSA* 1. No differences were obtained between groups in the size of the IGS fragment.

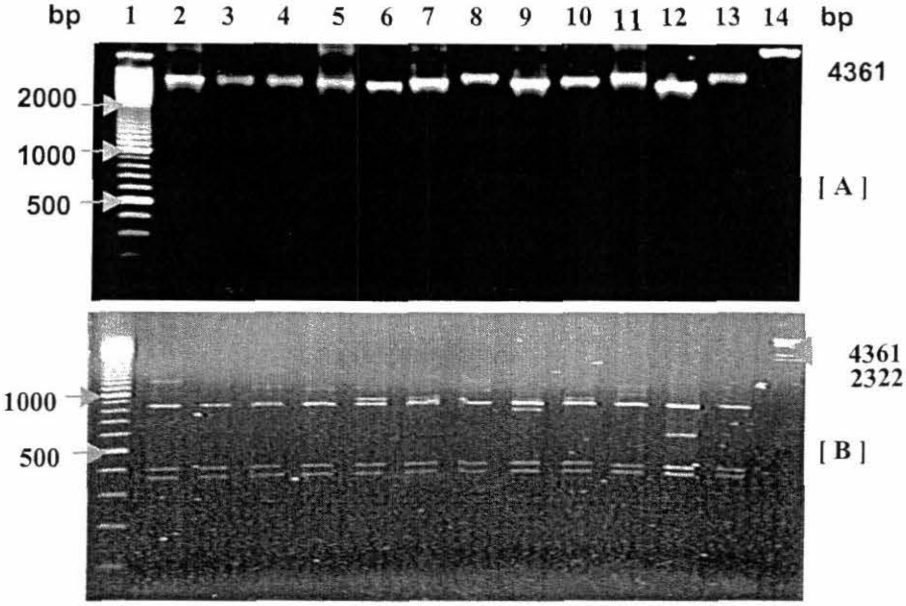


Figure 51. [A] Polymerase chain reaction (PCR) product following amplification with the intergenic spacer region (IGS) primers CLN12 and CLNTS1. [B] IGS profiles of *Phaeoisariopsis griseola* isolates resulting from restriction digestion of the IGS PCR product with the restriction enzyme *Rsa*I. Isolates in lanes 2-6 are Andean isolates, lanes 7-10 are Mesoamerican, and lanes 11-13 are Afro-Andean. Lane 1 corresponds to the molecular weight marker, the 100 bp DNA stepladder, and lane 14 to HIND III digested Lambda DNA.

Analysis of genetic differentiation showed that most of the genetic diversity was distributed within groups (81%) rather than between groups (19%). The AMOVA analysis showed that Andean and Afro-Andean *P. griseola* isolates belonged to the same group (Gst = 0.067), whereas the Mesoamerican group was distinct from both the Andean group (Gst = 0.41) and the Afro-Andean (Gst = 0.54) (Figure 52). These high levels of genetic differentiation signify the distance between the Andean and Mesoamerican group of *P. griseola*, further confirming the co-evolution concept. However, the low levels of genetic differentiation between the Andean and Afro-Andean groups show that these isolates represent recent events of genetic separation that has not occurred long enough to significantly separate them into two groups.

Similarly, cluster analysis separated isolates into two major groups, corresponding to Andean and Mesoamerican groups, and all isolates classified as Afro-Andean separated with the Andean group (Figure 53).

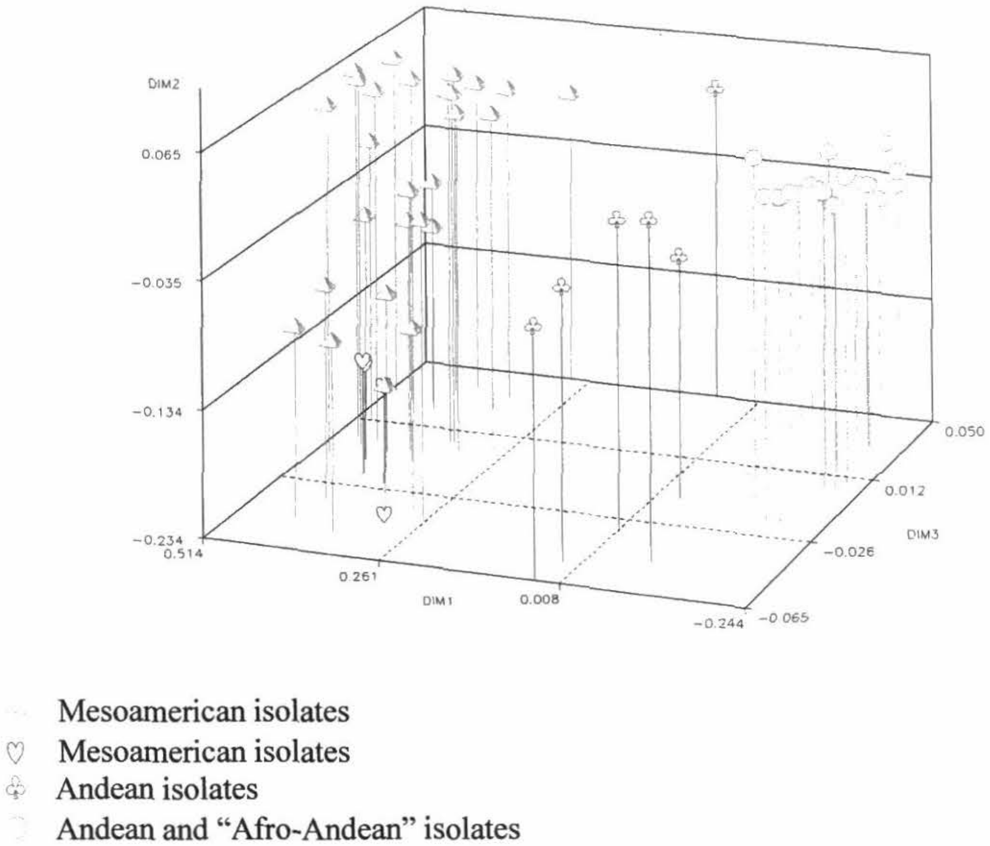


Figure 52. Multiple correspondence analysis of RAPD profiles of *Phaeoisariopsis griseola* isolates representative of Andean, Mesoamerican, and "Afro-Andean" groups.

Contributors: MA Henríquez, G Mahuku (IP-1); R Buruchara (IP-2)

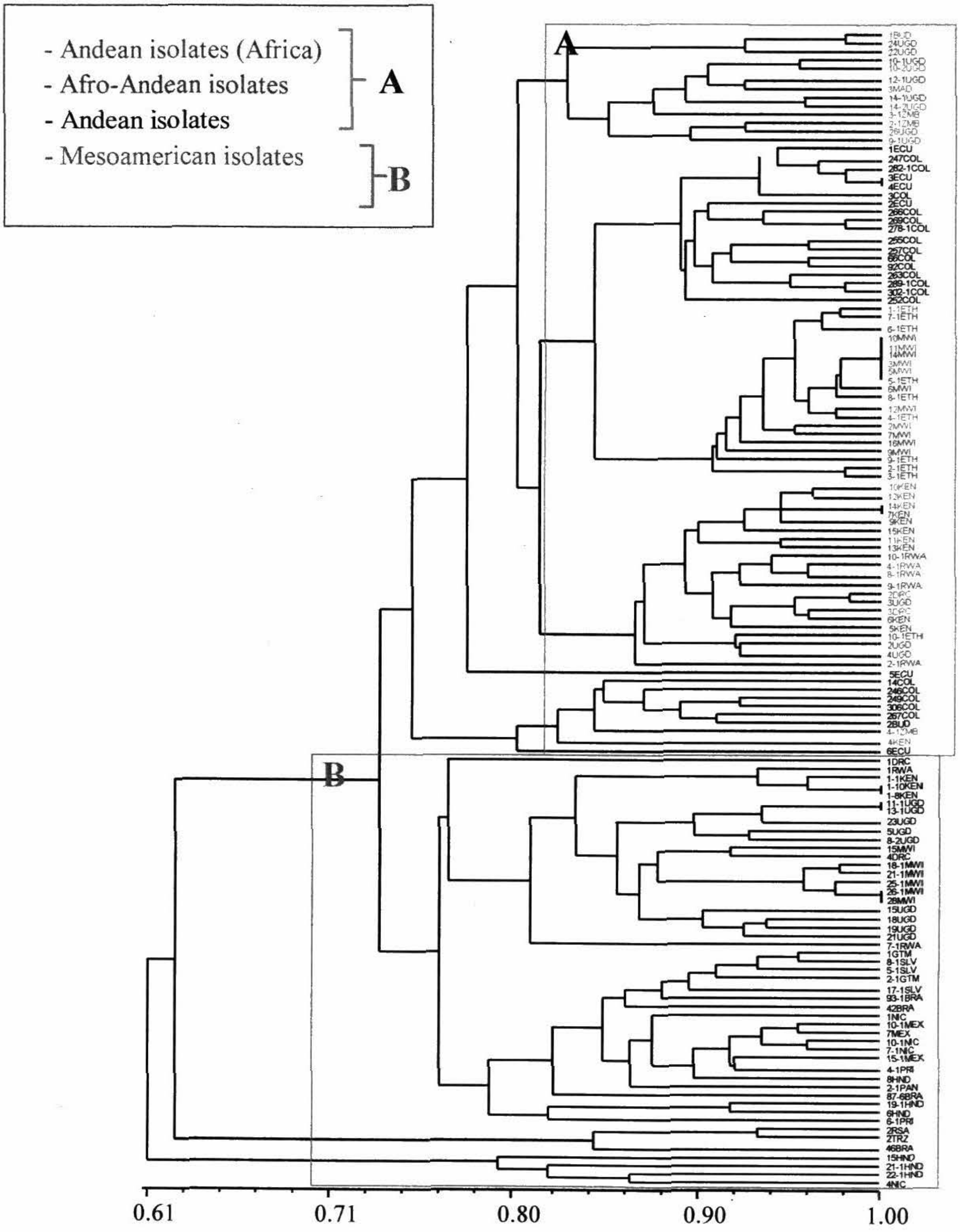


Figure 53. Dendrogram of *Phaeoisariopsis griseola* isolates based on UPGMA methods using the SAHN and TREE programs in NTSYS program using similarity coefficient calculated from combined IGS-RFLP data for five restriction enzymes. Dice's coefficient within the SimQual program of NTSYS-pc Version 1.8 (Exeter Software, Setauket, NY, USA) was used to calculate genetic similarities between isolates. (Note: acronyms are given in full at the end of this report.)

3.1.5 Characterization of whitefly-transmitted geminiviruses

Rationale: Whitefly-transmitted viruses, currently known as begomoviruses, are rapidly expanding their geographic range. Originally important only in lowland tropical regions with a prolonged dry season (particularly in Mexico, northern Central America, and the Caribbean) begomoviruses have been progressively impacting bean-producing regions in the humid tropics of the Americas. Costa Rica and Panama are good examples of regions where BGYMV has emerged in past years, despite the apparently unsuitable climatic conditions that affect the biology of the whitefly vector, *Bemisia tabaci*, in those countries. In South America, only the related species, BGMV, has been reported. This virus induces similar yellowing symptoms in common bean varieties, but it is genomically different to BGYMV.

The existence of whitefly-transmitted viruses in common bean has been known for at least two decades in Colombia. Galvez and co-workers reported on the occurrence of bean golden mosaic and bean dwarf mosaic in the municipality of El Espinal, department of Tolima[5].

Materials and methods: Golden mosaic-like symptoms have also been sporadically observed at CIAT at a very low incidence since the early 1980s. Recently, in CIAT fields, a few bean plants showing intense yellowing were tested with a monoclonal antibody that detects begomoviruses in general, confirming the presence of a whitefly-transmitted virus in the affected common bean plants. This virus was characterized at CIAT at the molecular level, as an isolate of BGYMV.

Results: The Colombian isolate had over 90% amino acid and nucleotide sequence homology with the known BGYMV isolated from Central America and the Caribbean, at the coat protein, replicase, and common region levels.

Conclusions: This is the first report of the presence of BGYMV in South America. However, it is unlikely that the virus will become economically important in the Cauca Valley of Colombia because of the marginal climatic conditions that predominate in this region for most of the year. Nevertheless, the virus may appear sporadically during the dry months of the year when *B. tabaci* populations tend to increase.

Contributors: C Muñoz (Instituto Colombiano para el desarrollo de la Ciencia y la Tecnología "Francisco José de Caldas" [COLCIENCIAS]); FJ Morales, M Castaño, CJ Alvarez

---

[5] Galvez GE, Castaño M, Belalcazar S. 1975. Presencia de los virus del mosaico dorado y del moteado clorótico del frijol en Colombia. Ascolfi Informa 1:3-4.

Progress towards achieving output milestones:

- 400 isolates of the ALS pathogen have been characterized using molecular and virulence markers and pathogen structure. This information is being used in looking for sources of resistance and developing gene deployment strategies.

- 400 isolates of *Xanthomonas campestris* pv. *phaseoli* were characterized using REP-PCR and RFLP of the 26S ribosomal genes and results show that XCP is highly distinct from XCPF. This information will contribute to the elucidation of races in this pathogen, and the development of resistant varieties.

- The "Afro-Andean" group is part of the Andean group that represents isolates resulting from point mutations in genes for virulence. This information contributes to the understanding of the mechanisms underlying emergence of virulence in *P. griseola*.

Activity 3.2 Characterizing disease and insect resistance genes

Highlights:

- 150 RILs were identified as having high levels of CBB resistance under both field and greenhouse conditions.
- 16 lines were identified that combine Andean and Mesoamerican ALS-resistance genes.
- Inheritance of ALS resistance to Andean and Mesoamerican *P. griseola* races in G 19833 and DOR 364 is different and complex being recessive for one race and dominant for another, depending on the source of resistance.
- Resistance to *Ascochyta* blight was found to be largely under additive gene control in *P. coccineus* although it tended to be recessive in *P. polyanthus*. From two to four genes appeared to control resistance.
- QTL mapping of resistance to *Thrips palmi* shows few genes controlling resistance to insect damage and reproductive adaptation under high infestation pressure.
- QTL mapping of ALS and anthracnose disease resistance shows clustering of resistance genes in the bean genome.
- Populations were developed to study the inheritance of ALS resistance.

3.2.1 Screening of a population derived from VAX 6 for resistance to common bacterial blight (*Xanthomonas campestris* pv. *phaseoli*)

Rationale: Common bacterial blight (CBB) is the most widely distributed disease of common bean that can cause yield losses of more than 40%. High levels of resistance to CBB have been introgressed from tepary bean, *P. acutifolius*, to develop a series of highly CBB-resistant *P. vulgaris* VAX lines, of which VAX 6 is especially resistant. However, its seed type and color is not desirable and resistance must be transferred to preferred grain and market class type. In order to maintain the same level of resistance as currently found in VAX 6, all the genes must be transferred to the same cultivar, and markers that are tightly linked to these genes are indispensable. Our objective was to screen RILs developed by crossing MAR 1 (CBB susceptible) x VAX 6 (CBB resistant) under field and greenhouse conditions to generate phenotypic data needed for QTL analysis and subsequent tagging of CBB resistance genes in VAX 6.

Materials and methods: VAX 6, MAR 1, and 223 RILs that were developed from a cross between VAX 6 (CBB resistant) and MAR 1 (CBB susceptible) were planted at Santander de Quilichao and inoculated three times using a local isolate of XCP. The first inoculation was done 25 days after planting and at weekly intervals thereafter. Four evaluations were taken starting 10 days after the first inoculation and using a 1 to 9 scale, where 1 represents no symptoms and 9 represents severe symptoms. Ratings of 1–3 are considered resistant, 4-6 intermediate, and >6 susceptible response. Similarly, the same RILs were screened in the greenhouse with the same XCP strain and using the same evaluation scale.

Results and discussion: To select the best XCP strain to use in field and greenhouse evaluations, the parents, MAR 1 and VAX 6, were screened with isolates collected in Santander de Quilichao. No differences were obtained in the levels of infection, but the *fuscans* variant of XCP consistently gave high disease ratings. Therefore XCP isolates were selected that are normally used for all inoculations in Santander de Quilichao. Most of the MAR 1 x VAX 6 RILS (76%) were resistant to XCP under field conditions, 21% were intermediate, and 3% susceptible (Figure 54). As expected, MAR 1 had a susceptible reaction (rating 7) while VAX 6 had a resistant reaction (rating 2). Under greenhouse conditions 78% of the RILS were resistant, 20% intermediate, and 2% susceptible (Figure 55). The field and greenhouse results were highly correlated (r = 0.94) showing the high levels of resistance that were introgressed into VAX 6. We are re-evaluating the RILS in the field with the same isolate, and making greenhouse evaluations with the *fuscans* variant of XCP. In addition, the parents are being screened with RAPD and microsatellite markers in order to identify polymorphic markers that can be used to screen the RILS to identify QTLs linked to resistance genes.

Contributors: G Mahuku, C Jara, H Terán, S Beebe

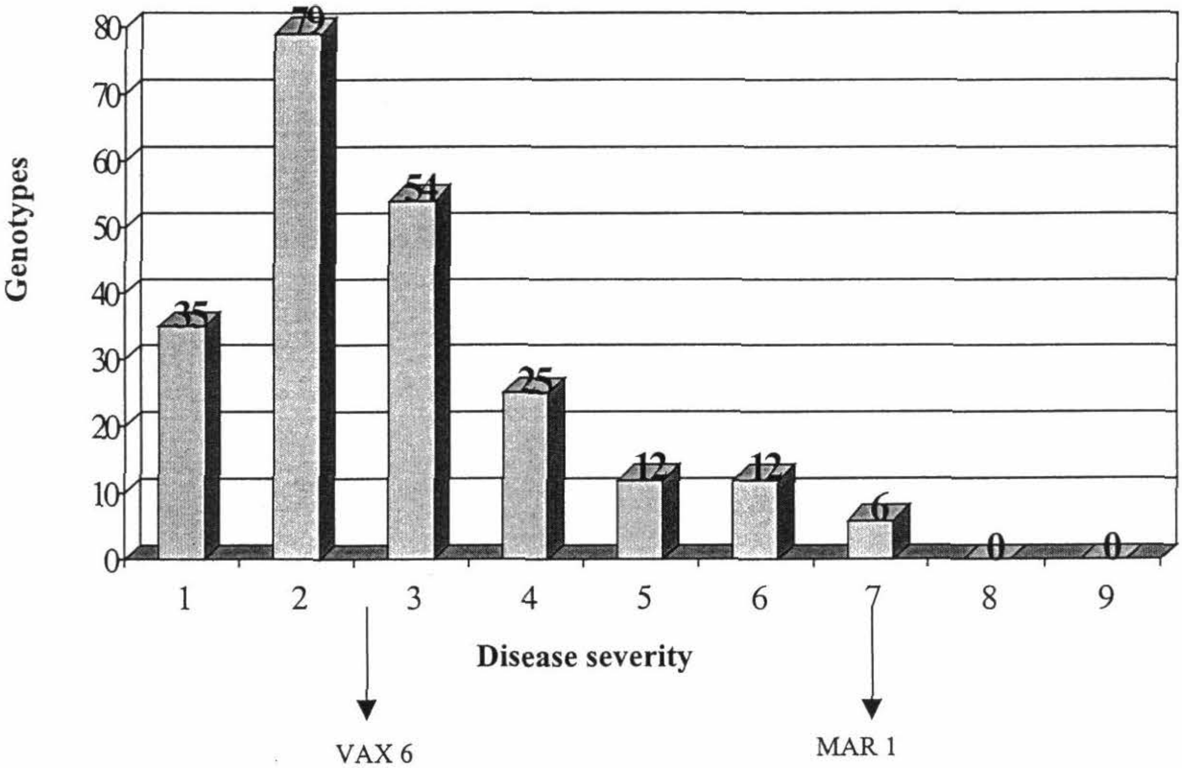


Figure 54. Response of 223 recombinant inbred lines of VAX 6 x MAR 1 to inoculation with *Xanthomonas campestris* pv. *phaseoli* under field conditions. Disease severity ratings of 1–3 are considered resistant, 4-6 intermediate, and >6 a susceptible response.

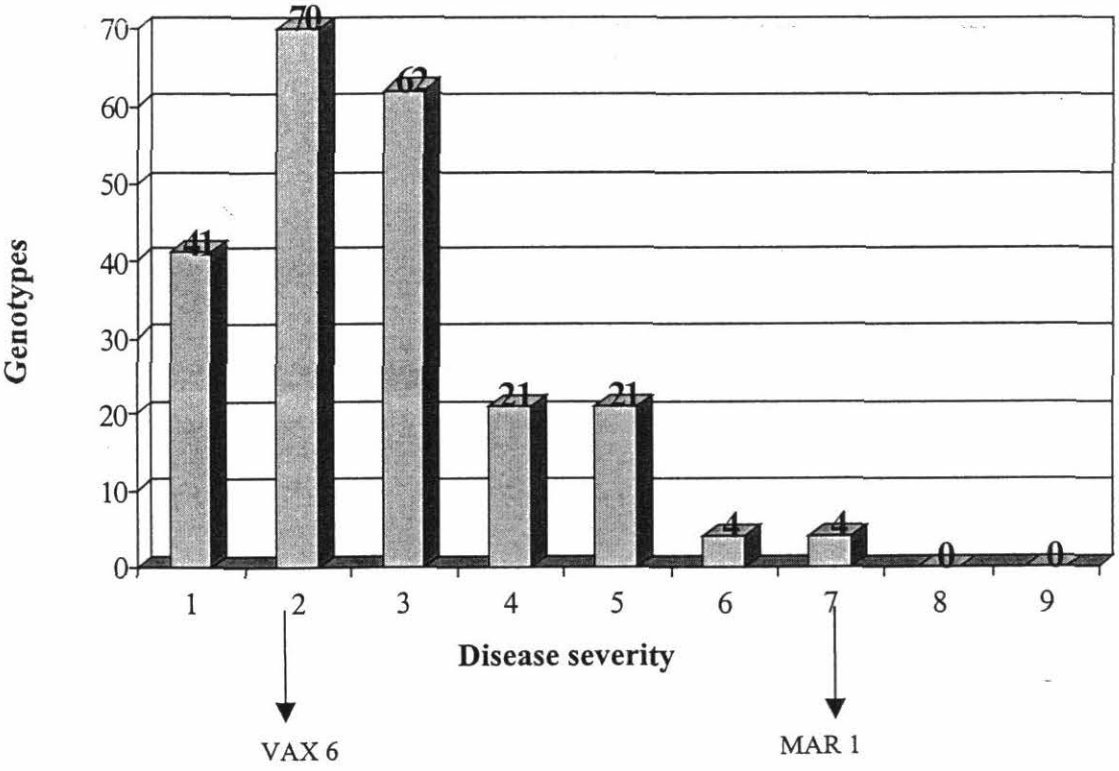


Figure 55. Response of 223 recombinant inbred lines of VAX 6 x MAR 1 to inoculation with *Xanthomonas campestris* pv. *phaseoli* under greenhouse conditions. Disease severity ratings of 1–3 are considered resistant, 4-6 intermediate, and >6 a susceptible response.

3.2.2 Inheritance of angular leaf spot resistance in the population VAX 6 x MAR 1

Rationale: Previous studies have shown that the variety MAR 1 is resistant to several ALS races including race 31-55, while the variety VAX 6 is not. In addition, MAR 1 has been shown to yield moderately well under low soil fertility, especially low P, and yields reasonably well under drought conditions although it has low levels of tolerance to *Macrophomina phaseolina*. We screened RILs that were developed by crossing MAR 1 (ALS resistant, but susceptible to CBB) and VAX 6 (susceptible to ALS, but highly resistant to CBB) for resistance to race 31-55 of ALS. These RILs present a very interesting population from which materials with resistance to multiple constraints (e.g., CBB, ALS, and low soil fertility) can be identified. This study was initiated to look at the nature and inheritance of resistance to ALS that is in MAR 1, develop markers that are tightly linked to the resistance genes, and identify materials that are resistant both to CBB and ALS.

