
Preface

The relevance of common bean (*Phaseolus vulgaris* L.) is determined by the fact that it is the most important grain legume for food consumption worldwide and has a role in sustainable agriculture owing to its ability to fix atmospheric nitrogen. It is a staple crop with a major societal importance as main source of proteins and nutrients in developing regions such as Africa and Latin America. Due to its domestication, it can be grown in a wide range of environments, from near sea level up to 3000 m above sea level, in arid, semiarid and tropical environments, and under high or moderate temperatures. Its main consumption is for its edible dry seed (dry beans) or unripe fruit (green beans). This double use determines that modern cultivars have been bred for different fruit characteristics such as those that influence the seed (shape, color, cooking ability, etc.) and the pod (length, tenderness, stringless, etc.) apart from common features as disease resistance, yield, precocity and plant architecture.

Common bean was domesticated in two geographically isolated and differentiated areas, according to multiple lines of evidence, generating two distinguishable gene pools, Mesoamerican and Andean, within a single species. The domestication of two independent lineages implicated a parallel evolution and introgression events with important implications for modern common bean crop improvement. In fact, common bean was likely domesticated concurrently with maize as part of the 'milpa' cropping system (featuring common bean along with maize and squash), which was adopted throughout the Americas. Common bean was introduced in Europe soon in the XVI century through Spanish and Portuguese trade routes, and independently introduced into Africa. Large variation of common bean evolved in Europe as a result of adaptation to new ecological and manmade conditions. In consequence, common bean has four well-identified centers of diversification, two in America, where it was domesticated, one in Europe, and one in Africa, where it was introduced after the discovery of America.

Common bean is also an important species from the scientific point of view. It has been widely used in research and breeding. Both Darwin and Mendel used this species in their research, and it was widely used as material for genetic experimentation and breeding during the early years of the development of genetics, at the beginning of the twentieth century. For example, the demonstration by Johansen that the phenotype is the result of the interaction between the genotype and the environment; or the direct

relationship between a quantitative and a qualitative character, seed size and seed coloration of the common bean seed, by Sax. A large corpus of genetic data on common bean has been generated throughout the twentieth century, now widely complemented and surpassed by the genomic information.

The recent release of the Andean and Mesoamerican common bean genomes is enabling a new wave of cutting-edge research, including epigenomics and translome analyses, in a crop that has fed billions of people for more than 5000 years. Moreover, the comparison of the Andean and the recently released Mesoamerican genome has initially revealed interesting differences. For example, the size and the number of genes in the Mesoamerican genome is smaller than the Andean genome. The availability of the genome sequence has completely changed the paradigm of the species' genetics and genomics.

Genomic information on the other domesticated or wild *Phaseolus* species range from scarce to null. However, the already sequenced genomes of common bean will help in sequencing and assembling the genomes of other species of the genus. In fact, common bean is one of the five domesticated species of the genus *Phaseolus*, a genus formed by a relatively large number of species with broader or narrower geographical distribution and some of them adapted to particular environments. The other four domesticated species are tepary bean (*P. acutifolius* A. Gray), runner bean (*P. coccineus* L.), lima bean (*P. lunatus* L.) and year-long bean (*P. dumosus* Macfad.), all four originated and domesticated in America. The genomic information from the other *Phaseolus* species will give more complete information on the evolutionary processes associated to domestication and on the adaptive processes to particular environments with special relevance for breeding strategies.

Genomic resources include not only data from the nuclear genome but also from organelle genomes. In particular, mitochondrial and chloroplast genomes gives complementary information on the evolutionary processes within common bean and between species within the genus *Phaseolus*. Genomics data allow knowing the whole set of genes implicated in a metabolic route, including the genes coding for the transcription factors implicated in their expression control, helping in the transcriptomic analyses of their expression under different environments or in different tissues. Likewise, they allow the analysis of the relationships between different metabolic routes and biological processes. A particular set of genes of interest in a crop mainly exploited by its seeds is the set of seed storage proteins, which determine a great part of the nutritive value of the main crop product. New tools will be likely developed from these data such as complete set of molecular markers, microarrays, etc., which will speed and facilitate assisted selection processes.

The present book summarizes data on the economic and scientific relevance of common bean, its relation with other species of the genus *Phaseolus*, and insists on the importance of the domestication events, parallel evolutionary history and further expansion of the cultivated forms. It also describes the numerous genetic and genomic resources available, the identified genes and quantitative trait loci (QTL) identified, as well examples

of the study of functionally related genes and future prospects. This book shows that these are exciting times for common bean research in a field with the potential to reduce the threat of food insecurity by releasing crops tolerant to biotic and abiotic stresses, increasing yields and enhancing the nutritional quality of beans.

León, Spain
Pontevedra, Spain
London, Canada

Marcelino Pérez de la Vega
Marta Santalla
Frédéric Marsolais



<http://www.springer.com/978-3-319-63524-8>

The Common Bean Genome

Pérez de la Vega, M.; Santalla, M.; Marsolais, F. (Eds.)

2017, XVIII, 295 p. 52 illus., 49 illus. in color., Hardcover

ISBN: 978-3-319-63524-8