Sustainable Agriculture and Food Security
Series Editor: Rajeev K. Varshney

Manish K. Pandey · Alison Bentley
Haile Desmae · Manish Roorkiwal
Rajeev K. Varshney *Editors*

Frontier Technologies for Crop Improvement

Springer

Chapter 8
Forward Breeding for Efficient Selection

Rajaguru Bohar, Susanne Dreisigacker, Hannele Lindqvist-Kreuze, Moctar Kante, Manish K. Pandey, Vinay Sharma, Sunil Chaudhari, and Rajeev K. Varshney

Abstract Global food security is the *numero uno* priority in the current global situation, threatened by a number of challenges catalyzed by accelerated climate change and population growth. Crop improvement coupled with the modern plant breeding approaches, such as genomic-assisted breeding, is a proven solution to meet the food security. One of the key mandates in the modern plant breeding program is to combine the power of genomic selection into the breeding pipeline employing a low-cost genotyping solution. Several SNP marker-based platforms are now available depending on the objectives and field of application; despite the

R. Bohar (✉)
CGIAR Excellence in Breeding (EiB), International Maize and Wheat Improvement Center (CIMMYT), c/o ICRISAT, Hyderabad, India
e-mail: R.Bohar@cgiar.org

S. Dreisigacker
International Maize and Wheat Improvement Center (CIMMYT), Veracruz, Mexico
e-mail: S.Dreisigacker@cgiar.org

H. Lindqvist-Kreuze · M. Kante
International Potato Center (CIP), Lima, Peru
e-mail: h.lindqvist-kreuze@cgiar.org; m.kante@cgiar.org

M. K. Pandey
Center of Excellence in Genomics and Systems Biology (CEGSB), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
e-mail: manish.pandey@icrisat.org

V. Sharma
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Telangana, India
e-mail: vinay.sharma@icrisat.org

S. Chaudhari
World Vegetable Center, South Asia, c/o ICRISAT, Hyderabad, India
e-mail: sunil.chaudhari@cgiar.org

R. K. Varshney
Murdoch's Centre for Crop and Food Innovation, State Agricultural Biotechnology Centre, Food Futures Institute, Murdoch University, Murdoch, WA, Australia
e-mail: rajeev.varshney@murdoch.edu.au

M. K. Pandey et al. (eds.), *Frontier Technologies for Crop Improvement*, Sustainable Agriculture and Food Security, https://doi.org/10.1007/978-981-99-4673-0_8

availability of different platforms, the public sectors face challenges in terms of funding and accessibility to the latest technology when compared to private sectors. Shared genotyping platform coupled with open breeding informatics involving different stakeholders with active support from donors will address several constraints faced by the public breeding program. Here, we summarize the available forward breeding genomic resources in the space of low-mid-density genotyping platform with special emphasis on shared services for four crop groups:

1. Wheat (cereal)
2. Potato (roots, tubers, and bananas (RTB crops))
3. Groundnut (grain legumes)
4. Vigna species (legumes)

Keywords Forward breeding · Genomics-assisted breeding · Marker-assisted selection · Single-nucleotide polymorphism · Genomic selection · Wheat · Potato · Groundnut · Vigna · Cowpea · Mung bean · Black gram

8.1 Introduction

Global food security is the *numero uno* priority in the current global situation, threatened by a number of challenges catalyzed by accelerated climate change and with the expected global population growth to bypass 9.75 billion figures, where more than 2.5 billion people reside in Africa by 2050 (FAOSTAT (2022)). Crop improvement coupled with the modern plant breeding approaches is one of the proven solutions to meet the food security along with number of other factors including, but not limited to exploiting the natural variations. Next-generation breeding, such as genomic-assisted breeding (GAB), employing molecular markers has a significant impact and is considered as a practical way forward to accelerate the crop improvement with specific focus to improved crop yield (Razzaq, Ali, et al. 2021). Importance of GAB is evident from the commitment made by the Consultative Group on International Agricultural Research (CGIAR) with its 2030 Research and Innovation Strategy (Action Area 3) to support the breeding optimization pipelines and implementation of GAB approaches (CGIAR 2021). Methods of plant breeding was positively changed by the implementation of molecular marker technology especially after the boom of the genomic sequencing era that enhanced the pace of crop improvement. From the era of restriction fragment length polymorphisms (RFLPs) to simple sequence repeats (SSRs) to single-nucleotide polymorphisms (SNPs), the marker technology rapidly advanced, and currently, SNPs is considered as the most advanced and commonly used marker systems in plant breeding application (Bohar et al. 2020). One of the key mandates in the modern plant breeding program is to combine the power of genomic selection (GS) into the breeding pipeline. Low-cost genotyping solution, which is affordable and meaningful, makes the practical application of GS integration. Many genotyping platforms are available, among which SNP genotyping method utilizing the high-throughput multiplexed approach is a predominantly used genotyping method, such as genotyping-by-sequencing (GBS). Though GBS is a preferred choice, it lacks

practical suitability, such as requirement of imputation to fill the missing data, and in turn requires a complex bioinformatics to suit the multiyear data interpretation. Diversity Arrays Technology's DArTag (Diversity Arrays Technology, Bruce, Australia), Integrated DNA Technologies' rhAmpSeq (Integrated DNA Technologies, Coralville, IA, USA), and Illumina's AmpliSeq (Illumina, San Diego, CA, USA,) are some of the commercially available pooled and multiplexed sequencing technology targeting the specific SNPs. Though the available platforms demand a high up-front cost for designing, they have a comparative advantage with GBS in terms of repeatability, heterozygotes identification, and requirement of less bioinformatics support (Sneller et al. 2021).

Several SNPs' marker-based platforms are now available, depending on the objectives and field of application such as the following: high-density SNP genotyping platforms (HDSG) for discovery studies and linkage mapping; medium-density SNP genotyping platforms (MDSG) for GS and background studies; and low-density SNP genotyping platforms (LDSG), such as Kompetitive Allele Specific PCR (KASP), for forward breeding application through marker-assisted selection (MAS), marker-assisted backcrossing (MABC), and quality control (QC) analysis (Roorkiwal et al. 2020). Despite the availability of different platforms, the public sectors face challenges in terms of funding and accessibility to latest technology when compared to private sectors. To tackle such situation, Xu et al. suggested that there should be coordinated efforts by the scientific community, particularly in developing countries backed by big donors, such as Bill and Melinda Gates Foundation (BMGF). These efforts, especially in the field of modernization of plant breeding through establishment of public–private partnerships, will improve the international crop improvement system (Xu et al. 2017; Cobb et al. 2019). Shared genotyping platform coupled with open breeding informatics involving different stake holders with active support from donors, such as BMGF, will address several constraints faced by the public breeding program. CGIAR's strategic approach in this direction includes the development of world-class shared genotyping service through High-Throughput Genotyping Project (HTPG) (http://cegsb.icrisat.org/high-throughput-genotyping-project-htpg/), the Genomics Open-Source Breeding Informatics Initiative (GOBii) (http://gobiiproject.org/), and the Excellence in Breeding (EiB) (https://excellenceinbreeding.org/) platform led by the CGIAR institutes with the able funding of the BMGF (Bohar et al. 2020). HTPG facilitated low-cost and high-throughput genotyping for CGIAR and National Agricultural Research Systems (NARS) led by ICRISAT (2016–2020) and further transitioned to genotyping/sequencing tools and services module of EiB platform through service provider, Intertek AgriTech (http://www.intertek.com/agriculture/agritech/) (Bohar et al. 2020).

EiB has been coordinating and supporting the use of genotyping by NARS and has launched shared genotyping services, such as EiB-LDSG and EiB-MDSG, for the benefit of national, CGIAR, and other breeding programs. Currently, the EiB shared services is functional with all CGIAR centers and their partner programs in rice, wheat, maize, several millets, legumes, and several other crops, which are readily deployable in the breeding programs with continuous addition of new crops and marker resources. These services are targeted at CGIAR and NARS

breeding institutions, aggregating demand across institutions to offer high-quality, low-cost genotyping with faster turnaround time of 10–15 business working days. Implementation of shared services is one among the six requests from the funder consortium Crops to End Hunger (CtEH), whose overall objective is to modernize CGIAR breeding programs and networks ensuring those programs deliver the highest possible rate of genetic gains in farmers' field (Hunt et al. 2021). The EiB-LDSG service (formerly HTPG) based on KASP platform, which is cost-effective up to 200 markers, is suited for applications including specific trait screening (foreground selection), QC, and MAS. The markers available for use in EiB-LDSG can be accessed at https://excellenceinbreeding.org/module3/kasp, which is continuously updated and improved (EiB-LDSG 2022). The EiB-MDSG service is a DArTAg genotyping method with a density of up to 4000 markers, primarily suited to GS applications, but can also be used for diversity studies, DNA fingerprinting, and MABC for background recovery analysis (EiB-MDSG 2022).

Success stories and publications incorporating the HTPG, EiB-LDSG, and/or EiB-MDSG are reported in several crops, such as groundnut (Parmar et al. 2021), potato (Kante et al. 2021; Sood et al. 2022), cassava (Le Thuy et al. 2021), sorghum (Mwamahonje et al. 2021), and banana (Garcia Oliveira et al. 2021). Here, we summarize the available forward breeding genomic resources in the space of low-mid-density genotyping platform with special emphasis on the resources available with EiB genotyping shared services for four crop groups: (1) wheat (cereal), (2) potato (roots, tubers, and bananas (RTB crops)), (3) groundnut (grain legumes), and (4) *Vigna* species (legumes).

8.2 Genomic Resources and Forward Breeding in Wheat

Wheat is a key food staple that provides around 20% of protein and calories consumed worldwide. The demand for wheat is projected to continue to grow over the coming decades, particularly in the developing world to feed an increasing population and, with wheat being a preferred food, continuing to account for a substantial share of human energy needs in 2050 (Wageningen 2016). Current annual genetic gains for grain yield of about 1% are being realized in the CIMMYT Global Wheat Program (GWP) for a number of target populations of environments (Crespo-Herrera et al. 2017, 2018; Honsdorf et al. 2018; Gerard et al. 2020). Thus, higher-yielding, more productive varieties continue to be released in developing countries, resulting in enhanced productivity (Lantican et al. 2016). In addition to grain yield improvement together with yield stability, key breeding objectives of the program (similar to others) are resistance/tolerance to biotic and abiotic stresses, end use, and nutritional quality characteristics. In order to keep up with the pressing future demands of wheat production and to adapt to changing environmental factors, wheat breeders overall and at CIMMYT are constantly turning to new and emerging technologies and breeding strategies. For example, advanced genetics and genomics tools are progressively deployed and related operating processes optimized (Fig. 8.1) (Dreisigacker et al. 2016, 2021).

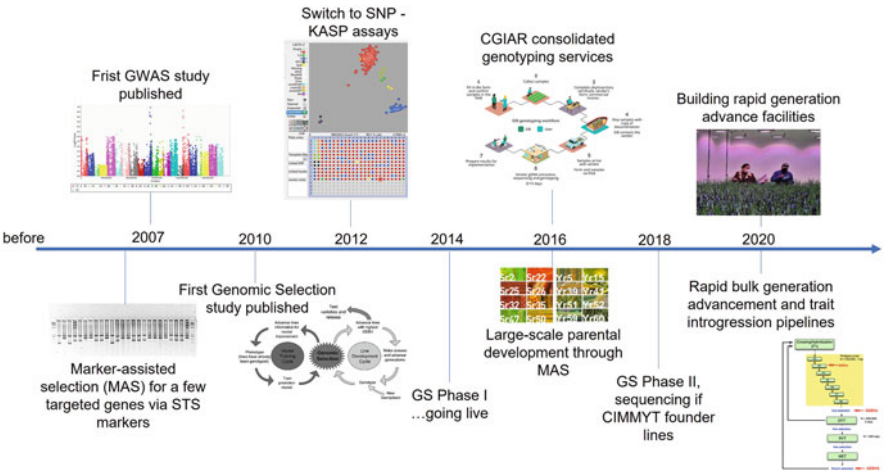

Fig. 8.1 Implementation of genetic and genomic tools in the CIMMYT Global Wheat Program

Marker-assisted forward and backcross breeding are approaches that can be successfully deployed in crops, mainly when (i) a target trait is rather difficult to manage in the field because it is expensive or time-consuming to measure, has low penetrance, or has complex inheritance; (ii) trait selection depends on specific environments or host developmental stages; (iii) recessive alleles during backcrossing need to be maintained or for speeding up backcross breeding in general; and (iv) pyramiding multiple monogenic traits or several QTL for single traits is looked for (Miedaner and Korzun 2012). However, often the number of markers per trait with enough information content about their relevance and usefulness to a breeding program is low. To increase response to selection using marker-assisted forward and backcross breeding in wheat, markers related to genes for disease resistance, end use, and nutritional quality are mainly used, because they show reasonable effect size. In the CIMMYT GWP, the targeted development of rust-resistant wheat germplasm is probably the most important example for which markers are adopted. The aim is to develop elite breeding lines that carry a combination of non-race-specific adult-plant resistance genes and race-specific genes, to avoid applying extremely high selection pressure on the pathogen that might endanger the avirulence of individual genes in developing countries. Rust research in the GWP has mapped and officially designated several rust genes (reviewed by Lan and Basnet 2016). Multiple pleiotropic non-race-specific genes (including *Lr34/Yr18/Sr57/Pm38*, *Lr46/Yr29/Sr58/Pm39*, and *Sr2/Yr30/Lr27/Pm*) are present in the CIMMYT wheat germplasm pool and build the basis of resistance against the three rusts (Singh et al. 2014). A larger number of race-specific stem and yellow rust resistance genes not present in CIMMYT germplasm have recently been introgressed into a set of elite genetic backgrounds via MABC to develop new parental lines (Table 8.1). In addition to rust, resistance to fusarium head blight (FHB) and Septoria tritici blotch are targets for forward breeding. For example, recombinant inbred lines that have the resistant *Fhb1* and *Sr2* alleles in coupled

Table 8.1 List of rust resistance genes introgressed via MAS for parental development

Trait	Source	Gene
Pleiotropic adult-plant resistance	RL6077/AOC-YR	*Lr67/Yr46/Sr55/Pm46*
	SUJATA	*Lr67/Yr46/Sr55/Pm46, YrSuj-7BL*
Stem rust resistance genes	SWSR22T.B.	*Sr22*
	KACHU/3/WHEAR//2*PRL/2*PASTOR	*Sr25*
	SHORT SR26 TRANS./4/3*CHIBIA//PRLII/CM65531/3/MISR 2/5/2*BAJ #1	*Sr26*
	SR32	*Sr32*
	W3763-SR35	*Sr35*
	SR47	*Sr47*
	SR50	*Sr50*
Stripe rust resistance genes	ALPOWA	*Yr39*
	CHUAN NONG 19	*Yr41*
	BLANCA GRANDE 515	*Yr5, Yr15*
	SUMMIT 515	*Yr5, Yr15*
	YR51#5515–1	*Yr51*
	KOELZ W 11192:AE	*Yr52*
	YR57#5474–6	*Yr57*
	IRAGI	*Yr59*
	LALBMONO1*4/PVN	*Yr60*

phase linkage in the background of the cultivar HARTOG were crossed with CIMMYT bread wheat lines and selected with molecular markers for both genes in addition to the use of pseudo-black chaff (PBC) as a phenotypic marker for the selection of *Sr2* (He et al. 2020). The *Fhb1*-resistant allele has previously been absent in CIMMYT germplasm as the gene is usually tightly linked in repulsion phase (the case where each homologous chromosome has one dominant and one recessive allele from the two genes) on chromosome 3BS and CIMMYT wheat breeding focused much time and energy on stem rust resistance. Durum wheat (*Triticum turgidum* subsp. *durum*) is also an important crop worldwide, while its production runs secondary to that of bread wheat. One aspect to consider is the relatively restricted food functionalities of durum wheat, primarily attributed to its kernel texture and gluten strength limitations (Morris et al. 2019). During the last few years, soft kernel durum was crossed with CIMMYT elite durum lines to produce soft kernel progeny with a high degree of genetic variance for milling and baking quality. Selection for the novel soft kernel types was routinely supported with associated KASP markers.