Materials and methods: The parents, VAX 6 and MAR 1, and 233 RILS, which were derived from a cross between VAX 6 (ALS susceptible) and MAR 1 (ALS resistant), were planted at Santander de Quilichao and inoculated three times using the ALS race 31-55 local. The first inoculation was done 25 days after planting and further inoculations at weekly intervals thereafter. Evaluations for disease severity were assessed four times, starting 2 weeks after inoculation, using a CIAT 1–9 scale, where 1 represents no visible symptoms and 9 represents severe symptoms and disease expression. Plants that had a rating of 3 or less were considered resistant, 4-6 intermediate, and a rating greater than 6, susceptible.

Results and discussion: Figure 56 shows the response of the 233 RILs to inoculation with *P. griseola*. Preliminary results showed that 40% of the plants were resistant, while 60% had a susceptible response. These materials will be screened again under field and greenhouse conditions using the same ALS race. We are generating molecular profiles of these materials for QTL analysis and identification of markers for MAS breeding.

Conclusions: Pending completion of study.

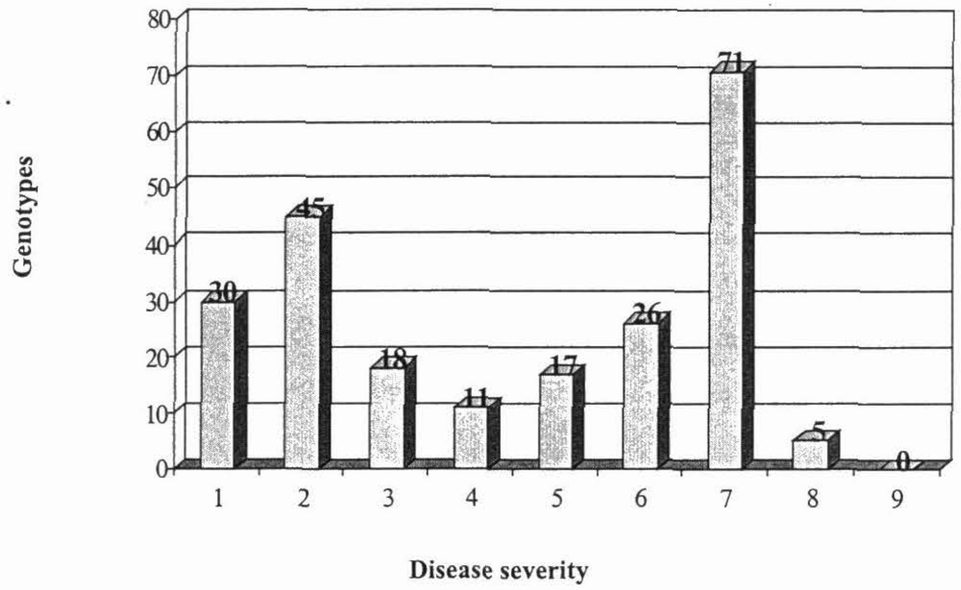


Figure 56. Response of 233 recombinant inbred lines derived from crossing MAR 1 x VAX 6 following inoculation with *Phaeoisariopsis griseola* under field conditions. Plants that had a rating of 3 or less were considered resistant, 4-6 intermediate, and a rating greater than 6, susceptible.

Contributors: G Mahuku, C Jara

3.2.3 Inheritance of angular leaf spot resistance in a population derived from DOR 364 x G 19833

Rationale: Pathogen characterization studies have shown that all *P. griseola* races can be separated into two major groups that correspond to the common bean gene pools. A unique opportunity exists of combining Andean and Mesoamerican genes to have broad spectrum and durable resistance to this pathogen. However, a clear understanding of the nature and inheritance of the identified sources of resistance (resistance genes) is necessary to fully take advantage of this host pathogen co-evolution to manage ALS of common bean. This is an ongoing study to understand the nature of inheritance of ALS resistance in common bean, with the ultimate objective of developing molecular markers that can be used to aid in transferring this resistance to well-adapted, market-class type bean.

Materials and methods: Eighty-seven RILs derived from a cross of DOR 364 (Mesoamerican variety) x G 19833 (Andean variety) were screened under greenhouse conditions using four *P. griseola* isolates. Two Andean and two Mesoamerican isolates were used in this study. With regard to these four isolates, DOR 364 is resistant to the Andean races of *P. griseola*, but highly susceptible to Mesoamerican races, while

G 19833 is highly resistant to the Mesoamerican races that were used, but susceptible to Andean races. The same isolates were used to screen F_1 (100 plants) and F_2 (100 plants) derived from DOR 364 x G 19833 crosses. Evaluations for disease severity were assessed using a CIAT 1–9 scale, where 1 represents no visible symptoms and 9 = severe symptoms and disease expression. Ratings of 1 to 3 were considered resistant and ratings >4 as susceptible.

Results and discussion: Sixteen of the RILS were resistant to the four isolates representing Mesoamerican and Andean races of *P. griseola* (Figure 57). These materials represent interesting sources of ALS resistance that combine Andean and Mesoamerican resistance genes that have been pyramided in the same material. These materials will be screened with more isolates from both Andean and Mesoamerican groups to establish the extent of activity and durability of this resistance. Table 38 shows the distributions of resistance and susceptibility following inoculation with Andean and Mesoamerican isolates of *P. griseola*, while Figure 58 shows the response distribution of F_1 populations following inoculation with Mesoamerican races of *P. griseola*. Preliminary analysis of the results is indicative of two genes conferring resistance to *P. griseola* acting in a dominant manner to Andean races, and in a recessive manner to Mesoamerican races. However, more information will be obtained following QTL analysis and evaluation of backcrosses to DOR 364 and G 19833.

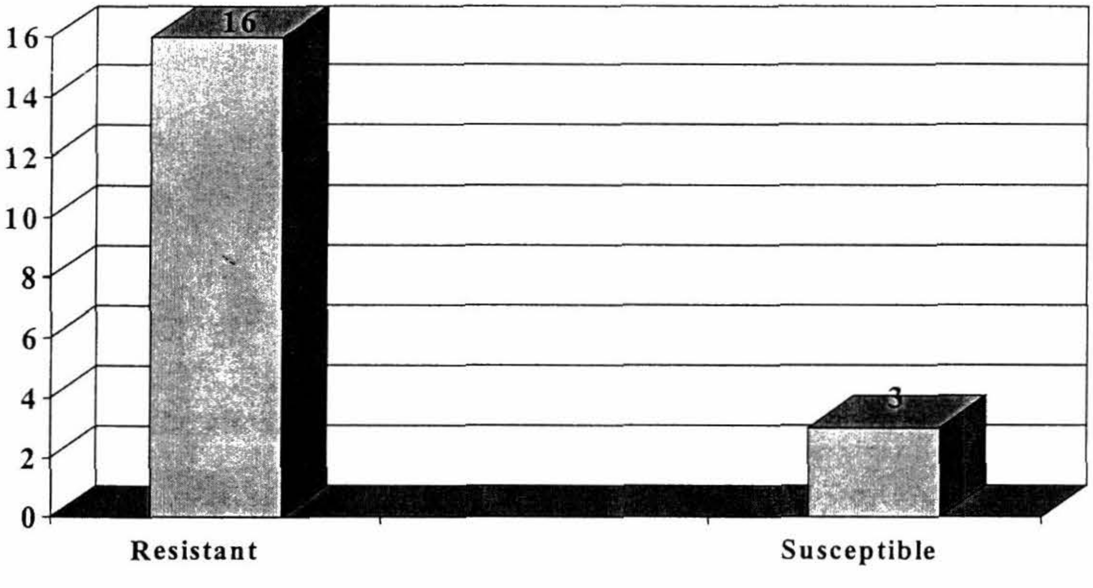


Figure 57. Proportion of DOR 364 x G 19833 recombinant inbred lines that were resistant and susceptible to Andean and Mesoamerican races of *Phaeoisariopsis griseola*.

Table 38. Response of DOR 364 x G 19833 recombinant inbred lines (RILs) and F_1 and F_2 families to inoculation with Andean and Mesoamerican races of *Phaeoisariopsis griseola*.

Isolate	Family	Materials evaluated	Resistant (R)	Susceptible (S)	Ratio	Expected ratio		
						1 gene	2 genes	3 genes
Andean	F_1	100	100	0	1R : 0S			
	F_2	100	87	13	6.7R : 1S	3R : 1S	15R : 1S	63R : 1S
	RILs	87	73	14	5.2R : 1S	1R : 1S	3R : 1S	7R : 1S
Mesoamerican	F_1	100	16	84	1R : 5.3S			
	F_2	100	14	86	1R : 6S	1R : 3S	1R : 15S	1R : 63S
	RILs	87	22	65	1R : 3S	1R : 1S	1R : 3S	1R : 7S

Similar results were observed in the evaluations of 100 plants each of the F_1 and F_2 populations. All F_1 materials were resistant to Andean races of *P. griseola*, while in the F_2 population, 13 were susceptible and 87 were resistant, thus indicating that resistance to this group of isolates might be controlled by two dominant genes (Table 38). F_1 plants that were inoculated with Mesoamerican isolates gave a 1:1 ratio of resistance to susceptible plants (Figure 58). However, in the F_2 population, 14 plants were resistant and 86 were susceptible (Table 38). These results show that recessive genes are conditioning resistance to this race.

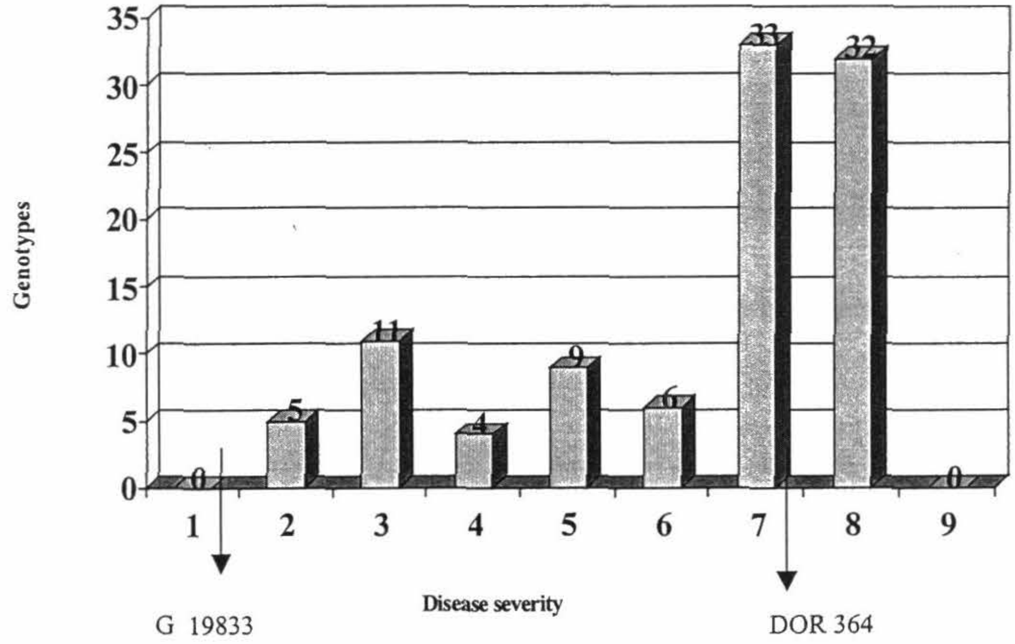


Figure 58. Response of DOR 364 x G 19833 F_1 populations inoculated with Mesoamerican races of *Phaeoisariopsis griseola*. Ratings of 1 to 3 were considered resistant and ratings >4 as susceptible.

Conclusions: The preliminary results reported here show the complex nature of inheritance of *P. griseola* resistance in the two genotypes under study. Resistance to the two major groups of *P. griseola* might be inherited differently, showing recessive genes for Mesoamerican isolates and dominant genes for Andean races. Preliminary analysis shows that at least two genes are conditioning resistance. In addition, there might be minor genes that are modifying the effect of the major genes in a race-specific manner. More information will be obtained following evaluations of the backcrosses to DOR 364 and G 19833, F_3 population, and QTL analysis of molecular profiles of the RILs.

Contributors: C Jara, G Mahuku, H Terán, S Beebe

3.2.4 Transfer of angular leaf spot resistance genes from Mesoamerican climbers to bush beans

Rationale: High levels of resistance to the most virulent and aggressive isolate of *P. griseola* (race 63-63) have been found in some materials from the highlands of Guatemala. Because of adaptation problems, this resistance has to be transferred to adaptable market-class type beans. In addition, the activity of these genes and the number and nature of this resistance has to be elucidated in order to take full advantage in using this resistance to manage ALS. This study is being conducted to transfer resistance genes from Mesoamerican climbers to Mesoamerican bush beans, to study the nature and inheritance of resistance in these climbers, and to develop populations for subsequent tagging of the genes with the broadest activity to facilitate transfer into other market-class type beans.

Materials and methods: Crosses were initiated to transfer ALS resistance in climbers (G 10474, G 10909, G 4691, G 18224, G 3991, and G 14301) into Mesoamerican bush types (G 4691, G 3991, and G 18224). In addition, crosses were made between these climbers and Sprite (a universal susceptible) to facilitate studying the nature and inheritance of ALS resistance in these materials. F_1 populations have been made and are currently being advanced to F_2 as well as backcrossed to resistant and susceptible (Sprite) parents.

Results and discussion: Results are pending evaluations and analysis of populations.

Conclusion: This study is in progress and results are pending evaluation of the generated populations.

Contributors: S Beebe, H Terán, C Jara, G Mahuku

3.2.5 Nature and inheritance of resistance in angular leaf spot differentials

Rationale: Because very little is known about the number of genes conditioning resistance in our differential materials, this has limited our ability to use virulence data to make inferences about our *P. griseola* populations. Knowledge of the resistance genes would facilitate precise definition of *P. griseola* races, their distribution, and relevance, and help in deploying resistant genes in ways that prolong their durability. Also, this would help in identifying the genes to combine for pyramiding in order to achieve long-lasting resistance.

Materials and methods: Crosses were made between PAN 72 and all the Mesoamerican differential varieties, and A 36 and all Andean differential varieties. F_1, F_2, and backcrosses to both the resistance and susceptible sources were recently completed. Host pathogen interactions are pending for this study.

Results and discussion: Results are pending evaluations of populations.

Contributors: G Mahuku, MW Blair, S Beebe

3.2.6 Inheritance of *Ascochyta* resistance

Rationale: Although *Ascochyta* blight is an important limitation in bean production in the moist highlands of the Andes and Africa, no good level of resistance has existed within the primary common bean gene pool until now, except for the variety ICTA Hunapú, which only recently was recognized as resistant. With the prospects of better sources of resistance, it is of interest to understand better the genetic control of this trait.

Materials and methods: Because the best resistance is found in the secondary gene pool, in *Phaseolus polyanthus* (PP) and in *P. coccineus* (PC), it was decided to study inheritance in resistant x susceptible crosses within and between these two species. A highly susceptible interspecific progeny with *P. coccineus* phenotype was identified and eventually coded as ASC 76. The F_1 generations of three crosses of ASC 7 x *P. coccineus* were evaluated in the field for their reaction to *Ascochyta* in seasons 1999B and 2000A, and the F_2 generation in the 2000A season (Table 39). Plants of the F_1 generation were replicated over time. This was possible because the plants were maintained alive between seasons by taking cuttings or by pruning old plants and taking data on regrowth. The F_2 generation was represented by the harvest of four F_1 plants of each cross, and the progeny of each F_1 plant was maintained as a separate subpopulation of 30 to 40 plants each. This permitted observations on possible segregation in the *P. coccineus* parent for resistance genes.

In the course of field evaluations, it was realized that a cross created for studying the resistance to BGYMV (G 35172 x G 35337, DRIN 13229) was also contrasting for resistance to *Ascochyta*. G 35172 is PC and G 35337 is PP. F_2 plants were being increased in the screenhouse to the F_3 generation, thus 144 F_2 plants were transplanted to the field and inoculated with *Ascochyta* for evaluation in the 1999B season. For this population, no F_1 plants were available, but as in the case of the other populations, harvests from individual F_1 plants were managed as subpopulations to observe possible segregation from the parents.

Statistical analysis was carried out as per Mathers and Jinks (1977)[6] for estimating gene number controlling a quantitative trait, according to the formula:

$$k \text{ (gene number)} = ((P2 - P1)/2)^2 / \sigma^2$$

Results: All resistant parents of the three ASC 76 crosses rated about 3 on a 9-point scale, and the susceptible ASC 76 rated 6.1 (Table 39). Disease reaction in F_1 plants was intermediate between those of the resistant and susceptible parents in every case. In two crosses, the F_1 rating was very close to the mid-parent value (4.5) that would be expected in the case of additive gene action. The exception was the F_1 of ASC 76 x G 35509, which presented a reaction more similar to the resistant parent. In other words, resistance in this F_1 behaved as if it were slightly dominant.

Table 39. Means and ranges of *Ascochyta* reaction in F_1 hybrids evaluated in inoculated field trials in Popayán 1999B – 2000A, and F_2 populations in 1999B.

	F_1 1999B		F_1 2000A		1999B 2000A	F_2 1999B	
	Range	Mean	Range	Mean	Mean F_1	Range	Mean
ASC 76 x G 35509	3 - 7	3.8	2 – 7	3.7	3.7	2.8 - 6.8	4.7
ASC 76 x G 35358	2 - 7	4.4	2 – 7	4.0	4.2	2.3 - 7.5	5.1
ASC 76 x G 35369	2 - 6	4.9	2 – 8	4.3	4.6	2.0 – 7.0	4.4
Parents:							
ASC 76	4 - 8	6.1	4 – 8	6.0	6.1		
G 35509	2 - 4	3.1	1 – 6	2.8	3.0		
G 35358	2 - 5	3.5	1 – 5	2.7	3.1		
G 35369	2 - 5	3.2	2 – 5	2.7	3.0		
Checks:							
G 35182	2 - 3	2.0	1 – 2	1.7	2.0		
ICTA Hunapu	4 - 6	4.4	3 – 6	4.1	4.2		
G 12727	5 - 7	6.0	5 – 8	6.4	6.2		

In the F_2 of the three *P. coccineus* crosses (Table 39) resistance continued to behave as if it were generally additive; even in the population of ASC 76 x G 35509 where some evidence of dominance was observed in F_1. Thus, the general conclusion of additive gene action is maintained.

---

[6] Mather K, Jinks JL. 1977. Biometrical genetics: the study of continuous variation. Cornell University Press, Ithaca, NY. 382 p.

The population of G 35172 x G 35337, however, presented a slightly different pattern. Because G 35337 is a *polyanthus*, it has higher resistance (rating of 2.1) than the *coccineus* accessions used for the *Ascochyta* inheritance studies. G 35172 (*coccineus*) rated 6.3. The mid-parent of the two would be about 4.2, but the three F_2 subpopulations all presented symptoms of 5.3 to 5.4, or well above the mid-parent and at the upper extreme of the F_2 populations involving *coccineus*. It appears that the resistance of *polyanthus* may tend to be recessive.

Because all four populations consisted of subpopulations derived from individual F_1 plants, each subpopulation was evaluated for mean and variance. In the populations involving a *coccineus* source crossed to ASC 76, those with G 35509 and with G 35358 presented uniform variances, but means were distinct. Thus, one subpopulation was eliminated from the analysis of each population and the remainder was evaluated jointly. In two of the populations, the estimate suggested that two genes might be segregating, while in the third population, three or four genes might differentiate the parents. In the case of the population G 35172 x G 35337, the variances were distinct; thus two subpopulations were analyzed jointly and the third separately. Here also, the variances suggested that two genes might be segregating in the analysis of two subpopulations, and only one gene in the third subpopulation. It is in fact feasible that a single population gives different results, because the parents are possibly heterozygous and segregating, such that subpopulations are distinct.

These estimates are in any case approximate, because the analysis carries with it several assumptions that are of questionable validity in virtually any genetic analysis, especially that all gene effects are equal. Nonetheless, the results were fairly uniform in concluding that resistance is controlled by a limited number of genes, but in most cases more than one gene. For practical breeding purposes, this information is useful and is about as detailed as most genetic information often is.

Conclusions: Results of the genetic studies suggest that the expression of resistance genes in general tends to be additive, although with different parents, resistance could express as slightly dominant in some cases and slightly recessive in others, especially with the *polyanthus* parent that was used. Gene number is probably in the range of 2 to 4. Given the progress in selecting for resistance in the breeding populations and an apparently acceptable heritability, the conclusion of additive gene action would tend also to be confirmed through the breeding efforts.

Contributors: S Beebe, C Cajiao, G Mahuku (IP-1); MC Duque (SB-2)

3.2.7 Quantitative trait locus mapping and heritability of resistance to *Thrips palmi* in common bean

A better understanding of the genetics of insect and disease resistance will lead to improved management of these pests. Basic to this endeavor is a thorough analysis of the QTL that provide pest resistance and how they are organized at the genome level. An appreciation of gene organization will allow plant breeders to use MAS more effectively to pyramid multiple resistance factors into bean varieties with commercial seed types.

Rationale: *Thrips palmi* is a damaging insect pest of common bean and other dicotyledonous crops that was introduced from Asia (Java, Indonesia) into the Americas during the last decade. Starting in the Caribbean, (Cuba, Dominican Republic, Haiti, and Puerto Rico) the species spread rapidly into the United States and northern South America (Brazil, Colombia, Ecuador, and Venezuela). The greatest damage inflicted on common bean production in Colombia is seen in climbing bean varieties that are grown for the fresh market (including snap beans and Cargamanto dry beans). Sequential plantings, common in the production of snap beans, is highly conducive to heavy infestations of thrips and whiteflies, which are synergistic in the damage that they inflict. Misuse of insecticides also can lead to resurgence in thrips populations. The first studies in integrated pest management (IPM) of thrips were conducted recently at CIAT (see IP-1 Project Annual Report). BAT 881 has been a bean genotype with the best thrips resistance. The objective of this research was to study the inheritance and location of QTL controlling the resistance derived from this variety in a RIL population derived from BAT 881 x G 21212.

Materials and methods: The BAT 881 x G 21212 population, consisting of 139 RILs, was evaluated over two seasons at a field site in Pradera, Valle, Colombia. In the first season (semester 1999A-April), the population was planted as an unreplicated trial; while in the second season (semester 1999B-July) it was planted in an RCBD with three repetitions. The parents of the population were included in both seasons. The bean genotypes PVA 773 and RAZ 136 were used as check varieties in the first season, while PVA 773 was used alone in the second season. Infestation by *Thrips palmi* was increased with an initial planting adjacent to a heavily affected snap bean field. The lines were evaluated on a per row basis using a 1-9 scale according to the CIAT standard evaluation (1 = resistant. 9 = susceptible). DNA was extracted from 95 of the RILs by a standard miniprep procedure. One hundred and fifty one RAPD markers were run on these individuals and the segregation information was analyzed to construct a genetic map using the software program MAPMAKER. Quantitative trait loci were identified through single-point regression analysis of the phenotypic data onto the marker genotypes using the software program qGENE.

Results and discussion: The population of RILs was normally distributed for thrips resistance, suggesting that the inheritance of resistance was truly quantitative (Figure 59). Some of the RILs outperformed either parent suggesting transgressive segregation had occurred, however the best lines were different in each season. BAT 881 was the more resistant parent for both resistance scores (damage score = 6.0 in 1999A and 7.5 in

1995B; reproductive adaptation = 7.0 in 1999A and 7.1 in 1999B). However, G 21212 was similar for its reproductive adaptation (9.0 in 1999A and 7.6 in 1999B), but inferior for its susceptibility to thrips damage (8.0 in 1999A and 8.2 in 1999B). Overall the correlation between seasons was moderate ($r = 0.277$ for damage score and $r = 0.371$ for reproductive adaptation), while the correlation between the two resistance scores within a season were high ($r = 0.873$ for 1999A and $r = 0.751$ for 1999B).

