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Contents

1 Acknowledgments

The IMIN team greatly appreciate the Australian Centre for International Agricultural Research (ACIAR) for supporting the concept of a network for mungbean researchers and with a long-term vision. The support provided by the organizations of the partner countries is very well acknowledged. Initial work in sub-Saharan African countries was supported by Foreign, Commonwealth & Development Office, UK.

2 Executive summary

1) Establish and coordinate an International Mungbean Improvement Network

The International Mungbean Improvement Network led by the World Vegetable Center (WorldVeg) was initially established with partners from Bangladesh, India, Myanmar and Australia. In 2020, Kenya, Tanzania and Uganda joined the network. Annual meetings were held in the partner countries. Contracts were signed with all the partner countries by WorldVeg, with provision for the exchange of germplasm through Standard Material Transfer Agreements. Fortnightly meetings (online) were conducted with the partners to monitor the project activities. The network also developed a newsletter called “Mung Central” to share the mungbean research updates among the stakeholders. So far eight editions of Mung Central have been released. The network has established links with strategic partners at both the national level in the partner countries and at the international level.

On April 23-24, 2019, WorldVeg in partnership with the Kasetsart University, Thailand, organized a regional workshop entitled “Enhancing farmers’ access to improved mungbean varieties and good agricultural practices in Southeast Asia”. The event brought together mungbean researchers from the public and the private sector from Cambodia, China, Indonesia, Laos PDR, Philippines, Thailand, Vietnam, as well as WorldVeg experts to exchange information and share knowledge about mungbean production and consumption in the region.

The network implemented capacity development of breeders including training on better breeding data management using a modern database, application of marker assisted selection and statistical methods in breeding, and adoption of integrated pest management (IPM) strategies.

The plant breeding data management system KDDart has been implemented with the network partners of IMIN1 in Asia. Training of the network partners in the use of this application on Android-based tablets for data entry, storage and exchange has strongly improved the breeding capacity of the network. The partners adopted experimental designs specifically suitable for field experiments, such as alpha-lattice designs for the evaluation of the mini-core collection (296 accessions). Data collected from trials accomplished at different locations in different countries were shared among the partners. The maintenance of pedigree information of the germplasm in the KDDart database has helped breeders in the network to select suitable parents. Training workshops were conducted regularly by WorldVeg for effective implementation of the database system. The KDDart team based in Australia (Diversity Arrays Pty Ltd) has been highly receptive to any queries from the implementing partners and this has enabled in further fine tuning the system.

2) Improve access to mungbean genetic diversity for breeders to source traits required for future elite varieties

The sharing of the mini-core collection (296 accessions) developed by WorldVeg with partners has been one of the major highlights of the IMIN1. The mini-core collection was screened for resistance to Mungbean Yellow Mosaic Disease (MYMD) and a range of other diseases such as powdery mildew, tan spot, halo blight and dry root rot in different partner countries in Asia and Africa and identified accessions resistant to these biotic stresses. These accessions are being used in the breeding programs.

The mini-core collection was submitted to genotyping by sequencing resulting in 24,000 single nucleotide polymorphism (SNP) markers. The population structure was analyzed and genome-wide association genetics analyses to map traits of interest such as disease

resistances and agronomic traits were initiated. Quantitative trait loci (QTLs) for morphological and developmental parameters were identified. In addition, loci associated with various disease resistances including MYMV have been found, but low significance levels due to the relatively small population size and low frequency of resistance alleles in the core collection require additional validation of these associations for reliable mapping and for future use in marker-assisted selection. QTLs for resistance to halo blight and powdery mildew in the mungbean nested association mapping (NAM) populations were identified. Genotyping data of the WorldVeg mini-core collection were combined with the data of the Australian Diversity Panel and a set of > 10,000 common single nucleotide polymorphic markers with low rate of missing data was defined. A diversity study over these two panels of mungbean lines was performed.

The capacity of the project team to perform genomic analyses was improved through training in multilocation trial data analysis and the use of genome-wide association tools. These works have resulted in obtaining the “Agricultural Greater Good” award of Illumina, allowing to re-sequence the whole core collection and other key materials on IMIN in the second phase of the project.

3) Develop improved mungbean germplasm and elite lines

WorldVeg shared AVMU lines (AVRDC mungbean line) with partners. In addition, varieties released in the partner countries were shared in the network. Ten of these varieties originated from India, ten from Bangladesh, five from Myanmar and ten from Australia. These lines were evaluated at multi-locations by the partners and promising accessions/lines were identified are at different stages of testing.

The project partners are actively engaged in the introgression of traits from donors identified during IMIN1.

In India, two breeding lines developed in IMIN1: IIPR 20-1 (AVMU 1683) and IIPR 20-2 (AVMU 1690) have been promoted to Advanced Varietal Trial 1 stage in the All India Co-ordinated Trials. Three AVMU lines (AVMU 1602, AVMU 1606 and AVMU 1608) with higher yields compared to reference variety BARImung 6 have been identified in Bangladesh for further testing (Regional Yield Trial) before potential release. In Myanmar, 7 AVMU lines (AVMU 1631, AVMU 1632, AVMU 1642, AVMU 1643, AVMU 1659, AVMU 1688 and AVMU 1690) and two high yielding mini-core accessions (VI000559 AG and VI004934 AG) will undergo further testing. Early maturing, high yielding mungbean lines with high iron content (AVMU 2014 and AVMU 2023) were preferred by farmers in Participatory Variety Selection in Kenya. Two AVMU lines (AVMU 1601 and AVMU 1693) preferred by Mungbean farmers in Tanzania were submitted for official release requisition by Tanzania Official Seed Certification Institute (TOSCI).