Breeding in Mexico routinely utilizes two crop seasons per year that cuts the breeding time by about half but also allows selection for a range of traits at contrasting field sites that have distinct daylength and temperature regimes. MAS is deployed in both crop-seasons. In 2020, a field screenhouse and rapid-generation advance (RGA) greenhouse facility at the CIMMYT Toluca research station were

constructed. Donor parents derived from the previous parental development pipelines are now used and crossed with selected elite lines for rapid introgression, pyramiding, and trait augmentation through RGA. The scaling-up marker-assisted forward and backcross breeding in the public sector has long been hampered by high genotyping costs and insufficient data management support. And still, the cost of genotyping for several high-throughput SNP platforms is inversely proportional to sample quantity, which in the case of smaller public sector organizations that have low individual demand partly impedes the routine deployment of molecular markers. In 2016, the HTPG project supported by the BMGF developed a shared industrial-scale service of low-density SNP genotyping serving the CGIAR and partner breeding programs. A low-cost, fast turnaround service (EiB-LDSG) was established by EIB platform. EiB-LDSG is routinely used in the CIMMYT GWP. Information on the wheat markers that are routinely applied is also available at https://excellenceinbreeding.org/module3/kasp.

8.3 Genomic Resources and Forward Breeding in Potato

To come up with a satisfactory variety, potato breeders must concentrate their efforts on selecting for a multitude of traits besides yield. Depending on the breeding program, goals as many as 12 traits have been proposed (Bonierbale et al. 2019). Although stacking of multiple genes is complicated in highly heterozygous tetraploid potato, it is possible to make progress through a dedicated MAS procedure (Bradshaw 2017; Stefańczyk et al. 2020; Rakosy-Tican et al. 2020). Furthermore, MAS facilitates the traits-based selection without heavy phenotypic evaluation at early stages, as compared to conventional breeding methods. In International Potato Center (CIP), the main breeding targets were for decades centered on disease resistance and climate resilience to achieve varieties that are productive under stressful conditions. The main diseases of potato in the breeding target areas of CIP are late blight (LB) caused by the oomycete *Phytophthora infestans* (Mont.) de Bary, potato virus Y (PVY), potato virus X (PVX), and potato leaf roll virus (PLRV). Molecular markers have been identified to trace the presence of many genes that provide control to these diseases (Nie et al. 2016; Fulladolsa et al. 2015; Ottoman et al. 2009; Whitworth et al. 2009; Tiwari et al. 2013), and significant time and cost savings can be achieved by using them instead of traditional phenotyping. We had calculated that the use of MAS for *Rladg* gene that provides resistance to PLRV (Mihovilovich et al. 2014; Velásquez et al. 2007) can save up to 88% of the costs as compared to phenotypic assays (RTB. 2019). This is particularly valuable for traits such as PLRV resistance that is extremely difficult to measure because the virus is phloem limited and thus infection assays require the use of vector insects or grafting to indicator plants (Mihovilovich et al. 2014). The *Rladg* assay that was developed at CIP is a gel-based SCAR marker (Mihovilovich et al. 2014) that is well suited for the screening of a relatively small number of samples. However, this screening method is not ideal for screening in the early breeding stages when

thousands of clones would be evaluated. Furthermore, a breeding program is usually interested in screening for more than one single trait, and therefore, screening for multiple markers in a single assay is more efficient. KASP offers an excellent cost-efficient option for breeding programs to develop custom sets of low-density markers for purposes, such as QC or MAS (Semagn et al. 2014; Caruana et al. 2021). Therefore, at CIP we started to convert some of the most important trait markers for our breeding program into KASP markers. The first trait markers converted and validated are two markers for PVY resistance and two for LB resistance (Kante et al. 2021). The PVY markers were designed for the *Ryadg* gene that is the main source of PVY resistance in CIP breeding populations (de Herrera et al. 2018). Based on high assay power and low error rate, the new markers work very efficiently in CIP breeding program (Kante et al. 2021). The LB markers were discovered in GWAS studies using CIP breeding germplasm and located in or near the QTL in chromosome 9 that has been shown to contain *R8* resistance gene (Lindqvist-Kreuze et al. 2014, 2021; Jiang et al. 2018). These markers have a variable performance, depending on the germplasm they are applied to, but have consistently good performance in the populations targeting LB as a main trait (Kante et al. 2021; M. Gastelo, pers. Comm). These markers are available at https://excellenceinbreeding.org/module3/kasp through EiB-LDSG. Other markers well worth pursuing as a KASP assay for disease resistance traits in CIP germplasm include at least gene *Rx* for PVX resistance and *Rladg* for PLRV resistance.

Another useful application for KASP markers is identity verification with the help of a set of QC markers. QC marker sets have been reported for maize, rice, and sweet potato (Gemenet et al. 2020a; Ndjiondjop et al. 2018; Semagn et al. 2012). Mislabeled genotypes at any stage of the breeding process are problematic and should be avoided as they waste time and resources and negatively affect genetic gains (Gemenet et al. 2020a). We selected a set of SNP markers from the SolCAP Infinium array that had discriminatory power to differentiate CIP breeding germplasm. Using the tetraploid calls, it was possible to discriminate full and half sibs with as few as 20 SNP markers (Kante et al. 2021). Several cases of mislabeling were discovered when this set of markers was applied to test the identity of clones across different stages (Kante et al. 2021). Although the KASP assay for a relatively low number of markers is cost-efficient, there is a need to carefully define the best approach for routine use of these markers in the breeding program. At the very least, the CIP breeding program will strive to verify the identity of the progenitors in the crossing block and the advanced clones that are shared with partners for variety evaluation.

The rate of progress in genetic gains by recurrent selection in potato is largely limited by the number of vegetative generations needed to complete all phenotyping (Bradshaw 2017). GS and genomic estimations of breeding values are a powerful tool that can shorten the breeding cycle of potato and lead to increased genetic gains for several traits (Ortiz 2020). Most studies published in potato GS up to date have utilized hybridization-based Illumina SNP SolCAP array (Stich and Van Inghelandt 2018; Enciso-Rodriguez et al. 2018; Endelman et al. 2018) or GBS (Sverrisdóttir et al. 2017; Caruana et al. 2019; Byrne et al. 2020). SolCAP array is a relatively

expensive assay keeping in mind that not all markers are applicable across different breeding populations (Slater et al. 2014). GBS can be more affordable particularly if sequencing depth is kept at a moderate level, but it is computationally intensive (Gemenet et al. 2020b). However, if one wishes to utilize the allele dosage information in the GS model, it is advisable to consider sequencing depth of 60–80x so that the different heterozygous states can be called reliably in autotetraploid potato (Uitdewilligen et al. 2013).

Targeted sequencing with selected SNP across the genome is therefore an attractive option to reduce the number of markers to a more manageable level allowing for a sufficient sequencing depth (Slater et al. 2014). DArTag is a targeted Diversity Arrays Technology (DArT, http://www.diversityarrays.com), genotyping method where a single oligonucleotide is used to capture selected SNPs or indels. Further advantage of this system is that the sequencing of the fragments allows for identification of other polymorphisms beyond the originally targeted SNP/indel and thus a capture of additional haplotypes. Tetraploid calls can be obtained from the raw read counts, even for samples with low read depth (<15). As part of the EiB-MDSG efforts, we developed such a reduced, but representative set of markers using previously available data points from the SolCAP SNP (Hamilton et al. 2011; Felcher et al. 2012) and SolSTW SNP (Uitdewilligen et al. 2013; Vos et al. 2015) genotyping efforts with CIP and Jeff Endelman's Lab at the University of Wisconsin potato germplasm. The marker selection and primer design yielded a set of 2503 markers, with a number of markers per chromosome ranging between 177 and 272. In a standard DArTag assay, these markers have a mean median read depth of 164, which allows for successful dosage calling in tetraploid potato. Like the KASP marker set, the DArTag marker set is in public domain and available for all interested breeding programs through EiB-MDSG. The mid-density DArTag marker set will allow a cost-effective genotyping of the breeding material for genomic prediction. Further, the inclusion of two trait markers for *Ryadg* and *Rysto* into the panel will allow a characterization of the breeding material without necessarily increasing the genotyping costs. Inclusion of more trait markers is and will allow a one-time genotyping of clones through the breeding cycle, for trait characterization and genomic prediction. CIP clones from intermediate trials DArTag genotyping for GS can be done from tuber and/or leaf samples, assuring therefore a rapid availability of molecular data of the prediction population.

8.4 Genomic Resources and Forward Breeding in Groundnut

Groundnut or peanut (*Arachis hypogaea* L.) is an important food and oil crop, cultivated across the tropics and subtropics regions. Globally, it is cultivated on an estimated 29.6 million hectares of area, producing 48.86 million tons (FAOSTAT 2022; http://www.fao.org/faostat/en/#data/QC). Moreover, half of groundnut crop

produce is used to extract oil, with the remaining eaten raw or processed. Groundnut is often referred to as the "poor man's almond" owing to its high nutritional content, like oil, protein, fiber, polyphenols, antioxidants, vitamins, and minerals. Gibbons began breeding work in groundnut around 1976. Groundnut breeding's major goal is to develop cultivars having high-yielding, early maturity, adaptability to specific conditions and production systems, resilience or endurance to environmental challenges, disease and insect resistance, and improved nutritional quality. Efforts to enhance groundnut breeding via genomics have been very successful, over the previous decades. Availability of genomic resources, such as extensive whole-genome assemblies and transcriptome assemblies, high-density saturated genetic maps, and, most interestingly, linked markers with traits of interest, has eased routine breeding programs (Pandey et al. 2020). Modern-day advanced breeding strategies, such as GS, speed breeding, or RGA, are projected to boost groundnut genetic gains (Parmar et al. 2021). Here, we commence by highlighting recent advances in groundnut genomics, with an emphasis on next-generation technologies.

8.4.1 Genomic Resources in Modern Era

Recent groundnut genomic advancements have enabled the emergence of a diverse array of advanced genomic methods and technologies for crop improvement. The groundnut researchers have succeeded in terms of leveraging genetic resources, notably during the past decade (Fig. 8.2). A wide range of genomic resources, including reference genomes assemblies, genome-wide genetic markers, expression atlas, genotyping platforms (low, mid, and high density), QC panels, and diagnostic markers, have facilitated the translational genomics in groundnut research.

8.4.2 Reference Genomes Assemblies

A reference genome provides a standardized, important basis for genomic and genetic research. Utilizing advanced sequencing technologies, a well-assembled and annotated genome has been developed, which facilitates the understanding of complex genome structure, aids gene discovery, and helps in the exploiting genetic resources for faster crop improvement (Pandey et al. 2020). In 2016, IPGI through Peanut Genome Consortium (PGC) completed the sequencing of two diploid ancestors (*A. duranensis* V14167 and *A. ipaensis* K30076) of cultivated groundnut (Bertioli et al. 2016) in order to solve the complexity associated with assembling chromosomal pseudomolecules. Meanwhile, the Diploid Progenitor Peanut A-Genome Sequencing Consortium (DPPAGSC) sequenced both diploid progenitor species, *A. duranensis* (Chen et al. 2016) and *A. ipaensis* (Lu et al. 2018). Furthermore, with the advent of next-generation sequencing (NGS) technology, it aided research in further improving, refining, and developing high-quality reference

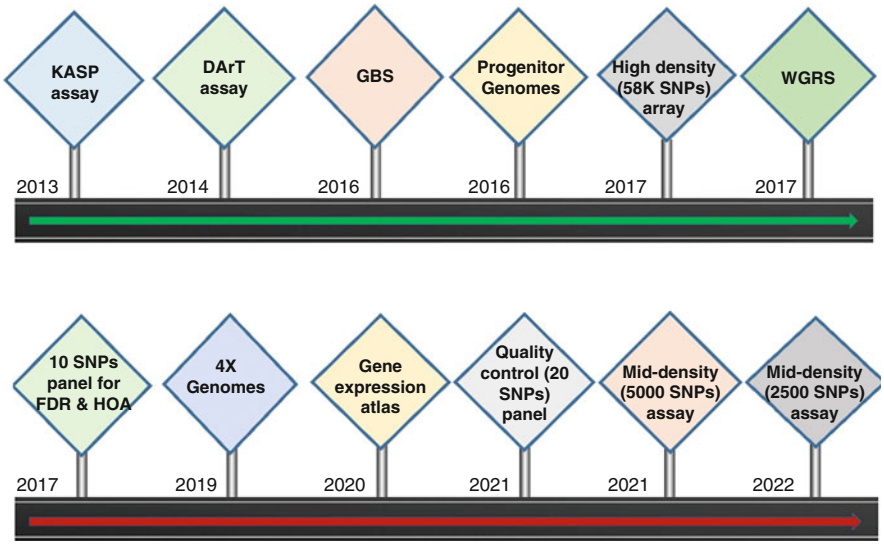

Fig. 8.2 A road map of significant developments in the field of groundnut genomics

genome assemblies for the cultivated tetraploid groundnut. In 2018, the genome assembly for the allotetraploid wild groundnut *A. monticola* was made publicly available (Yin et al. 2018). A major breakthrough among groundnut researchers took place with the availability of two reference genomes for subsp. *fastigiata* (Chen et al. 2019; Zhuang et al. 2019) and one for subsp. *hypogaea* (Bertioli et al. 2019). These reference genome assemblies revealed new knowledge on groundnut genes that have been impacted by domestication and breeding, highlighting breeding possibilities for future.

