

Phaseolus vulgaris (Beans)

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Beans usually refers to food legumes of the genus *Phaseolus*, family Leguminosae, subfamily Papilionoideae, tribe Phaseoleae, subtribe Phaseolinae. The genus *Phaseolus* contains some 50 wild-growing species distributed only in the Americas (Asian *Phaseolus* have been reclassified as *Vigna*). These species represent a wide range of life histories (annual to perennial), growth habits (bush to climbing), reproductive systems, and adaptations (from cool to warm and dry to wet). The genus also contains five domesticated species: in decreasing order of importance, common bean (*Phaseolus vulgaris* L.), lima bean (*P. lunatus* L.), runner bean (*Phaseolus coccineus* L.), tepary bean (*P. acutifolius* A. Gray), and year bean (*P. polyanthus* Greenman), with distinct adaptations and reproductive systems: mesic and temperate, predominantly self-pollinated; warm and humid, predominantly self-pollinated; hot and dry, cleistogamous; cool and humid, outcrossing; and cool and humid, outcrossing, respectively. Lima bean is phylogenetically more distant from the other domesticated species, which are sibling species and constitute a syngameon. The principal species economically and scientifically is common bean. It originated in Latin America where its wild progenitor (*P. vulgaris* var. *mexicanus* and var. *aborigineus*) has a wide distribution ranging from northern Mexico to northwestern Argentina. Large germplasm collections of domesticated and wild forms are located at CIAT, Cali, Colombia and USDA, Pullman, Washington, USA. The reference collection of Phaseolinae is located at the National Botanical Garden, Meise, Belgium.

Common bean is the most important legume worldwide for direct human consumption. The crop is consumed principally for its dry (mature) beans, shell beans (seeds at physiological maturity), and green pods. When consumed as seed, beans constitute an important source of dietary protein (22% of seed weight) that complements cereals for over half a billion people mainly in Latin America. Annual production of dry beans is around 15 million tonnes and average yield is 700 kg ha⁻¹, although yields in certain countries reach 2000–3000 kg ha⁻¹. The largest producers of

dry beans are Brazil, Mexico, China, and the USA. Annual production of green beans is around 4.5 million tonnes, with the largest production around the Mediterranean and in the USA.

Common bean was used to derive important principles in genetics. Mendel used beans to confirm his results derived in peas. Johannsen used beans to illustrate the quantitative nature of the inheritance of certain traits such as seed weight. Sax established the basic methodology to identify quantitative trait loci (for seed weight) via co-segregation with Mendelian markers (seed color and color pattern). The cultivars of common bean stem from at least two different domestications, in the southern Andes and Mesoamerica. In turn, their respective wild progenitors in these two regions have a common ancestor in Ecuador and northern Peru. This knowledge of the evolution of common bean, combined with recent advances in the study of the phylogeny of the genus, constitute one of the main current attractions of beans as genetic organisms. All species of the genus are diploid and most have 22 chromosomes ($2n = 2x = 22$). A few species show an aneuploid reduction to 20 chromosomes. The genome of common bean is one of the smallest in the legume family at 625 Mbp per haploid genome. Normal mitotic or meiotic chromosomes are very small (1–3 μm), metacentric or submetacentric. A karyotype has been developed for *P. vulgaris* and *P. coccineus* based on polytene chromosomes of the embryo suspensor cells. There are three or four rRNA loci (nucleolar organizing regions). *In situ* hybridization with radioactive or fluorescent probes have been performed on mitotic or polytene chromosomes for rRNA, telomeric, and single-copy sequences. Highly repeated sequences comprise some 20% of the genome. They are distributed primarily in highly heterochromatic regions and in chromosome ends. Satellite DNA is located mostly around centromeres. An as yet incomplete set of five trisomic stocks has been identified. A consensus molecular linkage map, correlating some 12 maps, has been established based on RFLP, RAPD, isozyme, AFLP, ISSR, microsatellite, and phenotypic markers. The average total map length is 1200 cM, consistent with the average number of chiasmata per bivalent (1.9). A single estimate of the average relationship of physical vs. physical distance gave 400 000 bp per cM, close to the genome-wide average of 500 000 bp per cM. The genome of common bean is colinear with that of *Vigna* sp. (also belonging to the subtribe of the Phaseolinae within the tribe Phaseoleae), but shows many rearrangements when compared to that of soybean (subtribe of the Glycininae within the tribe Phaseoleae). A retrotransposon family of the copia type has been described. Bacterial artificial chromosome libraries have been established for

common bean. Major genes or quantitative trait loci for the domestication syndrome (reduced seed dispersal and seed dormancy, compact growth habit, photoperiod insensitivity, seed size, color, and color pattern) have been located on the linkage map, as have clusters of resistance genes and resistance gene analogs (to viral, fungal, and bacterial diseases), and genes for *Rhizobium* nodulation, canning quality, and drought tolerance. In addition, several unmapped genes, especially for disease resistance and seed color and color pattern, have been tagged with molecular markers. Transformation systems have been established. These

include an *Agrobacterium*-mediated system in *P. acutifolius* and a biolistics method in *P. vulgaris*.

Further Reading

<http://agronomy.ucdavis.edu/gepts/geptslab.htm>

<http://www.ba.cnr.it/Beanref/>

<http://beangenes.cws.ndsu.nodak.edu:80/>

See also: 1122 (Rhizobium), 1664 (Glycine max (Soybeans)), 1638 (Transfer of Genetic Information from *Agrobacterium tumefaciens* to plants)