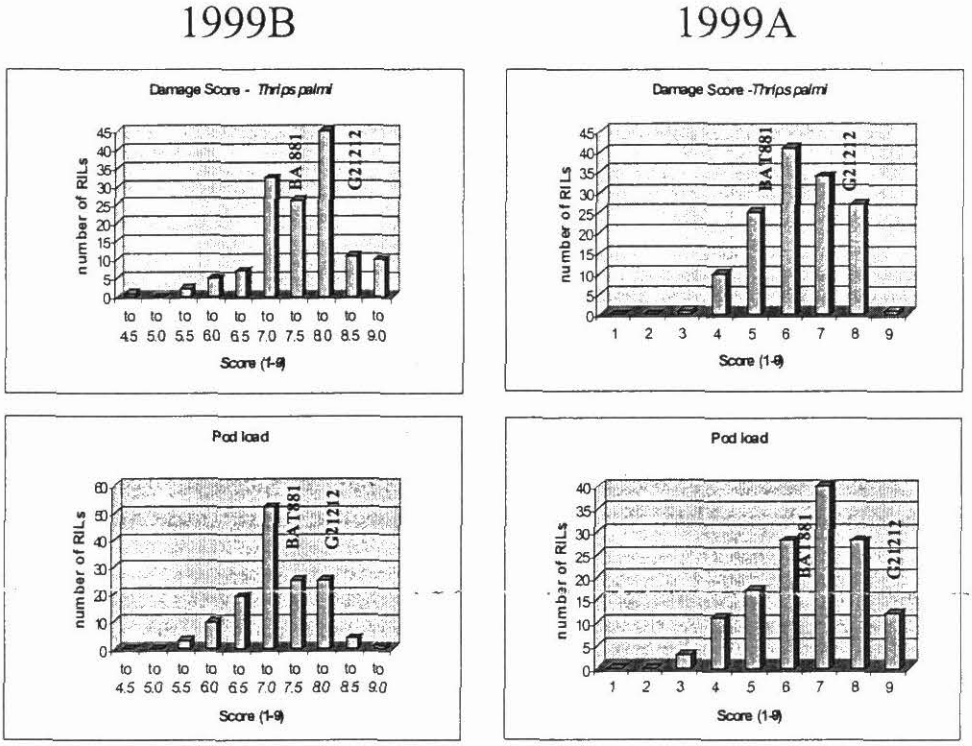


Figure 59. Population distribution for damage caused by *Thrips palmi* and pod load under heavy infestation in an unreplicated field trial conducted in Pradera, Valle, during two seasons (April - 1999A and July - 1999B).

Positive QTLs were found for thrips resistance in both seasons and were associated with both parents. However, it appeared that G 21212 was the principal source of QTLs for resistance to thrips damage, while both BAT 881 and G 21212 were the sources of QTLs for reproductive adaptation under thrips infestation. This varied from 1999A, when a mix of both genotypes provided QTLs for reproductive adaptation, to 1999B, when G 21212 provided all but one of the positive QTLs. An additional single QTL from BAT 881 provided resistance to damage in 1999B, but was unlinked to other markers. The existence of additive QTLs from both parents may explain why transgressive segregation was observed in some of the individual progeny.

Because the trial was replicated in 1999B, QTLs tended to be more highly significant for the 1999B data (up to F-value of 11.2) than for 1999A (maximum F-value of 6.5). In addition, in 1999B the inheritance of resistance appeared to be fairly simple: only one QTL each could be identified for resistance to damage and reproductive adaptation. The QTL for resistance to damage consisted of six significant markers on a single linkage group and was associated with the G 21212 allele. The QTL for reproductive adaptation was found on a different linkage group and was associated with the BAT 881 allele. This QTL was also observed in the data from the first season, but at a slightly different location along the linkage group.

Broad-sense heritabilities of thrips resistance were estimated on an entry mean basis for the replicated data from the second season. Heritabilities were about 61% for the damage score and 44% for the reproductive adaptation score. The corresponding estimates of narrow sense heritabilities would be similar given that the genotypes were all F_6-derived RILs in which most of the genetic variance is caused by additive rather than dominant gene action.

Conclusions and future plans: The inheritance of thrips resistance was not as complex as might have been expected and the existence of major QTLs will allow thrips resistance to be selected in segregating populations. The heritabilities estimated were relatively high, indicating that the trait can be selected without extensive genotype replication. However, the variability in QTLs detected from one season to the next indicates that GxE interactions may be important. Another population derived from the cross BAT 477 x DOR 364 will be analyzed for thrips resistance to confirm the magnitude of the heritability estimates and to identify whether the QTLs are common across both the BAT 881 x G 21212 and BAT 477 x DOR 364 populations. The four genotypes used to produce these two populations are from the same race of Mesoamerican beans, therefore it will be interesting to see how well the genes for thrips resistance identified in these studies can be transferred into other gene pools. We will attempt to pinpoint the exact location of the QTLs identified so far and may develop new SCAR markers for the most important QTLs. In addition, we will test the validity of microsatellite or SCAR markers for selection of thrips resistance.

Contributors: MW Blair, C Cardona, S Beebe, JM Bueno

3.2.8 Quantitative trait locus mapping of angular leaf spot and anthracnose disease resistance in the common bean cross DOR 364 x G 19833

Rationale: All together, several dozen major resistance genes have been tagged in common bean, mostly through bulked segregant or simple genetic linkage analysis with either RAPDs or SCARs. Reliable markers have been developed for the well-known genes for resistance to BCMV (*I*, *bc-3*, *bc-12*), BGMV (*bgm-1*), rust (*Ur-3*, *Ur-5*, *Ur-11*), and anthracnose (*Co-4*^{2} and *Co-2*). Most of the resistance genes studied have been simply inherited. Relatively fewer studies have looked at the QTLs controlling partial resistance to diseases. The objective of this research was to identify QTLs for resistance to two pathogens of common beans, *Colletotrichum lindemuthianum*, the causal agent of anthracnose, and *Phaeoisariopsis griseola*, the causal agent of ALS, in a well-characterized, genetic mapping population based on the cross DOR 364 x G 19833. Recombinant inbred lines from this population have been a highly useful resource for field and greenhouse studies because they are a genetically stable set of advanced lines that can be tested in replicated trials with a series of disease isolates.

Materials and methods: The 87 RILs of the DOR 364 x G 19833 population were tested with six isolates each of ALS (PG3COL, PG260COL, PGCRI, PG3ELS, PG14HND, and PG12MEX), and anthracnose (CL5DOM, CL20COL, CL43COL, CL77CRI, CL235COL, and CL289COL) by artificial inoculation in the greenhouse. Disease evaluation was done qualitatively by treating disease reaction as a binary trait; and assigning the RILs into a susceptible or resistant category. For six of the disease isolates (PG260COL, PG3ELS, PG14HND, CL20COL, CL43COL, and CL77CRI) data were also taken quantitatively and the individual plants were scored for resistance on a 1-9 scale according to the CIAT standard evaluation (where 1 = resistant and 9 = susceptible). The genetic map for the population consisted of 417 markers (AFLPs, microsatellites, RAPDs, and RFLPs) and was constructed using the software program MAPMAKER. The microsatellite markers were placed at a minimum LOD score of 2.5, while the rest of the markers had a minimum LOD score of 2.0. The QTL were identified using the software program qGENE by: (1) single-marker contingency analysis using chi-square tests comparing the genotypic classes to the categorical data from the qualitative disease evaluation; and (2) single-point regression analysis of the quantitative disease score data onto the marker genotypes. A probability threshold of $P = 0.0001$ was used for the individual marker tests to reduce overall type I error rate to $P = 0.05$, based on the full set of genetic markers used in the experiment.

Results: For anthracnose, significant QTLs were found on chromosome 3, 4, 10, and 11 (Figure 60). Three isolates (CL77CRI, CL20COL, and CL5DOM) uncovered the same resistance QTL on chromosome 3. One of these isolates (CL5DOM) also uncovered a QTL on chromosome 4. Another isolate (CL235COL) uncovered a second QTL for resistance on chromosome 4 proximal to the previous QTL. A fifth isolate (CL43COL) uncovered two QTLs, one on chromosome 10 and another on chromosome 11. No significant QTLs were detected using the isolate CL289COL.

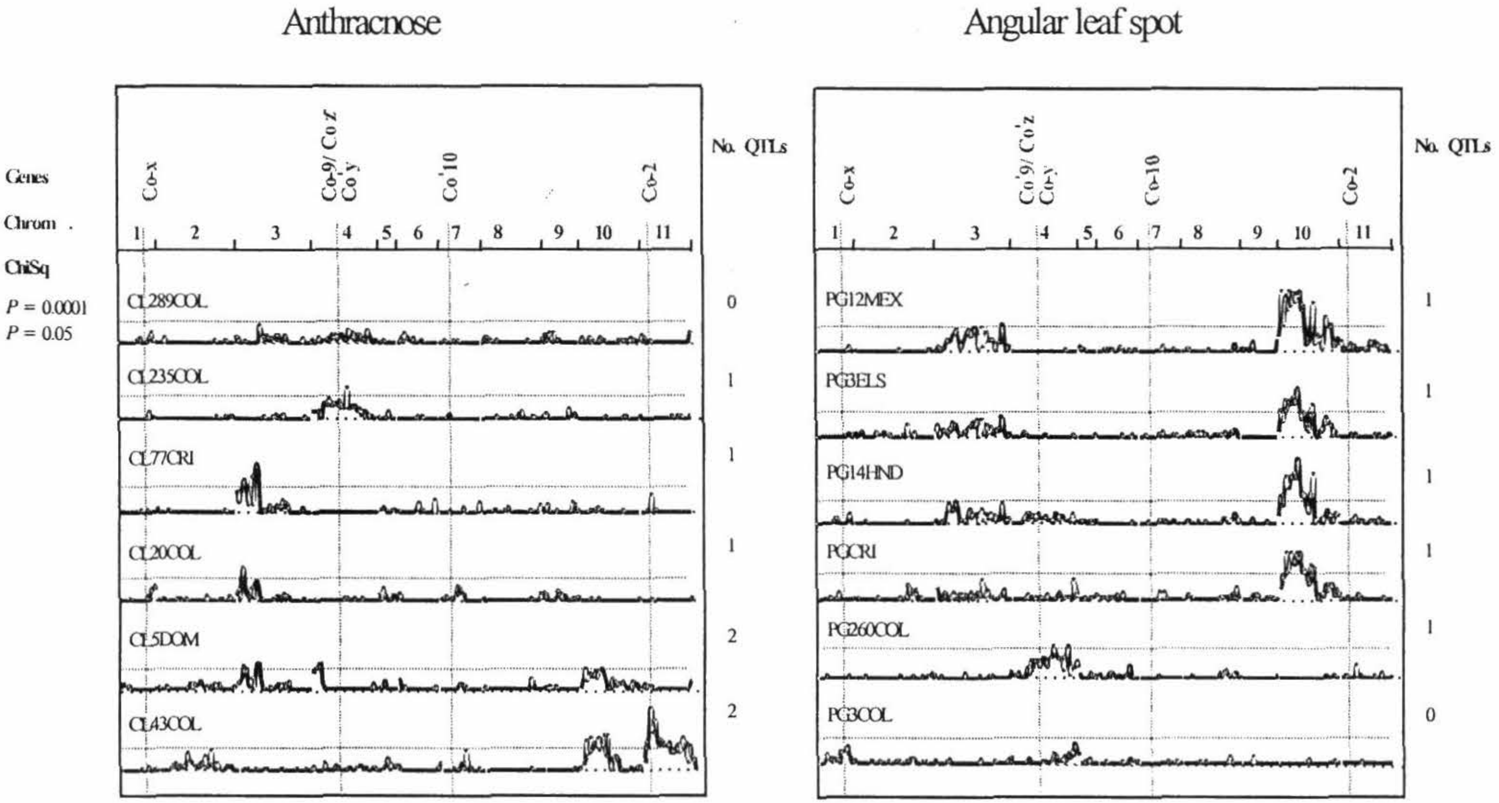


Figure 60. Location of quantitative trait loci (QTLs) for disease resistance identified in the population of DOR 364 x G 19833.

The QTLs on chromosome 4 coincided in location with known resistance factors for anthracnose (*Co-8*, *Co-y*, and *Co-z* cluster) and BGMV resistance. The QTL on chromosome 11 was probably a previously undescribed allele of the *Are* gene (renamed *Co-2*). The resistance QTLs on chromosomes 3 and 10 do not coincide with any previously mapped resistance genes in common bean, but may be allelic to the anthracnose genes that have been characterized and tagged, but not mapped (*Co-1*, *Co-4*, *Co-5*, and *Co-6*). Alternatively they may be allelic to the QTLs detected in the BAT 93 x JaloEEP 558 population studied by Geffroy et al.[7].

For ALS, significant QTLs were found on chromosomes 3, 4, and 10. Four isolates (PG12MEX, PG3ELS, PG14HND, and PGCRI) uncovered QTLs on chromosome 10 in the vicinity of the QTL for anthracnose described above. The isolate PG12MEX also detected a QTL at one end of chromosome 3. All along chromosome 3, minor genes appeared to be proportioning resistance against several isolates, but their effects were less significant. The isolate PG260COL uncovered a significant QTL on chromosome 4, while the isolate PG3COL uncovered no QTLs for resistance. The QTLs uncovered in this study may be alleles of the two ALS resistance genes, *Phg-1*, and *Phg-2*, which have been tagged with SCARs, but have not been localized on the genetic map of common bean.

Analysis of the quantitative data showed the same QTLs as those of the qualitative evaluation described above. For all the QTLs identified in this study, the positive effect was always from alleles of the resistant parent G 19833, not from those of the susceptible parent DOR 364. In contrast, a similar study showed that the DOR 364 provided resistance QTLs for BGMV.

Conclusions and future plans: The inheritance of resistance to both anthracnose and ALS appeared to be surprisingly simple in the DOR 364 x G 19833 population. A maximum of two chromosomes were involved in resistance to any single isolate and on the average only one significant QTL could be identified per inoculation. Quantum trait loci for disease resistance were found in five basic locations in the genome, both loci in areas that are already known to contain resistance genes and in areas where no resistance genes have been identified previously. A common QTL was found for resistance to both diseases. At resistance gene clusters, resistance genes are often found that function against multiple diseases and minor genes are found associated with major genes. Therefore, it is not surprising that the QTLs for resistance to the two diseases provided by G 19833 are clustered together with known resistance genes or with each other.

Contributors: MW Blair, S Beebe, C Jara, G Mahuku (IP-1); F Pedraza (SB-2)

---

[7] Geffroy V, Sévignac M, De Oliveira JCF, Fouilloux G, Skroch P, Thoquet P, Gepts P, Langin T, Dron M. 2000. Inheritance of partial resistance against *Colletotrichum lindemuthianum* in *Phaseolus vulgaris* and co-localization of quantum trait loci with genes involved in specific resistance. Mol. Plant Microbe Interact 13: 287-296.

3.2.9 Populations developed for pyramiding and analyzing angular leaf spot resistance genes in common bean

Rationale: Few of the genes involved in resistance to the ALS pathogen, *Phaeoisariopsis griseola,* have been studied systematically. The objective of this work was to create F_2 populations and Andean nearly isogenic lines to analyze ALS resistance genes from the differential varieties and new sources of resistance discovered by the Bean Pathology section.

Materials and methods: The study was initiated with a search for a susceptible Andean bush variety to use in crosses for the genetic studies. The genotypes A 36, AND 277, AND 279, Araucaria 80, CAL 96, CAL 143, G 4494, G 5849, G 18370, G 18355, K 20, and PVA 800 A were inoculated with four strains - two from Colombia and one each from Malawi and Ecuador. The genotype A 36 was selected as the standard susceptible, because in addition to being susceptible to all four strains it has several other advantages including high yield, commercial seed type, and good architecture for a type II bush bean. Genotypes AND 277, AND 279, CAL 96, and CAL 143 were selected as additional donor parents because they were resistant to some strains.

For the inheritance study, the 10 differential resistant lines were crossed within gene pools to the susceptible varieties PAN 72 (Mesoamerican) and A 36 (Andean). For isoline development, the Mesoamerican differentials were crossed across gene pools to the Andean lines, CAL 96, CAL 143, and AND 277. In an effort to pyramid various Andean genes for resistance, four additional Andean sources of resistance from Rwanda (G 20523, G 20743, G 22255, and G 22267) were crossed to four semi-commercial Andean red-mottled bush beans with partial resistance (AFR 735, AND 277, AND 279, and CAL 143). Table 40 summarizes the crosses.

Results and discussion: are pending.

Conclusions and future plans: F_1 plants will be selfed to produce F_2 populations and backcrossed to produce isolines, which will be used for inheritance studies in the most pertinent crosses. It will be interesting to see whether the genes found in these studies are at the same locations of QTLs found in the DOR 364 x G 19833 population. Backcrossing will continue to incorporate the resistance genes from the Mesoamerican differentials into the Andean recipient parents. The pyramiding strategy of crossing between Andean differentials and Andean resistance sources with Andean commercial or semi-commercial genotypes will be tested for efficacy.

Contributors: MW Blair, G Mahuku

Table 40. Crosses made for pyramiding and analysis of angular leaf spot resistance genes in Andean beans.

Type of cross / donor parent	Seed type	Recipient parent	Seed type
PAN 72 x Meso differential			
G 2858	2M,P	PAN 72	1,P
Flor de Mayo	3J,P	PAN 72	1,P
MEX 54	2,M	PAN 72	1,P
BAT 332	2,P	PAN 72	1,P
Cornell 49242	8,P	PAN 72	1,P
A 36 x Andean differentials			
Don Timoteo	7,G	A 36	6M,G
Montcalm	6,G	A 36	6M,G
Amendoim	5M,M	A 36	6M,G
G 5686	4M,M	A 36	6M,G
AND 277	6M,G	A 36	6M,G
AND 279	6M,G	A 36	6M,G
PVA 800 A	6M,G	A 36	6M,G
CAL 143	6M,G	A 36	6M,G
Andean bush x Andean bush			
G 20523	6,G	AFR 735	6M,G
G 20743	6,G	AND 279	6M,G
G 22255	6,G	AND 277	6M,G
G 22267	6,G	CAL 143	6M,G
Andean bush x Meso differentials			
G 2858	2M,P	CAL 96	6M,G
Flor de Mayo	3J,P	CAL 143	6M,G
MEX 54	2,M	AND 277	6M,G
BAT 332	2,P		
Cornell 49242	8,P		

Progress towards achieving output milestones:

- Lines (16) that combine Andean and Mesoamerican ALS resistance genes were identified.
- Inheritance of resistance to Andean and Mesoamerican *P. griseola* races in G 19833 and DOR 364 was found to be complex and different for the two races, being recessive for one race and dominant for another, depending on the source of resistance.
- Lines with high levels of CBB resistance were identified. These will be screened with strains of a diverse origin to establish their suitability to other areas where CBB is a problem.

Activity 3.3 Developing integrated pest management components

Highlights:

- Developed reliable sampling methods for *Thrips palmi* on beans and snap beans.
- Established an action threshold for *T. palmi* on snap beans.
- Identified levels of resistance to insecticides in whitefly (*Trialeurodes vaporariorum*) and thrips populations.
- Developed components and successfully tested management strategies for combined populations of whiteflies and thrips affecting snap beans.

3.3.1 Development of a knowledge base on *Thrips palmi* as a pest of beans and snap beans

Rationale: Information on *T. palmi* as a pest of beans is very scarce. Development of appropriate management strategies for a major insect pest such as *T. palmi* requires basic knowledge of its phenology and distribution in the plant. This knowledge is essential for developing appropriate sampling methodologies, which will in turn facilitate understanding the various ways whereby the insect injures the crop and the response of the crop to injury. Sampling is also an essential tool for making decisions on when and how to intervene in order to bring populations below recommended action thresholds. Because the spatial pattern of individuals in the habitat has a tremendous influence on the sampling plan, we first studied the patterns of aggregation of adult populations on dry beans and on snap beans. We then estimated the optimum sample size and developed a sequential sampling method for adult thrips. With this information, and the yield response of snap beans to insect attack (estimated from replicated plots in the field), an action threshold was calculated.

Materials and methods: Commercial-sized fields of snap beans and dry beans were sampled every 3 days for the duration of two consecutive cropping seasons. Samples were examined for the presence of adults and larvae of thrips. The data thus recorded were analyzed for aggregation, sample size, and sequential sampling determination. Using an effective insecticide and preliminary information on mean adult populations, differential levels of insect attack were established and maintained. Yield responses at different levels of attack were measured. Regression analysis was used to obtain a loss function with which to calculate action thresholds.

Results and discussion:

Sampling methods for *Thrips palmi*. We found that, most frequently, samples of *T. palmi* adults per leaflet taken from natural populations have a variance that exceeds the mean. This was the first indication of aggregation. Further analysis using Taylor's power law showed that thrips populations fit a linear relationship between the base-10 log of mean and variance (Figure 61). Furthermore, the index of dispersion (*b* in the regression equation) was always higher than 1, meaning that populations are highly clumped.

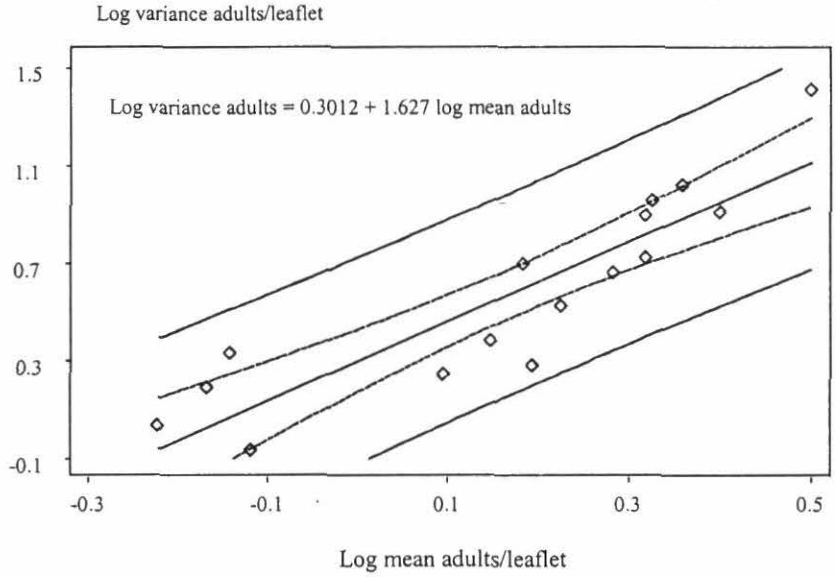


Figure 61. The relationship between mean and variance for adults of *Thrips palmi* per leaflet found on snap beans 49 days after planting.

Using values of *a* and *b* calculated from regression (Figure 61), we then calculated the optimum sample size at three levels of precision (Figure 62). The calculations showed that the required sample size at the 95% confidence level (the one that will assure us that our estimate is within 20% of the true value) is 40 leaflets taken at random in zigzag across the field.

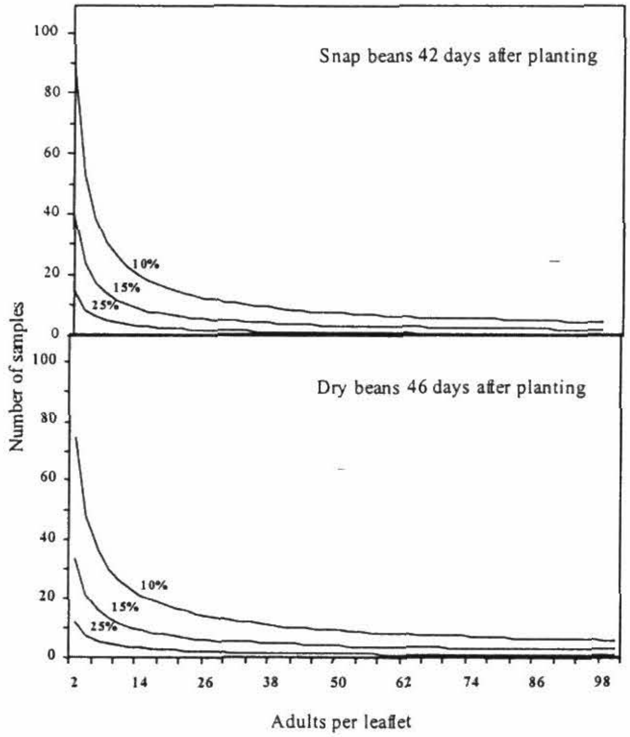


Figure 62. Estimates of optimum sample size for adults of *Thrips palmi* at three levels of precision.