8.4.3 Whole-Genome Resequencing and Genome-Wide Markers

Adoption of NGS approaches enabled the discovery and deployment of a diverse array of molecular markers in groundnut. Both diploid genomes (*A. duranensis* and *A. ipaensis*) were mined for markers, resulting in the discovery of 135,529 and 199,957 SSRs, respectively (Zhao et al. 2017). Additional comparative diploid genome study between *A. duranensis* and *A. ipansis* detected 515,223 InDels, i.e., 269,973 insertions and 245,250 deletions (Vishwakarma et al. 2017). Furthermore, high-coverage WGRS data for 41 distinct genotypes have been generated, resulting in the finding of 98,375 SNPs in the A-subgenome and 65,407 SNPs in the B-subgenome (Pandey et al. 2017a; Clevenger et al. 2017). Notably, 58,233 high-quality informative SNPs were employed to develop high-density genotyping platform, "Axiom_*Arachis*" Array (Pandey et al. 2017a). Nowadays, it is commonly

utilized in groundnut molecular breeding routine activities for mapping traits of interest and detection of associated genomic regions. Additionally, 300 diverse accessions of the ICRISAT groundnut reference set have been sequenced in order to explore genome-wide structural changes, diversity, and marker trait association studies (see Varshney et al. 2019). Similar initiatives are ongoing in the USA and China for diverse groundnut sets. Likewise, significant use of WGRS data has resulted in the discovery of unique alleles, signature sequences, and related markers.

8.4.4 Gene Expression Atlas

NGS not only advances genome sequencing and novel genome assembly development, but it also enhances genome annotation advancement via the RNA sequencing (RNA-seq) strategy. A groundnut subsp. *hypogaea* gene expression atlas was generated (Clevenger et al. 2017). This investigation generated gene expression data from 22 groundnut tissues and reported 8816 putative homeologous genes, over 9000 alternative splicing events, and over 6000 non-coding RNA. Similarly, the second groundnut transcriptome map has been generated using RNA-seq of 39 samples from various tissues and environments. This map represents 91.73% of all annotated genes (Zhuang et al. 2019). Subsequently, a gene atlas for subsp. *fastigiata* has been employed by utilizing the same subspecies tetraploid genome (Sinha et al. 2020). Furthermore, genome annotation expansion facilitates the integration of proteome and metabolome atlases. These findings will help us to better understand genomes that have more RNA genes than protein-coding ones. Crop trait development and expression will be better understood if the genome, metabolome, and epigenome are all studied in greater depth.

8.4.5 Rapid and Cost-Effective Genotyping Assays

The current crop genomics scenario has been transformed by NGS technologies, which give a multitude of sequence information with significant increases in coverage, speed, and expense. Such advances have permitted the design of low- to high-throughput genotyping platforms. SNPs are regarded the ideal marker due to genome-wide uniform distribution and cost-effectiveness. For the present, efficient and cost-effective genotyping platforms are being developed in groundnut genomics, which will be used according to the study's objective. For example: (a) High-density genotyping platform ("Axiom_*Arachis*" 58 K SNP arrays) has been developed and utilized in several studies, marker trait analysis, dense genetic map construction, and QTL analysis. (b) A mid-density assay (2500–5000 SNPs) has been successfully deployed in genetic mapping; QTL analysis (Bomireddy et al. 2022) is suggested for performing GS, genetic diversity assessment, and background selection; using Agri-seq 5 K assay, genotyping of about 3000 lines has been done so

far in order to optimize genomic prediction in groundnut breeding. Similar DArT-seq assay with 2500 SNPs has been developed and ready for deployment through EiB-MDSG. And (c) low-density assay (10–100 SNPs) can be effectively utilized for QC assessment and purity testing of founder parents, hybridity confirmation, and early generation selection through EiB-LDSG. Panel of highly informative 20 SNPs has successfully tested for quality check among founder parents of IC-Asia, IC-WCA, IC-ESA, ICAR-DGR, and UAS-Dharwad breeding (Unpublished). So far, QC panel has effectively used in hybridity testing of more than 700 F_1 plants (IC-Asia, ICAR-DGR, and UAS-Dharwad) and for determination of homozygosity among advanced breeding lines.

All the abovementioned genotyping assays are successfully deployed in routine breeding activities. In future, such genotyping platforms will become more widely used in breeding programs around the world and pave a new era of genomics in molecular breeding.

8.4.6 Sequencing-Based Trait Mapping

New inventions in sequencing and high-throughput genotyping have accelerated trait discovery studies significantly while also enabling candidate gene identification at a fast pace. The substantial decrease in the cost of sequencing and the increased advent of high reference genomes in groundnut have facilitated sequence-based trait mapping more feasible and time-effective, over the past 2–3 years. In fact, right now, sequencing-based mapping is now accomplished out by either sequencing the entire populations or pooling samples exhibiting extreme phenotypes of the desired trait (Varshney et al. 2019). Inside this aspect, the low-to high-density sequencing methodologies are being employed to develop high-density genetic maps and improve trait mapping precision in groundnut. Recently, the GBS method is employed to develop high-density maps, to perform QTL mapping and detection of candidate genes (Pandey et al. 2017c; Han et al. 2018; Dodia et al. 2019). By using SLAF-seq technology, two high-density maps (with 2266 and 2808 SNP loci) have been constructed, for QTL mapping of quality and growth habit traits (Hu et al. 2018; Li et al. 2019), respectively. Similar approach has been successfully deployed to develop dense map (with 7184 SNPs), which facilitates to narrow down the co-localized regions associated with seed size traits, resulting in the detection of trait-linked candidate genes. Additionally, same genetic map has been used for testa color trait mapping (Zhuang et al. 2019). Association mapping of 158 groundnut diverse accessions with 17,338 polymorphic SNPs has allowed to identify marker trait association for agronomic traits (Zhang et al. 2017). To obtain large number of polymorphic SNPs, the WGRS approach has been deployed in RIL population (Tifrunner GT-C20), which enabled the generation of high-density genetic maps (8869 to 11,106 SNP loci), fine mapping of genomic region, and candidate gene discovery for ELS, LLS, and TSWV resistance (Agarwal et al. 2018, 2019). However, both WGRS and GBS platforms have been extensively deployed for mapping

traits and identification of QTLs in groundnut, but each has its own shortcomings. Recent methods for trait mapping (QTL-seq, Indel-seq, Seq-BSA, MutMap, and BSR-seq) generally rely on high- and low-bulk sample pooled sequencing, which exhibits extreme phenotypes related to the trait of interest under investigation. Among all, the "QTL-Seq" approach has been effective in identifying genomic regions and candidate genes in groundnut (Pandey et al. 2017b; Clevenger et al. 2018; Luo et al. 2019; Zhuang et al. 2019; Kumar et al. 2020; Zhao et al. 2020). Such research efforts have been facilitating the development of diagnostic markers and will help in pyramiding of QTLs associated with traits of interest in groundnut breeding.

8.4.7 Genomics-Assisted Breeding to Accelerate Groundnut Breeding

The groundnut researcher has taken several initiatives over the past decade to provide efficient genetic resources for crop improvement. Groundnut achieved the status of crop with the plentiful of genomic resources, which enable identification of genes and associated markers used in GAB. Based on the available genomic resources, diagnostic markers for high-oleic acid and resistance to nematode, rust, and LLS have been effectively generated in groundnut. The three GAB procedures, notably MAS or MABC, marker-assisted recurrent selection (MARS), and GS, have proven the most effective in groundnut. The development of a nematode-resistant variety, NemaTAM, was the first successful use of MAS (Simpson et al. 2003). Later, by pyramiding the nematode resistance and high-oleic trait, employing molecular markers linked with these traits, a high-oleic "Tifguard High O/L cultivar" has been developed (Chu et al. 2011). Following that, favorable alleles (*ahFAD2A and ahFAD2B*) for oleic acid content from the donor parent SunOleic 95R were transferred to ICGV 06110, ICGV 06142, and ICGV 06420 using MAS (Pasupuleti et al. 2016). Similarly, utilizing the MABC approach, high-oleate lines have been developed in ICGV 05141 (Bera et al. 2018), GPBD 4 (Ndeve et al. 2019), and ICGV 06100 (Bera et al. 2018). In another study, high-oleate lines have been developed through MABC utilizing favorable alleles from parents (KN176, DF12, and KX016) (Huang et al. 2019). Likewise, work has been done in developing cultivars resistant to foliar diseases (rust and LLS) together on high-oleic background (Janila et al. 2016; Bera et al. 2018; Shasidhar et al. 2020). There have certain attempts to combine high-oleic acid with foliar disease resistance in GPBD 4, G 2–52, TMV 2, and JL 24, in addition to ICGV 06189 variety (Bhat et al. 2022). Among the molecular breeding lines developed through marker-assisted backcrossing for high oleic acid (Janila et al. 2016), two Virginia bunch high oleic varieties namely Girnar 4 (ICGV 15083) and Girnar 5 (ICGV 15090) and two Spanish bunch high oleic varieties namely GG 39 (ICGV 16697) and GG 40 (ICGV 16688) are released for cultivation in India. More recently, two elite

varieties, GPBD 4 and G-252, have been improved for oleic acid content using MABC (Jadhav et al. 2021). Now, development of groundnut backcross lines has been made more precise and efficient using the available genetic resources for LLS and rust resistance (Pandey et al. 2020). The first effort has been made by utilizing SSR markers to enhance resistance for rust in three susceptible varieties, ICGV 91114, JL 24, and TAG 24 (Varshney et al. 2014). Using two to three backcrosses and selfing, 200 backcross lines were selected. From these, 81 lines were examined in the field and found to be more resistant to rust. As contrast to susceptible parents, these lines produced far more pod yield (56–96%) in affected environments (Pasupuleti et al. 2016). With GPBD 4 as the donor, various attempts have been made to develop LLS- and rust-resistant backcross lines in JL 24 (Yeri and Bhat 2016) and TMV 2 (Kolekar et al. 2017; Ramakrishnan et al. 2020). Two foliar disease resistance varieties namely Improved JL 24 (DBG 3) and Super TMV 2 (DBG 4) using donor source GPBD 4 (Bhat et al. 2022) were developed using marker-assisted selection and released for cultivation in Karnataka state of India. The most of lines are being tested in multiple locations or on large-scale farms in order to facilitate varietal development (Bhat et al. 2022).

8.5 Genomic Resources and Forward Breeding in *Vigna* Species

The genus *Vigna* with around nine domesticated crops, viz., mung bean (*Vigna radiata* (L.) R. Wilczek *var. radiata*), black gram, (*V. mungo* (L.) Hepper), cowpea (*V. unguiculata* (L.) Walp), moth bean (*V. aconitifolia* (Jacq.) Marechal), azuki bean (*V. angularis* (Willd.) Ohwi & H. Ohashi), rice bean (*V. umbellata* (Thunb.) Ohwi & H. Ohashi), creole bean (*V. reflexo-pilosa*), tuber cowpea (*V. vexillata* (L.) A. Rich), and bambara groundnut (*V. subterranean* (L.) Verdc.), is one of the important genera contributing toward food and nutritional security across the world (Takahashi and Tomooka 2020). Except for mung bean, cowpea, and black gram, the other species have limited progress on development of genomic resources and use of forward breeding approaches for crop improvement. The forward breeding approaches have been successfully proven efficient in enhancing selection accuracies and intensity for complex traits in many crops, thus helping breeders in selecting individuals with the most desirable traits of the product profile. The initial efforts used isoenzymes, random amplified polymorphic DNA (RAPD), and RFLP markers and later shifted to microsatellite markers derived from various *Vigna* species for the construction of genetic maps and to find QTLs associated with the traits of interests. The recent advancement in whole-genome sequence has strongly improved the access to molecular markers for these crops. Several thousands of SNP markers have been produced by GBS and WGRS, which are being used to assess the diversity at the genomic level and for developing new genomic resources including diagnostic markers and tools for deployment in breeding programs. The genomic resources

available in cowpea (Muñoz-Amatriaín et al. 2017; Boukar et al. 2019), mung bean (Kim et al. 2015), and black gram (Bisht and Singh 2013) are discussed in detail in earlier studies. The important genomic resources that are useful for the genetic improvement of important *Vigna* crops through forward breeding approaches are summarized below.

8.5.1 Cowpea

Cowpea (*Vigna unguiculata*), 2n = 22 with a genome size of 620 MB, is one of the largely grown *Vigna* species in the dry agroecologies of the tropics in Latin America, Africa, and South Asia. The cultivated cowpea belonging to the cultivar group *Unguiculata* is divided into five cultivar groups, namely, *unguiculata*, *sesquipedalis* (yard-long-bean), *textilis*, *biflora*, and *melanophthalmus* (Padulosi and Ng 1997). Initial efforts for use of molecular markers for the cowpea improvement used RFLP (Fatokun et al. 1993), RAPD (Kaga et al. 1996; Simon et al. 2007), inter-simple sequence repeat (ISSR) (Ajibade et al. 2000), amplified fragment length polymorphisms (AFLPs) (Fang et al. 2007), and SSR (Gupta and Gopalakrishna 2010; Ogunkanmi et al. 2008) to characterize accessions belonging to the four subgenera of the genus *Vigna* and to study genetic diversity within cultivated as well as wild relatives of cowpea accessions. The world collection of landraces and African ancestral wild cowpea were characterized at molecular level with >1200 SNP markers. The study identified two major gene pools in cultivated cowpea in Africa, each with landraces mostly distributed in Western Africa (GP1) and Eastern Africa (GP2) (Huynh et al. 2013). GBS was used to discover more SNPs in cowpea that could be used to study genetic diversity, population structure, and phylogenetic relationships (Xiong et al. 2016).