3 Background

It was proposed to establish an International Mungbean Improvement Network as an investment under ACIAR's Crop Improvement and Management (CIM) research program, which aims to increase productivity for smallholder farmers and to foster sustainability in their cereal based cropping systems through research and the application of new technologies in crop improvement and agronomy.

This investment is aligned with the four key criteria of Australia's aid program and specifically addresses the following strategic performance targets:

Promoting Prosperity – improvement of mungbean productivity and grain quality creates access to new profitable markets for farmers

Engaging the Private Sector – seed and grain enterprises will be partners as a dynamic means of disseminating project outcomes and connecting smallholders to wider pulse markets

Reducing Poverty – as a cash crop mungbean increases the income of smallholder families through higher cash flow and profit

Empowering Women and Girls – the project will engage with women at the production level, in project management and in research and extension

Focusing on the Indo-Pacific Region – target countries are Bangladesh, Myanmar and India

Working with the most effective partners – a scoping study completed in December 2014 identified and has already engaged the public sector, NGOs and universities working in mungbean improvement and increasing livelihoods of smallholder farmers.

Rice-based farming systems in South and Southeast Asia are characterised by low system productivity, declining soil fertility, and small holding sizes. They are affected by environmental variability such as drought, flooding and heat waves. Farmer incomes increasingly depend on rotation crops rather than on the main crop rice. Short duration protein-rich legume crops such as mungbean can generate a significant part of farmers' income and contribute to the nutrition of resource-poor populations.

Diversification of rice cropping systems with mungbean is impeded by the lack of disease resistant and agronomically adapted mungbean varieties with high grain quality that meet market requirements. Although in a different production system, the Australian mungbean industry has many of the same production constraints as those found in Asia. Since crop improvement programs in Asia and Australia could benefit from the access to the same next generation breeding technologies, the co-ordinated and collaborative research proposed here targets mungbean farmers in South and Southeast Asia, as well as in Australia.

The global mungbean area is about 7.3 million ha and global output is about 5.3 million tons with India and Myanmar each supplying about 30% of this, China 16%, and Indonesia 5%. This short duration legume crop fits well into different cropping systems, fixes nitrogen from the atmosphere and thus improves soil fertility, and yields a nutritious grain in a short time. Globally, mungbean is in high demand, resulting in a large export potential and stable farm gate prices. The daily pulse availability in India has increased to 48 g per person, but is still below the recommended amount for a largely vegetarian population of 80 g per person (John et al 2021). Domestic demand for mungbean in India is expected to rise to 2.75 million t by 2030 (IIPR, 2011). Major exporters to India include Myanmar and Australia. Mungbean ranks third in area of cultivated pulses and total production in Bangladesh after grass pea (*Lathyrus sativus* L.) and lentils (*Lens culinaris* Medik.) (Bangladesh Department of Agricultural Extension, 2012). In Bangladesh, the per capita pulse consumption was only about 15.6 g per day (USDA, 2021), which is well below the rate recommended by FAO/WHO.

Traditional Asian mungbean cultivars had long growth duration, were low yielding and susceptible to virus diseases and insects. A joint research effort by AVRDC (now World

Vegetable Center) and Asian partners turned traditional mungbean into a short duration crop, with high and stable yields and resistance to *Cercospora* leaf spot, powdery mildew, and some *Mungbean yellow mosaic virus* (MYMV) strains. The adoption of these varieties led to a substantial increase in mungbean production and productivity in South and Southeast Asia. The greatest impact was evident where mungbean was grown in crop rotations, as the short maturity period made it a perfect fit for inclusion in cereal based cropping systems, such as rice-wheat-mungbean and rice-potato-mungbean practiced in Asia. For farmers in Punjab (India) growing short duration mungbean varieties increased their net return in rice-wheat-mungbean production systems by US $200 per ha as compared to rice-wheat systems (Sekhon et al., 2007). Adopters of improved mungbean varieties in Bangladesh increased their average yield by 40 % with an estimated benefit-cost ratio of 2.18 compared to non-adopters (Afzal et al., 2006).

The successful development and dissemination of improved mungbean varieties by AVRDC two decades ago had a significant impact in terms of increased production and cultivation area. The broad impact of these efforts are well documented in the IFPRI publication “The mungbean transformation: Diversifying crops, defeating malnutrition” (Shanmugasundaram et al., 2009). Since then progress has been limited, and Asian mungbean improvement has not seen the technical development from which more mainstream crops have benefited. Mungbean is an orphan crop, outside of the CGIAR mandate, and has lacked broad scale coordinated research. Consequently, increases in genetic gain and the development of improved varieties have lagged behind other crops. Greater investment in crop improvement, better access to genetic resources and modern breeding technologies are required to mobilize the full potential of mungbean as a food and cash crop for smallholder farmers. Increased pulse production and productivity is a priority in the target countries, and development of improved mungbean varieties is a key factor in achieving this.