The next step was to develop a sequential sampling method for *T. palmi* adult populations. This is a powerful tool used to categorize the pest population into density classes. If the population exceeds a pre-established action threshold, a curative treatment would be economically justified. Using an action threshold of seven adults per leaflet and values of *a* and *b* estimated from regression in Figure 61, we were able to develop decision lines (Figure 63). These lines are used to take decisions in the field. The number of samples taken is not fixed. Instead, after each sample, the cumulative number of insects is plotted on the graph. If the number falls above the upper line, treatment is necessary. If the number falls below the lower line, no treatment is necessary. In either case, sampling is stopped as soon as a line is crossed. If the cumulative number of insects sampled remains between the lines, sampling is continued.

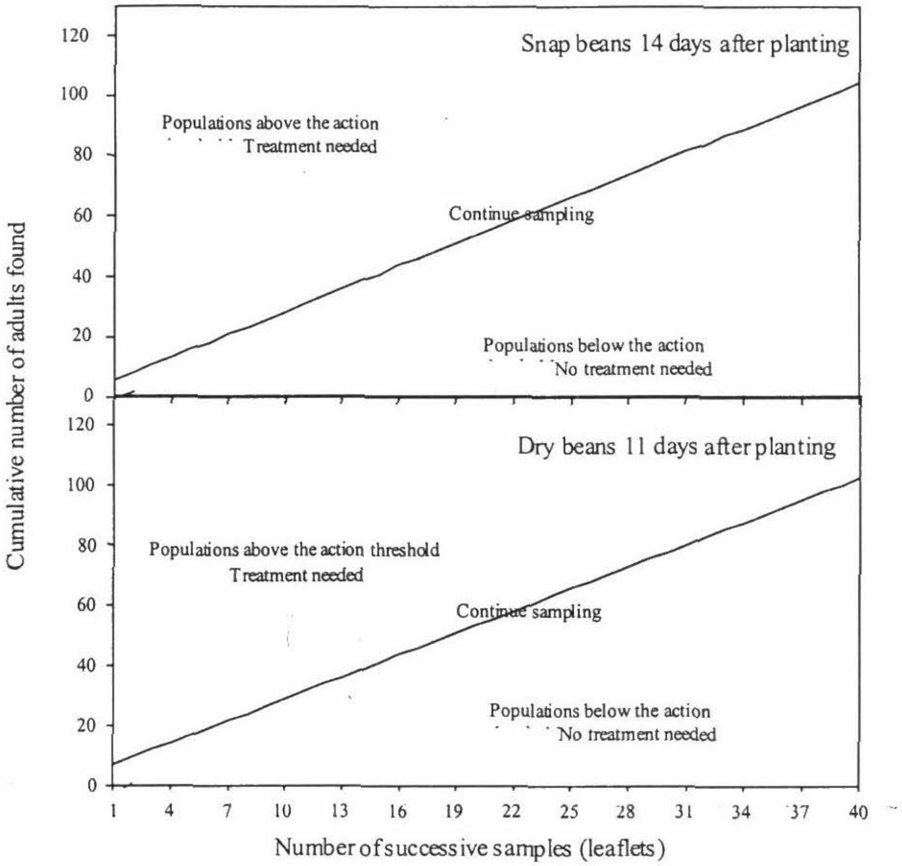


Figure 63. Sequential sampling plans for adults of *Thrips palmi* on dry beans and snap beans.

Contributors: J Osorio, C Cardona

Action thresholds for *T. palmi* on snap beans

Because insecticides are likely to remain the principal method of controlling *T. palmi*, decision aids for the rational and efficient use of insecticides can be important in the development of rational management strategies. One such tool is the action threshold, the level of population that warrants the economic use of a pesticide. In three consecutive trials, the response of snap beans to differential levels of attack by *T. palmi* adults was similar (Figure 64). The mean loss function (*b* in the regression) was 424 kg ha^{-1}. The action threshold calculated by means of the formula ranged from 7.1 to 8.0 adults per leaflet. Of course, the action threshold varies as the price of snap beans in the market changes (Figure 65).

$$\mathrm{AT} = \frac{\text{Cost of control}}{\text{Price of produce X loss function X efficiency of control}}$$

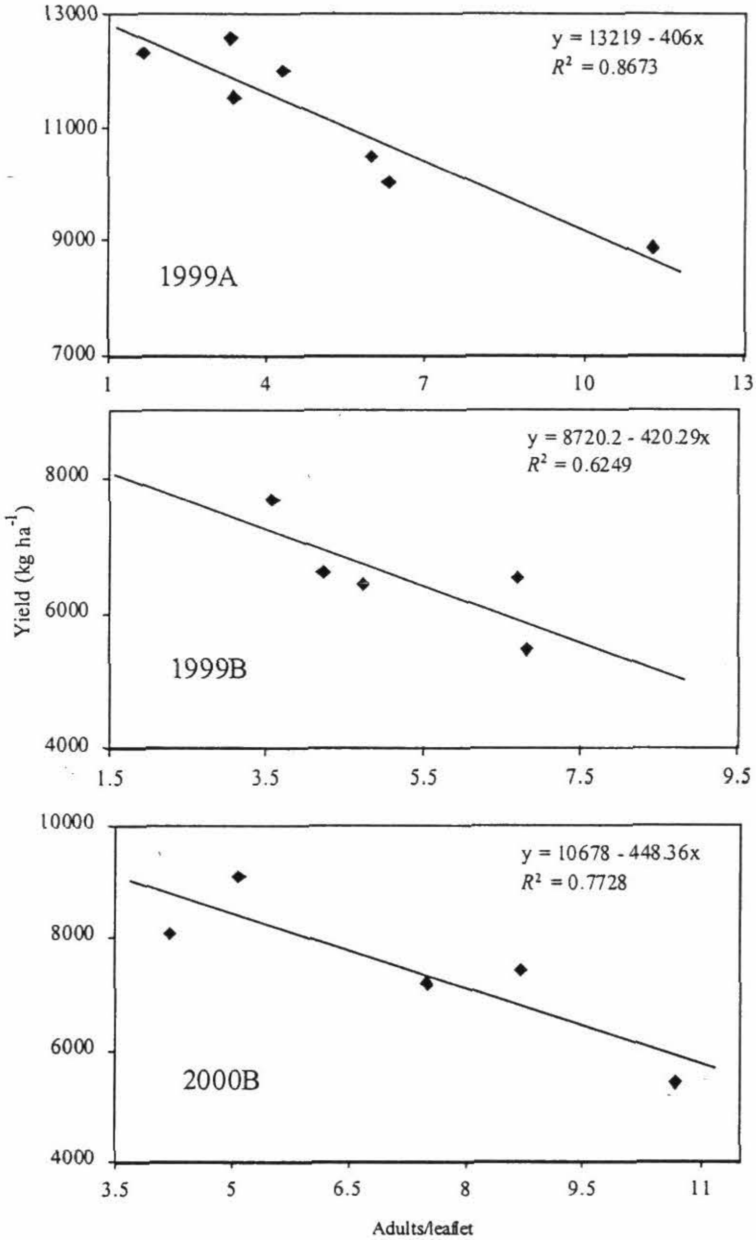


Figure 64. The relationship between adult *Thrips palmi* infestation and yields of snap beans.

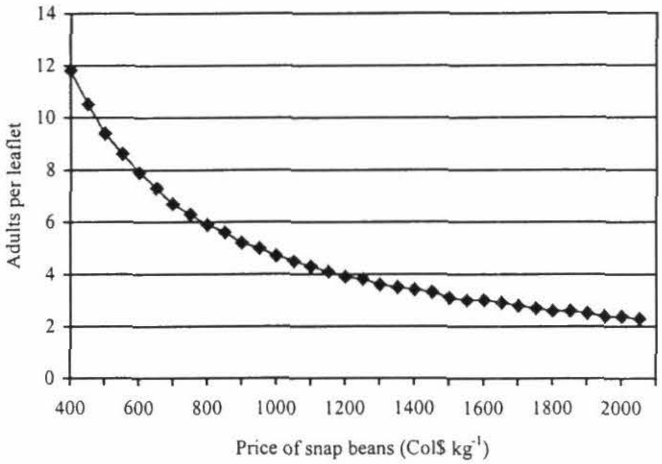


Figure 65. Action thresholds for *Thrips palmi* control as influenced by the market value of snap beans in a region of Colombia.

Losses in these trials were calculated. Results indicated that *T. palmi* is arguably one of the most important pests of snap beans. At high levels of population, the damage potential of thrips can be as high as 4.8 tons per hectare or almost 45% of the yield potential (Table 41).

Table 41. Yield losses caused by *Thrips palmi* on snap beans at varying levels of infestation.

Trial No./season	Level of infestation (adults/leaflet)	Losses	
		(t ha^{-1})	(%)
1/1999A	1.7	0.7	5.2
	3.3	1.3	10.1
	3.6	1.5	11.1
	4.1	1.7	12.6
	6.0	2.4	18.4
	6.3	2.6	19.3
	11.3 (Check)	4.6	34.7
2/1999B	3.6	1.6	18.0
	4.2	1.9	21.0
	4.8	2.1	24.0
	6.7	3.0	33.5
	6.8 (Check)	3.0	34.0
3/2000B	4.2	1.9	17.6
	5.1	2.3	21.4
	7.5	3.4	31.5
	8.7	3.9	36.5
	10.7 (Check)	4.8	44.9

Contributors: JM Bueno, J Díaz, C Cardona

Survey of thrips-affected areas in the Cauca Valley of Colombia

T. palmi has become a major pest of vegetables and beans in Colombia. A preliminary survey showed that snap beans, dry beans, pepper, melon, squash, and cucumber are the crops most affected by this pest in the Cauca Valley of Colombia. All farmers interviewed attempt chemical control. Conventional insecticides (organophosphates, carbamates, and pyrethroids) are ineffective. Some farmers are beginning to use new generation pesticides such as imidacloprid and compounds of biological origin such as abamectins and spinosad. Pesticides of biological origin can become powerful tools within an IPM system. Spinosad, for example, has shown a certain degree of selectivity for the control of thrips and there are no signs that *T. palmi* has become resistant to this new compound. Laboratory tests conducted at CIAT showed generalized susceptibility to spinosad in seven races tested, with a small increment of the LC_{50} (Figure 66) in Pradera, a hot spot for the insect where farmers usually abuse pesticides.

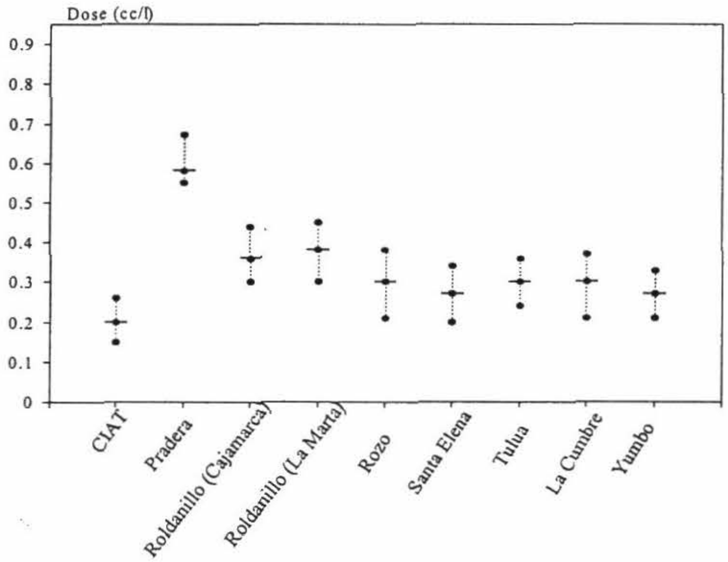


Figure 66. LC_{50} (−•−) and 95% fiducial limits (⁞) for nine races of *Thrips palmi* adults tested for toxicological response to spinosad. Two LC_{50} are considered significantly different if their 95% fiducial limits do not overlap.

Contributors: IC Durán, C Cardona

3.3.2 Monitoring of insecticide resistance levels in whitefly populations

Rationale: As indicated in the 1999 Annual Report, monitoring of insecticide resistance levels in adult populations of the greenhouse whitefly, *Trialeurodes vaporariorum*, is a major objective of the Systemwide Whitefly IPM Project. This work continued in 2000 with the calculation of baseline data for three additional insecticides and determination of diagnostic doses for five compounds. For the first time, we also calculated baseline data for nymphs of *T. vaporariorum* with three insecticides that are being used by farmers in Colombia and elsewhere.

Materials and methods: Baseline data and diagnostic dosages were calculated using mass rearings of susceptible strains of *T. vaporariorum* maintained at CIAT for several years. LC_{50} and LC_{90} values are calculated by exposing whitefly adults to increasing doses of a given insecticide in insecticide-coated vials and submitting the data to probit analysis. Once the baseline data are obtained, diagnostic doses (those causing mortalities of 95% or more in a susceptible strain) are tested. The diagnostic doses will be used to monitor resistance under field conditions by means of the insecticide-coated glass vials technique. Similar data are obtained for first instar nymphs using the dipping technique. Foliage is submerged for a few seconds in increasing concentrations of the insecticide tested, and mortality is recorded 72 h after treatment. Mortality data are used to calculate LC_{50} and LC_{90} values. Diagnostic doses are established as indicated above.

Results and discussion: Table 42 presents baseline data for monocrotophos, λ-cyhalothrin, and imidacloprid with the reference strain of *T. vaporariorum*. LC_{50} and LC_{90} values reflect toxicities to susceptible strains of whiteflies that have not been exposed to insecticides for over 10 years. Establishing baseline data for different insecticides is a fundamental step in resistance studies because the data thus obtained will serve for future comparisons in order to detect changes in insecticide resistance levels. Besides, calculation of baseline data permits the determination of diagnostic doses that can be used with less logistical difficulties in extensive monitoring of resistance such as the one carried out in the Andean zone.

Table 42. Toxicological responses of laboratory strains of *Trialeurodes vaporariorum* to five insecticides. Conventional insecticides were tested using insecticide-coated glass vials. Imidacloprid tests were conducted using the technique developed by Cahill et al[a].

Insecticide	N	LC_{50} (95% FL)[b]	LC_{90} (95% FL)[b]	Slope ± SEM	X^2
Monocrotophos	710	9.72 (6.77-13.37)	175.4 (115.5-299.8)	1.02 ± 0.08	4.80
λ cyhalothrin	714	9.38 (6.13-13.59)	264.9 (170.9-455.3)	0.88 ± 0.06	0.97
Imidacloprid	921	5.70 (4.6-6.9)	28.4 (20.9-44.9)	1.85 ± 0.22	7.80

a. Cahill M, Gorman K, Day S, Denholm I, Elbert A, Nauen R. Baseline determination and detection of resistance to imidacloprid in *Bemisia tabaci* (*Homoptera: Aleyrodidae*) 1996. Bull. Entomol. Res. 86: 343-349.

b. Imidacloprid in ppm. All others in µg a.i./vial.

Data in Table 42 and data obtained in 1999 were used to determine diagnostic doses for five insecticides. The diagnostic doses (those causing at least 95% corrected mortality) in Table 43 will be used in 2001 to monitor the occurrence of resistance under field conditions. The baseline data for nymphs of *T. vaporariorum* in Table 44 will be used in 2001 to calculate corresponding diagnostic doses and to initiate field monitoring of resistance.

Table 43. Toxicological responses of laboratory strains of *Trialeurodes vaporariorum* adults to varying doses of five insecticides. Conventional insecticides were tested using insecticide-coated glass vials. Imidacloprid tests were conducted using the technique developed by Cahill et al[a].

Insecticide	Doses[b]	Percentage corrected mortality	
		Test No. 1	Test No. 2
Monocrotophos	300	100.0	96.8
	20	46.3	43.7
	1	18.9	20.6
	0.3	7.4	10.2
λ-cyhalothrin	500	100.0	96.9
	50	51.6	61.1
	1.25	21.1	25.8
	0.16	8.4	6.9
Bifenthrin	5	100.0	96.9
	1.25	50.5	54.6
	0.3125	26.3	28.9
	0.0781	5.3	10.9
Carbofuran	5	97.5	96.5
	1.25	65.0	64.0
	0.3125	31.0	28.0
	0.0781	15.0	17.0
Imidacloprid	40	97.9	93.9
	5	47.4	43.3
	0.625	12.4	16.8
	0.156	3.1	5.6

a. Cahill M, Gorman K, Day S, Denholm I, Elbert A, Nauen R. Baseline determination and detection of resistance to imidacloprid in *Bemisia tabaci* (*Homoptera*: *Aleyrodidae*) 1996. Bull. Entomol. Res. 86: 343-349.

b. Imidacloprid in ppm. All others in µg a.i./vial.

Table 44. Toxicological responses of laboratory strains of *Trialeurodes vaporariorum* nymphs to three insecticides.

Insecticide	N	LC_{50} (95% FL)[a]	LC_{90} (95% FL)[a]	Slope ± SEM	X^2
Diafenthiuron	620	2.8 (0.8-6.3)	90-2 (40.0–346.8)	0.85 ± 0.1	11.30
Buprofezin 1st test	338	1.39 (0.98-1.87)	8.32 (5.7–14.0)	1.64 ± 0.18	3.90
Buprofezin 2nd test	600	0.5 (0.15-0.98)	7.68 (5.2-11.6)	1.01 ± 0.16	3.09
Imidacloprid	318	15.1 (9.5–22.2)	193.1 (118.2-382.0)	1.15 ± 0.12	5.30

a. Dosages in ppm of commercial formulation.

Contributors: I Rodríguez, C Cardona.

3.3.3 Management strategies for whiteflies and thrips

Rationale: Greenhouse whitefly and thrips have become the objects of excessive pesticide use by snap beans farmers. Insecticides will probably continue to be used until more biologically based management systems can be developed. However, with the information gathered so far on sampling methods, the action thresholds already developed for whitefly and thrips, and knowledge on the effectiveness of less toxic insecticides, systems can be developed that will at least contribute to reduce pesticide use. We report here on a series of field trials aimed at developing ways to reduce insecticide use in snap beans (see also the 1999 Annual Report).

Materials and methods: Different management tactics for whiteflies and thrips were compared using a Latin square design. There were five treatments:

(1) Seed treatment with imidacloprid;
(2) Imidacloprid applied as drench 15 days after planting;
(3) Timely application of imidacloprid or an equally effective insecticide when populations reach pre-established action thresholds;
(4) A simulation of farmers' current control practices; and
(5) Check (no insecticide use).

Whitefly and thrips populations were monitored twice a week. Yields and quality of the produce were recorded. Partial budget analysis was performed to compare benefit/cost ratios of the different treatments.

Results and discussion: As shown in Figures 67 and 68, significant differences occurred among treatments for levels of infestation, thus reflecting differential effectiveness of treatments in maintaining *T. vaporariorum* and *T. palmi* under control. Best results in two consecutive trials were obtained with the use of imidacloprid applied as drench 14-18 days after planting or as seed treatment at planting, followed by the timely application of effective foliar insecticides at pre-established action thresholds. Selective and timely use of insecticides resulted in a significant reduction in the number of applications per cropping season, from 7 in the "farmer's practices" treatment, to 2-3 in other treatments (Table 45). In terms of yields, the selective use of insecticides as seed treatment or as drench maintained adequate production levels. This is highly important. Our objective is to reduce pesticide use while maintaining yield levels. A management system that sacrifices yields for the sake of reducing insecticide use will not have impact in a farming community.

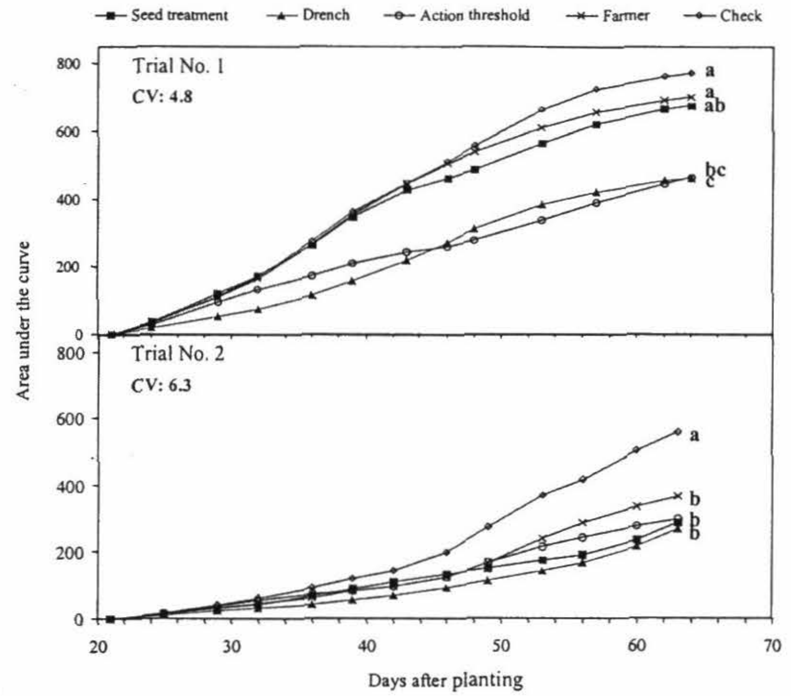


Figure 67. Areas under the curve for *Thrips palmi* larval populations on snap beans resulting from different management strategies. Letters show statistical differences at the 5% level (LSD Test). See text for explanation of treatments.

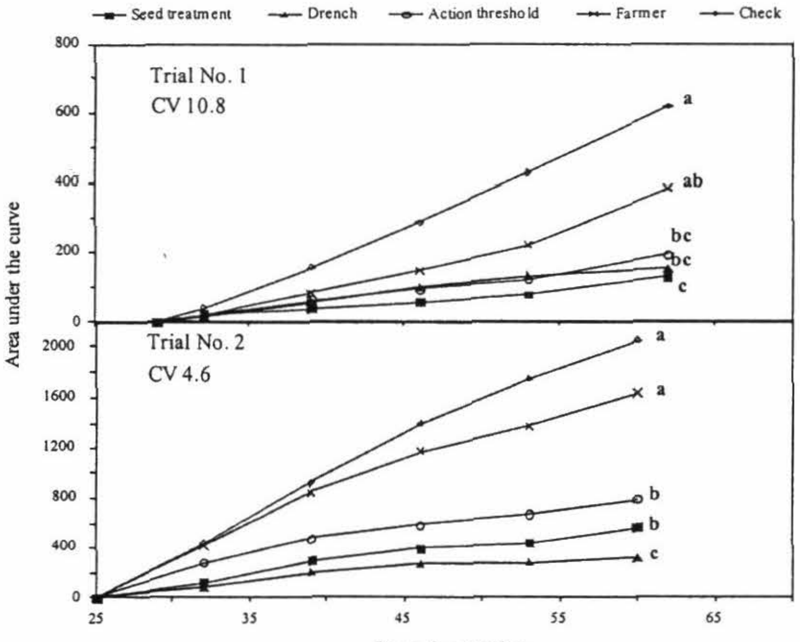


Figure 68. Areas under the curve for *Trialeurodes vaporariorum* nymphal populations on snap beans resulting from different management strategies. Letters show statistical differences at the 5% level (LSD Test). See text for explanation of treatments.

Table 45. Effect of different insect management strategies on damage levels and yields of snap beans; *Trialeurodes vaporariorum* and *Thrips palmi* acting together as key pests[a].

Treatment[b]	No. of applications		Farmers' appraisal[c]		Yield (t ha^{-1})		Percentage loss[d]	
	Trial 1	Trial 2	Trial 1	Trial 2	Trial 1	Trial 2	Trial 1	Trial 2
Seed treatment	3	2	3.6 ab	2.6 b	5.2 ab	10.3 a	25.7	-
Drench application	3	2	4.2 a	3.0 ab	7.0 a	10.0 a	-	2.9
Action threshold	4	3	3.2 bc	2.2 bc	4.0 b	8.4 a	42.8	18.4
Farmer's practices	7	7	2.6 c	4.2 a	4.0 b	9.6 a	4.3	6.8
Check	0	0	2.6 c	1.0 c	1.5 c	5.5 b	78.6	46.6

a. *Means followed by the same letter in a column are not significantly different at* $P = 0.05$.
b. See text for explanation.
c. On a scale of 1 (very poor) to 5 (excellent).
d. With respect to the best treatment.

