

Broadening the Genetic Base of Common Bean Cultivars
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Common bean (*Phaseolus vulgaris* L.) is attacked by pests and some highly variable pathogens that often cause severe yield losses. But genes for useful traits such as resistance to some pests (e.g., bruchids and leafhoppers) and diseases (e.g., Ascochyta blight, bean golden mosaic, common bacterial blight, web blight, and white mold), are not found in cultigens, are inadequately expressed, or the genetic base is very narrow indeed. Thus, there is increasing need for introgression of useful genes among different races, gene pools, and from wild populations of common bean (primary gene pool), and from related species (secondary and tertiary gene pools). This broadening of the genetic base of common bean cultivars is essential for developing durable resistance against diseases and insect pests, correcting cultivar defects, maximizing selection gains, facilitating introduction of crops into new growing environments, and developing new crops. Our objective is to briefly describe the research being done at CIAT for broadening the genetic base of common bean cultivars. CIAT researchers are using the following alternative approaches for broadening the genetic base of common bean cultivars:

Use of Primary Gene Pool: Cultigens. Owing to the fact that there are over 26,000 germplasm accessions of common bean available at CIAT and less than 5% of which have been used in breeding programs around the world thus far, greater emphasis must be given for its use. Table 1 lists some examples of traits for which substantial genetic improvement can be made from inter-gene-pool and interracial hybridization. The comparatively greater evolutionary differences between the two gene pools of *P. vulgaris* and apparent incompatibilities in occasional crosses often complicate the selection of useful recombinants for seed yield and other quantitative traits from biparental Andean x Middle American inter-gene-pool crosses, regardless of selection method used (pedigree, bulk, or single-seed descent). Nevertheless, high-yielding lines have been developed from inter-gene pool (1) and interracial populations (11). Similarly, plant architecture (4), water stress tolerance (11), and rust resistance (R. Stavely, personal communication, 1997) have been improved from interracial and inter-gene pool populations.

Wild *P. vulgaris*. Hybridization between cultivated and wild *P. vulgaris* populations has been carried out to study the inheritance of seed weight (7) and arcelin seed protein (8), determine the yield potential (12) and major genes involved in domestication (5), and transfer high levels of resistance to *Zabrotes subfasciatus* from wild bean accessions (2). Attempts are currently being made to introgress resistance to *Acanthoscelides obtectus* into cultivars.

Use of Secondary Gene Pool: We are currently transferring into common bean the extremely high levels of resistance to bean golden mosaic (BGM) found in *P. polyanthus* (G 35877) and *P. costaricensis* (DGD 2119). Resistance to common bacterial blight (caused by *Xanthomonas campestris* pv. *phaseoli*) (9) and to BGM (our unpublished results) has been transferred from *P. coccineus* into common bean. High levels of resistance to Ascochyta blight, halo blight, white mold (among other traits), and cold could also be expected from the members of this secondary gene pool.

Use of Tertiary Gene Pool: Very high levels of resistance to common bacterial blight were transferred into common bean from *P. acutifolius* (3, 6, 10). From the initial cross made at CIAT, high levels of resistance have also been transferred and pyramided (our unpublished results).

For common bean, the breeding and selection methods used for introgressing useful genes from distantly related races, gene pools, wild populations, and species from its secondary and tertiary gene pools often differ considerably from those commonly used for genetically narrow or elite x elite populations. From truly broad-based, and even from inter-gene-pool and interracial biparental populations, breeders can often expect no more than intermediate products or parental stocks. These may possess very high expression of specific traits but may lack, or insufficiently express, other necessary traits. Thus, these stocks must be used as parents in one or more subsequent crossings with elite lines to develop commercial cultivars. Some form of backcrossing is often used to transfer necessary genes. Examples are recurrent and congruity backcrossings, where either the desired parent(s) used in the initial cross or other elite parents of similar characteristics (e.g., market class, maturity,

growth habit, and adaptation) are crossed with one or more selfed (inbred-backcrossing) or unselfed generations.

The introgression of useful genes from distantly related genotypes often requires plant-to-plant hybridizations, and much larger population sizes. This is to ensure sufficient recombination and presence of useful genes in succeeding generations. Occasionally, bridging-parents and parents that can facilitate hybridization and recombinations between two apparently incompatible parents are also needed. Moreover, special attention may be needed, such as embryo rescue. Breeders must therefore keep the development of parental stocks and broadening the genetic base of cultivars separate from the development of populations for immediate cultivar improvement (elite x elite crosses). The latter group of populations usually have narrower ranges of variability but may segregate for multiple traits. The broad-based populations serve as a reservoir of useful genes for specific traits. For long-term, sustained genetic progress, a breeder must strike a balance between the resources and time available to developing the two groups of populations.

Availability of molecular markers; integrated linkage maps of different species in the primary, secondary, and tertiary gene pools; and use of *in situ* DNA hybridization should facilitate gene introgression from distantly related species. Similarly, availability of a reliable and repeatable transformation system in *P. vulgaris* should make gene transfers feasible from other gene pools and genera that, at present, cannot be accessed.

References

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Table 1. Some characters being improved through inter-gene-pool and interracial hybridization within cultivated common bean.

Character	Type of inter-gene-pool or interracial crosses
Seed yield	Mesoamerica/Jalisco/Durango
Earliness	Mesoamerica/Durango/Nueva Granada
Plant architecture	Mesoamerica/Nueva Granada
Water stress tolerance	Durango/Mesoamerica/Jalisco
Low soil fertility tolerance	Durango/Jalisco/Mesoamerica/Nueva Granada
Resistance to angular leaf spot, anthracnose, bean golden mosaic virus, and rust	Durango/Jalisco/Mesoamerica/Nueva Granada