Four QTLs on Vu01 with 24 to 95% PV associated with root-galling and egg masses per root system were reported most effective against resistance to root-knot nematode caused by *M. javanica* (Ndeve et al. 2019). The trait-specific SRR markers associated with different traits, such as seed size, pod fiber thickness, seed weight (Andargie et al. 2011), pod length (Kongjaimun et al. 2012), days to flower (Andargie et al. 2013), pod number per plant (Xuet al. 2013), and pod tenderness (Kongjaimun et al. 2012), were identified in different studies. Similarly, useful SNP markers were reported for cowpea bacterial blight (Agbicodo et al. 2010), foliar thrips (Lucas et al. 2012), leaf senescence (Xu et al. 2013), heat tolerance (Lucas et al. 2013a), seed size (Lucas et al. 2013b), aphid infestation (Huynh et al. 2015), and fusarium wilt (Pottorff et al. 2012) that could be deployed in the breeding programs. The microsatellite marker SSR1 was successfully used to transfer striga resistance gene from the breeding line IT93K-693-2 into three farmers' preferred varieties, viz., IT90K-372-1-2, KVx30–309-6G, and TN5–78 through MABC (Salifou et al. 2016). The resistance to three striga races SG1, SG3, and SG5 from IT97K-499-35 into an elite farmer preferred cowpea cultivar Borno Brown was successfully introgressed using three markers SSR-1, 61RM-2 and C42–26

(Omoigui et al. 2017). Around 28 introgression lines selected in the $BC1F_{2:4}$ generation with large seed size, brown seed coat color carrying marker alleles were evaluated in the field for resistance to striga resistance. The SSR-1 was identified as best for screening genotypes for striga resistance. A rare haplotype associated with large seeds at the Css-1 locus was successfully stacked from an African buff seed-type cultivar IT82E-18 (18.5 g/100 seeds) into a blackeye seed-type cultivar CB27 (22 g/100 seed) (Lucas et al. 2015). The foreground and background selections using genome-wide SNPs identified introgression lines with very large seed size (28–35 g/100 seeds) and desirable seed quality traits. For bacterial blight, one major QTL on linkage group (LG) Vu09 (qtlblb-1) accounting for 30.58% phenotypic variation (PV) and two QTLs, i.e., qtlblb-2 and qtlblb-3 on LG Vu04 with 10.77% and 10.63%, PV, respectively, were reported (Dinesh et al. 2016). The major QTL on Vu09 was successfully introgressed from cultivar V-16 into the bacterial leaf blight susceptible variety C-152 through marker-assisted backcrossing (MABC) (Dinesh et al. 2016).

A set of informative SNP panel, i.e., Cowpea iSelect Consortium Array with 51,128 SNPs, was developed to facilitate researchers with useful genomic resources (Muñoz-Amatriaín et al. 2017). The array was further used to develop a mid-density marker platform for cowpea with 2602 SNP markers distributed evenly throughout 11 chromosomes. The SNPs for the mid-density panel were selected based on iSelect data from 2714 diverse cultivated cowpea accessions with more weightage on 184 most commonly used accessions in African breeding programs while selecting these SNPs. This mid-density array is quite suitable for marker-assisted breeding, genomic-based predictions, QTL studies, molecular diversity analyses, and germplasm management applications. KASP fluorescence-based methodology offers rapid and cost-effective genotyping useful for target trait screening, QC, and MAS in the breeding programs across several crops. The KASP assay-based SNP markers were developed and being used in cowpea for screening against resistance to aphid infestation (Huynh et al. 2015) and bacterial blight (Agbicodo et al. 2010) (Table 8.2). The SNP-based foreground and background selections with KASP genotyping platform were successfully used to combine drought tolerance along with nematode and striga resistance into Moussa local, a cowpea variety from Burkina Faso, using MABC (Batieno et al. 2016). Six promising families were identified based on MAS and preliminary field testing for yield under well-watered and water-stress, and striga resistance field trials demonstrated the high efficiency of using SNP markers for foreground and background selections to combine target traits (Batieno et al. 2016). Around 17 KASP-based SNP markers were used to determine parental diversity and to confirm hybridity of cowpea crosses (Ongom et al. 2021). These QC markers differentiated 222 cowpea parental genotypes with mean efficiency of 37.9% and a range of 3.4–82.8%, revealing unique fingerprints of the parents. These markers demonstrated an effective application of KASP-based SNP assay in fingerprinting, confirmation of hybridity, and early detection of true F_1 plants (Ongom et al. 2021).

Table 8.2 Diagnostic trait-specific and QC SNP markers available for KASP genotyping platform useful for forward breeding in cowpea and mung bean

Target trait	SNP ID	Chr.	Position	SNP/ Indel	Favorable allele	Alternate allele	Reference
Cowpea							
Aphid resistance	snpVU0031	2	25,345,278–25,345,401	A/G	A	G	Huynh et al. (2015)
	snpVU0032	2	25,479,793-25,480,105	A/G	A	G	
	snpVU0024	5	3,748,293–3,748,425	A/T	A	T	
	snpVU0025	5	4,562,162–4,562,294	C/G	C	G	
Bacterial blight	snpVU0041	3	992,603–993,420	C/T	C	T	Agbicodo et al. (2010)
Quality control and hybridity test	snpVU0007	1	36,773,526–36,773,649	T/C	–	–	Ongom et al. (2021)
	snpVU0011	2	22,941,996–22,942,128	T/C	–	–	
	snpVU0018	4	16,415,787–16,415,919	A/G	–	–	
	snpVU0019	4	24,230,438–24,230,570	T/G	–	–	
	snpVU0001	5	399,824–399,956	C/G	–	–	
	snpVU0002	5	43,326,556–43,327,417	A/G	–	–	
	snpVU0009	6	30,511,313–30,511,445	A/C	–	–	
	snpVU0010	6	34,246,871–34,247,003	T/G	–	–	
	snpVU0003	7	4,914,544–491,665	T/C	–	–	
	snpVU0004	7	39,680,298–39,680,430	T/C	–	–	
	snpVU0008	8	34,271,840–34,271,972	A/G	–	–	
	snpVU0012	9	29,111,205–29,111,337	A/C	–	–	
	snpVU0013	9	37,010,557–37,010,817	A/T	–	–	
	snpVU0016	10	37,900,312–37,900,440	A/G	–	–	
	snpVU0017	10	967,432–967,564	C/G	–	–	
	snpVU0014	11	34,083,600–34,083,732	A/G	–	–	

(continued)

Table 8.2 (continued)

Target trait	SNP ID	Chr.	Position	SNP/ Indel	Favorable allele	Alternate allele	Reference
	snpVU0015	11	12,936,036–12,936,168	T/C	–	–	
Mung bean[a]							
Bruchid resistance	snpVR00001	5	5,178,332	G/A	G	A	Schafleitner et al. (2016)
	snpVR00002	5	5,179,402	T/C	T	C	
	snpVR00003	5	5,454,538	T/C	T	C	
	snpVR00004	5	5,622,070	G/A	G	A	
	snpVR00005	5	5,662,479	G/A	G	A	
	snpVR00006	5	5,730,691	G/A	G	A	
	snpVR00007	5	5,953,917	A/T	A	T	
	snpVR00008	5	5,974,663	C/T	C	T	
	snpVR00009	3	10,431,528	T/A	T	A	
	snpVR00010	4	15,255,162	T/G	T	G	

[a]SNPs for bruchid resistance in mung bean are being validated for their selection efficiency in the KASP platform

8.5.2 Mung Bean

Mung bean (*Vigna radiata* (L.) R. Wilczek *var. radiata*), an Asiatic *Vigna* species also known as green gram or moong, is grown in around 7.3 m ha worldwide with an average yield of 721 kg/ha (Nair and Schreinemachers 2020). It is one of the important food and cash crops in the rice-based farming systems of South and Southeast Asia with India and Myanmar together accounting for 60% of global produce of 5.3 m t. Other large producers are China, Indonesia, Thailand, Kenya, and Tanzania. The mung bean yellow mosaic disease (MYMD) and bruchid infestation are major biotic stresses initially focused to develop genomic resources for forward breeding approaches. The RAPD marker OPP 07_{895} was identified to be linked with MYMD resistance using bulk segregant analysis (Dharajiya and Ravindrababu 2019). Two QTLs, i.e., qMYMIV2 and qMYMIV7, with 31.42–37.60% and 29.07–47.36% PV, respectively, were reportedly linked to MYMD resistance (Alam et al. 2014). Four SSR markers, viz., CEDG275, CEDG006, CEDG041, and VES0503, linked to these QTLs could be useful for MAS. Other markers VrD1, CEDG228, CEDG044, and STSbr1 (Singh et al. 2017a, b) and CEDG293, DMB-SSR008, and DMB-SSR059 (Singh et al. 2020) were also reportedly linked with MYMD. Five QTLs with PV that ranged from 10.11 to 20.04% for MYMD resistance were detected on an interspecific recombinant inbred line (RIL) population of mung bean and rice bean. Of these, QTL qMYMV4–1 on LG4 was identified in the same marker interval across years (Mathivathana et al. 2019). The inter-simple sequence repeat, I85420, and ISSR-anchored resistance gene analog markers I42PL-229 and I42PL-222 were successfully used for MAS of powdery mildew (PM) resistance in mung bean. Of these,

I42PL229 was used for negative selection, where I85420 and I42PL-222 were used for positive selection with around 94% selection accuracies when confirmed resistance using detached leaf assay (Chathiranrat et al. 2018). Diagnostic derived cleaved amplified polymorphic sequences (dCAPS1, 2, and 3) and cleaved amplified polymorphic sequences (CAPS) markers (CAPS1, 2, 3, 4, 6, 8, 9, 11, 12, 13, and 14) were reported for resistance to bruchid infestation on LG3, LG4, and LG5 with selection efficiency of over 93% (Schafleitner et al. 2016). Among these, 10 promising markers information used to design SNP markers and their KASP assay to deploy in the breeding program (Table 8.2). These markers are being validated for their selection efficiency using a diverse set of genotypes. The genomic regions qZn-4-3 and qFe-4-1 on LG4 between flanking markers PVBR82-BM210 and qZn-11-2 and qFe-11-1 on LG11 between flanking markers BM141-BM184 were reported for Zn or Fe concentration (Singh et al. 2017a, b). Around 43 SNPs were found to be highly associated with seven seed mineral concentrations traits, including Fe and Zn through genome-wide association study. A total of six genomic regions, one with Fe (five associated SNPs) and five with Zn (7 associated SNPs), were found to be associated with PV ranging from 13 to 22% (Wu et al. 2020).

8.5.3 Black Gram

Black gram is a highly nutritious grain legume crop, mainly grown in the South and Southeast Asian countries, including Afghanistan, Bangladesh, India, Myanmar, Pakistan, Sri Lanka, and Thailand, with India contributing over 70% of global black gram production (Kaewwongwal et al. 2015). The efforts of development linkage map in black gram during the initial years used RFLP and AFLP markers (Chaitieng et al. 2006; Gupta et al. 2008). The efforts were also made to identify and deploy SSR markers available in other crops, such as cowpea (Gupta and Gopalakrishna 2010), mung bean, adzuki bean (Gupta and Gopalakrishna 2009), and common bean (Souframanien and Reddy 2015). The discovery of NGS technologies such as Illumina paired-end sequencing resulted in 17.2 million paired-end reads, and 48,291 transcript contigs (TCS) were used for gene discovery and development of 1840 SSRs that could be used for developing linkage maps and linked molecular markers for target traits (Souframanien and Reddy 2015). In black gram, the efforts on identification of QTLs and molecular markers are limited to MYMD (Souframanien and Gopalakrishna 2006; Maiti et al. 2011; Gupta and Gopalakrishna 2013) and bruchid infestation (Souframanien et al. 2010; Somta et al. 2019). An ISSR marker, ISSR8111357, linked to the MYMD resistance gene with a 6.8 cM distance identified, was sequenced to design a sequence characterized amplified region (SCAR) primer to deploy for MAS (Souframanien and Gopalakrishna 2006). The SSR marker CEDG180 linked to MYMD resistance was also reported (Gupta and Gopalakrishna 2013). Two major QTLs governing resistance to MYMD disease in black gram reported on LG2 and LG10 with 20.90 and 24.90% PVE, respectively (Vadivel et al. 2021). The validation of these QTLs in

two other mapping populations identified as qmymv10_60 of LG10 with better selection efficiency could be useful for the MAS/MABC in black gram. Two loci, YR4 and CYR1, were identified associated with resistance to *Mung bean Yellow Mosaic India Virus* (MYMIV) in mung bean, of these CYR1 also co-segregated with MYMIV-resistant F_2, F_3 progenies of black gram (Maiti et al. 2011).

Two QTLs, viz., Cmrae1.1 and Cmrae1.2, were reported for bruchid adult emergence on LG3 and LG4, respectively (Souframanien et al. 2010). However, six QTLs were identified, with two QTLs (Cmrdp1.1 and Cmrdp1.2) on LG 1, three QTLs (Cmrdp1.3, Cmrdp1.4, and Cmrdp1.5) on LG 2, and one QTL (Cmrdp1.6) on LG 10, capturing 8.4 to 16.4% phenotypic variation for developmental period (Souframanien et al. 2010). The draft genome of black gram was sequenced using hybrid genome assembly with Illumina reads and third-generation Oxford Nanopore sequencing technology (Souframanien et al. 2021). It opens tremendous opportunities for the development of marker resources, along with the discovery of QTLs/genes and molecular markers for desirable traits. The genome analysis identified 42,115 genes with a mean coding sequence length of 1131 bp, of which around 80.6% are annotated. Besides, a total of 166,014 SSRs, including 65,180 compound SSRs, were also identified (Jegadeesan et al. 2021). The genome sequence of black gram is expected to provide greater insights and facilitate the identification of genes and QTLs linked to economically important traits for accelerating the genetic gain in black gram. The QTL qCm_PDS2.1 for percent damaged seeds and qVmunBr6.1 (24.32–28.76% PV) and qVmunBr6.2 (15.26–17.37%) for bruchid infestation severity progress mapped on LG 6 in mung bean. Two QTLs, i.e., qVmunBr6.1 and *qVmunBr6.2*, that are new loci for *C. maculatus* resistance in *Vigna* species will be useful for widening the genetic base of bruchid resistance in black gram (Somta et al. 2019). The SSR markers CEDG030 and CEDG248 were successfully used for hybridity test and ingression of MYMD resistance from rice bean to black gram (Sehrawat et al. 2016). Another successful example of the introgression of QTLs for MYMD resistance on LG2 and LG10 from resistant donor Mash 1008 into the popular black gram variety MDU 1 uses the MABC approach. Nine advanced backcross lines were identified with significant superior performances over recurrent parent MDU1 for yield and MYMD resistance (Subramaniyan et al. 2021).