Contributors: I Rodríguez, JM Bueno, C Cardona

Progress towards achieving output milestones:

- We have greatly increased the body of knowledge on both *T. palmi* and *T. vaporariorum* as pests of beans and snap beans.

- This knowledge is being used to achieve output milestones: to develop and implement management systems aimed at reducing pesticide use.

99637

Output 4. Improved cultivars and management practices developed and tested in partnership with IP-2 Project (Africa), NARS, and Regional Networks

Activity 4.1 Supporting breeding programs in NARS, Regional Networks, farmers' associations, and CIALs with germplasm and technical knowledge

Highlights:

- Evaluation of red-mottled, and red- and cream-speckled bean genotypes by farmer-led research committees (CIALs) in Colombia has identified broadly adapted bush bean varieties for mid-elevation ecosystems.
- Characterization of on-farm diversity of local common bean varieties in Nicaragua showed greater than expected genetic variability, which will be correlated with agro-morphological variability in the upcoming season.
- The IPHIS database was published for the first time with bean pedigrees, and remaining pedigrees are now incorporated into the IPHIS format.
- A project on breeding for aluminum resistance in bean was approved.
- Continuous support was given to breeding programs in PROFRIJOL, the Andean zone, and African networks.
- Seed was distributed to all collaborating partners.

4.1.1 Evaluation of bean genotypes through farmer-led research committees (CIALs)

Rationale: Participatory research with farmers can expedite the process of variety release. Feedback from producers on the advantages and disadvantages of varieties is critical to the success of any breeding program. Knowledge of the germplasm and the genetic management systems employed by farmers can help plant breeders to tailor varieties to their needs. Selections made at the farm or community level can benefit greatly from a precise description of the genetic variability present; which in turn can determine the need for infusion of new germplasm from plant breeding or genetic resources programs. On-farm testing exposes potential varieties to the range of abiotic and biotic stresses that the crop will face in a "real-life" situation as well as to the agronomic management practices that the farmer will apply to crops on a "day-to-day" basis. Farmers in Colombia grow beans under a range of agroecosystems and have different germplasm needs for these different growing environments. On-farm testing can help to find the perfect niche between germplasm and grower that will satisfy the common goal of the farmer and the plant breeder to create and use valuable new genetic resources.

Materials and methods: Farmer participatory research organizations (CIALs) planted bean variety trials during several growing seasons (1999-2000) in three regions of southwest Colombia:

(1) Pescador / Carpintero (Cauca) - initiating with six farms in two locations and with additional farms in El Jardín and Frontino the following season, supported by the CIAT- Participatory Research in Agriculture (IPRA) program and Consorcio Interinstitucional para una Agricultura Sostenible en Laderas (CIPASLA).

(2) Caicedonia (Valle) - initiating on three farms and supported by the local extension service (Unidad Municipal de Asistencia Técnica Agropecuaria [UMATA]), the CIAT-IPRA Program, and the departmental Coffee Growers' Committee (Comité de Cafeteros del Valle).

(3) Restrepo (Valle) - initiating on four farms and supported by a local NGO (Fundación para la Investigación y el Desarrollo Agro-industrial Rural [FIDAR]).

Monocultures of beans were followed by rotations with maize / vegetables and cassava in Restrepo, Pescador, and Carpintero; while in Caicedonia the bean varieties were planted in double rows as an intercrop in between pruned coffee bushes. From 10 to 22 varieties and advanced lines were tested at any one location. The plots consisted of four or five 5-m rows. The genotypes included red-mottled "Calima", large red "Radical", and cream-speckled "Sugar" types (Table 46). All the genotypes were bush beans with a general adaptation to altitudes of 1000 to 2000 m. The crop cycle of the bean varieties was 80 to 100 days depending on the prevailing weather conditions. The farmer committees evaluated the varieties for vegetative characteristics during the season and for yield and seed characteristics at harvest.

Results and discussion: Several red-mottled and red-seeded lines performed well over various sites. Several of the CIALs preferred the genotypes AFR 188, AFR 612, BRB 181, and CAL 96 over the current check varieties Calima, Guarzo, and Caucaya. The farmers in Caicedonia achieved the highest yields because fertility within the coffee-intercropping experiments was high due to residual fertilizer from the coffee harvest. In this setting, many of the varieties yielded well even under high plant densities. This system made efficient use of space with two rows of beans separated by 0.4-m spacing between coffee rows separated by 2-m spacing. In Restrepo, the plantings were plagued by drought. However, AFR 612 performed very well in two plots with irrigation and new farmers were interested in joining the effort. The Restrepo CIAL presently consists of eight farmers (six men and two women of different ages). During their experiments, the farmers from the Restrepo CIAL were invited to visit the CIAT research plots in Darien. Their criteria for plant and seed types were taken into consideration for the selection of promising material from over 1000 advanced $F_{6:7}$ lines derived from gamete selection. Their priorities were for commercial seed types, especially dark red seed colors. Although they were willing to accept varieties that had moderate levels of disease infection, any lines with light red seed color were eliminated.

Table 46. Genotypes tested in the Comités de Investigación Agrícola Local (CIALs) across three locations in southwest Colombia.

Locations	Bean genotypes			
	Red-mottled		Large red	Cream-speckled
Trial 1	A 36		AFR 188	
Caicedonia	AFR 612		ICA Cerinza	
Pescador/Carpintero	AND 279		Chocho	
	CAL 96		Guarzo	
	CAL 143			
	Caucaya			
Trial 2	AFR 735	CAL 181	AND 1088	SEQ 1027
Caicedonia	AND 1085	Caucaya	BRB 189	SEQ 1035
	AND 1089	POA 10	BRB 219	SEQ 1036
	AND 1090	POA 12	DFA 2	SEQ 1038
	BRB 189	SEQ 1039	SEQ 1033	SEQ 1040
	CAL 180	SEQ 1040		
Trial 3	AFR 612		AFR 188	
Restrepo	CAL 96		AND 1088	
	CAL 143		BRB 181	
	Caucaya		Chocho	
	Calima		SEQ 1033	
			SEQ 1031	
Trial 4	300 advanced $F_{6:7}$ lines			
Restrepo	AFR 612		AFR 188	
	CAL 96		BRB 181	
	Calima		Chocho	
	300 advanced $F_{6:7}$ lines			
	AFR 612		AFR 188	
	CAL 96		BRB 181	
	Calima		Chocho	

Future plans: The varieties selected by the CIALs in the initial trials are being tested in validation trials using larger plots (10 rows x 10 m). In the future, the best varieties may be grown in commercial plots for seed production to satisfy the local demand for new varieties among other farmers. Angular leaf spot was observed to be the primary disease in the bean fields of Restrepo during the previous season. We are expanding the range of germplasm available to the farmer committee in Restrepo and are planning a disease-resistance screening trial with them for the current season. With their help, we selected a group of 300 CIAT advanced $F_{6:7}$ red-mottled lines with good seed color for early on-farm testing. Most of these genotypes are derived from crosses that included parents that were resistant to ALS, anthracnose, and BCMV. The genotypes will be planted between spreader rows of the susceptible local check variety, Calima, and near a large bean field that contains the farmer's variety. Genotypes that are successful in this on-farm trial will be put into replicated and inoculated trials in CIAT plots in Darien, and subsequently the best lines will be distributed to other CIALs and collaborators.

Contributors: MW Blair (IP-1); I Roa (CIAT-IPRA Project);
C Gallego, J Restrepo (FIDAR, Cali, Colombia)

4.1.2 Characterization of on-farm diversity of local common bean varieties in Nicaragua

Rationale: Common bean (*Phaseolus vulgaris* L.) is a self-pollinated crop with a very low rate of out-crossing. It is commonly assumed that in such a crop, modern varieties grown on medium to large farms are maintained as pure lines while traditional landrace varieties grown on small farms are maintained as populations of mixed genotypes. In this study we attempt to describe the amount of genetic variation at the molecular level that is found within and between on-farm populations (here referred to as local varieties) collected from farmers in different geographical regions of Nicaragua. Seed color is an important commercial trait in Nicaragua, and farmers predominantly grow small, red-seeded beans, although they also have landraces that have brown- or cream-colored seed. Within these seed classes, seed size and pigment tones vary slightly. The genes underlying these differences in seed appearance are not well understood, but the discovery of allelic variation at molecular markers may give some clues as to how farmers maintain the diversity in their seed stocks.

Materials and methods: Thirty-three local varieties representing three seed classes (30 small red, three brown/ cream) were genotyped with bean microsatellite markers (Table 47). Seven Nicaraguan varieties that are part of the CIAT Core Collection were used as controls for gel-to-gel variation. Of the five most genetically diverse local varieties, 40 seeds were grown out in the screenhouse. The single plant selections are being grown in the field in Nicaragua as pure lines to distinguish phenotypic differences related to the genetic variability.

Results and discussion: The results indicate that microsatellites were ideal markers for detecting DNA polymorphisms in the closely related, but somewhat divergent, genotypes of Nicaraguan farmers. The genetic markers facilitated the differentiation of subpopulations within all the local varieties even when the individuals within the variety were all similar in terms of seed color and other phenotypic characteristics. This intra-population diversity was not correlated with agroclimatological zones or other variables. Although most of the individuals were homozygous for most loci, the frequency of heterozygous individuals in several of the populations was higher than 10%. This suggests that out-crossing had occurred at the farm level and that gene flow between diverse individuals within the population, or between adjacent populations from neighboring farms, might be important. The presence of individuals with different alleles is proof that farmers are planting genetic mixtures or populations rather than pure line varieties. These results suggest that traditional farmer-managed local varieties are reservoirs of genetic diversity and highlight the importance of preserving genetic resources by *in situ* conservation.

Table 47. Characteristics of the 21 local varieties from Nicaragua tested in this study.

Variety	Local name	Site	Department	Grain color
V1	Chile Rojo	Santa Rosa, Condega	Estelí	Red
V5	Rojo Criollo	La Zopilota, Diriomo	Granada	Red
V6	Rojo Criollo	Palo Quemado, Diriomo	Granada	Red
V7	Rojo Criollo	Palo Quemado, Diriomo	Granada	Red
V9	Rojo Criollo	El Guarumo, Nandaime	Granada	Red
V10	Rojo Criollo	La Orilla, Nandaime	Granada	Red
V11	Rojo Criollo	La Granadilla, Nandaime	Granada	Red
V12	Kaki	El Horno	Matagalpa	Dark brown
V16	Rojo Criollo	Santa Cruz, Estelí	Estelí	Red
V17	Chile Rojo	Condega	Estelí	Red
V18	Rojo Criollo	San Fco del Gamalote, Juigalpa	Chontales	Red
V19	Mono	Pantasma	Jinotega	Light brown
V21	Gualiceño	Pantasma	Jinotega	Light green
V22	Chile Rojo	Yali, Condega	Estelí	Red
V23	Vaina Roja	Estelí	Estelí	Red
V24	Chile Pando	Yali, Condega	Estelí	Red
V26	Rojo Criollo	Monte Grande, Nandaime	Granada	Red
V27	Rojo Pajiso	Santa Lucía	Boaco	Red
V28	Rojo Criollo	Santa Lucía	Boaco	Red
V29	Ligero Nacional	Santa Lucía	Boaco	Red
V30	Bayo	El Loro, San Juan del Sur	Rivas	Light yellow

Conclusions and future plans: On-farm trials of single-plant selections (pure lines) from the mixed varieties are being grown in Nicaragua to determine the morphological variability associated with the genetic diversity identified in this study. The introgression and mixing of improved, BGMV-resistant, modern varieties into the local populations will be studied by comparing the microsatellite fingerprints of varieties released in Nicaragua in the last 20 years to the alleles observed in this study. The amount of genetic variability present in today's landraces will be compared to that of the "same" varieties stored in gene banks in CIAT and in Nicaragua to determine the changes that occur over time with *in vitro* germplasm storage.

Collaborators: MW Blair (IP-1); E Gaitán, J Tohme (SB-2); OJ Gómez (Ministerio de Agricultura, Nicaragua); U Gullberg, B Frankow-Lindberg (Sveriges Lantbruks Universitet [SLU], Uppsala, Sweden)

4.1.3 Populations created and distributed

Rationale: Breeding has traditionally been a collaborative effort between CIAT and national programs, combining the strengths of the several institutions. The Center has been a source of both segregating populations and fixed lines. Reduced budgets require that efficient systems be created that exploit comparative advantages. The strength of

CIAT lies in the genetic variability housed in the gene bank, the novel gene combinations that have been created, and the capacity to create large numbers of populations.

Materials and methods: Populations were created including parental genotypes that had proven their worth across sites, and under multiple stresses in CIAT's trials and in the international nursery for this purpose. These include A 774 and VAX 1, among others. Populations were screened in the F_2 generation for resistance to diseases and for agronomic worth. In the subsequent generation, seed was planted at CIAT headquarters for clean seed increase for distribution. With the revival of the breeding program in Guatemala, a set of black seeded populations was sent that were prescreened in Colombia under fertility stress at the Santander de Quilichao site. With the initiation of collaboration with a Haitian NGO, these same populations were shipped to Haiti also. The same strategy was used to select populations of red-seeded beans for Costa Rica.

Results: Among nine populations planted in Haiti, four or five were promising in terms of potential to select superior plants. This modus operandi will be explored in the next few years to determine if it can optimize efficiency in the breeding program. The inferior populations would be weeded out in Colombia and generations advanced to near homozygosity (F_5 or so), while the latter phases of selection (line development and family testing) are practiced in individual countries. We would like to work molecular markers into this scheme as well, whereby we would apply markers in early generations to increase the frequency of desirable genes in populations that pass to NARS.

Conclusions: are pending.

4.1.4 Databases

Rationale: The interchange of information about genetic resources and improved germplasm is as important as the germplasm itself in assuring adequate use of that germplasm in breeding programs and in production. The Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT) and the International Rice Research Institute (IRRI) are developing a crop generic, integrated model of International Crop Information System (ICIS). The model is centered on the germplasm, in particular on the pedigree management and agronomic data generated on improved lines. Pedigrees are managed within the Germplasm Management System (GMS) and agronomic data with the Data Management System (DMS). We have been working on adapting bean pedigrees and data to the ICIS model for 2 years.

Materials and methods*:* CIAT data are stored in Oracle and are available internally, but are not accessible to partners outside of CIAT. Data include pedigrees of over 40,000 crosses and genealogies of over 6000 bred lines. These have resulted from more than 20 years of work involving six different breeders using essentially the same notation system, but each with variations. These data represent the raw material for ICIS. Last year we reported that these data had been adapted to the ICIS model.

Results: Early in 2000, IRRI and CIMMYT published the first CD-ROM of ICIS. It included a database on bean crosses, which was designated IPHIS (for *Phaseolus*). The IPHIS first edition carried about 30,000 crosses and 5000 pedigrees, with a second edition soon to be released, which should carry all CIAT crosses. The ICIS translates pedigrees into dendrograms or "trees", which visually display the parentage of a line over its several generations of crossing and selection, and this aspect of IPHIS is fully functional. The second edition of IPHIS should also contain evaluation data on the lines that passed through the bean team evaluations and the international trials.

Conclusion: The publication of IPHIS represents a milestone in the progress of data management and in user access to CIAT data on pedigrees. We expect this to be a highly popular item among national programs.

Contributors: S Beebe, H Terán, C Cajiao, A Hoyos (IP-1);
F Rojas, AF Guerrero (Databases)

4.1.5 Data analysis of the International Bean Yield and Adaptation Nursery (IBYAN)

Rationale: For nearly 20 years, the IBYAN was distributed and planted in bean production regions around the world. These data are stored at CIAT, and represent a substantial bank of biological information on the adaptation of bean to contrasting environments. Last year we reported on the application of the SEQRET program to the IBYAN data, to group environments based on crop yield response. However, the SEQRET program did not permit analysis of much of the IBYAN data because of restrictions on the minimum number of sites in which a variety must be planted to be included in the analysis, or the minimum number of years and common varieties to include for a site. These problems are common in multi-locational analysis, because the same trial is seldom planted over several years, and thus data matrices are invariably incomplete. This year, a novel data analysis technique was developed with the Land Use Project that overcomes many of these restrictions and permits analysis of highly incomplete matrices.

Materials and methods: A highly modified leader cluster algorithm was written that can create a dimension independent distance measure in the variable dimensioned subspaces. The crux to the working of this algorithm is, we think, what is known as the "Small World" or the "Kevin Bacon" effect. The essence of the game is to link any Hollywood actor to Kevin Bacon by the pairings of actors working together in films in the least number of steps. Thus: Charlie Chaplin acted with "X" in Limelight, "X" acted with "Y" in The Great Escape, "Y" acted with Kevin Bacon in "The Most Mindless Film Ever Made". The link from Chaplin to Bacon is made in three steps even though many thousands of actors have worked in Hollywood. This is becoming widely researched in the investigation of network connectivity. The important result is that regular networks should show a very poor connectivity on large scales, but by adding a few long-range connections the performance of a regular network can be made to approximate very closely to a truly random network.

The tool was developed with a set of simulated data, starting with a full matrix and eliminating data progressively until the limits were found of how little data could give the right results. The tool was then applied to bean yield data over sites. Over the years of its existence, from 1978 to 1987, the black-seeded IBYAN was the trial that had the longest history and the widest distribution. Therefore our statistical analysis focussed on the black IBYAN, obtaining clusters of environments based on response of bean varieties. Once the black bean trials were analyzed by this method, the coordinates of the resulting clusters of sites were fed into the FloraMap program to visualize similar environments.

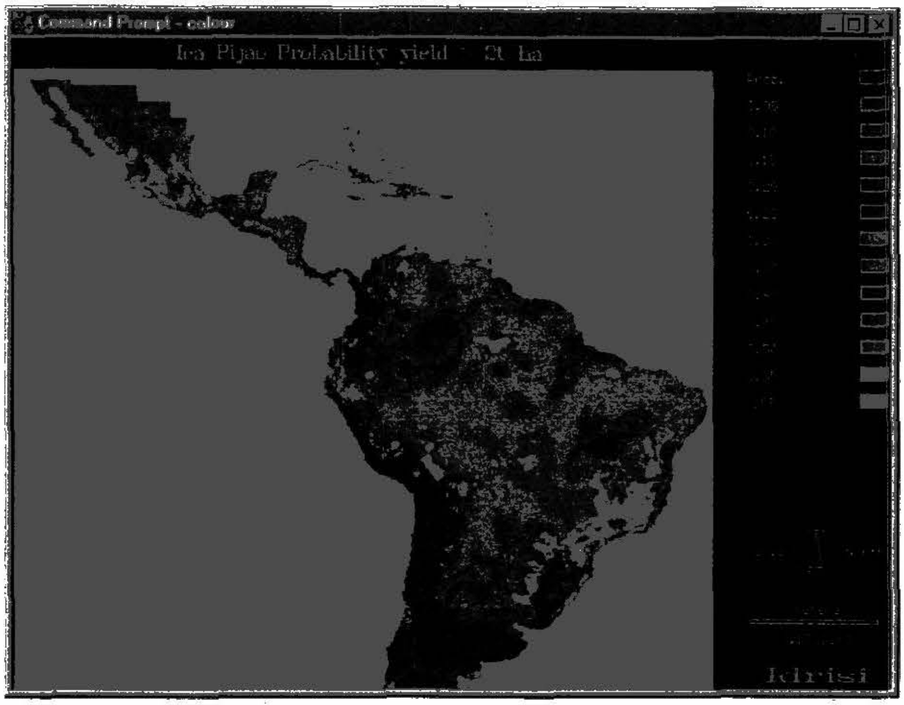
Results: A novel method of data analysis was developed that permits the analysis of very sparse matrices in which many of the data in a site x variety matrix do not exist. A simulated data matrix suggests that as little as 15% of the data can produce the same clustering of sites as a full matrix. Other multi-variate methods discard sites or varieties that are incomplete in the matrix, but this method permits including many more sites in the analysis and the classification of these in relation to other sites. We think that this represents a vast improvement over previous analyses and is a great contribution to multi-locational analysis. The mapping exercise produced maps that were logical, and climatically similar regions were mapped. This resulted in regions that could be associated with contrasting altitudes or latitudes, and were in some degree discrete. This suggests that the multi-locational analysis had in fact extracted differential response to environments.

Additionally, the yield patterns of two well-known varieties, ICA Pijao and Porrillo, were compared and the probability functions developed as described above. Experience suggests that Pijao adapts better at moderate temperatures while Porrillo performs well under high temperatures. In the two maps, although they are similar, some subtle differences show that confirm this empirical experience (Figure 69). Porrillo is shown to be adapting down to the Pacific coast of El Salvador, which is exactly where it was originally selected (and named! Porrillo is a site in coastal El Salvador); while Pijao is doing better in the central, higher (800-1000 m) environments of Central America. In the broad swathe of the hot, Brazilian cerrados, Porrillo is better.

Conclusions: A promising, novel data analysis was developed that permits grouping environments despite very incomplete data matrices. This could be a breakthrough in the analysis of multi-locational trials. An initial attempt to apply the FloraMap program to the clusters so derived suggested that even with year-round climate comparisons that are used in FloraMap, some logical patterns could be discerned.

The Australian Center for International Agricultural Research (ACIAR) funded this research.

Contributors: P Jones (PE-4); S Beebe (IP-1)



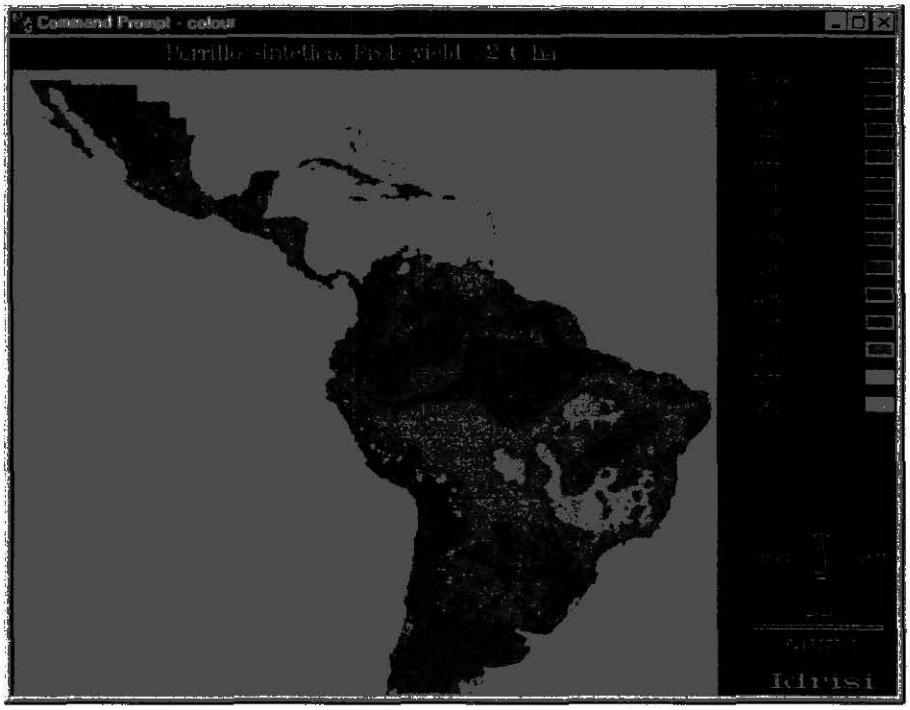


Figure 69. Maps of adaptation ranges of two closely related black bean varieties, ICA Pijao and Porrillo.

