

Genetic Resources of *Phaseolus* Beans

Their maintenance, domestication, evolution, and utilization

edited by

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1. INTRODUCTION

Experiments on intraspecific genetic variability of plant species have revealed complex spatial patterns of variability among and within populations ranging from clines at one end, and ecotypes, to the other (for a review, see BRIGGS and WALTERS, 1984).

A cline represents a continuous gradation in the expression of a trait resulting from a variety of causes such as a continuously varying environment or genetic drift associated with limited migration (for examples, see BRIGGS and WALTERS, 1984: p. 168; AMMERMAN and CAVALLI-SFORZA, 1984). Traits showing clinal variation include quantitative traits with a more complex genetic control, exemplified by the variability for plant height and frost tolerance in *Achillea* sp. (CLAUSEN et al., 1948). They also include traits controlled by single loci with a major effect, such as the genes coding for lotaustralin (a cyanogenic glucoside) and linamarase (the enzyme releasing HCN from lotaustralin) in *Trifolium regens* in Europe (DADAY, 1954a and b).

As defined by WILLIAMS (1964: p. 305), ecotypes are distinct populations resulting from the genotypic response of individuals of a species to a particular habitat

" The most important distinction with the clinal distribution is the discontinuity of variation. Depending on the cause of the discontinuity, edaphic, climatic, biotic, and geographic ecotypes have been recognized.

Cultivated plants are also subject to ecotypic differentiation. Compared to natural evolution operating on their wild relatives, however, crop evolution includes an additional dimension resulting from human intervention. This added dimension includes selection for adaptation to agroecosystems (e.g. loss of dormancy, even germination, non-shattering inflorescences or fruits, competition in dense stands, even ripening, etc.), selection for adaptation to a broad range of new environments outside the centers of domestication, and repeated founder effects taking place during selection and migration.

Starting with domestication and during subsequent evolution, a more or less discontinuous variation was created in crop plants. These discrete variants have been called variously agro-ecotypes (GREGOR, 1933), ecogeographical races (e.g., rice: CHANG, 1976a and b; 1985),

or races (e.g., maize: GOODMAN and Bird, 1977; sorghum: HARLAN and de WET, 1972; HARLAN and STEMLER, 1976). Following HARLAN and de WET's (1971) terminology, a race is a " ... biological unit with some genetic **integrity** ... and a distinct cohesion of morphology, geographic distribution, ecological adaptation, and frequently of breeding behavior ... ; ... it originated in some geographic region at some time in the history of the crop .. .". Morphological, physiological, cytogenetic, genetic, and phytopathological traits, as well as isozymes and seed proteins have been used to characterize crop races. Perhaps one of the best studied cases is the differentiation of Asian rice (~ sativa L.) into the indica (tropical) and japonica (temperate) ecogeographic races or subspecies (see section 4, this chapter). Another example is given by the races of teosinte, the wild relative of maize (SMITH et al., 1981, 1982, and 1984).

In this chapter, I will review genetic evidence suggesting the existence of two major gene pools or geographic races in common bean and I will then discuss these findings in the light of previous morphological, biochemical, physiological, and phyto-pathological observations. A comparison will then be made with Asian rice and alfalfa, also exhibiting two major geographic races. Finally, I will outline some future research orientations.

2. GEOGRAPHIC DISTRIBUTION OF GENES INDUCING F1 HYBRID WEAKNESS IN CULTIVATED COMMON BEAN

Electrophoretic screening of phaseolin seed protein has revealed a parallel geographic distribution pattern of phaseolin types in wild and cultivated common beans; this has led us to postulate multiple centers of domestication for this crop plant (GEPTS, 1984; GEPTS ~ al., 1986; GEPTS and BLISS, 1986; GEPTS, this volume). Domestication in Middle America lead to small-seeded, 'S' phaseolin cultivars, whereas in Colombia, it lead to small-seeded, 'B' phaseolin cultivars. In the southern Andes (Peru and Argentina) on the other hand domestication gave rise to large-seeded, 'T' (and possibly 'A', 'C', and 'H') phaseolin cultivars. Because of the geographic differentiation of phaseolin, it became possible to follow the dissemination of common bean cultivars from their centers of domestication to other regions of the world (GEPTS, 1984; GEPTS et al., 1986; GEPTS and BLISS, 1986; GEPTS, this volume).