8.6 Future Prospects

Despite the availability of several SNP markers, the public sectors face several challenges compared to private sectors when it comes to accessibility of these platform for implementation. Shared genotyping platform are expected to address several constraints faced by the public breeding program and will enable the implementation of genotyping tools into routine breeding operation. Availability of several LDSG-based trait and QC markers for forward breeding especially for QC and MAS and the MDSG-based medium density SNP panel will be useful for diversity studies, DNA fingerprinting, and MABC for background recovery analysis

and GS applications in wheat, potato, and groundnut crops. The *Vigna* species crops were previously considered to be an orphan crop due to the limited availability of genomic resources compared to other legume and cereal crops. However, the recent progress on draft genome sequencing of mung bean (Kang et al. 2014), cowpea (Lonardi et al. 2019), black gram (Jegadeesan et al. 2021), and azuki bean (Kang et al. 2015) would help in accelerating the development of genomic resources and varietal improvement through forward breeding in *Vigna* crops. Collecting and resequencing *Vigna* species from different geographical areas would help researchers investigate allelic variation in beneficial traits that can be mined from wild relatives. These new resources would also open the door to genomic research in other *Vigna* species. More focus should be given to bring the identified markers on a cost-effective genotyping platform, i.e., KASP for their deployment in the breeding program. Utilization of 100-150 SNPs using DArTag panels for QC in potato and sweet potato (polyploids in general) would help streamline the QC implementation in a cost-effective manner. The enhanced precision and selection intensities for different complex target traits using diagnostic cost-effective molecular markers would accelerate the rate of genetic gains in crops and help breeders in developing the market preferred varieties.

References

Agarwal G, Clevenger J, Kale SM, Wang H, Pandey MK, Choudhary D, Yuan M, Wang X, Culbreath AK, Holbrook CC, Liu X, Varshney RK, Guo B (2019) A recombination bin-map identified a major QTL for resistance to tomato spotted wilt virus in peanut (*Arachis hypogaea*). Sci Rep 9(1):1–13. https://doi.org/10.1038/s41598-019-54747-1

Agarwal G, Clevenger J, Pandey MK, Wang H, Shasidhar Y, Chu Y, Fountain JC, Choudhary D, Culbreath AK, Liu X, Huang G, Wang X, Deshmukh R, Holbrook CC, Bertioli DJ, Ozias-Akins P, Jackson SA, Varshney RK, Guo B (2018) High-density genetic map using whole-genome resequencing for fine mapping and candidate gene discovery for disease resistance in peanut. Plant Biotechnol J 16(11):1954–1967. https://doi.org/10.1111/pbi.12930

Agbicodo EM, Fatokun CA, Bandyopadhyay R, Wydra K, Diop NN, Muchero W, Ehlers JD, Roberts PA, Close TJ, Visser RGF, van der Linden CG (2010) Identification of markers associated with bacterial blight resistance loci in cowpea [*Vigna unguiculata* (L.) Walp.]. Euphytica 175(2):215–226. https://doi.org/10.1007/s10681-010-0164-5

Ajibade SR, Weeden NF, Chite SM (2000) Inter simple sequence repeat analysis of genetic relationships in the genus Vigna. Euphytica 111(1):47–55. https://doi.org/10.1023/A:1003763328768

Alam AM, Somta P, Srinives P (2014) Identification and confirmation of quantitative trait loci controlling resistance to mungbean yellow mosaic disease in mungbean [Vigna radiata (L.) Wilczek]. Mol Breed 34:1497–1506

Andargie M, Pasquet RS, Gowda BS, Muluvi GM, Timko MP (2011) Construction of a SSR-based genetic map and identification of QTL for domestication traits using recombinant inbred lines from a cross between wild and cultivated cowpea (*V. unguiculata* (L.) Walp.). Mol Breed 28(3):413–420. https://doi.org/10.1007/s11032-011-9598-2

Andargie M, Pasquet RS, Muluvi GM, Timko MP (2013) Quantitative trait loci analysis of flowering time related traits identified in recombinant inbred lines of cowpea (*Vigna unguiculata*). Genome 56(5):289–294. https://doi.org/10.1139/gen-2013-0028

Batieno BJ, Danquah E, Tignegre J-B, Huynh B-L, Drabo I, Close TJ, Ofori K, Roberts P, Ouedraogo TJ (2016) Application of marker-assisted backcrossing to improve cowpea (Vignaunguiculata L. Walp) for drought tolerance. Journal of Plant Breeding and Crop Science 8(12):273–286. https://doi.org/10.5897/JPBCS2016.0607

Bera SK, Kamdar JH, Kasundra SV, Dash P, Maurya AK, Jasani MD, Chandrashekar AB, Manivannan N, Vasanthi RP, Dobariya KL, Pandey MK, Janila P, Radhakrishnan T, Varshney RK (2018) Improving oil quality by altering levels of fatty acids through marker-assisted selection of ahfad2 alleles in peanut (Arachis hypogaea L.). Euphytica 214(9):1–15. https://doi.org/10.1007/S10681-018-2241-0/FIGURES/8

Bertioli DJ, Cannon SB, Froenicke L, Huang G, Farmer AD, Cannon EKS, Liu X, Gao D, Clevenger J, Dash S, Ren L, Moretzsohn MC, Shirasawa K, Huang W, Vidigal B, Abernathy B, Chu Y, Niederhuth CE, Umale P et al (2016) The genome sequences of *arachis duranensis* and *arachis ipaensis*, the diploid ancestors of cultivated peanut. Nat Genet 48(4): 438–446. https://doi.org/10.1038/ng.3517

Bertioli DJ, Jenkins J, Clevenger J, Dudchenko O, Gao D, Seijo G, Leal-Bertioli SCM, Ren L, Farmer AD, Pandey MK, Samoluk SS, Abernathy B, Agarwal G, Ballén-Taborda C, Cameron C, Campbell J, Chavarro C, Chitikineni A, Chu Y et al (2019) The genome sequence of segmental allotetraploid peanut *Arachis hypogaea*. Nat Genet 51(5):877–884. https://doi.org/10.1038/s41588-019-0405-z

Bhat RS, Venkatesh Jadhav MP, Patil PV, Shirasawa K (2022) Genomics-assisted breeding for resistance to leaf spots and rust diseases in Peanut. Accelerated Plant Breeding 4:239–278. https://doi.org/10.1007/978-3-030-81107-5_8

Bisht IS, Singh M (2013) Genetic and genomic resources of grain legume improvement: 10. Asian Vigna

Bohar R, Chitkineni A, Varshney RK (2020) Genetic molecular markers to accelerate genetic gains in crops. BioTechniques 69(3). https://doi.org/10.2144/btn-2020-0066

Bomireddy D, Gangurde SS, Variath MT, Janila P, Manohar SS, Sharma V, Parmar S, Deshmukh D, Reddisekhar M, Reddy DM, Sudhakar P, Reddy BVB, Varshney RK, Guo B, Pandey MK (2022) Discovery of major quantitative trait loci and candidate genes for fresh seed dormancy in groundnut. Agronomy 12(2). https://doi.org/10.3390/AGRONOMY12020404

Bonierbale MW, Amoros WR, Salas E, De Jong W (2019) Potato breeding. In: The potato crop: its agricultural, nutritional and social contribution to humankind. Springer International Publishing, pp 163–217. https://doi.org/10.1007/978-3-030-28683-5_6

Boukar O, Belko N, Chamarthi S, Togola A, Batieno J, Owusu E, Haruna M, Diallo S, Umar ML, Olufajo O, Fatokun C (2019) Cowpea (*Vigna unguiculata*): genetics, genomics and breeding. Plant Breed 138(4):415–424. https://doi.org/10.1111/PBR.12589

Bradshaw JE (2017) Review and analysis of limitations in ways to improve conventional potato breeding. Potato Res 60(2):171–193. https://doi.org/10.1007/s11540-017-9346-z

Byrne S, Meade F, Mesiti F, Griffin D, Kennedy C, Milbourne D (2020) Genome-wide association and genomic prediction for fry color in potato. Agronomy 10:90. https://doi.org/10.3390/AGRONOMY10010090

Caruana BM, Pembleton LW, Constable F, Rodoni B, Slater AT, Cogan NOI (2019) Validation of genotyping by sequencing using transcriptomics for diversity and application of genomic selection in tetraploid potato. Front Plant Sci 10. https://doi.org/10.3389/fpls.2019.00670

Caruana BM, Rodoni BC, Constable F, Slater AT, Cogan NOI (2021) Genome enhanced marker improvement for potato virus Y disease resistance in potato. Agronomy 11(5):832. https://doi.org/10.3390/agronomy11050832

CGIAR System Organization (2021) CGIAR 2030 research and innovation strategy: transforming food, land, and water systems in a climate crisis. Montpellier, France: CGIAR System Organization. Available at https://hdl.handle.net/10568/110918. Accessed 20 April 2022

Chaitieng B, Kaga A, Tomooka N, Isemura T, Kuroda Y, Vaughan DA (2006) Development of a black gram [Vigna mungo (L.) hepper] linkage map and its comparison with an azuki bean

[*Vigna angularis* (Willd.) Ohwi and Ohashi] linkage map. Theor Appl Genet 113(7): 1261–1269. https://doi.org/10.1007/S00122-006-0380-5/TABLES/3

Chathiranrat N, Nitisit S, Chaiyapan C, Wansuriwong N, Papan P, Tantasawat PA (2018) Selection of mungbean resistant to powdery mildew in BC_1F_1 progenies based on ISSR and ISSR-RGA markers. Int J Adv Sci Engg Technol 6:2321–9009. http://iraj.in

Chen X, Li H, Pandey MK, Yang Q, Wang X, Garg V, Li H, Chi X, Doddamani D, Hong Y, Upadhyaya H, Guo H, Khan AW, Zhu F, Zhang X, Pan L, Pierce GJ, Zhou G, Krishnamohan KAVS et al (2016) Draft genome of the peanut A-genome progenitor (*arachis duranensis*) provides insights into geocarpy, oil biosynthesis, and allergens. Proc Natl Acad Sci U S A 113(24):6785–6790. https://doi.org/10.1073/PNAS.1600899113

Chen X, Lu Q, Liu H, Zhang J, Hong Y, Lan H, Li H, Wang J, Liu H, Li S, Pandey MK, Zhang Z, Zhou G, Yu J, Zhang G, Yuan J, Li X, Wen S, Meng F et al (2019) Sequencing of cultivated Peanut, *Arachis hypogaea*, yields insights into genome evolution and oil improvement. Mol Plant 12(7):920–934. https://doi.org/10.1016/J.MOLP.2019.03.005

Chu Y, Wu CL, Holbrook CC, Tillman BL, Person G, Ozias-Akins P (2011) Marker-assisted selection to pyramid nematode resistance and the high oleic trait in Peanut. The Plant Genome 4(2):110–117. https://doi.org/10.3835/PLANTGENOME2011.01.0001

Clevenger J, Chu Y, Chavarro C, Agarwal G, Bertioli DJ, Leal-Bertioli SCM, Pandey MK, Vaughn J, Abernathy B, Barkley NA, Hovav R, Burow M, Nayak SN, Chitikineni A, Isleib TG, Holbrook CC, Jackson SA, Varshney RK, Ozias-Akins P (2017) Genome-wide SNP genotyping resolves signatures of selection and Tetrasomic recombination in Peanut. Mol Plant 10(2):309–322. https://doi.org/10.1016/J.MOLP.2016.11.015

Clevenger J, Chu Y, Chavarro C, Botton S, Culbreath A, Isleib TG, Holbrook CC, Ozias-Akins P (2018) Mapping late leaf spot resistance in Peanut (*Arachis hypogaea*) using QTL-seq reveals markers for marker-assisted selection. Front Plant Sci 9. https://doi.org/10.3389/fpls.2018.00083

Cobb JN, Juma RU, Biswas PS, Arbelaez JD, Rutkoski J, Atlin G, Hagen T, Quinn M, Ng EH (2019) Enhancing the rate of genetic gain in public-sector plant breeding programs: lessons from the breeder's equation. Theor Appl Genet 132(3):627–645. https://doi.org/10.1007/S00122-019-03317-0

Crespo-Herrera LA, Crossa J, Huerta-Espino J, Autrique E, Mondal S, Velu G, Vargas M, Braun HJ, Singh RP (2017) Genetic yield gains in CIMMYT's international elite spring wheat yield trials by Modeling the genotype × environment interaction. Crop Sci 57(2):789–801. https://doi.org/10.2135/cropsci2016.06.0553

Crespo-Herrera L, Crossa J, Sci JH-E-C (2018) Genetic gains for grain yield in CIMMYT's semi-arid wheat yield trials grown in suboptimal environments. ScienceopenCom 58(5):1890–1898. https://doi.org/10.2135/cropsci2018.01.0017

Dharajiya DT, Ravindrababu Y (2019) Identification of molecular marker associated with mungbean yellow mosaic virus resistance in mungbean [*Vigna radiata* (L.) Wilczek]. Vegetos 32(4):532–539. https://doi.org/10.1007/s42535-019-00063-y

Dinesh HB, Lohithaswa HC, Viswanatha KP, Singh P, Rao AM (2016) Identification and marker-assisted introgression of QTL conferring resistance to bacterial leaf blight in cowpea (Vigna unguiculata (L.) Walp.). Plant Breed 135(4):506–512

Dodia SM, Joshi B, Gangurde SS, Thirumalaisamy PP, Mishra GP, Narandrakumar D, Soni P, Rathnakumar AL, Dobaria JR, Sangh C, Chitikineni A, Chanda SV, Pandey MK, Varshney RK, Thankappan R (2019) Genotyping-by-sequencing based genetic mapping reveals large number of epistatic interactions for stem rot resistance in groundnut. Theor Appl Genet 132(4): 1001–1016. https://doi.org/10.1007/S00122-018-3255-7