The further expansion of mungbean has also been impeded by non-availability of seed of improved varieties, poor crop management practices and pests and diseases. Among diseases, new strains of MYMV and the lack of varieties resistant to bruchids (*Callosobruchus* spp.), the major insect pest of stored grain, have been the main reasons for the limited expansion of mungbean cultivation. New varieties with resistances derived from various sources are required to address newly emerging strains, species or biotypes of important pests or pathogens.

The Australian mungbean breeding program, established in 2003, has demonstrated that large genetic gains for mungbean are possible and have a major impact on the local pulse industry. Building on the recent developments from the Australian mungbean breeding program and germplasm curation efforts by AVRDC, the project aimed to strengthen mungbean improvement capacity in the target countries. Efficient collaboration among mungbean researchers and breeders, multilocation trials on a core germplasm set and systematic data management unlock the trait diversity of mungbean for pre-breeding. Farmer-participatory selection ensure that farmer-accepted lines are channelled into variety development processes. Better mungbean varieties will increase productivity, allow cultivation to expand to new areas and make the crop more profitable for farmers. Increased system productivity and sustainability through integration of profitable short duration mungbean varieties will contribute to poverty alleviation for smallholder farmers and will improve livelihoods of resource-poor rural populations in the target countries.

The goal of the project has been to build a successful mungbean improvement network that will sustain and attract new members and investors beyond the timeframe of the project, with the network’s main role to facilitate germplasm exchange and coordinate research and development activities. The researchers trained by the project will be part of the personnel resource that will implement the next generation of mungbean improvement. The project is demonstrating the impact of genetic improvement of a rotation crop on overall system productivity and smallholder farmers’ livelihoods. The project outcomes are the starting point

for a wider collaboration in the Indo-Pacific region to target research towards crop diversification options for better income, nutrition and environment.

4 Objectives

The project was planned to unlock the potential of mungbean to improve system productivity and livelihoods. The goal of the project has been to build a successful network that will attract new members and investors in mungbean research and continue beyond the timeframe of the project. The network has coordinated and performed research resulting in the development and release of new mungbean varieties that are widely adopted and raise the profitability of smallholder farms and the sustainability of local production systems. Three objectives were defined:

4.1 Objective 1: Establish and coordinate an International Mungbean Improvement Network

Activities

1.1: Set-up the International Mungbean Improvement Network, establish a Reference Group and Coordination Group to develop research solutions for specific constraints, conduct annual meetings.

1.2: Establish a communication infrastructure for the network including a web page and a newsletter and regular online meetings of the Coordination Group.

1.3: Select and roll-out a curated plant breeding information management system for evaluation data sharing and analysis.

1.4: Organise workshops for phenotype and genotype data handling, analysis, and manage a small grants system for training of network member scientists.

1.5: Develop and implement mechanisms for germplasm exchange among the partner institutions and countries to guarantee the transfer of germplasm and breeding materials among network partners.

1.6: Monitoring and evaluation of the project progress after 2 and 3.5 years after project initiation.

4.2 Objective 2: Improve access to mungbean genetic diversity for breeders to source traits required for future elite varieties

Activities

2.1: Deploy a set of 300 genetically diverse mungbean lines (mini-core collection) to project partners, perform post entry quarantine where necessary (Australia, India), multiply seed, develop a phenotyping plan (trial design, phenotyping protocols, data to be collected).

2.2: Perform multi-location appraisal (3 environments per country) of the mini-core collection and quantify the tolerance to abiotic and biotic stresses present in the lines – data collection, analysis and sharing following agreed phenotyping protocols.

2.3: Genotype the mini-core collection at high density using the best possible service provider. Single nucleotide polymorphisms are physically mapped to the published mungbean whole genome sequence and deposited in the plant breeding information system.

2.4: Carry out a genome-wide association study of disease, pest and abiotic stress tolerance traits measured during the multi-location evaluation of the mini-core collection to define useful genes for improving trait diversity of mungbean breeding populations.

2.5: Screen the mungbean mini-core collection for additional key biotic traits (halo blight, tan spot, powdery mildew), white fly, stem fly and aphids and screen a sub set of the collection for abiotic traits (heat stress).The screening will be conducted in the major agro-ecological regions (hot spots) in the target countries where mungbean is grown and/or likely to expand.

2.6: Continue to build capacity to implement the database management system successfully within the Network, with evaluation data from multi-locations in partner countries and also pedigree information including adoption of standardized pedigree information across the network.

2.7: Shortlist traits, markers-associated with these traits and validation, develop backcross and initiate nested association mapping populations to maximize the benefit of new pest and disease resistance traits and grain quality traits in breeding.

2.8: Share Nested Association Mapping (NAM) populations (2000 lines) and Australian Diversity Panel (430 lines) developed in Australia under MTA with the World Vegetable Center. Scope and plan future coordinated phenotyping activities and projects.

2.9: Explore the effect of elevated CO_2 on host-pathogen interactions, dry root rot disease severity and on expression of defence response genes in mungbean, (MSc research project, Lovely Professional University, Punjab).