In a similar way, phaseolin was used as a marker to identify the origin of genes involved in F1 hybrid weakness. Over the years, several scientists have reported crosses between specific genotypes resulting in weakly growing or lethal and sterile F1 plants. Symptoms exhibited by these plants include a "crippled" morphology (COYNE, 1965), retarded growth, chlorosis of the trifoliolate leaves, reduced root growth, and formation of adventitious roots on the hypocotyl (SHII et Qi., 1980 and 1981; SINGH, 1983; SINGH and GUTIERREZ, 1984), chlorotic primary leaves, absence of trifoliolate leaves, degeneration of the tap

root, and development of adventitious roots on the stem just above the soil level (YORK and DICKSON, 1975), apical chlorosis, leaf rolling and seedling wilt (PROVVIDENTI and SCHROEDER, 1969), and absence of roots (T. OSBORN and F.A. BLISS, pers. comm.).

Genetic analysis showed this F₁ hybrid weakness to be controlled by two complementary genes, whether dominant (YORK and DICKSON, 1975), semi-dominant (SHII et al., 1980), or recessive (COYNE, 1965; PROVVIDENTI and SCHROEDER, 1969). Grafting experiments indicated that the complementary genes controlled a shoot and a root factor, respectively, in the case studied by SHII et al. (1981). Alleviation of reduced root growth by exogenous cytokinin applications pointed to a biochemical lesion affecting hormonal metabolism (SHII et al., 1981).

Determination of phaseolin type by one-dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis revealed that in each of the crosses giving rise to F₁ hybrid weakness, one of the parents had an 'S' phaseolin type and the other either a 'T' or a 'C' phaseolin type (Table 1) (GEPTS and BLISS, 1985). Seed size analysis showed that 'S' phaseolin cultivars had significantly smaller seeds than 'T' or 'C' phaseolin cultivars (GEPTS and BLISS, 1985).

F hybrid weakness appeared, therefore, only in crosses involving a small-seeded, 'S' phaseolin parent, on one hand, and a large-seeded, 'T' or 'C' phaseolin, on the other. Control experiments showed that crosses within the small-seeded, 'S' phaseolin cultivar group or the large-seeded, 'T' or 'C' phaseolin group, did not lead to F₁ hybrid weakness (SINGH, 1983; SINGH and GUTIERREZ, 1984). Given the geographic origin of the different phaseolin types and seed sizes, it is possible to conclude that F₁ hybrid weakness appeared only in crosses between a Middle American and an Andean cultivar.

It should be stressed that several crosses between small-seeded, 'S' phaseolin type cultivars and large-seeded, 'T' or 'C' phaseolin cultivars give normal progenies. It is therefore unlikely that phaseolin or seed size genes are directly involved in the expression of F₁ hybrid weakness. Genes determining F₁ hybrid weakness may, however, be linked genetically to the phaseolin or any seed size loci.

The highly deleterious nature of F hybrid weakness represents a high selection pressure against its continued existence and could explain why the two complementary genes are not observed jointly within the same region (Middle America or the Andes). However, as suggested by LEVIN (1978), there is no evidence that complementary genes responsible for F₁ hybrid weakness evolved specifically to reduce or eliminate introgression. They may be genes coding for essential metabolic functions in non-hybrid plants and which lead only incidentally to the production of inviable hybrid plants. Common bean breeding programs, by crossing genotypes of widely different origin, effectively bridge the geographical gap and this, in turn, leads to more frequent observations of F₁ hybrid weakness.