Dreisigacker S, Crossa J, Pérez-Rodríguez P, Montesinos-López OA, Rosyara U, Juliana P, Mondal S, Crespo-Herrera L, Govindan V, Singh RP, Braun H-J (2021) Implementation of genomic selection in the CIMMYT global wheat program, findings from the past 10 years. Crop Breeding, Genetics and Genomics 3(2):e210004. https://doi.org/10.20900/cbgg20210005

Dreisigacker S, Sukumaran S, Guzmán C, He X, Lan C, Bonnett D, Crossa J (2016) Molecular marker-based selection tools in spring bread wheat improvement: CIMMYT experience and prospects, pp 421–474. https://doi.org/10.1007/978-3-319-27090-6_16

EiB-LDSG (2022). Available: https://excellenceinbreeding.org/toolbox/services/low-density-genotyping-services-introduction. Accessed April 20, 2022

EiB-MDSG (2022). Available: https://excellenceinbreeding.org/toolbox/services/mid-density-genotyping-service. Accessed April 20, 2022

Enciso-Rodriguez F, Douches D, Lopez-Cruz M, Coombs J, de los Campos, G. (2018) Genomic selection for late blight and common scab resistance in tetraploid potato (*Solanum tuberosum*). G3 Genes|Genomes|Genetics 8(7):2471–2481. https://doi.org/10.1534/g3.118.200273

Endelman JB, Carley CAS, Bethke PC, Coombs JJ, Clough ME, da Silva WL, De Jong WS, Douches DS, Frederick CM, Haynes KG, Holm DG, Miller JC, Muñoz PR, Navarro FM, Novy RG, Palta JP, Porter GA, Rak KT, Sathuvalli VR et al (2018) Genetic variance partitioning and genome-wide prediction with allele dosage information in autotetraploid potato. Genetics 209(1):77–87. https://doi.org/10.1534/genetics.118.300685

FAOSTAT (2022). Available: http://www.fao.org/faostat/en/#data. Accessed April 20, 2022

Fang J, Chao CCT, Roberts PA, Ehlers JD (2007) Genetic diversity of cowpea [Vigna unguiculata (L.) Walp.] in four West African and USA breeding programs as determined by AFLP analysis. Genet Resour Crop Evol 54:1197–1209

Fatokun CA, Danesh D, Young ND, Stewart EL (1993) Molecular taxonomic relationships in the genus Vigna based on RFLP analysis. Theor Appl Genet 86(1):97–104. https://doi.org/10.1007/BF00223813

Felcher KJ, Coombs JJ, Massa AN, Hansey CN, Hamilton JP, Veilleux RE, Buell CR, Douches DS (2012) Integration of two diploid potato linkage maps with the potato genome sequence. PLoS One 7(4):e36347. https://doi.org/10.1371/journal.pone.0036347

Fulladolsa AC, Navarro FM, Kota R, Severson K, Palta JP, Charkowski AO (2015) Application of marker assisted selection for potato virus Y resistance in the University of Wisconsin Potato Breeding Program. Am J Potato Res 92(3):444–450. https://doi.org/10.1007/s12230-015-9431-2

Garcia Oliveira AL, Ayele L, Uwimana B, Storr S, Tadesse T, Ng EH, Swennen R, Bohar R, Debaene J, Quinn M (2021) Access to genetic analysis accelerates banana breeding in East Africa. Available:https://excellenceinbreeding.org/news/access-genetic-analysis-accelerates-banana-breeding-east-africa. Accessed April 20, 2022

Gemenet DC, Kitavi MN, David M, Ndege D, Ssali RT, Swanckaert J, Makunde G, Craig Yencho G, Gruneberg W, Carey E, Mwanga RO, Andrade MI, Heck S, Campos H (2020a) Development of diagnostic SNP markers for quality assurance and control in sweetpotato [*Ipomoea batatas* (L.) lam.] breeding programs. PLoS One 15(4):e0232173. https://doi.org/10.1371/JOURNAL.PONE.0232173

Gemenet DC, Lindqvist-Kreuze H, De Boeck B, da Silva Pereira G, Mollinari M, Zeng Z-B, Craig Yencho G, Campos H (2020b) Sequencing depth and genotype quality: accuracy and breeding operation considerations for genomic selection applications in autopolyploid crops. Theor Appl Genet 133:3345–3363. https://doi.org/10.1007/s00122-020-03673-2

Gerard GS, Crespo-Herrera LA, Crossa J, Mondal S, Velu G, Juliana P, Huerta-Espino J, Vargas M, Rhandawa MS, Bhavani S, Braun H, Singh RP (2020) Grain yield genetic gains and changes in physiological related traits for CIMMYT's high rainfall wheat screening nursery tested across international environments. Field Crop Res 249:107742. https://doi.org/10.1016/j.fcr.2020.107742

Gupta SK, Gopalakrishna T (2009) Genetic diversity analysis in blackgram (*Vigna mungo* (L.) Hepper) using AFLP and transferable microsatellite markers from azuki bean (*Vigna angularis* (Willd.) Ohwi & Ohashi). Genome 52(2):120–129. https://doi.org/10.1139/G08-107

Gupta SK, Gopalakrishna T (2010) Development of unigene-derived SSR markers in cowpea (Vigna unguiculata) and their transferability to other Vigna species. Genome 53(7):508–523. https://doi.org/10.1139/G10-028/SUPPL_FILE/G10-028SUPPL.PDF

Gupta SK, Gopalakrishna T (2013) Advances in genome mapping in orphan grain legumes of genus *Vigna*. Ind J Genetics Plant Breed 73(1):1. https://doi.org/10.5958/j.0019-5200.73.1.001

Gupta SK, Souframanien J, Gopalakrishna T (2008) Construction of a genetic linkage map of black gram, Vigna mungo (L.) hepper, based on molecular markers and comparative studies. Genome 51(8):628–637. https://doi.org/10.1139/G08-050

Hamilton JP, Hansey CN, Whitty BR, Stoffel K, Massa AN, Van Deynze A, De Jong WS, Douches DS, Buell CR (2011) Single nucleotide polymorphism discovery in elite north american potato germplasm. BMC Genomics 12(1):302. https://doi.org/10.1186/1471-2164-12-302

Han S, Yuan M, Clevenger JP, Li C, Hagan A, Zhang X, Chen C, He G (2018) A snp-based linkage map revealed QTLs for resistance to early and late leaf spot diseases in peanut (*Arachis hypogaea* L.). Front Plant Sci 9:1012. https://doi.org/10.3389/FPLS.2018.01012/BIBTEX

He X, Brar GS, Bonnett D, Dreisigacker S, Hyles J, Spielmeyer W, Bhavani S, Singh RP, Singh PK (2020) Disease resistance evaluation of elite CIMMYT wheat lines containing the coupled *Fhb1* and *Sr2* genes. Plant Dis 104(9):2369–2376. https://doi.org/10.1094/PDIS-02-20-0369-RE

de Herrera MR, Vidalon LJ, Montenegro JD, Riccio C, Guzman F, Bartolini I, Ghislain M (2018) Molecular and genetic characterization of the Ryadg locus on chromosome XI from Andigena potatoes conferring extreme resistance to potato virus Y. Theor Appl Genet 131(9):1925–1938. https://doi.org/10.1007/s00122-018-3123-5

Honsdorf N, Mulvaney MJ, Singh RP, Ammar K, Burgueño J, Govaerts B, Verhulst N (2018) Genotype by tillage interaction and performance progress for bread and durum wheat genotypes on irrigated raised beds. Field Crop Res 216:42–52. https://doi.org/10.1016/j.fcr.2017.11.011

Hu XH, Zhang SZ, Miao HR, Cui FG, Shen Y, Yang WQ, Xu TT, Chen N, Chi XY, Zhang ZM, Chen J (2018) High-density genetic map construction and identification of QTLs controlling oleic and linoleic acid in peanut using SLAFseq and SSRs. Sci Rep 8(1):5479. https://doi.org/10.1038/s41598-018-23873-7

Huang B, Qi F, Sun Z, Miao L, Zhang Z, Liu H, Fang Y, Dong W, Tang F, Zheng Z, Zhang X (2019) Marker-assisted backcrossing to improve seed oleic acid content in four elite and popular peanut (Arachis hypogaea L.) cultivars with high oil content. Breed Sci 69(2):234–243. https://doi.org/10.1270/jsbbs.18107

Hunt LA, Garcia Oliveira AL, William HM, Ng EH, Das B, Kwemoi DB, Asante MD (2021) African breeding programs leap forward by accessing new genotyping data. Available: https://excellenceinbreeding.org/news/african-breeding-programs-leap-forward-accessing-new-genotyping-data. Accessed April 20, 2022

Huynh B-L, Ehlers JD, Ndeve A, Wanamaker S, Lucas MR, Close TJ, Roberts PA (2015) Genetic mapping and legume synteny of aphid resistance in African cowpea (*Vigna unguiculata* L. Walp.) grown in California. Mol Breed 35(1):36. https://doi.org/10.1007/s11032-015-0254-0

Huynh B, Close TJ, Roberts PA, Hu Z, Wanamaker S, Lucas MR, Chiulele R, Cissé N, David A, Hearne S, Fatokun C, Diop NN, Ehlers JD (2013) Gene pools and the genetic architecture of domesticated cowpea. Plant Genome 6(3). https://doi.org/10.3835/plantgenome2013.03.0005

Jadhav MP, Patil MD, Hampannavar M, Venkatesh DP, Shirasawa K, Pasupuleti J, Pandey MK, Varshney RK, Bhat RS (2021) Enhancing oleic acid content in two commercially released peanut varieties through marker-assisted backcross breeding. Crop Sci 61(4):2435–2443. https://doi.org/10.1002/CSC2.20512

Janila P, Pandey MK, Shasidhar Y, Variath MT, Sriswathi M, Khera P, Manohar SS, Nagesh P, Vishwakarma MK, Mishra GP, Radhakrishnan T, Manivannan N, Dobariya KL, Vasanthi RP, Varshney RK (2016) Molecular breeding for introgression of fatty acid desaturase mutant alleles (*ahFAD2A* and *ahFAD2B*) enhances oil quality in high and low oil containing peanut genotypes. Plant Sci 242:203–213. https://doi.org/10.1016/J.PLANTSCI.2015.08.013

Jegadeesan S, Raizada A, Dhanasekar P, Suprasanna P (2021) Draft genome sequence of the pulse crop blackgram [*Vigna mungo* (L.) hepper] reveals potential R-genes. Sci Rep 11(1):1–10. https://doi.org/10.1038/s41598-021-90683-9

Jiang R, Li J, Tian Z, Du J, Armstrong M, Baker K, Tze-Yin Lim J, Vossen JH, He H, Portal L, Zhou J, Bonierbale M, Hein I, Lindqvist-Kreuze H, Xie C (2018) Potato late blight field

resistance from QTL dPI09c is conferred by the NB-LRR gene R8. J Exp Bot 69(7):1545–1555. https://doi.org/10.1093/jxb/ery021

Kaewwongwal A, Kongjaimun A, Somta P, Chankaew S, Yimram T, Srinives P (2015) Genetic diversity of the black gram [Vigna mungo (L.) Hepper] gene pool as revealed by SSR markers. Breed Sci 65(2):127–137

Kaga A, Tomooka N, Egawa Y, Hosaka K, Kamijima O (1996) Species relationships in the subgenus Ceratotropis (genus Vigna) as revealed by RAPD analysis. Euphytica 88(1):17–24. https://doi.org/10.1007/BF00029261

Kang YJ, Kim SK, Kim MY, Lestari P, Kim KH, Ha BK, Jun TH, Hwang WJ, Lee T, Lee J, Shim S, Yoon MY, Jang YE, Han KS, Taeprayoon P, Yoon N, Somta P, Tanya P, Kim KS et al (2014) Genome sequence of mungbean and insights into evolution within Vigna species. Nat Commun 5(1):1–9. https://doi.org/10.1038/ncomms6443

Kang YJ, Satyawan D, Shim S, Lee T, Lee J, Hwang WJ, Kim SK, Lestari P, Laosatit K, Kim KH, Ha TJ, Chitikineni A, Kim MY, Ko J-M, Gwag J-G, Moon J-K, Lee Y-H, Park B-S, Varshney RK, Lee S-H (2015) Draft genome sequence of adzuki bean, Vigna angularis. Sci Rep 5(1): 8069. https://doi.org/10.1038/srep08069

Kante M, Lindqvist-Kreuze H, Portal L, David M, Gastelo M (2021) Kompetitive allele specific PCR (KASP) markers for potato: an effective tool for increased genetic gains. Agronomy 11(11):2315. https://doi.org/10.3390/agronomy11112315

Kim SK, Nair RM, Lee J, Lee S-H (2015) Genomic resources in mungbean for future breeding programs. Front Plant Sci 6. https://doi.org/10.3389/fpls.2015.00626

Kolekar RM, Sukruth M, Shirasawa K, Nadaf HL, Motagi BN, Lingaraju S, Patil PV, Bhat RS (2017) Marker-assisted backcrossing to develop foliar disease-resistant genotypes in TMV 2 variety of peanut (*Arachis hypogaea* L.). Plant Breed 136(6):948–953. https://doi.org/10.1111/pbr.12549

Kongjaimun A, Kaga A, Tomooka N, Somta P, Shimizu T, Shu Y, Isemura T, Vaughan DA, Srinives P (2012) An SSR-based linkage map of yardlong bean [*Vigna unguiculata* (L.) Walp. Subsp. unguiculata sesquipedalis group] and QTL analysis of pod length. Genome 55(2):81–92. https://doi.org/10.1139/g11-078

Kumar R, Janila P, Vishwakarma MK, Khan AW, Manohar SS, Gangurde SS, Variath MT, Shasidhar Y, Pandey MK, Varshney RK (2020) Whole-genome resequencing-based QTL-seq identified candidate genes and molecular markers for fresh seed dormancy in groundnut. Plant Biotechnol J 18(4):992–1003. https://doi.org/10.1111/pbi.13266

Lan C, Basnet BR. (2016) Overview of bi-parental QTL mapping and cloning genes in the context of wheat rust. In S. Dreisigacker, Sehgal D, Reyes Jaimez AE, Luna Garrido B, Muñoz Zavala S, Núñez Ríos C, & Mollins JMall S (Eds.), CIMMYT wheat molecular genetics: laboratory protocols and applications to wheat breeding (pp. 39–46). CIMMYT

Lantican MA, Braun HJ, Payne TS, Singh RP, Sonder K, Baum M, van Ginkel M, Erenstein O (2016) Impacts of international wheat improvement research, 1994–2014. International Maize and Wheat Improvement Center (CIMMYT), Mexico, DF, Mexico