4.1.6 Distribution of seed to partners

I. **International nurseries**

- A. Observational Nurseries (IBN)
  (Formed by advanced lines Andean type)
- B. Specialized Nurseries *Empoasca*
- C. Snap Bean Germplasm

II. **Dry bean breeding nurseries**

III. **Germplasm characterization**

IV. **Others**

DIFALS	(Angular Leaf Spot Differentials)
DIFANT	(Anthracnose Differentials)
DIFFUS	(*Fusarium* Differentials)
DIFRUST	(Rust Differentials)

I. **International Nurseries**

A. Observational Nurseries

Nursery	Country	No. of lines	Institution
2000 IBN (Andean types)	Bolivia	40	Universidad Autónoma Gabriel René Moreno (UAGRM)
	Colombia	99	Corporación Colombiana de Investigación Agropecuaria (CORPOICA)
		20	Corporación para el Fomento de los Comités de Investigación Agrícola Local, Colombia (CORFOCIAL)
		60	Federación Nacional de cultivadores de Céreales (FENALCE)
		20	Ministry of Education (MINEDUCACION)
		40	UMATA
		39	Universidad de Nariño (UDENAR)
	Ecuador	40	Instituto Nacional Autónomo de Investigaciones Agropecuarias (INIAP)
	Haiti	31	Organization for the Rehabilitation of the Environment (ORE)

B. Specialized Nurseries

Nursery	Country	No. of lines	Institution
Single crossing (individual selections) and backcrossing of Berna x EMP 419	Canada	161 (35 kg)	University of Guelph

C. Snap Bean Germplasm

Institution	Country	No. of lines	Collaborator
ORE	Haiti	78	E Magloire, L Eugene
	Honduras	20	L Brizuela
University of Nairobi	Kenya	70	P Kimani
Chitedze Agricultural Research Station	Malawi	69	RM Chirwa

II. Dry Bean Breeding Nurseries

Nursery	Country	No. of lines	Institution
Bean nursery of red-seeded lines	Bolivia	39	UAGRM
	Honduras	18	Dirección de Investigación de Ciencias y Tecnología Agrícola (DICTA)
	Honduras	39	EAP-Zamorano
	Peru	39	Comisión para la Promoción de Exportaciónes (PROMPEX)
	Puerto Rico	39	University of Puerto Rico
Bean nursery of red-seeded lines and sources of BGMV	Dominican Republic	23	Secretaría de Estado de Agricultura (SEA)
BGMV-resistant parents and advanced lines	Haiti	11	ORE
Bred lines	Haiti	5	Instituto Interamericano de Cooperación para la Agricultura (IICA)
BRB lines	Colombia	38	CORPOICA
Climbing accessions from Rwanda	Haiti	35	ORE
Core Collection accessions	Costa Rica	10	Ministry of Agriculture

II. **Dry Bean Breeding Nurseries** (continued)

Nursery	Country	No. of lines	Institution
Common bean lines	England	69	University of Reading
	Hawaii	8	University of Hawaii
	Peru	98	Universidad Nacional Agraria "La Molina" (UNALM)
	Uganda	4	Kawanda Research Station
Common bean lines – CBB	China	19	Inst. Germplasm Resources
Common bean lines – Low P	Brazil	2	Instituto Agronômico de Campinas (IAC)
	Haiti	45	ORE
	USA	11	University of Pennsylvania
Common bean lines – races	Costa Rica	26	University of Costa Rica
	USA	17	University of California
Common bean lines Andean type	China	32	Inst. Germplasm Resources
Common bean lines Ñuña germplasm	Guatemala	6	Instituto de Ciencia y Tecnología Agrícolas (ICTA)
Common bean lines Pinto type	Puerto Rico	60	University of Puerto Rico
	USA	60	Colorado State University
Common bean lines White type	Peru	10	PROMPEX
Common bean lines for registration in Crop Science	USA	9	University of Idaho
DOR 364 RILs	USA	175	University of Pennsylvania
Early lines of common bean	Canada	36	University of Saskatchewan
F_1 hybrids	Guatemala	45	ICTA
	USA	3	Oregon State University
F_2 populations for BGMV	Haiti	12	IICA
F_2 populations of G 2333 x G 23338	USA	1	Michigan State University
F_2 populations of single crosses	Iran	6	Seed Plant Improvement Institute (SPII)

II. Dry Bean Breeding Nurseries (continued)

Nursery	Country	No. of lines	Institution
F_2 populations of triple crosses	Iran	12	SPII
F_3 bulks bush Cargamantos	Iran	48	SPII
F_3 bulks early Cargamantos	Colombia	67	CORPOICA
F_3 bulks late Cargamantos	Colombia	62	CORPOICA
F_3 families of G 35172 x G 35337	Guatemala	103	ICTA
F_3 segregating populations – Cranberry type	Iran	66	SPII
F_4 segregating populations	Costa Rica	7	Ministry of Agriculture
	Guatemala	9	ICTA
	Haiti	9	ORE
F_6/ F_8 advanced red-mottled bush bean lines	Haiti	35	ORE
Interspecific crosses families	Guatemala	516	ICTA
	Mexico	516	
P. coccineus and *P. polyanthus* core accessions	Guatemala	248	ICTA
	Mexico	124	
	Puerto Rico	69	University of Puerto Rico
Potential parents	Costa Rica	263	Ministry of Agriculture
	Guatemala	16	ICTA
	USA	559	University of Idaho
Resistance sources of CBB	USA	57	United States Department of Agriculture (USDA)- Agricultural Research Service (ARS)- Irrigated Agriculture Research and Extension Center (IAREC)
Resistance sources of common bean lines	USA	76	University of Idaho

II. **Dry Bean Breeding Nurseries** (continued)

Nursery	Country	No. of lines	Institution
Resistance sources of *Fusarium*	USA	5	Colorado State University
Resistance sources of halo blight, cold, heat	Iran	30	SPII

III. Germplasm Characterization

Nursery	Country	No. of lines	Institution
Core Collection accessions	Bolivia	9	UAGRM
	Haiti	10	ORE
Core Collection climbing accessions	Haiti	14	ORE
DOR 364 x G 19833 recombinant inbred lines (RILs)	England	32	University of Reading
	USA	89	University of Pennsylvania
DOR 364 x G 19833 F_2 populations	England	40 seed	University of Reading
G 2333 x G 19839 RILs	England	32	University of Reading
	USA	86	University of Pennsylvania
G 24404 x Radical-Cerinza backcrosses families	Colombia	100	CORPOICA
Local variety – single plant selections	Nicaragua	240	Universidad Agraria

IV. Others

Nursery	Country	No. of lines		Institution
DIFALS (angular leaf spot differentials)	Bolivia	1 set	(4 checks)	Instituto de Investigaciones Agrícolas (IIA) "El Vallecito"
	Costa Rica	2	(200 g)	Universidad de Costa Rica
	Colombia	12		CORPOICA
	Peru	12		UNALM
DIFANT (anthracnose differentials)	Bolivia	1 set	(4 checks)	IIA "El Vallecito"
	Colombia	12		UDENAR
		12		CORPOICA
	Costa Rica	12	(700 g)	Universidad de Costa Rica
	Slovenia	12		Agricultural Institute
	South Africa	12	(500 g)	Dept. of Plant Pathology
	Ecuador	12		Instituto Nacional Autónomo de Investigaciones Agropecuarias (INIAP)
	Peru	12		Universidad Nacional Cajamarca
		12		UNALM
DIFFUS (*Fusarium* differentials)	Uganda	9		Kawanda Research Station
	USA	9		Colorado State University
DIFRUST (Rust differentials)	Ecuador	20		INIAP
	Bolivia	3	(50 g)	IIA "El Vallecito"
	Colombia	20		UDENAR
Resistance sources of angular leaf spot (ALS)	Brazil	25	(500 g)	Centro Nacional de Pesquisa de Arroz e Feijão (CNPAF)/ Empresa Brazileira de Pesquisa Agropecuária (EMBRAPA)
	Haiti	19	(450)	ORE
	Uganda	26	(1500 g)	Kawanda Research Station
Resistance sources of anthracnose (ANT)	Peru	4		Universidad Nacional Cajamarca
Resistance sources of root rots	Uganda	4	(200 g)	Kawanda Research Station
Xanthomonas campestris pv. *phaseoli* lyophilized bubbles	Cuba	60	(300)	Instituto de Investigaciones Horticolas

Contributors: IP-1 Team

Activity 4.2 Collaborative projects developed and executed with NARS and Regional Networks

Highlights:

- CIAT scientists participated in the planning of activities of PROFRIJOL, the Andean zone, and African Networks.
- *Individual training* of national scientists was provided.
- Joint collaboration and concept notes were prepared.

4.2.1 Regional bean project for Central America (PROFRIJOL)

In 1980, CIAT established a formal regional research project in Central America with funding from the Swiss Development Cooperation (SDC). The project has evolved to the point that today its operative administration is in the hands of an Executive Committee of five members that in turn carries out the decisions of the General Assembly in which all participating countries are represented. The Bean Project Manager represents the CIAT-based Bean Team on the Executive Committee. Furthermore, CIAT headquarters gives administrative backstopping in financial management.

With regard to research, priorities are set in consultation with NARS in a joint planning session. All CIAT activities are coordinated with the planning matrix, and CIAT delivers a yearly work plan relating goals to budget allotments. Thus, CIAT activities are totally coordinated with the regional project structure and CIAT functions as a full partner with NARS.

The project structure involves five main subprojects:
(1) Improved bean varieties of the Mesoamerican gene pool, including red- and black-seeded types;
(2) Improved bean varieties of the Andean gene pool, for use in the Caribbean basin and Panama;
(3) Support to breeding efforts, including analysis of genetic variability of pathogens, broadening the genetic base of resistance, and developing molecular markers for traits;
(4) Developing improved crop management techniques including soil conservation and fertility management; and
(5) Socioeconomic studies including adoption and impact studies.

CIAT participates directly (with project funds) in subprojects 1 and 3, and indirectly (with core funds) in subproject 2. Technical results are presented in the respective sections under output.

The IP-1 team members participated in the Project Planning by Objectives (PPO) for preparation of the next phase of PROFRIJOL and the following contributions are to be made and are consistent with the overall plan for the next phase:

- Varietal improvement in both black and red small-seeded beans. Emphasis on resistance to biotic constraints (BGMV, ALS, anthracnose, *Apion*, CBB, BSMV, BCMV, and web blight), and abiotic constraints (drought and low soil fertility).
- Pathogen diversity, specifically, ALS and anthracnose.
- Marker-assisted selection for BGMV and CBB.
- Germplasm characterization.
- Collaboration (mainly by supplying populations) with participatory breeding initiatives in the region.
- Artesanal seed production (with emphasis on seed quality, especially in relation to phytosanitary standards).
- Statistical analysis of Ensayo regional de Rendimiento (ECAR) trials.

In addition, CIAT's IP-1 Project will be an important member of a foundation, tentatively called Fundación Regional de Investigación y Desarrollo Agropecuario (FRIDA). The SDC donor is planning to create FRIDA with CIMMYT, national programs, the private sector, and other partners interested in bean research in Central America and the Caribbean.

In 1999, SDC approved a new phase of PROFRIJOL. This will last for 2 years and its continuity will depend on the outcome of FRIDA. An agreement between SDC, CIMMYT, and CIAT to create FRIDA was signed with the aim of promoting the establishment of this foundation. A Task Force led by a Swiss consultant will examine the logistical, legal, and operational issues of the sustainability and feasibility of establishing FRIDA. There will also be an Advisory Group (one member each from CIAT, CIMMYT, SDC, PROFRIJOL, and the Programa Regional de Maíz [PRM]). This group will be in charge of providing guidance, and will establish the terms of reference and monitor progress. During 2000, two FRIDA Task Force meetings were attended. Meanwhile, activities within PROFRIJOL will continue as per the PPO approved in Guatemala City in 1999.

Contributors: C Cardona (IP-1); A Viana (PROFRIJOL)

4.2.2 Regional bean project for the Andean zone (PROFRIZA)

The Regional Bean Project for the Andean Zone (PROFRIZA) has operated since 1988. Until 30 June 1998, PROFRIZA was one of CIAT's regional projects; on 1 July 1998, it became a project of the SDC, an entity that has financed this project from the beginning. The continuous technical and scientific support, which CIAT provided, ended on 31 December 1999. However, CIAT will continue to include bean as a mandated crop because of its importance as a staple food for large sectors of the Latin American rural and urban populations. For this reason, CIAT sent a project proposal to the SDC for beans and other legumes for year 2000 and beyond. The proposal is entitled "Consortium for promoting the production and marketing of grain legumes in the Andean Region". The SDC has agreed to fund legume research and promotion in the region for the next 3 years on a separate bilateral basis with each country.

Bilateral bean projects for the Andean Region (Ecuador, Peru, and Bolivia)

The national bean programs of Bolivia, Ecuador, and Peru continued to be important partners for the CIAT bean project this year. The regional PROFRIZA project, which previously linked the countries formally into a network, ended. However, the programs remain in contact with one another and with the CIAT bean project. In the new phase of the bean project for the region, the national programs are interested in continuing their strong historical ties and close interaction with the CIAT bean project. Germplasm from CIAT has been instrumental in the past successes of these programs and will continue to be important to their advances. Each national program has prepared rough drafts of the new bilateral projects, and in the new format CIAT will be subcontracted for germplasm and specific services that are of interest to the country.

As part of the planning stage for this project, visits were made during the past year to each of the principal sites for bean research in the region. The plant breeder for Andean beans visited Peru during the irrigated winter season on the northern coast / sierra (Chiclayo and Cajamarca) and visited Bolivia during the winter season in the Inter-montane valleys (Santa Cruz and Cochabamba). The purpose of these trips was to discuss breeding strategies, observe the Vivero de Padres Donanates de Genes Necesarios (VIPADOGEN) and IBN 1996 nurseries, and to see CIAT germplasm that has been released recently as varieties. Both the bean pathologist and Andean breeder visited sites in Ecuador (Chota, Ibarra, Bolivar, and Quito) during the first semester plantings to observe bush and climbing bean trials, collect pathogen isolates, and consult on future breeding goals and methodologies.

Breeding of Andean and Mesoamerican beans, IPM, and MAS are highly important areas of research for the new phase of the project. Joint breeding objectives across the region are needed to get the most varieties from each program. Bolivia covers lowland breeding and Ecuador covers highland breeding, while CIAT covers the full range of adaptation zones including mid-elevation breeding. Peru has no formal breeding programs, but has plant breeders placed in Universities and at the export board. Therefore, CIAT can continue to contribute to the national programs with germplasm and research. New interest has been expressed in applications of biotechnology to plant breeding in the region. The program in Bolivia plans to invest in some equipment for DNA extraction and in a screenhouse where they can carry out controlled inoculations and pathotyping. The DNA extraction will be used for collaborative work with CIAT on MAS and pathogen strain characterization. Ecuador has a modest laboratory working on molecular markers and genetic diversity characterization and is interested in applying MAS for resistance breeding.

Germplasm exchange has continued over the last year. An Andean bean nursery of advanced lines with commercial seed types was distributed to Ecuador and Bolivia for their upcoming planting seasons. The most important genetic resources for the region are the traditional commercial classes, new seed classes with export potential, and sources of disease and insect resistance. Although Colombian bean researchers are no longer within a formal Andean network, they can benefit from the germplasm developed in the region. For example, 10 local and regional research entities in Colombia have received the same CIAT advanced lines as their counterparts in Ecuador and Bolivia and will be trying them at the same time.

Training has been an important benefit of the regional network. A course was offered during the past year for the principal bean researchers from the region in modern techniques of the use of MAS and pathogen characterization in plant breeding and pathology. Training and regional collaboration will continue in the upcoming year with a visit to CIAT of a student from Ecuador for anthracnose isolation, inoculation, and resistance breeding.

Possibilities for joint fund-raising and collaborations in the region are promising. Many donors would be receptive to projects presented to them by the national programs. Future projects might revolve around specialty grain types and small-scale farmers who are growing beans for commercial and export production (as on the Peruvian coast and Bolivian lowlands). The Peruvian government is interested in capitalizing on and conserving their genetic resources, especially popping beans or ñuñas and the yellow- and white-seeded Canario and Caballero beans typical of Peru. Ecuador has started work in participatory plant breeding and export production. Bolivia has an interest in expanding bean production at higher elevations.

Contributors: MW Blair, O Voysest, G Mahuku, C Cardona

4.2.3 Joint collaboration and concept notes

Projects approved

The Administration Generale de la Coopération au Développement (AGCD)-Belgium approved a project, "Broadening the genetic base of common beans (*Phaseolus vulgaris* L.) through biotechnology", to extend activities carried out previously with Ghent University on interspecific hybridization and transformation.

The Belgian government tentatively approved a project, "Integration of biofertilisation in bean cultivation by optimizing the use of the *Rhizobium*-bean symbiosis", to work with Mexico and with the Catholic University of Leuven on the topic of symbiotic nitrogen fixation (SNF). This will permit follow-up on the gene tagging work initiated several years ago to improve SNF under conditions of low P availability.

The Federal Ministry for Economic Cooperation and Development (BMZ), Germany, approved a collaborative project entitled "An integrated approach for genetic improvement of aluminum resistance of crops on low-fertility acid soils". Four other CIAT projects (IP-2, SB-2, IP-5, and PE-2), one network (Pan-Africa Bean Research Alliance [PABRA]),and two systemwide programs (Soil Water Nutrient Management [SWNM] and Systemwide Livestock Program [SLP]-TROPILECHE) are collaborating to explore aluminum tolerance in bean and *Brachiaria*. The bean component includes on-site selection of aluminum-resistant genotypes in Africa, and will serve to maintain contact between headquarters and African breeders.

Another collaborative project with IP-2 was prepared and the Rockefeller Foundation approved funding. The project is entitled "Increasing food security and rural incomes in eastern, central, and southern Africa through genetic improvement of bush and climbing beans". It will start in 2001 and finish in 2003.

The Wallace Genetic Foundation, Inc. approved a 1-year grant to support "The development of molecular markers for breeding of common beans".

The USDA- Pan American Development Foundation (PADF) Hurricane Georges Recovery Program (HGRP) for Haiti gave the bean project funds for a project.

Another project for Haiti, "RFP No. 521-00010 for the Haiti Hillside Agricultural Program", was approved, funded by the United States Agency for International Development (USAID).

Projects submitted

The project "Sustainable management of P and N to improve production and quality of peanut (*Arachis hypogea* L.) in Latin America" was submitted to the European Union with partners in Belgium, France, Scotland, Spain, Cuba, Argentina, Mexico, and Brazil. It will permit exploring further applications in the use of FloraMap in predicting crop productivity across environments.

"Broadening the genetic base of common beans (*Phaseolus vulgaris* L.) through biotechnology", the same project that was approved by AGCD-Belgium with Ghent University, was submitted for extension.

A request was made for extension of the project "Interspecific solutions to intractable problems of common bean: Understanding the genome of the secondary gene pool to facilitate interspecific transfer of genes and broadening the genetic base of common bean". This has been ongoing for the past 4 years, in partnership with Gembloux University, to exploit the diversity of *P. coccineus* and *P. polyanthus*.

The proposal "Breeding beans for resistance to drought, mites, and root rots for Iran" was submitted for extension of collaboration with the Ministry of Agriculture of Iran.

The proposal "Food security for Central America and the Caribbean through a regional collaborative bean research network", funding of PROFIJOL 2001-2003, was submitted to SDC.

Projects in preparation

"Real digestibility and stimulating effect of phaseolin, the bean storage protein, on endogenous secretion in rats", a proposal developed with the Universidad Nacional de Palmira to study the effects of different morphotypes of phaseolin protein on endogenous protein loss from the gut, is to be submitted to the Volkswagon Foundation.

"Exploiting diversity among gene pools of common bean for underprivileged farmers in the highlands of Mesoamerica and Ecuador", a pre-proposal developed with NARS of Guatemala, Mexico, and Ecuador, and with Michigan State University, was submitted to the McKnight Foundation. It is intended to extend the benefits of breeding to farmers that have been bypassed by past efforts in varietal development.

"Breeding staple crops for improved micronutrient value", a concept note, was submitted to the Gates Foundation to improve the nutritional status of bean consumers in Africa and Middle America.

"Mineral-rich grains for better nutrition: Beans with higher zinc and iron for African farmers and consumers", a concept note, was developed for submission to USAID-Uganda.

Concept notes prepared

- "Plan de fomento para reactivar la producción de frijol en Colombia", prepared with FENALCE.
- Safeguarding bean farmers' health from pesticide abuse through IPM approaches through COLCIENCIAS.
- "Recuperación y utilización de los recursos fitogenéticos del Perú: Mejoramiento del frijol reventón (ñuña/poroto) y caballero" submitted to the Ministry of Agriculture of Peru, for the regions of Cajamarca, La Libertad, Ancash, Ayacucho, Apurimac, and Cusco.
- "Estrategias de manejo de insectos plaga y enfermedades para pequeños productores de habichuela en suelo de planicia aluvial de piedemonte en el Valle del Cauca", a project submitted to Progama Nacional de Transferencia de Tecnología (PRONATTA), Colombia, together with CORPOICA.
- Sustainable soil-crop-pest management strategies for integrating staple food crops with high value crops in hillside environments.

- Identification of dry bean germplasm tolerant to soil zinc deficiency for cultivar development for low-input sustainable agriculture.

- Phosphorus efficiency in common bean (*Phaseolus vulgaris* L.) in east and south African agroecosystems.

- Root rot problems: impact of beneficial soil microorganisms and soil nutrient management strategies in bean cropping systems.

- Increasing economic and food security for African households headed by women in sub-Saharan Africa.

- Integrating nutrient and pest management approaches for agroecosystem health sustainability.

Contributors: S Beebe, MW Blair, C Cardona, G Mahuku, IM Rao

Activity 4.3 Supporting NARS and Regional Network researchers on soil and crop management

Highlights:

- Partners are evaluating a set of 49 genotypes for their adaptation to abiotic constraints such as drought, aluminum toxicity, and low nutrient supply.

- Partners are evaluating a set of 19 genotypes for their response to ALS.

4.3.1 Evaluate elite bean genotypes for their tolerance to low fertility conditions in soil on farmer fields in Costa Rica, Mexico, Cuba, and Haiti

Collaborators in Mexico are evaluating a set of 49 promising genotypes for tolerance to low fertility in soil. Collaborators are:

Mexico: Javier Cumpian Gutierez, Instituto Nacional de Investigaciones Forestales Agrícolas y Pecuarias (INIFAP), and Cd. Isla, Veracruz.
Cuba: German Hernandez, Ministerio de Agricultura (MINAG), and Quivican.
Costa Rica: Rodolfo Araya, Univ. of Costa Rica, Alajuela.
Haiti: Eliassaint Magloire, Organization for the Rehabilitation of the Environment (ORE), and Camp-Perrin.

Mexico: The most promising genotypes identified from the acid soil site in Veracruz, Mexico based on grain yield were: A 774, G 983, CAP 4, MAR 1, MAM 38, and

G 13755. These genotypes not only were adapted to acid Al-toxic soil conditions, but also were responsive to lime and fertilizer inputs. Among the plant attributes measured, number of pods per plant was identified as an important trait related to seed yield.

Costa Rica: Evaluation in Costa Rica was carried out at two sites (Fraijanes and Alajuela) with two levels of P supply (no P application and 200 kg ha^{-1} P application). At Fraijanes, V 8025, A 321, G 19833, DICTA 17, G 11640, and A 752 were identified as outstanding genotypes for their adaptation to low P-supply in soil. Among these six genotypes, A 321 was also highly responsive to P application. At the Alajuela site, CAP 4, A 774, FEB 192, Carioca, and FEB 190 were identified as low-P adapted genotypes. Among these five genotypes, FEB 190 was also highly responsive to P application.

Cuba: Field evaluation of 49 genotypes resulted in identifying eight promising genotypes (A 321, A 774, G 92, DICTA 17, FEB 190, CAP 4, SEA 13, and MAM 46) with adaptation to soil and climatic conditions of Quivicán. Seed multiplication of these materials is in progress.

Haiti: Field studies are in progress at two sites, an acid soil site at Deron (mid-altitude) and a high temperature site in the lowlands at Camp-Perrin. Genotypes that looked promising for acid soil conditions were BAT 304, BAT 477, BAT 881, FEB 192, ICTA-Ostua, BH 21134-66, DOR 364, DOR 390, G 18479, G 21212, BT-21138-98, and Tio Canela. Genotypes that showed better adaptation to high temperature stress were A 774, BAT 304, BAT 477, DOR 364, DOR 390, BT-21138-98, Tio Canela, and Quimbaya.