TABLE 1. Phaseolin type of parental genotypes involved in F₁ hybrid weakness (GEPTS, 1984; GEPTS and BLISS, 1985)

Source	Parent A		Parent B	
	Genotype	Phaseolin	Genotype	Phaseolin
COYNE (1965)	PI209806	'T'	GN Nebraska	'S'
SHII <i>et al.</i> (1980)	Cuilapa 72	'S'	Bolivia 6	'T'
YORK and DICKSON (1975)	PI165435	'S'	('Maestro' 'Spartan Arrow'	'T' 'C'
OSBORN and BLISS (pers. comm.)	BBL 274	'T'	Rosinha 6-1	'S'
SINGH (1983); SINGH and GUTIERREZ (1984)	'Carioca'	'S'	(G7623 ^a (G5066 (G7633 ('Tortolas Diana'	'C' 'T' 'T' 'C'
	G623	'C'	('Carioca' (G7148 (BAT332 ^b (BAT1061	'S' 'S' 'S' 'S'
	BAT332	'S'	(G153 (G568 (G623 (G5066 (G5129 (G7613 (G7633 (Línea 23 ^c ('Tortolas Diana'	'C' 'T', 'C' 'C' 'T' 'T' 'T' 'T' 'T' 'T' 'C'

^a G: Accession number of the *Phaseolus* world collection at the Centro Internacional de Agricultura Tropical (CIAT), Cali, Colombia

^b Breeding line of CIAT

^c Breeding line of the Instituto Colombiano Agropecuario, Palmira, Valle, Colombia

Cases of F1 hybrid weakness controlled by complementary genes have also been described in rice and wheat. OKA (1957) observed that hybrid inviability arising in intervarietal *Oryza sativa* crosses was under the control of two complementary dominant or recessive genes. Hybrid necrosis in *Triticum aestivum* is controlled by two complementary genes - Ne_1 and Ne_2 - whereas grass clump dwarfness is controlled by three complementary dominant genes - D_1 , D_2 , and D_3 . In both cases, the genes involved had different geographic distributions (ZEVEN, 1976).

The simple genetic control of F hybrid weakness in *P. vulgaris* may be indicative of incipient geographical speciation within this species. Further divergence on an evolutionary time scale may lead to more pronounced and genetically and physiologically more complex isolation barriers.

3. A MIDDLE AMERICAN AND AN ANDEAN GEOGRAPHIC GENE POOL IN CULTIVATED COMMON BEAN

The appearance of F1 hybrid weakness in crosses involving an Andean cultivar, on one hand, and a Middle American cultivar on the other, reflects the geographical isolation between the cultivars of the two regions. On an evolutionary time scale, this isolation may have led to genetic divergence and the establishment of two distinct gene pools. A gene pool is defined here as a set of genotypes characterized by:

- 1) a circumscribed geographic distribution;
- 2) specific allele frequencies: some alleles may be found predominantly or exclusively in one or the other gene pool;
- 3) similar allele associations: specific alleles of different genes may be associated with each other more often than random assortment would predict; this association may be due to phylogenetic relatedness, genetic linkage, selection, founder effects, as well as physiological or developmental constraints;
- 4) differential adaptation to climatic, edaphic, and biotic conditions; and
- 5) potential or actual reproductive isolation with some or all other gene pools.

Morphological, phytopathological, biochemical, and adaptation data, in addition to the genetic data just presented, point to the existence of a Middle American and an Andean gene pool (Table 2).