Le Thuy CT, Becerra Lopez-Lavalle LA, Vu NA, Hy NH, Nhan PT, Ceballos H, Newby J, Tung NB, Hien NT, Tuan LN, Hung N, Hanh NT, Trang DT, Ha TT, Ham LH, Pham XH, Quynh TN, Rabbi IY, Kulakow PA, Zhang X (2021) Identifying new resistance to cassava mosaic disease and validating markers for the CMD2 locus. Agriculture 11(9):829. https://doi.org/10.3390/agriculture11090829

Li L, Yang X, Cui S, Meng X, Mu G, Hou M, He M, Zhang H, Liu L, Chen CY (2019) Construction of high-density genetic map and mapping quantitative trait loci for growth habit-related traits of peanut (Arachis hypogaea L.). Front Plant Sci 10:745. https://doi.org/10.3389/fpls.2019.00745

Lindqvist-Kreuze H, De Boeck B, Unger P, Gemenet D, Li X, Pan Z, Sui Q, Qin J, Woldegjorgis G, Negash K, Seid I, Hirut B, Gastelo M, De Vega J, Bonierbale M (2021) Global multi-environment resistance QTL for foliar late blight resistance in tetraploid potato with tropical adaptation. G3 Genes|Genomes|Genetics 11(11). https://doi.org/10.1093/g3journal/jkab251

Lindqvist-Kreuze H, Gastelo M, Perez W, Forbes GA, de Koeyer D, Bonierbale M (2014) Phenotypic stability and genome-wide association study of late blight resistance in potato genotypes adapted to the tropical highlands. Phytopathology 104(6):624–633. https://doi.org/10.1094/PHYTO-10-13-0270-R

Lucas MR, Ehlers JD, Roberts PA, Close TJ (2012) Markers for quantitative inheritance of resistance to foliar thrips in cowpea. Crop Sci 52(5):2075–2081

Lonardi S, Muñoz-Amatriaín M, Liang Q, Shu S, Wanamaker SI, Lo S, Tanskanen J, Schulman AH, Zhu T, Luo M, Alhakami H, Ounit R, Hasan AM, Verdier J, Roberts PA, Santos JRP, Ndeve A, Doležel J, Vrána J et al (2019) The genome of cowpea (*Vigna unguiculata* [L.] Walp.). Plant J 98(5):767–782. https://doi.org/10.1111/tpj.14349

Lu Q, Li H, Hong Y, Zhang G, Wen S, Li X, Zhou G, Li S, Liu H, Liu H, Liu Z, Varshney RK, Chen X, Liang X (2018) Genome sequencing and analysis of the peanut B-genome progenitor (*arachis ipaensis*). Front Plant Sci 9. https://doi.org/10.3389/FPLS.2018.00604/FULL

Lucas MR, Ehlers JD, Huynh B-L, Diop N-N, Roberts PA, Close TJ (2013a) Markers for breeding heat-tolerant cowpea. Mol Breed 31(3):529–536. https://doi.org/10.1007/s11032-012-9810-z

Lucas MR, Huynh B-L, da Silva Vinholes P, Cisse N, Drabo I, Ehlers JD, Roberts PA, Close TJ (2013b) Association studies and legume synteny reveal haplotypes determining seed size in *Vigna unguiculata*. Front Plant Sci 4. https://doi.org/10.3389/fpls.2013.00095

Lucas MR, Huynh B-L, Roberts PA, Close TJ (2015) Introgression of a rare haplotype from southeastern Africa to breed California blackeyes with larger seeds. Front Plant Sci 6. https://doi.org/10.3389/fpls.2015.00126

Luo H, Pandey MK, Khan AW, Guo J, Wu B, Cai Y, Huang L, Zhou X, Chen Y, Chen W, Liu N, Lei Y, Liao B, Varshney RK, Jiang H (2019) Discovery of genomic regions and candidate genes controlling shelling percentage using <scp>QTL</scp> −seq approach in cultivated peanut (*Arachis hypogaea* L.). Plant Biotechnol J 17(7):1248–1260. https://doi.org/10.1111/pbi.13050

Maiti S, Basak J, Kundagrami S, Kundu A, Pal A (2011) Molecular marker-assisted genotyping of Mungbean yellow mosaic India virus resistant germplasms of Mungbean and Urdbean. Mol Biotechnol 47(2):95–104. https://doi.org/10.1007/s12033-010-9314-1

Mathivathana MK, Murukarthick J, Karthikeyan A, Jang W, Dhasarathan M, Jagadeeshselvam N, Sudha M, Vanniarajan C, Karthikeyan G, Yang T-J, Raveendran M, Pandiyan M, Senthil N (2019) Detection of QTLs associated with mungbean yellow mosaic virus (MYMV) resistance using the interspecific cross of *Vigna radiata* × *Vigna umbellata*. J Appl Genet 60(3–4):255–268. https://doi.org/10.1007/s13353-019-00506-x

Miedaner T, Korzun V (2012) Marker-assisted selection for disease resistance in wheat and barley breeding. Phytopathology 102(6):560–566. https://doi.org/10.1094/PHYTO-05-11-0157

Mihovilovich E, Aponte M, Lindqvist-Kreuze H, Bonierbale M (2014) An RGA-derived SCAR marker linked to PLRV resistance from *Solanum tuberosum* ssp. andigena. Plant Mol Biol Report 32(1):117–128. https://doi.org/10.1007/s11105-013-0629-5

Morris CF, Kiszonas AM, Murray J, Boehm J, Ibba MI, Zhang M, Cai X (2019) Re-evolution of durum wheat by introducing the hardness and *Glu-D1* loci. Frontiers in Sustainable Food Systems 3. https://doi.org/10.3389/fsufs.2019.00103

Muñoz-Amatriaín M, Mirebrahim H, Xu P, Wanamaker SI, Luo M, Alhakami H, Alpert M, Atokple I, Batieno BJ, Boukar O, Bozdag S, Cisse N, Drabo I, Ehlers JD, Farmer A, Fatokun C, Gu YQ, Guo Y, Huynh B et al (2017) Genome resources for climate-resilient cowpea, an essential crop for food security. Plant J 89(5):1042–1054. https://doi.org/10.1111/tpj.13404

Mwamahonje A, Eleblu JSY, Ofori K, Feyissa T, Deshpande S, Garcia-Oliveira AL, Bohar R, Kigoni M, Tongoona P (2021) Introgression of QTLs for drought tolerance into farmers' preferred sorghum varieties. Agriculture (Switzerland) 11(9). https://doi.org/10.3390/agriculture11090883

Nair R, Schreinemachers P (2020) *Global Status and Economic Importance of Mungbean* (pp. 1–8). https://doi.org/10.1007/978-3-030-20008-4_1

Ndeve AD, Santos JRP, Matthews WC, Huynh BL, Guo Y-N, Lo S, Muñoz-Amatriaín M, Roberts PA (2019) A novel root-knot nematode resistance QTL on chromosome *Vu01* in cowpea. G3 Genes|Genomes|Genetics 9(4):1199–1209. https://doi.org/10.1534/g3.118.200881

Ndjiondjop MN, Semagn K, Zhang J, Gouda AC, Kpeki SB, Goungoulou A, Wambugu P, Dramé KN, Bimpong IK, Zhao D (2018) Development of species diagnostic SNP markers for quality control genotyping in four rice (*Oryza* L.) species. Molecular Breeding 38(11):131. https://doi.org/10.1007/s11032-018-0885-z

Nie X, Sutherland D, Dickison V, Singh M, Murphy AM, De Koeyer D (2016) Development and validation of high-resolution melting markers derived from Ry_{sto} STS markers for high-throughput marker-assisted selection of potato carrying Ry_{sto}. Phytopathology 106(11): 1366–1375. https://doi.org/10.1094/PHYTO-05-16-0204-R

Ogunkanmi L, Ogundipe O, Ng N, Fatokun C (2008) Genetic diversity in wild relatives of cowpea (*Vigna unguiculata*) as revealed by simple sequence repeats (SSR) markers. J Food Agric Environ 6(4):263–268

Omoigui LO, Kamara AY, Moukoumbi YD, Ogunkanmi LA, Timko MP (2017) Breeding cowpea for resistance to *Striga gesnerioides* in the Nigerian dry savannas using marker-assisted selection. Plant Breed 136(3):393–399. https://doi.org/10.1111/pbr.12475

Ongom PO, Fatokun C, Togola A, Salvo S, Oyebode OG, Ahmad MS, Jockson ID, Bala G, Boukar O (2021) Molecular fingerprinting and hybridity authentication in cowpea using single nucleotide polymorphism based Kompetitive allele-specific PCR assay. Front Plant Sci 12. https://doi.org/10.3389/fpls.2021.734117

Ortiz R (2020) Genomic-led potato breeding for increasing genetic gains: achievements and outlook. Crop Breeding, Genetics and Genomics 2:e200010. https://doi.org/10.20900/cbgg20200010

Ottoman RJ, Hane DC, Brown CR, Yilma S, James SR, Mosley AR, Crosslin JM, Vales MI (2009) Validation and implementation of marker-assisted selection (MAS) for PVY resistance (*Ry adg* gene) in a tetraploid potato breeding program. Am J Potato Res 86(4):304–314. https://doi.org/10.1007/s12230-009-9084-0

Padulosi S, Ng NQ (1997) Origin, taxonomy, and morphology of Vigna unguiculata (L.) Walp. In: Singh BB, Mohan Raj DR, Dashiell KE, Jackai LEN (eds) Advances in cowpea research. Japan International Research Center for Agricultural Sciences and International Institute of Tropical Agriculture, Ibadan, Nigeria, pp 1–12

Pandey MK, Agarwal G, Kale SM, Clevenger J, Nayak SN, Sriswathi M, Chitikineni A, Chavarro C, Chen X, Upadhyaya HD, Vishwakarma MK, Leal-Bertioli S, Liang X, Bertioli DJ, Guo B, Jackson SA, Ozias-Akins P, Varshney RK (2017a) Development and evaluation of a high density genotyping 'Axiom_*Arachis*' Array with 58 K SNPs for accelerating genetics and breeding in groundnut. Sci Rep 7(1):1–10. https://doi.org/10.1038/srep40577

Pandey MK, Khan AW, Singh VK, Vishwakarma MK, Shasidhar Y, Kumar V, Garg V, Bhat RS, Chitikineni A, Janila P, Guo B, Varshney RK (2017b) QTL-seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut (*Arachis hypogaea* L.). Plant Biotechnol J 15(8):927–941. https://doi.org/10.1111/pbi.12686

Pandey MK, Pandey AK, Kumar R, Nwosu CV, Guo B, Wright GC, Bhat RS, Chen X, Bera SK, Yuan M, Jiang H, Faye I, Radhakrishnan T, Wang X, Liang X, Liao B, Zhang X, Varshney RK, Zhuang W (2020) Translational genomics for achieving higher genetic gains in groundnut. Theor Appl Genet 133(5):1679–1702. https://doi.org/10.1007/S00122-020-03592-2

Pandey MK, Bhat RS, Janila P, Guo B, Varshney RK (2017c) Genetic dissection of foliar disease resistance using next-generation sequencing approaches in groundnut. In: 9th international conference advances in arachis through Genomics & Biotechnology (AAGB), pp 14–17

Parmar S, Deshmukh DB, Kumar R, Manohar SS, Joshi P, Sharma V, Chaudhari S, Variath MT, Gangurde SS, Bohar R, Singam P, Varshney RK, Janila P, Pandey MK (2021) Single seed-based high-throughput genotyping and rapid generation advancement for accelerated groundnut genetics and breeding research. Agronomy 11(6):1226. https://doi.org/10.3390/agronomy

Pasupuleti J, Pandey MK, Manohar SS, Variath MT, Nallathambi P, Nadaf HL, Sudini H, Varshney RK (2016) Foliar fungal disease-resistant introgression lines of groundnut (*Arachis hypogaea* L.) record higher pod and haulm yield in multilocation testing. Plant Breed 135(3):355–366. https://doi.org/10.1111/PBR.12358

Pottorff M, Wanamaker S, Ma YQ, Ehlers JD, Roberts PA, Close TJ (2012) Genetic and physical mapping of candidate genes for resistance to fusarium oxysporum f.sp. tracheiphilum race 3 in cowpea [*Vigna unguiculata* (L.) Walp]. PLoS One 7(7):e41600. https://doi.org/10.1371/journal.pone.0041600

Rakosy-Tican E, Thieme R, König J, Nachtigall M, Hammann T, Denes T-E, Kruppa K, Molnár-Láng M (2020) Introgression of two broad-Spectrum late blight resistance genes, Rpi-Blb1 and Rpi-Blb3, from Solanum bulbocastanum dun plus race-specific R genes into potato pre-breeding lines. Front Plant Sci 11. https://doi.org/10.3389/fpls.2020.00699

Ramakrishnan P, Manivannan N, Mothilal A, Mahaingam L, Prabhu R, Gopikrishnan P (2020) Marker assisted introgression of QTL region to improve late leaf spot and rust resistance in elite and popular variety of groundnut (*Arachis hypogaea* L.) cv TMV 2. Australas Plant Pathol 49(5):505–513. https://doi.org/10.1007/s13313-020-00721-9

Razzaq A, Kaur P, Akhter N, Wani SH, Saleem F (2021) Next-generation breeding strategies for climate-ready crops. Front Plant Sci 12:620420. https://doi.org/10.3389/fpls.2021.620420

Roorkiwal M, Bharadwaj C, Barmukh R, Dixit GP, Thudi M, Gaur PM, Chaturvedi SK, Fikre A, Hamwieh A, Kumar S, Sachdeva S, Ojiewo CO, Taran B, Wordofa NG, Singh NP, Siddique KHM, Varshney RK (2020) Integrating genomics for chickpea improvement: achievements and opportunities. Theor Appl Genet 133(5):1703–1720. https://doi.org/10.1007/S00122-020-03584-2

RTB (2019) Making an impact. Annual report 2018. www.rtb.cgiar.org/2018-annual-report

Salifou M, Tignegre JBLS, Tongoona P, Offei S, Ofori K, Danquah E (2016) Introgression of striga resistance gene into farmers' preferred cowpea varieties in Niger. Int J Plant Breed Genet 3(6): 233–240