2.10: Development of Quantitative PCR assay for screening of Mungbean genotypes against dry root rot caused by *Macrophomina phaseolina*, (MSc research work, Ramakrishna Mission Vivekananda Educational and Research Institute (RKMVERI) Narendrapur, Kolkata).

2.11: Screening a subset of the mini-core collection at varying levels of CO_2 for the nutritional content of the grains

4.3 Objective 3: Develop improved mungbean germplasm and elite lines

Activities

3.1: Strengthen mungbean improvement programs in the target countries, coordinate research activities and germplasm exchange within the network. Mungbean germplasm in general and breeding lines developed from the project will be exchanged amongst all project partners. In addition germplasm of related species will also be exchanged between the network partners.

3.2: Make available plant breeding methods and marker-assisted selection tools to network members.

3.3: Broaden the genetic diversity available to breeders. Thirty crosses made to black gram and other *secondary genepool* donors, backcrossing to fix desired traits in adapted backgrounds.

3.4: Provide network member breeders improved mungbean lines with desirable traits (at least 10 lines per tier)

Tier 1: Mungbean lines with MYMV resistance genes pyramided, lines with synchronised maturity, high yield and short duration lines for mechanical harvest

Tier 2: Lines with improved tolerance to terminal heat stress

Tier 3: interspecific hybrids of mungbean with black gram and rice bean

3.5: Make available mungbean lines to the network partners with: MYMV resistance genes pyramided with synchronised maturity and high yield, bruchid resistance, powdery mildew resistance and short duration lines suitable for mechanical harvesting with improved tolerance to terminal heat stress.

3.6: Test newly developed lines in target environments by public, private and non-governmental organisations.

3.7: Conduct stakeholder meetings in partner countries to define the profiles of mungbean products and packaging of traits into varieties, adopting a standardized, best practice approach agreed to by network stakeholders.

3.8: Conduct farmer-participatory evaluation of selected mungbean breeding accessions from the mini-core collection and elite mungbean lines developed by WorldVeg as part of IMIN, in arid and semi-arid mungbean growing areas of Kenya, Tanzania and Uganda.

5 Methodology

Establish and coordinate an International Mungbean Improvement Network

The International Mungbean Improvement Network was established with partners from India, Bangladesh, Myanmar and Australia and is coordinated by the World Vegetable Center. The first annual project meeting was held in New Delhi from 8-11 November, 2016, which included a database training program for implementing KDDart by Diversity Arrays Pty Ltd, Canberra. A representative of East West Seeds was also invited to the annual meeting to discuss the industry perspective of mungbean seed production.

The second annual project meeting was held in Dhaka from 30-31 May, 2017. A representative of ACI Seeds, Bangladesh, participated with the meeting and reported on the current work of ACI on mungbean. At this meeting, the participants formally decided to welcome both Kasetsart University, Thailand and East West Seeds to the network.

The third annual meeting of the network was held in Nay Pyi Taw, Myanmar from 2-4 May, 2018. This was attended from representatives from all the partner countries. In addition, representatives from Agricultural Mechanisation Department (AMD), Myanmar, Yezin Agricultural University (YAU), Myanmar and Myanmar ICCO Cooperation attended the meeting.

The fourth Annual meeting was held at Kanpur, India from September 8-10, 2019. The meeting was attended by representatives from all the partner countries. Besides the regular partners, retired scientists who had earlier worked towards mungbean improvement in India also attended the meeting.

The network has established links with strategic partners at both the national level in the partner countries and at the international level.

On April 23-24, 2019, WorldVeg in partnership with the Kasetsart University, Thailand, organized a regional workshop entitled “Enhancing farmers’ access to improved mungbean varieties and good agricultural practices in Southeast Asia”. The event brought together mungbean researchers from the public and the private sector from Cambodia, China, Indonesia, Laos PDR, Philippines, Thailand, Vietnam, as well as WorldVeg experts to exchange information and share knowledge about mungbean production and consumption in the region.

The network implemented capacity development of breeders including training on better database management, application of marker assisted selection, statistical methods in breeding and adoption of IPM strategies.

The network is using KDDart for collection, curation and sharing of data. The KDDart database is an open-source platform that develops software applications for breeding and pre-breeding purposes. This integrates three diverse types of data i.e. phenotypic, genotypic, and environmental. In the mungbean breeding program, two major tools (KDSmart and KDManage) of the database have been utilized to record and store the data. KDSmart is an android based application to record data from the field. The recorded data can be exported from KDSmart to KDManage. KDManage is an administrative tool on how various activities of breeding trials and data need to be organized. The data exported from KDSmart can be curated and uploaded into the cloud with the help of KDManage. Also, the data stored in KDManage can be accessed by all the partners of the project. Regular workshops have been conducted by WorldVeg with support of staff from KDDart on the implementation of the database management system.