CIAT (1980) classified the growth habits of common bean cultivars in four categories: determinate bush upright (type I), indeterminate bush upright (type II), indeterminate bush prostrate (type III), and indeterminate climber (type IV) (for a description of these four growth habits, see also SINGH, 1982). Whereas the four growth habits are found both in Middle America and in the Andes, cultivars of the Andes -

TABLE 2. Evidence suggesting a Middle American and an Andean gene pool in common bean (for further explanations, see text)

Type of evidence	Source
1. Morphology	
* seed size and correlated effects on leaf size and internode length	KAPLAN, 1956; EVANS, 1973 and 1976; GEPTS et al., 1986
2. Phytopathology	
* dominant I gene for BCMV resistance	S. TEMPLE, pers. comm.
* rust (<i>Uromyces phaseoli</i>) resistance	STAVELY, 1982 and 1984
3. Biochemistry	BASSIRI and ADAMS, 1978
* isozymes	GEPTS et al., 1986; GEPTS and BLISS, 1986;
* phaseolin	GEPTS, this volume
4. Genetics	GEPTS and BLISS, 1985
* reproductive isolation	GHADERI et al., 1982 (see Fig. 1)
5. Adaptation	
* environmental reaction measured by yield	

the average have larger seeds than Middle American cultivars. For example, both 'cranberry' and 'pinto' cultivars exhibit a type III growth habit. 'Cranberry' beans originated in the Andes and have larger seeds than 'pinto' beans which originated in Middle America. In addition, seeds are usually correlated with larger leaves and internodes with concomitant effects on the overall habit.

The dominant I allele conferring resistance against systemic infection by bean common mosaic virus (BCMV or bean virus 1) (ALI, 1950; DRIJFHOUT et al., 1978) is found exclusively among certain groups of land races of Middle American origin, including the small-seeded, black cultivars, as well as the 'mulatinhos', 'chumbinho', and 'Carioca' types from Brazil. Andean landraces and certain American landrace groups such as the light red, small-seeded types, the 'azufrados', and the 'bayos' do not carry this allele. It has been introduced successfully by breeding, however, into cultivars of both Middle American and Andean origin, such as 'navies', 'bayos', 'great northerns', 'pintos', 'red kidneys', 'white kidneys', and snap beans (S. TEMPLE, pers. comm.).

Coevolution between the common bean plant and associated organisms, such as pathogens, pests, and *Rhizobium phaseoli*, may have led to analogous gene pools in these organisms. STAVELY (1982 and 1984) observed that 'red kidney' and snap beans, whose origin has been traced to the Andes based on phaseolin type, growth habit, and seed size, had similar reactions to a set of 20 races of common bean rust (*Uromyces phaseoli*) compared to cultivars of different origin. The pathogen and the host may therefore have different genes for virulence and resistance, respectively, in Middle America and in the Andes. It may be worthwhile investigating whether a combination of genes for resistance from the two regions provides a more stable resistance than a combination of genes from the same region.

If coevolution is operating in the *R. vulgaris* - *R. phaseoli* symbiosis, *R. phaseoli* might also consist of a Middle American and an Andean group of strains. Coevolution might lead to a specificity between the common bean host and the *Rhizobium* symbiont operating at several levels: recognition and competition for nodule sites, degree of adhesion to the root surface, degree of nodulation (number, size, and distribution), time to nodulation, nitrogenase activity, percentage of plant nitrogen derived from the atmosphere, etc. (F.A. BLISS and P. GRAHAM, pers. comm.). Knowledge of coevolutionary relationships may allow us to better match the host and symbiont genotypes to achieve maximum levels of N₂ fixation. One or the other region may have produced host-*Rhizobium* combinations adapted to specific stress conditions, such as low pH or high temperature in soils.