Schafleitner R, Huang S, Chu S, Yen J, Lin C, Yan M, Krishnan B, Liu M, Lo H, Chen C, Chen LO, Wu D, Bui T-GT, Ramasamy S, Tung C, Nair R (2016) Identification of single nucleotide polymorphism markers associated with resistance to bruchids (*Callosobruchus* spp.) in wild mungbean (*Vigna radiata* var. sublobata) and cultivated V. radiata through genotyping by sequencing and quantitative trait locus analysis. BMC Plant Biol 16(1):159. https://doi.org/10.1186/s12870-016-0847-8

Sehrawat N, Yadav M, Bhat KV, Saıram RK, Jaıwal PK (2016) Introgression of mungbean yellow mosaic virus resistance in *Vigna mungo* (L.)hepper and purity testing of F1 hybrids using SSRs. Turk J Agric For 40(1):95–100

Semagn K, Babu R, Hearne S, Olsen M (2014) Single nucleotide polymorphism genotyping using Kompetitive allele specific PCR (KASP): overview of the technology and its application in crop improvement. Mol Breed 33(1):1–14. https://doi.org/10.1007/s11032-013-9917-x

Semagn K, Beyene Y, Makumbi D, Mugo S, Prasanna BM, Magorokosho C, Atlin G (2012) Quality control genotyping for assessment of genetic identity and purity in diverse tropical maize inbred lines. Theor Appl Genet 125(7):1487–1501. https://doi.org/10.1007/s00122-012-1928-1

Shasidhar Y, Variath MT, Vishwakarma MK, Manohar SS, Gangurde SS, Sriswathi M, Sudini HK, Dobariya KL, Bera SK, Radhakrishnan T, Pandey MK, Janila P, Varshney RK (2020) Improvement of three popular Indian groundnut varieties for foliar disease resistance and high oleic acid using SSR markers and SNP array in marker-assisted backcrossing. Crop J 8(1):1–15. https://doi.org/10.1016/J.CJ.2019.07.001

Simon MV, Benko-Iseppon A-M, Resende LV, Winter P, Kahl G (2007) Genetic diversity and phylogenetic relationships in *Vigna* Savi germplasm revealed by DNA amplification fingerprinting. Genome 50(6):538–547. https://doi.org/10.1139/G07-029

Simpson CE, Starr JL, Church GT, Burow MD, Paterson AH (2003) Registration of 'NemaTAM' Peanut. Crop Sci 43(4):1561–1561. https://doi.org/10.2135/cropsci2003.1561

Singh CM, Pratap A, Gupta S, Biradar RS, Singh NP (2020) Association mapping for mungbean yellow mosaic India virus resistance in mungbean (*Vigna radiata* L. Wilczek). 3Biotech 10(2): 33. https://doi.org/10.1007/s13205-019-2035-7

Singh N, Mallick J, Sagolsem D, Mandal N, Bhattacharyya S (2017a) Mapping of molecular markers linked with MYMIV and yield attributing traits in mungbean. Indian J Genet Plant Breed 78(1):118. https://doi.org/10.5958/0975-6906.2018.00014.7

Singh RP, Herrera-Foessel S, Huerta-Espino J, Singh S, Bhavani S, Lan C, Basnet BR (2014) Progress towards genetics and breeding for minor genes based resistance to Ug99 and other rusts in CIMMYT high-yielding spring wheat. J Integr Agric 13(2):255–261. https://doi.org/10.1016/S2095-3119(13)60649-8

Singh V, Yadav RK, Yadav NR, Yadav R, Malik RS, Singh J (2017b) Identification of genomic regions/genes for high iron and zinc content and cross transferability of SSR markers in mungbean (*Vigna radiata* L.). Legume Res Intern J 40(6). https://doi.org/10.18805/lr.v40i04.9006

Sinha P, Bajaj P, Pazhamala LT, Nayak SN, Pandey MK, Chitikineni A, Huai D, Khan AW, Desai A, Jiang H, Zhuang W, Guo B, Liao B, Varshney RK (2020) Arachis hypogaea gene expression atlas for fastigiata subspecies of cultivated groundnut to accelerate functional and translational genomics applications. Plant Biotechnol J 18(11):2187–2200. https://doi.org/10.1111/PBI.13374

Slater AT, Cogan NOI, Hayes BJ, Schultz L, Dale MFB, Bryan GJ, Forster JW (2014) Improving breeding efficiency in potato using molecular and quantitative genetics. Theor Appl Genet 127(11):2279–2292. https://doi.org/10.1007/s00122-014-2386-8

Sneller C, Ignacio C, Ward B, Rutkoski J, Mohammadi M (2021) Using genomic selection to leverage resources among breeding programs: consortium-based breeding. Agronomy 11(8): 1555. https://doi.org/10.3390/AGRONOMY11081555

Somta P, Chen J, Yundaeng C, Yuan X, Yimram T, Tomooka N, Chen X (2019) Development of an SNP-based high-density linkage map and QTL analysis for bruchid (Callosobruchus maculatus F.) resistance in black gram (*Vigna mungo* (L.) hepper). Sci Rep 9(1):1–9. https://doi.org/10.1038/s41598-019-40669-5

Sood S, Bhardwaj V, Chourasia KN, Kaur RP, Kumar V, Kumar R, Sundaresha S, Bohar R, Garcia-Oliveira AL, Singh RK, Kumar M (2022) KASP markers validation for late blight, PCN and PVY resistance in a large germplasm collection of tetraploid potato (*Solanum tuberosum* L.). Sci Hortic 295. https://doi.org/10.1016/j.scienta.2021.110859

Souframanien J, Gopalakrishna T (2006) ISSR and SCAR markers linked to the mungbean yellow mosaic virus (MYMV) resistance gene in blackgram [*Vigna mungo* (L.) hepper]. Plant Breed 125(6):619–622. https://doi.org/10.1111/j.1439-0523.2006.01260.x

Souframanien J, Gupta SK, Gopalakrishna T (2010) Identification of quantitative trait loci for bruchid (Callosobruchus maculatus) resistance in black gram [*Vigna mungo* (L.) hepper]. Euphytica 176(3):349–356. https://doi.org/10.1007/S10681-010-0210-3/FIGURES/2

Souframanien J, Reddy KS (2015) De novo assembly, characterization of immature seed transcriptome and development of genic-SSR markers in black gram [*Vigna mungo* (L.) hepper]. PLoS One 10(6):e0128748. https://doi.org/10.1371/journal.pone.0128748

Stefańczyk E, Plich J, Janiszewska M, Smyda-Dajmund P, Sobkowiak S, Śliwka J (2020) Marker-assisted pyramiding of potato late blight resistance genes *Rpi-rzc1* and *Rpi-phu1* on di- and tetraploid levels. Mol Breed 40(9):89. https://doi.org/10.1007/s11032-020-01169-x

Stich B, Van Inghelandt D (2018) Prospects and potential uses of genomic prediction of key performance traits in tetraploid potato. Front Plant Sci 9. https://doi.org/10.3389/FPLS.2018.00159/FULL

Subramaniyan R, Kulanthaivel V, Narayana M, Angamuthu M, Kothandaraman SV (2021) Marker-assisted backcross breeding for enhancing Mungbean yellow mosaic virus (MYMV) disease resistance in blackgram [*Vigna mungo* (L.) hepper] cv MDU 1. Physiol Mol Plant Pathol 116:101732. https://doi.org/10.1016/j.pmpp.2021.101732

Sverrisdóttir E, Byrne S, Sundmark EHR, Johnsen HØ, Kirk HG, Asp T, Janss L, Nielsen KL (2017) Genomic prediction of starch content and chipping quality in tetraploid potato using genotyping-by-sequencing. Theor Appl Genet 130(10):2091–2108. https://doi.org/10.1007/S00122-017-2944-Y

Takahashi Y, Tomooka N (2020) Taxonomy of mungbean and its relatives (pp. 27–41). https://doi.org/10.1007/978-3-030-20008-4_3

Tiwari JK, Siddappa S, Singh BP, Kaushik SK, Chakrabarti SK, Bhardwaj V, Chandel P (2013) Molecular markers for late blight resistance breeding of potato: an update. Plant Breed 132(3): 237–245. https://doi.org/10.1111/pbr.12053

Uitdewilligen JGAML, Wolters AMA, D'hoop BB, Borm TJA, Visser RGF, van Eck HJ (2013) A next-generation sequencing method for genotyping-by-sequencing of highly heterozygous autotetraploid potato. PLoS One 8(5). https://doi.org/10.1371/JOURNAL.PONE.0062355

Vadivel K, Manivannan N, Mahalingam A, Satya VK, Vanniarajan C, Ragul S (2021) Identification and validation of quantitative trait loci of Mungbean yellow mosaic virus disease resistance in Blackgram [*Vigna mungo* (L). Hepper]. Legume Res Int J 1:1–7. https://doi.org/10.18805/LR-4459

Varshney RK, Pandey MK, Bohra A, Singh VK, Thudi M, Saxena RK (2019) Toward the sequence-based breeding in legumes in the post-genome sequencing era. Theor Appl Genet 132(3):797–816. https://doi.org/10.1007/S00122-018-3252-X/FIGURES/1

Varshney RK, Pandey MK, Janila P, Nigam SN, Sudini H, Gowda MVC, Sriswathi M, Radhakrishnan T, Manohar SS, Nagesh P (2014) Marker-assisted introgression of a QTL region to improve rust resistance in three elite and popular varieties of peanut (*Arachis hypogaea* L.). Theor Appl Genet 127(8):1771–1781. https://doi.org/10.1007/S00122-014-2338-3/FIGURES/3

Velásquez AC, Mihovilovich E, Bonierbale M (2007) Genetic characterization and mapping of major gene resistance to potato leafroll virus in *Solanum tuberosum* ssp. andigena. Theor Appl Genet 114(6):1051–1058. https://doi.org/10.1007/S00122-006-0498-5

Vishwakarma MK, Kale SM, Sriswathi M, Naresh T, Shasidhar Y, Garg V, Pandey MK, Varshney RK (2017) Genome-wide discovery and deployment of insertions and deletions markers provided greater insights on species, genomes, and sections relationships in the genus arachis. Front Plant Sci 8:2064. https://doi.org/10.3389/FPLS.2017.02064/BIBTEX

Vos PG, Uitdewilligen JGAML, Voorrips RE, Visser RGF, van Eck HJ (2015) Development and analysis of a 20K SNP array for potato (*Solanum tuberosum*): an insight into the breeding history. Theor Appl Genet 128(12):2387–2401. https://doi.org/10.1007/s00122-015-2593-y

Wageningen FSC (2016) Multi-level mapping and exploration of wheat production and consumption and their potential contribution to alleviation of poverty, malnutrition and gender inequality. Final Report WHEAT Competitive Grant. Wageningen University Food Security Center Study, The Netherlands

Whitworth JL, Novy RG, Hall DG, Crosslin JM, Brown CR (2009) Characterization of broad Spectrum potato virus Y resistance in a *Solanum tuberosum* ssp. andigena-derived population and select breeding clones using molecular markers, grafting, and field inoculations. Am J Potato Res 86(4):286–296. https://doi.org/10.1007/s12230-009-9082-2

Wu X, Islam ASMF, Limpot N, Mackasmiel L, Mierzwa J, Cortés AJ, Blair MW (2020) Genome-wide SNP identification and association mapping for seed mineral concentration in mung bean (Vigna radiata L.). Front Genet 11. https://doi.org/10.3389/fgene.2020.00656

Xiong H, Shi A, Mou B, Qin J, Motes D, Lu W, Ma J, Weng Y, Yang W, Wu D (2016) Genetic diversity and population structure of cowpea (*Vigna unguiculata* L. Walp). PLoS One 11(8): e0160941. https://doi.org/10.1371/journal.pone.0160941

Xu P, Wu X, Wang B, Hu T, Lu Z, Liu Y, Qin D, Wang S, Li G (2013) QTL mapping and epistatic interaction analysis in asparagus bean for several characterized and novel horticulturally important traits. BMC Genet 14(1):4. https://doi.org/10.1186/1471-2156-14-4

Xu Y, Li P, Zou C, Lu Y, Xie C et al (2017) Enhancing genetic gain in the era of molecular breeding. J Exp Bot 68(11):2641–2666. https://doi.org/10.1093/jxb/erx135

Yeri SB, Bhat RS (2016) Development of late leaf spot and rust resistant backcross lines in Jl 24 variety of groundnut (*Arachis hypogaea* L.). Electron J Plant Breed 7(1):37. https://doi.org/10.5958/0975-928X.2016.00005.3

Yin D, Ji C, Ma X, Li H, Zhang W, Li S, Liu F, Zhao K, Li F, Li K, Ning L, He J, Wang Y, Zhao F, Xie Y, Zheng H, Zhang X, Zhang Y, Zhang J (2018) Genome of an allotetraploid wild peanut *Arachis monticola*: a de novo assembly. GigaScience 7(6):1–9. https://doi.org/10.1093/GIGASCIENCE/GIY066

Zhao C, Qiu J, Agarwal G, Wang J, Ren X, Xia H, Guo B, Ma C, Wan S, Bertioli DJ, Varshney RK, Pandey MK, Wang X (2017) Genome-wide discovery of microsatellite markers from diploid progenitor species, *A. duranensis* and *A. Ipaensis*, and their application in cultivated peanut (*a. hypogaea*). Front Plant Sci 8:1209. https://doi.org/10.3389/FPLS.2017.01209/BIBTEX

Zhao Y, Ma J, Li M, Deng L, Li G, Xia H, Zhao S, Hou L, Li P, Ma C, Yuan M, Ren L, Gu J, Guo B, Zhao C, Wang X (2020) Whole-genome resequencing-based QTL-seq identified *AhTc1* gene encoding a R2R3- MYB transcription factor controlling peanut purple testa colour. Plant Biotechnol J 18(1):96–105. https://doi.org/10.1111/pbi.13175

Zhang X, Zhang J, He X, Wang Y, Ma X, Yin D (2017) Genome-wide association study of major agronomic traits related to domestication in peanut. Front Plant Sci 8:1611. https://doi.org/10.3389/fpls.2017.01611

Zhuang W, Chen H, Yang M, Wang J, Pandey MK, Zhang C, Chang W-C, Zhang L, Zhang X, Tang R, Garg V, Wang X, Tang H, Chow C-N, Wang J, Deng Y, Wang D, Khan AW, Yang Q et al (2019) The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. Nat Genet 51(5):865–876. https://doi.org/10.1038/s41588-019-0402-2