Contributors: IM Rao, S Beebe, H Terán

4.3.2 Evaluate elite bean genotypes for their tolerance to drought on farmer fields in Nicaragua

A set of 49 promising genotypes was planted along with a regional yield trial, to obtain baseline data on drought tolerance or susceptibility of regional breeding lines in relation to some well-known drought tolerant genotypes. Evaluation at San Diego identified G 18479, G 21212, and SEA 13 as promising materials for adaptation to drought. A bred line, SEA 5, was affected by BGMV and therefore was not among the best performers.

Contributors: IM Rao, S Beebe, H Terán

4.3.3 Evaluate genotypes for their response to angular leaf spot

A set of 19 potential sources of resistance is being evaluated for resistance to ALS in Nicaragua, Honduras (Juan Carlos Rosas, Zamorano), El Salvador, Bolivia, Costa Rica (Carlos Araya, University of Costa Rica), and Haiti (ORE, Camp-Perrin, Haiti).

Results from Honduras have shown that the lines G 5686, G 6727, G 8152, G 14301, AFR 702, AFR 703, and AFR 735 have high levels of resistance.

Haiti: Little incidence of ALS was observed partly because the trials were established under very high temperatures and low rainfall. The conditions were not conducive for disease incidence. These materials will be screened again during the main October season. The genotype AFR 702 showed very good heat tolerance.

Contributors: G Mahuku, C Jara

Activity 4.4 Supporting human resource development in NARS and Regional Networks

Highlights:

- CIAT bean project scientists actively participated in international conferences and meetings that they attended.
- Individual and group training of national and international scientists was provided.
- A marker database was constructed for an RAPD survey of Andean common bean germplasm.
- Colombian research and extension agents identified regional bean production problems.
- The Web page for IP-1 in English and Spanish was updated and expanded http://www.ciat.cgiar.org/projects/ip-1/bar_ip1.htm.

4.4.1 Trips and attendance at meetings

The breeder and plant nutritionist visited Cuba to evaluate bean trials during February.

The bean-breeding assistant visited Guatemala and Costa Rica to evaluate bean fields in April.

The team entomologist, plant nutritionist, breeder, and pathologist, together with the research assistants in breeding and germplasm characterization laboratory attended the

XLVI annual meeting of the Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA) and the PROFRIJOL general assembly meeting in San Juan, Puerto Rico, during May.

The breeder and plant pathologist visited Iran in July-August to present a course on bean breeding-pathology, to familiarize themselves with the production constraints, to identify areas for collaboration, and to review field trials.

The breeder, plant pathologist, and plant nutritionist visited Haiti to familiarize themselves with bean production in Haiti and to evaluate bean trials during September.

The Project Manager made the following trips:

- To Guatemala in February to attend the First FRIDA Task Force and in July for the Second FRIDA Task Force.
- To Haiti in April in order to become acquainted with the Germplasm Improvement and On-Farm Adaptive Research Program and to plan the activities conducted in collaboration with ORE.
- To Bogota in July to elaborate the National Plan on Legumes with FENALCE and CORPOICA.

The breeder visited the following countries:

- Mexico, in September 1999, to familiarize himself with highland bean production and coordinate activities.
- El Salvador, in October 1999, to review field trials including heat tolerance studies.
- The Philippines, in October 1999, to the Consultative Group on International Agricultural Research (CGIAR) workshop on nutritional quality, IRRI.
- Brazil, in November 1999, to attend the national bean meeting, Reunião Nacional de Pesquisa de Feijão (RENAFE).
- Nicaragua and Honduras, in December 1999, to review field trials.
- East Lansing, Michigan, USA, in April 2000, to attend the Meeting of Bean /Cowpea Collaborative Research Support Project (CRSP), to plan the renewal phase.
- Guatemala, in April 2000, to evaluate bean fields.
- Cuba, in May 2000, to attend the planning session for a project to be submitted to the European Union.

The Andean breeder/germplasm specialist made the following visits:

- Peru, in November 1999, to discuss breeding strategies and to observe nurseries.
- San Diego, California, USA, in January 2000, to attend the Plant and Animal Genome (PAG)VII - genomics conference.
- Bolivia, in March 2000, to discuss breeding strategies and to observe nurseries.

- Ecuador, together with the plant pathologist in May 2000, to observe bush and climbing bean trials, collect pathogen isolates, consult on future breeding goals and methodologies, and discuss possible areas of collaboration.
- USA, in June 2000, to attend a tour of MAS facilities in Novartis, Monsanto, University of Minnesota, and Washington University.

Bean breeding supported the participation of the ICIS Workshop at CIMMYT, Mexico.

The plant nutritionist gave a seminar on abiotic stress adaptation of common bean to MSc students of the National University, Palmira and to UMATA technicians from Colombia.

4.4.2 Training and courses

- Active participation of the breeder and the plant pathologist was given to the workshop for the PROFRIZA network held at CIAT from October 25 to November 5, 1999. The workshop was entitled "Curso internacional para mejoradores y patólogos de la región Andina - Técnicas modernas en el mejoramiento y estudios de patología de frijol" and was addressed to the 22 bean researchers from the Andean zone (Colombia, Bolivia, Peru, and Ecuador).

- The plant pathologist gave a talk on the use of microsatellites in population genetics studies of plant pathogens during a course on "Técnicas moleculares aplicadas a la identificación de la resistencia a enfermedades en diferentes cultivos" held at CIAT 9–12 December 1999.

- A Legume Planning Workshop on "Discusión de un plan nacional de investigación, transferencia de tecnología y promoción del comercio de leguminosas alimenticias" was held at CIAT, 16-17 March. Researchers from CORPOICA (Regionals 1, 4, 5, 6, and 7), FENALCE, and UDENAR attended this workshop.

- Plans for the fieldwork of a Cuban MSc student were solidified during a visit to La Habana in May. The student will carry out a physiological analysis of lines derived from the cross of DOR 364 x BAT 477, the latter of which has expressed resistance to multiple abiotic stresses. The study will reveal the physiological relationship between resistances to low P, nitrogen, and drought stress.

- Twenty-two legume researchers from Colombia and Ecuador participated in "Primer curso avanzado de producción y gerencia de proyectos sobre el cultivo de frijol" held at CIAT from 12 to 23 June.

- A bean breeding-pathology course was given to Iranian bean scientists on bean breeding and pathology in Karaj, Iran, from July 29 to August 4.

- Researchers and extension workers from Bolivar, Colombia, visited CIAT from 11-15 September, for a training course in bean production.

- The plant pathologist participated in training a Cuban scientist, using molecular techniques (DNA extraction, REP-PCR) to characterize the CBB pathogen.

4.4.3 PhD, MSc, and pregraduate thesis students

- An Argentinean PhD candidate was hosted for 2 weeks to prepare data analysis for his thesis work, involving a statistical analysis of multi-locational trials carried out over a 15-year period in the northwest of Argentina. The study will help to orient a strategy for future bean trials in the region.

- A PhD student from the Universidad del Valle is conducting his research on molecular characterization of NL4 BCMV strain.

- A PhD student from the Ecology and Crop Production Science Department of SLU, Uppsala, Sweden and Universidad Nacional Agraria, Nicaragua, made an analysis of on-farm genetic diversity in Nicaragua, where he is a germplasm specialist with the University.

- A PhD student from the University of Wageningen, The Netherlands, finished her thesis research on biological control of whiteflies.

- A PhD student from ETHZ, Zurich is conducting her thesis research on host plant resistance to *Thrips palmi*.

- Two MSc students from the Universidad Nacional are finishing their thesis research. One is conducting a study on " Efectividad de método de selección por gametos en la F_1 de cruzas múltiples para resistencia a enfermedades en frijol común *P. vulgaris* L." The other thesis is on "Análisis de la herencia en la resistencia a *Phaeoisariopsis griseola*, hongo causante de la mancha angular en 87 líneas recombinantes de frijol común, *Phaseolus vulgaris* L.

- A visiting scientist from ETHZ, Zurich is conducting a 6-month training period in bruchid management.

- A pregraduate student from the University of Tolima was supervised and completed his laboratory work toward obtaining his undergraduate agronomist degree. His thesis involved the identification of QTL for agronomic traits that had been introgressed from wild bean to cultivated bean.

- A pregraduate student from the University of Tolima is conducting her project on a wild QTL study to see whether cultivated beans of Andean and Mesoamerican gene pools can be improved via crosses with wild bean accessions from divergent gene pools.

- A pregraduate student from the Universidad del Valle started his thesis studies on using molecular markers to study the genetic diversity of *Colletotrichum lindemuthianum*.

- A pregraduate student from the Universidad Nacional is finishing her thesis on Pathogen diversity of the ALS pathogen, *Phaeoisariopsis griseola*.

- Two new undergraduate students from the Universidad del Valle have begun their thesis research. One is studying the inheritance of micronutrient content in bean seeds, especially for the minerals iron and zinc; the other is testing microsatellite markers from other legumes, such as soybean and cowpea, in common bean.

- Two pregraduate students from the Universidad Nacional are finishing their theses on ecology and phenology of *Thrips palmi* as a pest of beans and snap beans.

4.4.4 Databasing

Molecular genetics database constructed for an RAPD survey of Andean common bean germplasm

Rationale: We are developing a database to store the information from the RAPD analysis of genetic diversity of the Core Collection of Andean common beans. Our first step was to find a software system for storing, handling, and presenting images within a relational database. Fortunately, a new version of the Oracle software, v. 7.3.2, has been released that has these capabilities and has a more user-friendly interface and the capacity to be loaded onto the Web. As a relational database, Oracle has the advantage of being an efficient program for organizing and managing data; it has multiple layers of relational structure and is based on a series of data tables. This software provides a set of tools for building new interfaces for a database and asking new questions of that database. The three principal components are tools to generate worksheets, reports, and graphic images. The program DEVELOPER/2000, part of the Oracle suite, has a Web-compatible format that uses windows and buttons to allow for interactive searches and queries. Oracle software is the standard program for databasing the information from the breeding programs at CIAT. We hope that this preliminary database will be the basis for collecting genotypic information on common bean, and will be a dynamic analysis tool allowing researchers to ask such questions as: How many polymorphisms can I expect when comparing two varieties that might be potential parents? Which polymorphisms distinguish one variety from another?

Materials and methods: Using the software package Quantity One from Biorad, 330 photographs of RAPD banding patterns were scanned and analyzed. These represented 10 primers run on 680 genotypes. The annotated gel images were loaded into the database using the Oracle graphics development tool and the estimated band sizes were loaded using the Oracle worksheet development tool. The finished database has three main windows for "gel", "accession", and "bands". Each of these has a datasheet format with columns and entries. The "gel" window indicates the center of origin for the genotypes, the molecular technique and the primer used, and shows all of the genotypes run together in a given gel. Clicking on a genotypes entry brings up all the sized bands for that individual. Embedded windows are used to call additional items such as the gel images. The "accession" window can be used to compare the markers present in two genotypes. Activities are realized either through the menu bar or action buttons. A console line indicates the status and location of the user. The first version of this database was written in Spanish.

Future plans: Future plans are to load additional molecular marker data into the present database. We hope to place the database on the Internet using Microsoft Interdev or with the Oracle software tool, Web-DB. With either system, the database can be accessed from any type of computer, via common Web-browsers such as Netscape or Internet Explorer. To date, the database contains RAPD fingerprints, but could also accommodate data from other multiple-copy marker systems such as AFLP fingerprints. The information stored in this Oracle database could be amenable to incorporation into databases that use other software applications. The basic components of this database will be easy to transfer to ICIS (http://www.cgiar.org/icis), which is the database system for managing and integrating genetic resource, crop improvement, and crop management information of the CGIAR-system. The IPHIS database has been developed at CIAT to hold bean-breeding data. Molecular data are foreseen to be an important part of these databases in the future. It would also be important for this database to be interactively linked with the BeanGenes database (http://beangenes.cws.ndsu.nodak.edu/), which was established by the USDA-Plant Genome program to specialize in the genetic information relating to common bean. To realize the maximum potential of a molecular marker database, it should also be linked with other existing databases that contain germplasm data on *Phaseolus* including SINGER (http://singer.cgiar.org), the principal database on genetic resources held in the CGIAR system and GRIN (http://www.ars-grin.gov/npgs/). The potential for linkages between all these databases is shown schematically in Figure 70.

Collaborators: MW Blair, M Muñoz, S Beebe, AF Guerrero, F Rojas

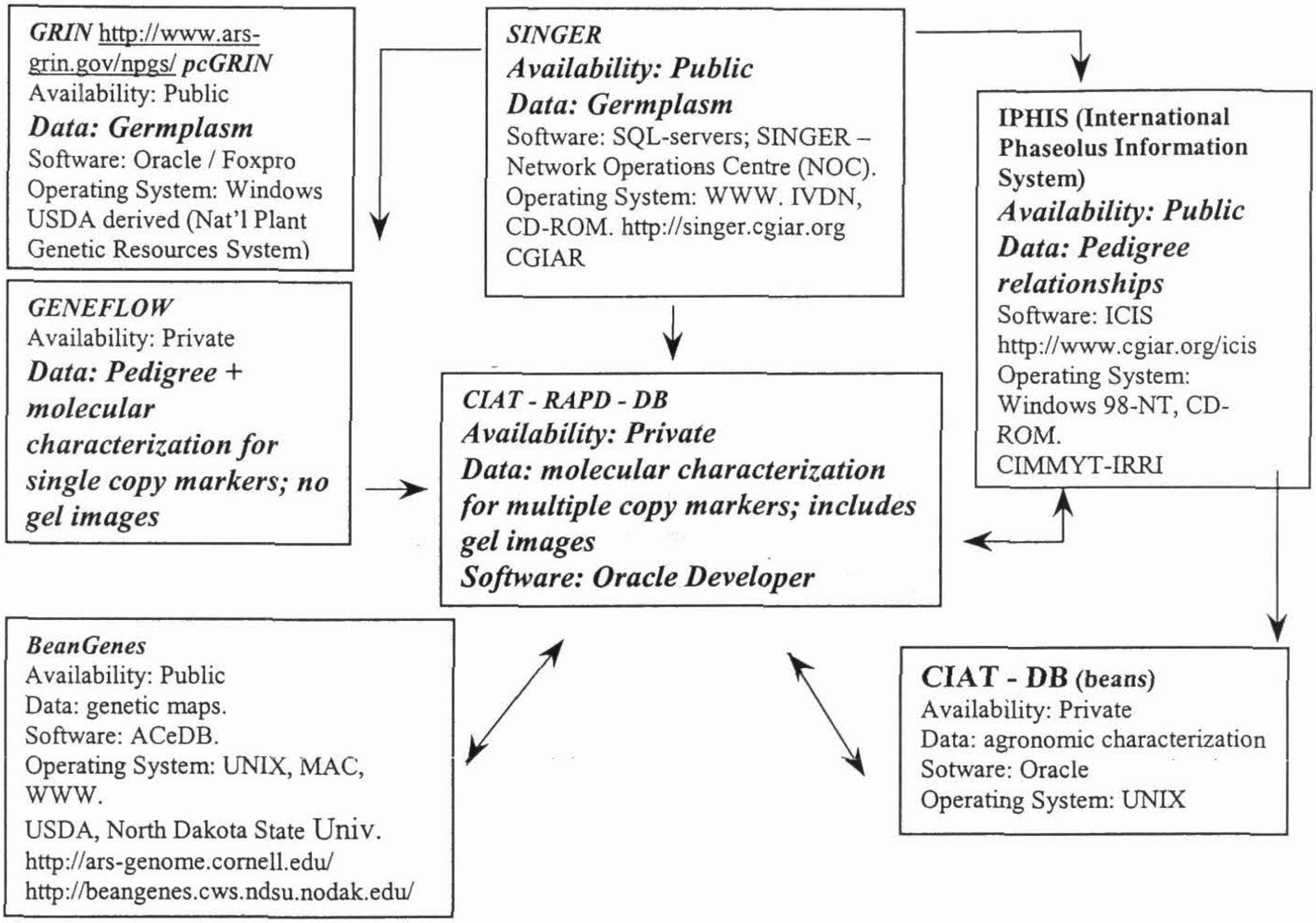


Figure 70. Databases for common bean germplasm and genetic information. Web sites are given for those databases available on the Internet.

Identification of regional bean production problems by Colombian research and extension agents

Rationale: A workshop sponsored by the Colombian Ministry of Agriculture was held in June 2000 for researchers and extension agents from all over Colombia who had an interest in bean production. As part of the exchange that developed during the workshop, the idea was born of a questionnaire to assess the current situation of bean production in Colombia. The objective of this report is to summarize the data collected from the Colombian researchers and extension agents.

Materials and methods: The questionnaire was distributed to 20 participants. Questions came under nine headings: area planted, grain preferences and varieties, planting dates, cropping systems, diseases, insects, market opportunities, nursery management, and germplasm interests. Where appropriate, the answers were given separately for bush versus climbing beans. The participants were from private (FENALCE - 5; NGOs -3) and public institutions (ICA/CORPOICA - 6; SEA - 1; UMATA - 3) and came from seven departments of Colombia (Antioquia - 3; Boyacá - 1; Cauca - 2; Huila - 3; Nariño - 4; Norte Santander - 1; Santander -2; Tolima -1). FENALCE is the national cereal and legume producers association, ICA/CORPOICA is the national research service and the UMATAs are local extension services. The information was tabulated according to the departments from which the participants came.

Results: All participants answered the questionnaire enthusiastically and completely. In the first question, they estimated the area planted across their regions. These estimates were comparable to previous estimates from the Ministry of Agriculture for the areas in beans for each department. The breakdown between bush and climbing beans across the departments showed that bush beans predominate, but that climbing bean production is substantial in the departments of Antioquia, Boyacá, and Nariño. Climbing beans are also found in departments that are not believed to have as much climbing bean, such as Cauca, Huila, and Tolima. The other surprise was the interest in expanding the hectares of bush beans, especially at lower elevations, in traditional climbing bean growing departments, such as Antioquia and Nariño.

Table 48 shows the varieties of bush and climbing beans identified by the participants as important for their regions. While most of the bush bean varieties were modern releases from ICA, most of the climbing beans were landraces. Two breeding programs at the University of Nariño and at the La Selva experiment station are addressing the paucity of improved climbing bean varieties. In addition, an interesting program run by a group of farmers in Nariño, in conjunction with CORPOICA, is selecting better-yielding varieties from local landraces of climbing beans.

Table 48. Bean varieties identified by participants as important in seven departments of Colombia.

Department	Bush		Climber	
	Variety	Origin	Variety	Origin
Antioquia	Uribe Rosado	ICA	Cargamanto	ICA
	Citara	ICA	Cargamanto Rojo	Local
	Quimbaya	ICA	Cargamanto Blanco	Local
	Regional	Local	--	--
	Radical	ICA	--	--
	Llanogrande	ICA	--	--
Boyacá	Rovirense	ICA	Bola Roja	ICA
	ARS-59	ICA	--	--
Cauca	Cerinza	ICA	Bola Roja	Local
	Caucaya	ICA	Cargamanto	Local
	Cacha	Local	--	--
Huila	Diacol Calima	ICA	Bolón Rojo	Local
	Diacol Catio	ICA	Cargamanto Rojo	Local
	Radical	Local	Variedad	Local
	Cajamarca	Local	Sabanero morado	Local
	Calima	ICA	--	--
	Bola Roja	Local	--	--
Nariño	Bachue	ICA	Rumichaca	ICA
	Cerinza	ICA	--	--
	Guaitara	ICA	--	--
Norte Santander	Zaragoza	Local	--	--
Santander	Froilan	ICA	--	--
	Guanenta	ICA	--	--
	Rovirense	ICA	--	--
	ARS-59	ICA	--	--
Tolima	Caucaya	ICA	Bola Roja	ICA
	ICA-60	ICA	Cargamanto Rojo	Local
	Algarrobo	Local	--	--

The planting dates identified by the participants varied depending on the region. At higher elevations in Nariño and Antioquia, planting dates were more likely to be once a year, but in any month. At lower elevations, they were associated with the bimodal rainfall, except in the irrigated areas of Santander. A range of cropping systems were mentioned, however, bush beans were usually planted as a monocrop while climbing beans, when not grown on trellises, were sometimes planted as an intercrop with maize.

Table 49 shows the diseases and insects mentioned most often by participants for bush or climbing beans. Anthracnose was the most important disease of both bean systems. Rust was the second most important disease in bush beans, but not in climbers, followed by ALS and *Ascochyta*. Leaf feeders, including the Chrysomelids, were the most important insects in bush beans, while pod borers were more important in climbing beans. Other important insects were *Empoasca* and Cutworms. According to the participants, the price received at the farm was about 60%-70% the price of beans sold by the intermediaries.

Table 49. Frequency of diseases and insects mentioned by participants as important in bush and climbing beans in seven departments of Colombia.

Pathogens	Bush	Climber	Insects	Bush	Climber
Anthracnose	82.4	76.5	Aphids	17.6	5.9
Ascochyta	23.5	35.3	Borers	11.8	17.6
Ashy stem blight	17.6	11.8	Cutworms	29.4	29.4
Angular leaf spot	23.5	35.3	*Empoasca*	41.2	29.4
BCMV[a]	5.9	5.9	Leaf feeders	52.9	23.5
Fusarium wilt	0.0	5.9	Leaf miners	5.9	5.9
Powdery mildew	11.8	5.9	Pod borers	23.5	47.1
Root rots	17.6	17.6	Slugs	23.5	5.9
Rust	35.3	17.6	Thrips	17.6	17.6
Web blight	23.5	0.0	Whiteflies	17.6	23.5

a. BCMV = bean common mosaic virus.

Conclusions and future plans: We plan to use the information collected to help orient the Andean bean breeding program at CIAT and to make recommendations that can be used in the national plan for research in pulse crops, which is being formulated this year by government and non-governmental agencies. Increased attention to climbing beans and resistance to diseases such as anthracnose and *Ascochyta* blight are needed.

Contributors: MW Blair, P Zamorano, C Cardona

Publications

Book and Journal

Beebe S, Skroch PW, Tohme J, Duque MC, Pedraza F, Nienhuis J. 2000. Structure of genetic diversity among bean landraces of Mesoamerican origin based on Correspondence Analysis of RAPD. Crop Sci. 40:264-273.

Goossens A, Quintero C, Dillen W, De Rycke R, Valor JF, De Clercq J, Van Montagu M, Cardona C, Angenon G. 2000. Analysis of bruchid resistance in the wild common bean accession G02771: no evidence for insecticidal activity of arcelin 5. J Exp Bot 51: 1229-1236.

Mahuku G, Henríquez MA. 2000. Molecular markers dispute the existence of the "Afro-Andean" subgroup of the bean angular leaf spot pathogen, *Phaeoisariopsis griseola*. Phytopathology 90: S49 (abstract).

Manzano MR, van Lenteren JC, Cardona C, and Drost YC. 2000. Developmental time, sex ratio, and longevity of *Amitus fuscipennis* MacGown & Nebeker (Hymenoptera: Platygasteridae) on the greenhouse whitefly. Biol Control 18: 94-100.

Rao IM, Terry N. 2000. Photosynthetic adaptation to nutrient stress. In: Yunus M, Pathre U, Mohanty P, eds. Probing photosynthesis: Mechanism, regulation and adaptation. Taylor and Francis, UK. p 378-396.

Singh SP, Morales FJ, Miklas PN, Terán H. 2000. Selection for bean golden mosaic resistance in intra- and interracial bean populations. Crop Sci 40:1565-1572.

Tohme J, Beebe S, Iglesias C. 1999. Molecular characterization of the CIAT bean and cassava core collections. In: Johnson RC, Hodgkin T, eds. Core collections for today and tomorrow. International Plant Genetic Resources Institute (IPGRI), Rome, Italy. p 28-36.

Welch RM, House WA, Beebe S, Cheng Z. 1999. Genetic selection for enhanced bioavailable levels of iron in bean (*Phaseolus vulgaris* L.) seeds. J Agr Fd Chem 48:3576-3580.