GHADERI et al. (1982) studied the environmental reaction as assessed by yield - of 98 cultivars in 8 locations of Michigan (USA). Using canonical analysis, three groups were

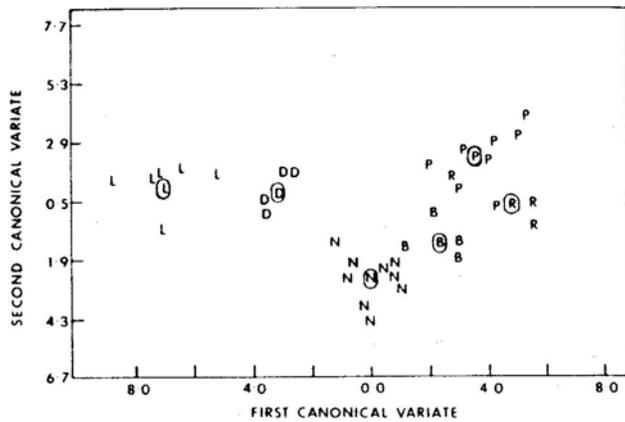


FIGURE 1. Canonical analysis of environmental response, as measured by yield, of dry bean cultivar classes of the USA (from Ghaderi et al., 1982).

L: 'light red kidney'; D: 'dark red kidney'; N: 'navy'; B: 'tropical blacks'; P: 'pinto'; and R: 'red Mexican'. Circled letters represent cultivar class averages.

recognized, each consisting of two classes: 'light and dark red kidney', 'navy' and 'tropical black', and 'pinto' and 'red Mexican' (Fig. 1). The first canonical variate separated the 'red kidneys' from the other two groups. The second canonical variate separated the 'navies' and 'tropical blacks' from the 'pintos' and 'red Mexicans'.

Phaseolin type, seed size, and growth habit indicate that the 'red kidneys' originated in the Andes, whereas the other groups originated in Middle America. Therefore, the contrasting environmental adaptations of these groups can be explained by their different evolutionary origin, in particular the difference between 'red kidneys' and the two other groups. These data also show that heterogeneity in environmental reactions occurs among groups of the same evolutionary origin (i.e. 'navies' and 'tropical blacks' vs. 'pintos' and 'red Mexicans'). It may be useful to examine the range of environmental adaptations both within and between the Middle American and Andean gene pools, and to compare these ranges with the environmental reaction of the wild common beans of the two regions.

BASSIRI and ADAMS (1978) performed an isozyme analysis on a series of USA cultivars belonging to different commercial seed type categories. Only the esterases and peroxidases had good band resolution and were sufficiently polymorphic to assess genetic relationships. Based on the number of polymorphic bands shared by each cultivar pair, a banding

similarity index was calculated. I averaged these banding similarity indices for each pairwise commercial class comparison (Table 3).

The 'red kidney' class and 'Michigan Cranberry' were closely related to each other, as were the 'navy', 'great northern', 'tropical black', 'pinto' and 'red Mexican' classes. Phaseolin type, seed size, and growth habit indicate that the former originated in the Andes, whereas the latter originated in Middle America. Isozymic differences reflect the different origin of the two groups; geographical isolation led to the appearance of different genes or alleles (or combinations thereof) in Middle America and in the Andes.

The evidence presented so far is suggestive of the existence of a Middle American and an Andean common bean gene pool. By analogy with Asian rice, these gene pools could be called "mesoamericanus" and "andinus", respectively.

4. COMPARISON WITH ASIAN RICE AND ALFALFA

Asian rice (*Oryza sativa* L.) and alfalfa (or lucerne; *Medicago sativa* L.) provide two examples of a similar organization of the cultivated germplasm into two entities with contrasting characters.

In rice, the japonica and indica ecogeographical races¹ can be separated on the basis of geographic distribution, morphological, physiological, genetic, cytogenetic, biochemical, and phytopathological data (LU and CHANG, 1980; TAKAHASHI, 1984; SECOND, 1985).

The indica (or 'hsien') race is a tropical race with native distribution mainly in southern Asia, including south China; the japonica (or 'keng') race represents a temperate race and is encountered mostly in northern China, Japan, the Philippines, and Taiwan.

The two races can be distinguished by a complex of morphological traits including vegetative characters, such as plant height, tillering tendency, and leaf shape and color, and reproductive characters, such as grain shape, pubescence of the hull, degree of grain shedding and the presence of awns (CHANG, 1980; TAKAHASHI, 1984).