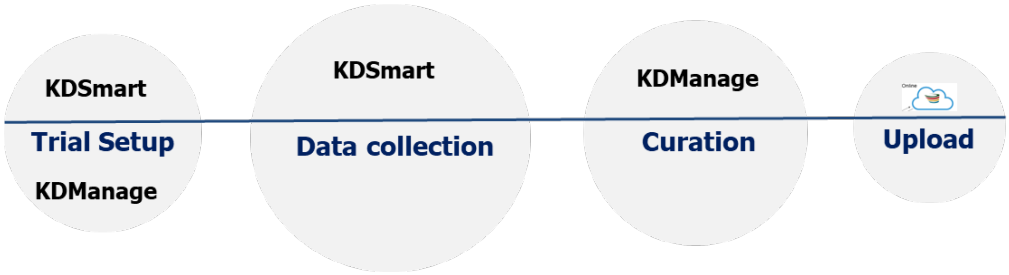


Figure 1. A work-flow chart of the KDDart database

Improve access to mungbean genetic diversity for breeders to source traits required for future elite varieties

The WorldVeg mini-core collection (296 accessions) was shared with all the partners of the network. In addition, it was also shared with interested national organisations/partners in other mungbean projects for multi-location testing and phenotyping for agronomic, biotic and abiotic stresses.

Table 1. Details of trials conducted with mungbean mini-core and Australian Diversity Set across different sites in Asia and Australia during 2016-2021.

No.	Country	Location	Year	Season	Population	Trial Type	Lines#
1	Australia	Emerald	2017	Summer	Mini-core	Mini-core Evaluation	330
2	Australia	Hermitage	2017	Summer	Mini-core	Screening against Halo Blight	330
3	Australia	Hermitage	2017	Summer	Mini-core	Screening against Powdery Mildew	320
4	Australia	Hermitage	2017	Summer	Mini-core	Screening against Tan spot	330
5	Australia	Emerald	2018	Summer	Mini-core	Mini-core Evaluation for Early Maturity	80
6	Australia	Emerald	2018	Summer	Mini-core	Mini-core Evaluation forLate Maturity	145
7	Australia	Emerald	2018	Summer	Mini-core	Mini-core Evaluation for Medium Maturity	110
8	Australia	Hermitage	2018	Summer	Mini-core	Mini-core Evaluation for Early Maturity	78
9	Australia	Hermitage	2018	Summer	Mini-core	Screening against Halo Blight	320
10	Australia	Hermitage	2018	Summer	Mini-core	Mini-core Evaluation for Late Maturity	150
11	Australia	Hermitage	2018	Summer	Mini-core	Mini-core Evaluation for Medium Maturity	112
12	Australia	Hermitage	2018	Summer	Mini-core	Screening against Powdery Mildew	252
13	Australia	Hermitage	2018	Summer	Mini-core	Screening against Tan spot	252
14	Australia	Redlands	2020	Summer	Mini-core and Diversity Set	Screening against Halo Blight and Powdery Mildew	774
15	Australia	Tosari	2020	Summer	Mini-core and Diversity Set	Screening against Powdery Mildew	774

16	Australia	Hermitage	2021	Summer	Mini-core and Diversity Set	Screening against Powdery Mildew	756
17	Australia	Redlands	2021	Summer	Mini-core and Diversity Set	Screening against Halo Blight	756
18	Bangladesh	Barisal	2017	*Kharif_1*	Mini-core	Mini-core evaluation	280
19	Bangladesh	Gazipur	2017	*Kharif_1*	Mini-core	Mini-core evaluation	295
20	Bangladesh	Ishwardi	2017	*Kharif_1*	Mini-core	Mini-core evaluation	297
21	Bangladesh	Barisal	2018	*Kharif_1*	Mini-core	Mini-core evaluation	296
22	Bangladesh	Gazipur	2018	*Kharif_1*	Mini-core	Mini-core evaluation	296
23	Bangladesh	Ishwardi	2018	*Kharif_1*	Mini-core	Mini-core evaluation	296
24	Bangladesh	Gazipur	2019	*Kharif_1*	Mini-core	Mini-core evaluation	300
25	Bangladesh	Ishwardi	2019	*Kharif_1*	Mini-core	Mini-core evaluation	300
26	Bangladesh	Madaripur	2020	*Kharif_2*	Mini-core	Mini-core evaluation	201
27	Bangladesh	Rangpur	2020	*Kharif_2*	Mini-core	Mini-core evaluation	300
28	Bangladesh	Gazipur	2021	*Kharif_1*	Mini-core	Mini-core evaluation	300
29	India	Hyderabad	2016	Post-Rainy	Mini-core	Mini-core Evaluation	297
30	India	Hyderabad	2016	Rainy	Mini-core	Mini-core Evaluation	297
31	India	Hyderabad	2017	Post-Rainy	Mini-core	Mini-core Evaluation	297
32	India	Hyderabad	2017	Rainy	Mini-core	Mini-core Evaluation	296
33	India	ICAR-IIPR Kanpur	2017	Rainy	Mini-core	Mini-core Evaluation	296
34	India	Hyderabad	2018	Rainy	Mini-core	Mini-core Evaluation	300
35	India	ICAR-IIPR Kanpur	2018	Rainy	Mini-core	Mini-core Evaluation	300
36	India	ICAR-IIPR Dharwad	2019	Rainy	Mini-core	Mini-core Evaluation	296
37	India	ICAR-IIPR Kanpur	2019	Summer	Mini-core	Mini-core Evaluation	300
38	India	ICAR-IIPR Kanpur	2020	Rainy	Mini-core	Mini-core Evaluation	297
39	India	ICAR-IIPR Dharwad	2021	Summer	Mini-core	Mini-core Evaluation	300
40	India	ICAR-IIPR Kanpur	2021	Summer	Mini-core	Mini-core Evaluation	300
41	Myanmar	Yezin	2017	Monsoon	Mini-core	Mini-core Evaluation	296
42	Myanmar	Yezin	2019	Monsoon	Mini-core	Mini-core Evaluation	172

Table 2. Details of mungbean mini-core evaluation trials conducted across seven countries in Sub-Saharan Africa during 2018-19.

