The mungbean genome sequence: a blueprint for *Vigna* improvement

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Mungbean (*Vigna radiata* L.) (family Fabaceae) is a diploid ($2n = 2x = 22$) pulse crop, cultivated predominantly in South East Asia. The genus *Vigna* also contains several major agriculturally important legumes like black gram (*V. mungo*), rice bean (*V. umbellata*), moth bean (*V. aconitifolia*) and adzuki bean (*V. angularis*). The grains are rich in protein and minerals and hence form important component of human diet. Mung bean is reported to be domesticated in India approx. 4,000–6,000 years ago. India is the largest producer of mung bean in the world, followed by China and Myanmar. The crop is gaining wider acceptance in India, because of short life cycle fitting well in intercropping with rice and wheat-based cropping system, besides being a nitrogen fixer. With the advances and affordability of genome sequencing technologies, generation of genomic resources of this valuable pulse shall go a long way in complementing modern breeding activities[1].

Recently, the draft genome sequence of mungbean (*Vigna radiata* L.) was released in November 2014 as a result of endeavour from a consortia of twelve institutions, led by Suk-Ha-Lee, Seoul National University, Korea[2]. Two next generation sequencing platforms HiSeq2000 and GS FLX+ were used to sequence and assemble the information into 11 pseudo chromosomes. Genome sequence information of wild relative of mungbean (*V. radiata* var. *sublobata*), its tetraploid relative, creole bean (*V. reflexpilosa* var. *glabra*) and the transcriptome sequence of 22 accessions belonging to 18 *Vigna* species, were also deciphered. Further, a genetic map based on F6 population of 190 recombinant inbred lines (RIL) was also constructed based on genotyping by sequencing (GBS) strategy. The 421 Mb (80%) assembled genome coupled with sequence information of related *Vigna* species provides meaningful insights into the evolutionary history of *Vigna* spp. (particularly subgenus *Ceratotropis*) based on comparative genomics strategy.

Like other recently sequenced crops, repetitive and transposable elements covered the bulk of the genome. For instance, the LTR retrotransposons (*Gypsy* and *Copia*) were more abundant as compared to DNA transposons (CACTA, Mutator, PIF-Harbinger, etc.). Higher proportion of repetitive elements was found in domesticated species than in wild accessions[3–5]. Assembled transcripts based on RNA-seq analysis represent 97% match with 248 eukaryotic core proteins, implicating completeness of genome sequence[6]. Gene prediction tools annotated 22,427 protein coding genes either in unitary or solitary clusters and 2,310 protein non-coding genes (tRNA, rRNA, miRNA, snRNA, etc.). Comparative analysis indicated 160 unique *Vigna* specific gene clusters, apart from common 6,799 gene clusters shared between other plant species, i.e. thale cress (*Arabidopsis thaliana*), barrel medic (*Medicago truncatula*), rice (*Oryza sativa*) and soybean (*Glycine max*)[7].

A rich repertoire of molecular markers was deciphered from the draft genome sequences. A total of 2,922,833 single nucleotide polymorphisms (SNPs) differentiate wild and cultivated species, corresponding to a SNP frequency of 6.78 per 1 kb. However, SNP frequency was comparatively lesser (1.8 SNPs per 1 kb) among mungbean genotypes with only 775,831 SNPs being identified. Further, simple sequence repeat (SSR) markers (200,808) were reported that can provide valuable resources for breeding programmes related to biotic and abiotic stresses.

Presence of well conserved macrosyntenic blocks indicates closer relationship of *Vigna* to *Glycine max*, as compared to other members of the Fabaceace family. Comparison of collinear blocks within the mung bean genomes implicate only one whole genome duplication (WGD) event that shaped the current genome of cultivated mungbean. In contrast, the tetraploid relative of mungbean has almost double the gene content than cultivated mungbean, implicating two rounds of duplication. Based on comparative genome analysis, a syntenic relationship was revealed for the quantitative trait

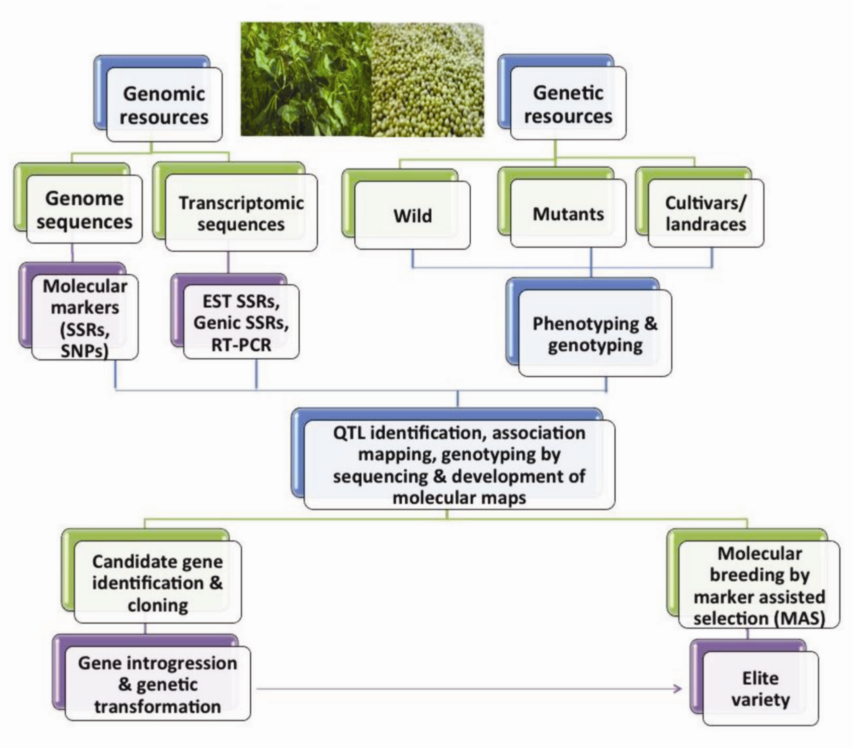

Figure 1. Application of genomic and genetic resources for mungbean improvement.

loci (QTL) of soybean (*G. max*) related to seed size/germination and bruchid (storage pest) resistance[8].

Owing to short life cycle and small genome size, mungbean may be used as model pulse for genetic studies on crop domestication and species divergence. This study adds valuable genomic resources that can be effectively utilized to accelerate breeding programmes for *Vigna* improvement (Figure 1). Thus, the whole genome sequence information opens a wide platform to understand the molecular and genetic mechanisms of important traits.

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