Physiologically, indica and japonica cultivars can be separated by their tolerance to cool temperatures and to drought (TAKAHASHI, 1984). They are further distinguished by F1 sterility and restrictions to recombination in crosses between the two types (CHANG, 1980; SECOND, 1982).

MORISHIMA (1969) established that rice blast (*Piricularia oryzae* Cav.) strains she had studied could be classified into two groups: the indica group which had been isolated in India, Pakistan, Thailand, Indonesia, and Vietnam, and was pathogenic on indica type varieties; the japonica group

1. Some authors (e.g. CHANG, 1976a and b; TAKAHASHI, 1984) recognize a third - secondary - race: javanica

TABLE 3. Averages of banding similarity indices for commercial dry bean classes of the USA

Commercial class	'red kidney'	'Michigan Cranberry'	'navy'	'great northern'	'tropical black'	'pinto'	'red Mexican'
No. of cultivars	8	1	6	6	4	2	3
'red kidney'		15.9	10.0	8.8	9.8	10.4	10.7
'Michigan Cranberry'			11.5	9.0	10.5	10.0	9.7
'navy'				14.2	15.7	13.6	12.2
'great northern'					15.3	14.4	13.7
'tropical blacks'						16.0	14.5
'pinto'							16.7

a Modified from BASSIRI and ADAMS (1978)

which had been collected in Japan and was pathogenic on japonica rice cultivars.

A multivariate analysis of isozyme data revealed two cultivar groups corresponding to the indica and japonica types (SECOND, 1982). The javanica type recognized by certain authors appeared to have been derived from the japonica type. Based on F1 pollen sterility relationships, two extreme groups were identified. They had each a limited isozyme diversity but were complementary in that, considering the 15 most polymorphic isozymes (out of 40), most combinations of electromorphs observed could theoretically be obtained by recombination between them. These groups were thus considered to represent the indica and japonica ancestral isozyme combinations (SECOND, 1982). Additional biochemical traits distinguishing the indica from the japonica types include the phenol reaction and the amylose content of the grain (TAKAHASHI, 1984).

It should be kept in mind, however, that numerous intermediates exist between the indica and japonica races (SECOND, 1982) and that within each race, further subdivisions can be recognized. For example, among the indica types of the Ganges delta, three subtypes have evolved corresponding to the winter (boro), summer (aus) and autumn (aman) growing season (CHANG, 1980). Rice cultivars have also been categorized according to the water regime: deep water, shallow (or irrigated), and dryland (or upland or rainfed) (CHANG, 1980).

According to SECOND (1982 and 1985), the indica and japonica subspecies arose through independent domestication events, in tropical South Asia and in China, respectively. Hybridization between the two subspecies and with the local wild rice populations led to the appearance of numerous races within each subspecies. OKA (1974), on the other hand, suggested a monophyletic origin for cultivated rice. After domestication, the two types became differentiated because of different selection pressures. CHANG (1976a and b; 1980) assumed that the indica race was domesticated first and gave rise to the japonica race.

The genetic variability of alfalfa (*Medicago sativa* L.) is organized around two polar variants. *M. sativa* subsp. *sativa* and *M. sativa* subsp. *falcata* (L.) Arcangeli, between which a continuum of intermediate types exists (*M. sativa* subsp. *x varia* (Martyn) Arcangeli). Subspecies *sativa* and *falcata* differ geographically, morphologically, ecologically, and agronomically (SMALL and BROOKES, 1984).

Subspecies *sativa* is distributed in the Middle East and around the Black Sea and the Caspian Sea, whereas subspecies *falcata* is found in Eurasia, from northern Europe to Siberia. The two subspecies differ in growth habit, branching, root system, flower color, and degree of pod coiling (GUNN et al., 1978; SMALL and BROOKES, 1984). Subspecies *sativa* originates from a continental more arid climate with soils characterized by a high pH, high levels of bases, and a low water table; subspecies *falcata* is found in environments with colder, more humid climates, with acid,

leached soils (IVERSON and MEIJER, 1967).