Country	Site	Year of Evaluation	Collaborating Institute
Tanzania	Arusha	2018	Tanzania Agricultural Research Institute (TARI), Selian
	Arusha	2019	World Vegetable Center, Eastern and Southern Africa, Duluti, Arusha, Tanzania
Uganda	Serere	2018 & 2019	National Agricultural Research Organization-National Semi Arid Resources Research Institute (NARO-NaSARRI)
Kenya	Katumani	2018	Kenya Agricultural and Livestock Research Organization (KALRO), Nairobi Kenya
	Kampi Mawe	2019	
Benin	Cotonou	2018 & 2019	World Vegetable Center, West and Central Africa – Coastal and Humid Regions, Benin
Ghana	Kumasi	2018 & 2019	CSIR-Crops Research Institute, Kumasi-Ghana
Mali	Bamako	2018 & 2019	World Vegetable Center, West and Central Africa – Dry Regions, Samanko Research Station, Bamako, Mali
Nigeria	Ibadan	2018 & 2019	National Horticultural Research Institute (NIHORT), Ibadan, Nigeria

At each trial site, morphological and developmental parameters were collected and the response to locally prevalent diseases was scored in the germplasm, using standardised methods. The collected data have been used to perform genome-wide association studies by combining the evaluation data with marker data produced for the core collection. For developmental parameters such as flowering time and seed set, as well as for grain quality parameters (seed lustre) associations with genetic loci have been established. For other parameters, including disease responses, the significance of the identified associations was low. For validating the associations, for the most important traits such as MYMV and powdery mildew resistance, segregating bi-parental populations were produced by crossing a resistant with a susceptible parent for QTL mapping in the F_2 or later generations.

Develop improved mungbean germplasm and elite lines

Improved lines developed by WorldVeg were shared with all the partners of the network. In addition, it was also shared with interested national organisations for multi-location testing and phenotyping for agronomic, biotic and abiotic stresses.

The project partners in IMIN1 were provided with the following materials from WorldVeg:

- AVMU lines: ICAR-IIPR (183 lines). BARI (276 lines), DAR (312 lines), DAF (274 lines), KALRO (322 lines), TARI (121 lines) and NARO (105) for initial seed multiplication and further testing, including ones with resistance to all the three major species/strains of MYMD, early maturity, heat stress tolerance, improved iron content and good sprouting quality)

- Released varieties were shared among the partner countries: India (10), Bangladesh (10), Myanmar (5) and Australia (10).

6 Achievements against activities and outputs/milestones

6.1 Objective 1: Establish and coordinate and International Mungbean Improvement Network

No.	Activity	Outputs/ Milestones	Completion date	Comments
1.1	Form the network	International Mungbean Improvement Network established with partners from India, Bangladesh, Myanmar and Australia.	Feb 2016	The project inception was meeting held on 22-23 Feb in Kanpur, India. The first annual project meeting was held in New Delhi from 8-11 November, 2016, The second annual project meeting was held in Dhaka from 30-31 May, 2017.
		International Mungbean Improvement Network established with partners from India, Bangladesh, Myanmar and Australia.	May 2017	The third annual project meeting was held in Nay Pyi Taw, Myanmar from 2-4 May, 2017.
		International Mungbean Improvement Network was initially established with partners from Bangladesh, India, Myanmar and Australia. In 2020, Kenya, Tanzania and Uganda joined the network.	June 2019	A workshop was held in Yangon, Myanmar on 7-8 February, 2019, organized by Department of Agricultural Research (DAR), Myanmar. Participants in the workshop included representatives from DAR, Yezin Agricultural University (YAU), Myanmar Pulses, Beans & Sesame Merchants Association, Myanmar Awba Group, ICCO and farmers from Yangon region. Workshop was held at the ICAR-Indian Institute of Pulses Research, Kanpur from 10th – 11th February 2019 involving all the major stakeholders in the mungbean industry including researchers, millers, farmers and traders.

No.	Activity	Outputs/ Milestones	Completion date	Comments
1.2	Establish a communication infrastructure	Regular fortnightly skype/zoom meetings are being conducted with active participation by partner countries.	March 2016	The first and second editions of the 'Mung Central' newsletter were released, with the latest in March 2017.
			October 2017	The third edition of the 'Mung Central' newsletter was released.
			August 2018	The fourth edition of the 'Mung Central' newsletter was released.
			July 2019	The fifth edition of the 'Mung Central' newsletter was released.
			April 2020	The sixth edition of the 'Mung Central' newsletter was released.
			December 2020	The seventh edition of the 'Mung Central' newsletter was released.
			July 2021	The eight edition of the 'Mung Central' newsletter was released.
				Project activities are regularly updated on the website: https://avrdc.org/intl-mungbean-network/