Other

Morales F. 2000. El mosaico dorado y otras enfermedades del frijol común causadas por geminivirus transmitidos por mosca blanca en la América Latina: 1960-2000 40 años de investigación colaborativa. Centro Internacional de Agricultura Tropical (CIAT), Cali, Colombia. 169 p.

Workshop and Conference

Blair MW. 2000. La importancia de los marcadores moleculares y estudios del genoma en el fitomejoramiento. Invited speaker, paper presented at the International Alliance for Sustainable Agriculture (IASA) and Santa Catalina Experiment Station, Quito, Ecuador.

Blair MW. 2000. Selección asistida por marcadores en frijol. Invited speaker, paper presented at Universidad Nacional de Cajamarca, Cajamarca, Peru.

Blair MW, Gonzalez AV, Iriarte G, Buendía HF, Beebe S. 2000. Análisis molecular de poblaciones derivadas de retrocruzas avanzadas entre accesiones silvestres y variedades cultivadas de frijol común (*Phaseolus vulgaris* L.) XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 47.

Blair MW, Pedraza F, Beebe S, Weeden N. 2000. Nuevos marcadores moleculares para la selección asistida de caracteres múltiples del frijol (*Phaseolus vulgaris* L.). XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 45.

Cardona C. 1999. El manejo integrado de plagas en frijol: análisis y perspectivas. Conference paper presented at VI Meeting of Reunião Nacional de Pesquisa de Feijão (RENAFE), 21-26 Nov 1999, Salvador, Bahía, Brazil. 13 p.

Gomez OJ, Blair MW, Gullberg U, Frankow-Lindberg B, Gaitán E, Tohme J. 2000. Diversidad genética de variedades locales de frijol en Nicaragua. XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 53.

Jara C, Castellanos G, Mahuku G. 2000. Estado actual y proyección de la investigación relacionada con la mancha angular del frijol. Presented at the XXI Congreso Asociación Colombiana de Fitopatología y Ciencias Afines (ASCOLFI), 30 Aug-1 Sept 2000, CIAT, Palmira, Colombia.

Jara C, Castellanos G, Beebe S, Mahuku G. 2000. Un método rápido de invernadero para seleccionar germoplasma del frijol por resistencia a Macrophomina phaseolina y su aplicación para el mejoramiento a estres de sequía. XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 71.

Mahuku G, Henríquez, MA. 2000. Molecular markers dispute the existence of the "Afro-Andean" subgroup of the bean angular leaf spot pathogen, *Phaeoisariopsis griseola*. American Phytopathological Society (APS) annual meeting, 12-17 Aug 2000, New Orleans.

Mahuku G, Jara C, Castellanos G. 2000. La mancha angular de frijol: Donde estamos y para donde vamos. XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 69.

Osorno JM, Beebe S, Blair MW, Hoyos A, Terán H. 2000. Aumento en la productividad del frijol comun, mediante la introgresión de materiales silvestres. XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 48.

Quintero C, Terán H, Tohme J. 2000. Selección asistida por marcadores en el esquema de selección gamética en fríjol común en CIAT, Cali, Colombia. XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 52.

Rao IM, Troy P, Beebe S, Ricaurte J. 2000. Identificación de genotipos de fríjol común (*Phaseolus vulgaris* L.) con mejor adaptación a sequía. XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 56.

Rengifo J, Gonzalez AV, Muñoz M, Blair MW, Beebe S. 2000. Análisis de dos poblaciones de líneas recombinantes para el estudio de la herencia del contenido de minerales (hierro y zinc) en semilla de frijol (*Phaseolus vulgaris* L.). XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 46.

Ricaurte J, Terán H, Rao IM, Beebe S. 2000. Evaluación de genotipos de fríjol común (*Phaseolus vulgaris* L.) bajo estrés moderado de sequía. XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 55.

Terán H, Quintero C, Morales FJ, Beebe S. 2000. Selección de líneas rojas de frijol mediante el mejoramiento asistido por marcadores moleculares en CIAT, Cali, Colombia: caso mosaico dorado. XLVI Annual Meeting Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios (PCCMCA), 1-5 May 2000, San Juan, Puerto Rico. Proceedings Summary. p 50.

List of Donors

Australia:	Australian Center for International Agricultural Research (ACIAR)
Belgium:	Administration Generale de la Coopération au Développement (AGCD) Belgian Administration for Development Cooperation (BADC)
Canada:	Crop Development Centre, University of Saskatchewan (CDC) Canadian International Development Agency (CIDA) International Development Research Centre (IDRC)
Colombia:	Instituto Colombiano para el desarrollo de la Ciencia y la Tecnología "Francisco José de Caldas" (COLCIENCIAS)
Denmark:	Danish International Development Agency (DANIDA)
France:	Ministère des Affaires Etrangères (MAE)
Germany:	Bundes Ministerium Für Wirtschaftliche Zusammenarbeit und Entwicklung (BMZ)
Iran:	Seed and Plant Improvement Research Institute (SPII) Ministry of Agriculture, Islamic Republic of Iran
Peru:	Government of Peru (Ministry of Agriculture)
Switzerland:	Eidgenössische Technische Hochschule-Zentrum – Zentrum für Internationale Landwirtshaft (ETHZ-ZIL) Swiss Development Cooperation (SDC)
United Kingdom:	Department for International Development (DFID)
United States of America:	Colorado State University (CSU) International Food Policy Research Institute (IFPRI) Rockefeller Foundation United States Agency for International Development (USAID) Wallace Genetic Foundation, Inc

Contracts

Agricultura en Evolución, compañía (AgrEvo)
Asociación Colombiana de Productores de Flores (ASOCOLFLORES)
Dow Chemical Corp., Colombia
Francisco Terasawa Semente e Genética (FT Seeds), Brazil

Special Collaborative Projects

Title	Donor[a]	Country
Common bean germplasm trait evaluation and multivariate analyses	ACIAR	Australia
Genetic Improvement of *Phaseolus vulgaris* using exotic bean germplasm and biotechnology	AGCD	Belgium
Interspecific solutions to intractable solutions problems to common bean	AGCD/ BADC	Belgium
Development of common bean germplasm lines adapted to Western Canada	CDC	Canada
Meeting demand for beans in Sub-Saharan Africa in sustainable ways – PABRA (see IP-2 Project)	CIDA/ SDC/ USAID/ DFID	Canada Switzerland USA United Kingdom
Whitefly Project	DANIDA	Denmark
An integrated approach for genetic improvement of aluminum resistance of crops on low-fertility acid soils	BMZ	Germany
Genetic improvement of common bean cultivars adapted to higher latitudes in Iran	SPII – Ministry of Agriculture	Iran
Contribution of the government of Peru for "ñuñas" in highlands	Ministry of Agriculture	Peru
Bean Research Network for the Andean Zone – PROFRIZA	SDC	Switzerland
Regional collaborative bean network for Central America, Mexico and the Caribbean – PROFRIJOL	SDC	Switzerland
Assessing the impact of adapted germplasm on the phosphorus fertility of low phosphorus –supplying tropical soils	ETHZ	Switzerland
Genetic plant resources as a core element to safeguard bean harvest	ETHZ	Switzerland
Integrated Pest Management in grain legumes	ETHZ	Switzerland
Resistance to *Thrips palmi* in beans	ZIL	Switzerland
Improved beans for Africa and Latin America	DFID	United Kingdom
Comparison of alternative selection methods for improvement of pinto bean cultivars resistant to principal biotic factors	CSU	USA
Work on genetic variability among genotypes in the bean core collection	IFPRI	USA
Increasing food security and rural incomes in eastern, central, and southern Africa through genetic improvement of bush and climbing beans	Rockefeller Foundation	USA
A coordinated effort to mark and map important genes in commom bean: Universities of California, Cornell, Michigan State, North Dakota and Puerto Rico	USAID	USA
Germplasm improvement on-farm adaptive research program in Haiti	USAID/ PADF	USA
The development of molecular markers for the breeding of sustainable pest resistance in common beans: a novel strategy	Wallace Genetic Foundation, Inc.	USA

a. For acronyms used see page 187.

List of Collaborating Partners

Ing. Oscar Vizgarra, EEA "Obispo Colombres", Tucumán, Argentina
Dr Alain Goossens, University of Gent, Belgium
Dr Jozef Vanderleyden, Catholic University of Leuven, Leuven , Belgium
Ing. Juan Ortubé, Instituto de Investigaciones Agrícolas "El Vallecito", Santa Cruz, Bolivia
Ing. Carlos Rivadeneira, Universidad Autónoma Gabriel Rene Moreno, Santa Cruz, Bolivia
Dr Walter Cuadros, Sementes FT, Curutiba, Brazil
Dr Art Schaafsma, University of Guelph, Canada
Ing. Oscar Checa, CORPOICA-University of Nariño, Pasto, Colombia
Dr Pascal Leterme, Universidad Nacional de Palmira, Colombia.
Dr Aristóbulo López, CORPOICA, Tibaitatá, Colombia
Ing. Gloria Esparanza Santana, CORPOICA Rionegro, Antioquia, Colombia
Dr Edmundo García, CORPOICA, Palmira, Colombia
Dr Helga Blanco Metzler, University of Costa Rica, San José, Costa Rica
Ing. Carlos Manuel Araya, National University, Heredia, Costa Rica
Ing. Rodolfo Araya, University of Costa Rica, San Jose, Costa Rica
Ing. Benito Faure, EE "Liliana Dimitrova", Ministry of Agriculture, La Habana, Cuba
Ing. German Hernandez, EE "La Renee", Instituto de Suelos, MINAG, Quivican, Cuba
Ing. Julio César Nin, SEA-CIAS, San Juan de la Maguana, Dominican Republic
Ing. Eduardo Peralta, INIAP, Ecuador
Ing Carlos Atilio Perez, CENTA, El Salvador
Dr J Drevon, INRA, Montpellier, France
Ing. Juan José Soto, ICTA, Guatemala, Guatemala
Ing. Eliassaint Magloire, ORE, Camp-Perrin, Haiti
Ing. Levael Eugene, USAID/PADF Project, Haiti
Ing. Emmanuel H. Prophète, CRDA, Ministery of Agriculture, Port-au-Prince, Haiti
Ing Danilo Escoto, DICTA, Tegucigalpa, Honduras
Dr Juan Carlos Rosas, Escuela Agrícola Panamericana (Zamorano), Honduras.
Dr Jorge Acosta, INIFAP, Texcoco, Edo. Mexico, Mexico
Ing. Javier Cumpian Gutierrez, Veracruz, Mexico
Dr Ramón Garza, INIFAP, Texcoco, Mexico
Ing. Ernesto Lopez, INIFAP, Veracruz, Mexico
Ing. Aurelio Llano, INTA/CNIA, Managua, Nicaragua
Ing Ms.C. Julio Molina, INTA, Estelí, Nicaragua
Prof. Bal Ram Singh, Agric. Univ. of Norway, Aas, Norway
Ing Edwin Lorenzo, IDIAP, David, Chiriquí, Panama
Ing. Angel Valladolid, PROMPEX, Lima, Peru
Dr James Beaver, University of Puerto Rico, Mayaguez, Puerto Rico
Dr Deidre Fourie, ARC-GCRI, South Africa
Prof. Silvia Dorn, ETH University Zurich, Switzerland
Dr Emmanuel Frossard, ETH, University Zurich, Switzerland
Dr Astrid Oberson, ETH, University Zurich, Switzerland
Dr Peter Graham, University of Minnesota, USA
Dr James D. Kelly, Michigan State University, USA
Dr Jonathan Lynch, Pennsylvania State University, USA.
Dr Norman Weeden , University of Montana, USA

Project Staff List

Senior staff

Beebe, Stephen, PhD, Breeder, Geneticist
Blair, Matthew, PhD, Germplasm Characterization Specialist/Bean Breeder
Cardona, César, PhD, Entomologist, Bean Project Manager
Abelardo Viana, Economist, Regional Coordinator: PROFRIJOL (stationed in Guatemala, Guatemala)
Mahuku, George, PhD, Plant Pathologist
Morales, Francisco, Virologist
Rao, Idupulapati, PhD, Plant Nutritionist/Physiologist
*Voysest, Oswaldo, PhD, Agronomist, Regional Coordinator PROFRIZA

Administrative assistant

Giraldo, Isabel Cristina, Economist, Office of Bean Project Manager

Research associates and assistants

Bueno, Juan Miguel, Ing. Agr., Entomology
Cajiao, César, Ing. Agr., Andean Bean Genetics
Castaño, Mauricio, Ing. Agr., Virology Research Unit
Giraldo, Martha Cecilia, Bioch., Germplasm Characterization Lab.
*González, Alma Viviana, Bioch., Germplasm Characterization Lab.
Jara, Carlos Eduardo, Ing. Agr., Phytopathology
*Osorno, Juan Manuel, Ing. Agr., Mesoamerican Bean Genetics
Pedraza, García Fabio, Biol., Germplasm Characterization Lab.
*Rendón, Francisco, Ing. Agr., Entomology
*Rengifo, Judith, Biol., Germplasm Characterization Lab.
Ricaurte, José Jaumer, Ing. Agr. Plant Nutrition
Rodriguez, Isaura, Ing. Agr., Entomology
Terán, Henry, Estat. Mesoamerican Bean Genetics

Secretaries

Arenas, Beatriz, Entomology
Zamorano, Patricia, Breeding/Germplasm Characterization

Technicians

Castellanos, Guillermo, Pathology
Cerón, Carlos Alberto, Mesoamerican Bean Genetics
Cuasquer, Juan Bosco, Pathology
*Garzón, Francisco de Paula, Entomology
Gómez, Ivan, Germplasm Characterization
Grajales, Miguel Angel, Mesoamerican Bean Genetics
Hoyos, Agobardo, Germplasm Characterization
Joaqui, Orlando, Mesoamerican Bean Genetics
Morales, Héctor, Entomology
Ortíz, Guillermo, Germplasm Characterization
Valor, Jose Flower, Entomology
Vargas, Luis Alberto, Mesoamerican Bean Genetics
Zuleta, Jesús María, Mesoamerican Bean Genetics

Trainees

*Durán, Isabel Cristina, Dow AgroSciences of Colombia, Entomology
*Gómez, Oscar, Nicaragua, Germplasm Characterization Lab.
Muñoz, Mónica Cecilia (COLCIENCIAS trainee), Germplasm Characterization Lab.

PhD Students and MSc Thesis

Bravo, Enrique, Colombia, Virology Research Unit
Frei, Andrea, Switzerland, Entomology
Manzano, María del Rosario, Colombia, Entomology
*Schmale, Kristina, Germany, Entomology

Visiting Scientists

Daniela Schaerer, Switzerland, Entomology

Pregraduate Thesis Students

Astudillo, Carolina, Universidad del Valle, Colombia, Germplasm Characterization Laboratory.
Buendía, Héctor Fabio, Universidad del Tolima, Colombia, Breeding
Díaz John, Universidad Nacional, Colombia, Entomology
Guerrero, Alberto Fabio, Universidad Javeriana, Colombia, Breeding
Henríquez, Maria Antonia, Universidad Nacional, Colombia, Pathology
Iriarte, Gloria Astrid, Universidad del Tolima, Colombia, Germplasm Characterization Laboratory.
Osorio, Juliana, Universidad Nacional, Colombia, Entomology
Pantoja, Wilfredo, Universidad del Valle, Colombia, Germplasm Characterization Lab.
Riascos, Jhon Jaime, Universidad del Valle, Colombia, Pathology

*Left in 2000

List of Acronyms and Abbreviations Used

ACIAR	Australian Center for International Agricultural Research
AFLP	amplified fragment length polymorphism
AGCD	Administration Generale de la Coopération au Développement, ISABU, Burundi
AgrEvo	Agricultura en Evolución, compania
AID	Agency for International Development
ALS	angular leaf spot
AMOVA	analysis of molecular variance
ANT	anthracnose
ARC	Agricultural Research Council of GCRI, South Africa
ARO	advanced research organization
ARS	Agricultural Research Service, USDA, Washington
ASCOLFI	Asociación Colombiana de Fitopatología y Ciencias Afines
ASOCOLFLORES	Asociación Colombiana de Productores de Flores
BADC	Belgian Administration for Development Cooperation
BCMV	bean common mosaic virus
BCMNV	bean common mosaic necrosis
BGMV	bean golden mosaic virus
BGYMV	bean golden yellow mosaic virus
BMZ	Bundesministerium für Wirtschaftliche Zusammenarbeit und Entwicklung (*Federal Ministry for Economic Cooperation and Development*), Germany
BOL	Bolivia
BSMV	bean severe mosaic virus
CATIE	Centro Agronómico Tropical de Investigación y Enseñanza, Costa Rica
CBB	common bacterial blight
CCMV	cowpea chlorotic mottle virus
CDC	Crop Development Centre, University of Saskatchewan, Canada
CENTA	Centro Nacional de Tecnología Agropecuaria, El Salvador
CGIAR	Consultative Group on International Agricultural Research
CIAL	Comité de Investigación Agrícola Local (*farmer-led research committee*)
CIAS	Centro de Investigaciones Agrícolas del Sureste, SEA, Dominican Republic
CIDA	Canadian International Development Agency
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo, Mexico
CIPASLA	Consorcio Interinstitucional para una Agricultura Sostenible en Laderas, Colombia
CL	*Colletotrichum lindemuthianum*
CNIA	Centro Nacional de Investigación Agropecuaria, Nicaragua
CNPAF	Centro Nacional de Pesquisa de Arroz e Feijão, Brazil
COL	Colombia

COLCIENCIAS	Instituto Colombiano para el desarrollo de la Ciencia y la Tecnología “Francisco José de Caldas
CORFOCIAL	Corporación para el Fomento de los Comités de Investigación Agrícola Local, Colombia
CORPOICA	Corporación Colombiana de Investigación Agropecuaria
CPSMV	cowpea severe mosaic virus
CRDA	Centre Recherche de Agriculture, Haiti
CRSP	Collaborative Research Support Project of USAID
CSU	Colorado State University, USA
DANIDA	Danish International Development Agency
DFID	Department for International Development, UK
DICTA	Dirección de Investigación de Ciencias y Tecnología Agrícola, Honduras
DIFALS	Angular Leaf Spot Differentials nursery
DIFANT	Anthracnose Differentials nursery
DIFFUS	*Fusarium* Differentials nursery
DIFRUST	Rust Differentials nursery
DMS	Data Management System of ICIS
EAP	Escuela Agrícola Panamericana, Zamorano, Honduras
ECAR	Ensayo regional de Rendimiento, PROFRIJOL
EEA	Estación Experimental Agroindustrial
EMBRAPA	Empresa Brazileira de Pesquisa Agropecuária
ERIC	enterobacterial repetitive intergenic consensus REP-PCR primers
ETHZ	Eidgenössische Technische Hochschule-Zentrum, Switzerland
ETHZ-ZIL	ETHZ– Zentrum für Internationale Landwirtshaft
FENALCE	Federación Nacional de cultivadores de Céreales, Colombia
FIDAR	Fundación para la Investigación y el Desarrollo Agroindustrial Rural, Colombia
FRIDA	Fundación Regional de Investigación y Desarrollo Agropecuario
FT Seeds	Francisco Terasawa Semente e Genética, Brazil
GCRI	Grain Crops Research Institute, South Africa
G x E	genotype x environment
GMS	Germplasm Management System of ICIS
HFI	high fertilizer input
HGRP	Hurricane Georges Recovery Program of USDA for Haiti
HTI	Haiti
IAC	Instituto Agronômico de Campinas, Brazil
IAREC	Irrigated Agriculture Research and Extension Center, USA
IASA	International Alliance for Sustainable Agriculture
IBN	International Bean Nursery
IBYAN	International Bean Yield and Adaptation Nursery
ICIS	International Crop Information System
ICTA	Instituto de Ciencia y Tecnología Agrícolas, Guatemala City, Guatemala
IDIAP	Instituto de Investigación Agropecuaria, Panama
IDRC	International Development Research Center, Canada

IFPRI	International Food Policy Research Institute
IGS	intergenic spacer region
IIA	Instituto de Investigaciones Agrícolas, Bolivia
IICA	Instituto Interamericano de Cooperación para la Agricultura
INIAP	Instituto Nacional Autónomo de Investigaciones Agropecuarias, Ecuador
INIFAP	Instituto Nacional de Investigaciones Forestales Agrícolas y Pecuarias, Mexico
INRA	Institut National de Recherche Agronomique, France
INTA	Instituto Nacional de Tecnología Agropecuaria, Nicaragua
IPEL	Instituto Peruano de Leguminosas de Grano
IPHIS	International *Phaseolus* Information System, an ICIS
IPM	integrated pest management
IPRA	Investigación Participativa en Agricultura / Participatory Research in Agriculture of CIAT
IRRI	International Rice Research Institute, Philippines
MAE	Ministère des Affaires Etrangères, France
MAS	marker-assisted selection
MINAG	Ministerio de Agricultura, Cuba
MINEDUCACION	Ministry of Education, Colombia
MWI	Malawi
NARIs	national agricultural research institutes
NARS	national agricultural research systems
NFI	no fertilizer input
NGO	nongovernmental organization
NIC	Nicaragua
NOC	Network Operation Center
NTSYS	numerical taxonomy system (a type of computer package)
ORE	Organization for the Rehabilitation of the Environment, Haiti
PABRA	Pan-Africa Bean Research Alliance
PADF	Pan American Development Foundation of USDA
PAG	Plant and Animal Genome conference, USA
PC	*Phaseolus coccineus*
PCCMCA	Programa Cooperativo Centroamericano para el Mejoramiento de Cultivos Alimenticios, Guatemala
PCR	polymerase chain reaction
PG	*Phaeoisariopsis griseola*
PP	*Phaseolus polyanthus*
PPO	Project Planning by Objectives
PRM	Programa Regional de Maíz, Guatemala
PROFRIJOL	Proyecto Regional de Frijol para C entro América, México y el Caribe
PROFRIZA	Proyecto Regional de Frijol para la Zona Andina, CIAT
PROMPEX	Comisión para la Promoción de Exportaciónes, Peru
PRONATTA	Progama Nacional de Transferencia de Tecnología, Colombia
QTL	quantitative trait locus or loci

RAM	random amplified microsatellites
RAPD	random amplified polymorphic DNA (a technique for mapping genomes)
RCBD	randomized complete block designs
RENAFE	Reunião Nacional de Pesquisa de Feijão
REP-PCR	repetitive extragenic palindromic polymerase chain reaction
RFLPs	DNA restriction fragment length polymorphisms
RILs	recombinant inbred lines
SAHN	sequential, agglomerative, hierarchic, and nonoverlapping clustering methods
SCAR	sequence characterized amplified region molecular markers
SDC	Swiss Development Cooperation
SEA	Secretaría de Estado de Agricultura, Dominican Republic
SLP	Systemwide Livestock Program
SLU	Sveriges Lantbruks Universitet (Swedish University of Agricultural Science)
SNF	symbiotic nitrogen fixation
SPII	Seed Plant Improvement Institute, Iran
SPS	single plant selections
SSR	simple sequence repeat
SWNM	Soil Water Nutrient Management Program (SWP of the CGIAR)
TNC	total nonstructural carbohydrates
TROPILECHE	Sistemas de Alimentación a base de leguminosas mejoradas para pequeños productores con ganado de doble proposito en América Latina tropical ("Improved legume-based feeding system for smallholder dual-purpose cattle production in tropical Latin America"), a CGIAR project
TZA	Tanzania
UAGRM	Universidad Autónoma Gabriel René Moreno, Bolivia
UDENAR	Universidad de Nariño, Colombia
UMATAs	Unidades Municipales de Asistencia Técnica Agropecuaria, Colombia
UNALM	Universidad Nacional Agraria "La Molina", Peru
UPGMA	unweighted pair-group distance method of averaging
USAID	United States Agency for International Development, Washington
USDA	United States Department of Agriculture
VIPADOGEN	Vivero de Padres Donanates de Genes Necesarios
XCP	*Xanthomonas campestris phaseoli*
XCPF	*X. campestris phaseoli* pv. *Fuscans*
ZIL	Zentrum für internationale Landwirtshaft (Centre for International Agriculture)