Hybridization between the two parental types has led to the existence of numerous hybrid forms (subsp. x varia) representing a wide range in the relative proportion of both parent subspecies. A correlation has been observed between the relative contribution of the parental forms and nodulation by *Rhizobium meliloti* (GIBSON, 1962), resistance to the seed chalcid *Brucophagus roddi* (SMALL and BROOKES, 1982), accumulation of calcium and sulphur (SMALL and LEFKOVITCH, 1982), and cold tolerance and photoperiod sensitivity (IVERSON and MEIJER, 1967).

The examples of common bean, rice, and alfalfa illustrate that variability in crop plants is distributed non-randomly. Groups of genotypes (variously called gene pools, races, subspecies, etc.) can be identified which show characteristic geographic distributions, allele frequencies, allele associations, and environmental adaptations. The existence of these gene pools reflects the evolutionary forces that have shaped the crop and is probably the result of the mutually reinforcing effects of selection, migration and genetic drift, operating before, during, and after domestication. During the evolution of a crop (starting with the domestication process), humans have selected plants not only for specific agricultural ecosystems, but also to suit their particular needs or tastes. Through human migrations, crops were introduced into new areas and became adapted to a much wider range of environments compared to their wild relatives. The types thus selected were further carefully maintained by selection against any aberrant type arising by mutation or accidental hybridization. Throughout these processes of selection and migration, genetic drift acted on traits not directly under selection causing an additional reduction in genetic variability within and among each of the gene pools and thus accentuating the discontinuous distribution of genetic variability. It should be noted, however, that migrations also provide opportunities for hybridizations between gene pools leading to the often observed intermediate types.

Identification of gene pools, besides providing information on the evolution of a crop, also should lead to a more efficient management of genetic resources and breeding programs.

5. FUTURE RESEARCH PROSPECTS

A more systematic characterization is needed of the variability of the Middle American and Andean gene pools, among both wild and cultivated common beans, to determine to what extent:

- 1) the variability in the cultivated forms reflects that in the wild forms from which they were derived. How strong a reduction in variability does domestication represent? Is it worthwhile to use wild forms more actively in breeding programs to increase the available genetic variability?

2) the variability in the two gene pools overlap. Can breeding objectives be achieved more efficiently by favoring within-gene pool or between-gene pool (or both) hybridization and selection? The answer to this question depends on the degree of overlap in variability between the two gene pools, on the level of recombination, and the ease of recovering useful segregants in the progenies.

Traits to be considered include resistances to diseases and pests and environmental adaptation (e.g., tolerance to high or low temperature and drought; tolerance to low pH, high aluminum soils; photoperiod insensitivity, etc.). Particular attention to the possibility of coevolution between the common bean and associated organisms such as pathogens and *R. phaseoli*. Through coevolution, Middle American and Andean gene pools for these organisms may have appeared with important consequences for common bean breeding. Non-agronomic traits such as isozymes or restriction fragment length polymorphisms in nuclear and cytoplasmic genomes may also provide useful information.

During these studies, it should be possible to identify sub-gene pools within each gene pools, as well as intermediate forms between gene pools.

6. SUMMARY

Genetic evidence (reproductive isolation) is presented suggesting the existence of a Middle American ("mesoamericanus", and an Andean ("andinus") gene pool in cultivated common bean. This evidence correlates well with independently obtained morphological, phytopathological, isozyme, and adaptation data. An analogy is drawn with Asian rice and alfalfa where a comparable division of the cultivated germplasm into two entities is observed. The existence of these two gene pools is a consequence of the geographic isolation between Middle American and Andean *P. vulgaris* and further emphasized by selection, migration, and genetic drift operating under human influence.

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