No.	Activity	Outputs/ Milestones	Completion date	Comments
1.3	Adopt a single information management system for curation, sharing and analysis of project data	A contract for provision of the KDDart software suite and support has been signed. One orientation/training session was conducted in November 2016, concurrent with the project's annual meeting in Delhi. Follow-up training is scheduled in mid-October 2017. Follow-up trainings for the implementation of KDDart were conducted.	December 2016 December 2017 October 2021	The project reviewed four tenders that included both public and private sector contributors. The KDDArT suite (Diversity Arrays, Canberra) was selected by project partners as being best placed to provide the network with the most cost effective and flexible solution with the greatest range of functionality. The KDDArT suite (Diversity Arrays, Canberra) was selected by project partners for collection, curating and sharing of the data. One orientation/training session was conducted in November 2016, concurrent with the project's annual meeting in Delhi. A follow-up training was conducted in October 2017 in Hyderabad, India. Network is using KDDArT for collection, curation and sharing of phenotype data. The network is using KDDart for collection, curation and sharing of phenotype data. Follow up trainings are being conducted in the partner countries to fix problems encountered during the implementation.
1.4	Perform workshops and manage a small training grants system for network member scientists	25 breeders trained 25 production specialists trained 100 extension service officers trained	November 2017 June 2019	Training on plant breeding methods and the application of statistical methods in plant breeding was conducted from 23-27 October 2017 at the WorldVeg South Asia office, Hyderabad. 24 scientists from the network participated in this training. A report and feedback on the training is included in the appendix. Supported by the small grants program Dr. Aditya Pratap from ICAR-IIPR joined the molecular breeding group at WorldVeg HQ to work on genome-wide association mapping in mungbean during November 2017. Follow up trainings on KDDart conducted in India. Bangladesh and Myanmar. Extension officers (over 300) trained on Good Agricultural Practices in India, Bangladesh and Myanmar.

No.	Activity	Outputs/ Milestones	Completion date	Comments
1.5	Develop and implement mechanisms for germplasm exchange among the partner institutions and countries	Exchange of germplasm has been incorporated in the sub contracts between the World Vegetable Center and the national Partners.	May 2017 June 2019	MTAs were signed between World Vegetable Center and the partner countries Material Transfer Agreement between QUT and World Vegetable Center was signed on 10 June, 2019
1.6	Assess the project progress	The second annual report has been prepared and submitted. Mid-term review of the project held during 2-4 May 2018, Nay Pyi Taw, Myanmar. Follow up on the recommendations from the mid-term review of the project held during 2-4 May 2018, Nay Pyi Taw, Myanmar.	July 2017 May 2018 June 2019	To be reviewed by the Program Manager The review team from ACIAR was led by Dr. Eric Huttner, Research Program Manager and Ms. Emily Lamberton, Research Officer, Crops Cluster during the third annual meeting of the project. Based on the mid-term review recommendations product pipeline workshops were conducted in Myanmar Bangladesh and India.
1.7	Conduct product pipeline workshops in the partner countries involving all the major stakeholders	Mungbean products suitable for different market segments identified	December 2020	Virtual workshop on Demand-led Breeding Approaches for market segmentation and designing mungbean product profiles with mungbean researchers from Asia and Africa held on 8-9 December 2020
1.8	Conduct workshop on database management, marker assisted selection and pest & disease management	Capacity building of participants from all the target countries	October 2021	Follow up trainings on KDDart conducted in India. Bangladesh and Myanmar and during 2020-21 via online (with participation of 32 researchers).
1.9	Project review	Final report of the first phase prepared	October 2021	Final report (draft) prepared and submitted

6.2 Objective 2: Improve access to mungbean genetic diversity for breeders to source traits required for future elite varieties

No.	Activity	Outputs/ milestones	Completion date	Comments
2.1	Deploy a set of biodiverse mungbean lines	The mungbean mini-core collection (296 accessions) has been made available to the project partners by the World Vegetable Center. In addition, 5-10 released varieties have been exchanged between the partner countries	July 2016	The mini-core was multiplied in the partner countries and seed for multilocation trials was produced. At some sites, strong MYMD pressure affected seed production and the evaluation of other traits than MYMV resistance. Therefore, the set also needs to be planted on sites with less MYMD pressure to ensure seed availability and facilitate the evaluation of a broad range of traits. **India:** Seeds of 296 accessions of the mungbean mini-core collection sent by WorldVeg were received at ICAR-National Bureau of Plant Genetic Resources, New Delhi in October 2015. The seed was released to IIPR in February 2017 after completing post entry quarantine at NBPGR. Simultaneously one set was also supplied to IIPR by WorldVeg South Asia, Hyderabad in July 2016. While one evaluation trial was conducted during the monsoon season (July-October, 2016), a replicated evaluation trial was conducted during spring (April-June), 2017 at IIPR, Kanpur . **Bangladesh:** Evaluation of 296 mungbean genotypes from the mini-core collection for seedling vigor, resistance to MYMD and CLS was carried out at three different locations in Bangladesh (Barisal, Ishurdi and Gazipur) by the Bangladesh Agricultural Research Institute (BARI). **Myanmar**: Evaluation of the mini-core collection was carried out during spring (Feb-April) 2016 and 2017. **Australia:** The mini-core collection was released from post entry quarantine and field increased in tropical north Queensland over the southern

				winter of 2016. Quantities of up to 400 g of seed were produced. Seed from 15 international varieties from Bangladesh, Myanmar and Australia have been increased. Replicated foliar disease nurseries (halo blight, powdery mildew, and tan spot) were completed in the 2016/17 summer season (see attachment). The replicated yield and agronomic evaluation of the mini core and shared international varieties was conducted at Emerald in the semi-arid tropics of central Queensland between February and May. Samples are still to be processed for this trial.
			May 2018	A seed increase of the mini-core and shared international varieties was sown and hand-harvested in southern Queensland in order to provide pure seed for all subsequent project years. It is expected that upon processing of samples that 400g seed will be available for future use.
			June 2018	The mini-core collection deployment and multiplication in the partner countries was accomplished and reported in the progress report 2017.
			December 2020	Seed of the some of the accessions of the mini-core collection was provided to partners in India, Myanmar and Bangladesh during 2018/19 based on their additional requirements. In addition, the mini-core collection was shared with Kasetsart University, Thailand. **Kenya, Tanzania and Uganda:** The mini-core collection was shared with partners in Kenya (KALRO), Tanzania (TARI) and NARO (Uganda) during 2016-18, as part of a FCDO Project.

2.2	Carry-out multi-location appraisal of the biodiverse mungbean lines	Field performance data with emphasis on abiotic and biotic stress tolerance available from at least 12 locations	May 2018 June 2019 October 2021	Standardized and agreed protocols were developed and shared with partners to maintain consistency in data collection and for analysis. Multi-location appraisal of the mini-core collection has been continued at three locations in each of the four partner countries. Multi-location appraisal of the mini-core collection has been continued in each of the four partner countries. In addition, evaluation has been continued in Hyderabad and in Taiwan for resistance to pests and diseases. Screening of the mini-core accessions at WorldVeg led to the identification of resistance to anthracnose, powdery mildew, Cercospora Leaf Spot and thrips. Dry root rot resistant accessions identified by WorldVeg were field tested in Myanmar, which led to the confirmation of high levels of resistance in 4 accessions. More details in Appendix, section 10. Multi-location testing of the mini-core conducted in Kenya, Tanzania and Uganda conducted.
2.3	Genotype the mini-core collection	Genotyping by sequencing resulted in 24,000 Single nucleotide polymorphic markers for the mini-core collection. A set of 8,000 high quality markers with good sequencing depth and low missing data rate (<25%) was chosen for the molecular analyses of the germplasm set.	July 2016	Genotyping by sequencing (GBS) of the mungbean mini-core was fully accomplished and reported in the 2017 progress report. The GBS raw data of this experiment were merged with the raw data obtained from the Australian diversity panel and a combined diversity and structure analysis was performed. The combination of these datasets will provide increased benefits to the network and greater synergy to the Australian arm of this project in phenotyping for emergent foliar diseases.
2.4	Carry-out association mapping of disease and	Structure and linkage disequilibrium decay distance analysis has been accomplished in the germplasm panel.	August 2020	The population structure of the germplasm panel was analysed with various software tools. The linkage disequilibrium decay distance calculated for the

	abiotic stress tolerance traits	Genome-wide association genetics analyses (GWAS) have been performed using all available phenotypic data. For morphological (e.g. seed size, luster and color) and developmental traits (e.g. flowering time) QTLs have been identified. For resistance to diseases such as MYMV similar loci were found associated with resistance for trial sites in Bangladesh and Myanmar, while different loci were associated with MYMD resistance in India.	September 2021	germplasm panel was relatively large (100 kb) indicating that around 5,000 evenly spread markers should be sufficient to capture each linkage block. The TASSEL (Bradbury et al., 2007) pipeline has been routinely used for GWAS (Kusmec and Schnable 2018). In addition, the R-based GAPIT (Lipka et al., 20212) software was adopted for GWAS to allow using a broader set of GWAS models. The significance levels of most disease resistance QTLs are low, requiring additional validation in bi-parental populations.
2.5	New populations developed in Australia shared with the World Vegetable Center	Nested Association Mapping (NAM) populations (2000 lines) and Australian Diversity Panel (430 lines) developed in Australia is shared with the World Vegetable Center	September 2021	A part of the collection has been received by WorldVeg West and Central Africa, Cotonou, Benin. A subset has been grown for DNA extraction. Shipment of the material required seed propagation under quarantine conditions to avoid possible spread of *Pseudomonas syringe* from the plantlets. The second and last batch of this material which is proven to be free of *P. syringae* is currently shipped from Australia to Taiwan. Australian Diversity Panel has been despatched to WorldVeg Taiwan via DAF and the Australian Grains Genebank. The NAM populations were seed increased under glasshouse conditions over 2020/21 and will arrive with WorldVeg Taiwan before the end of 2021.
2.6	Screening of a subset of the mini-core collection at varying levels of CO_2 : effect on the nutritional content of the grains	Data collected will be analysed and a manuscript prepared for submission to an open access journal	October 2021	A set of 50 genotypes that includes a subset of mini-core collection (37 accessions), popular varieties from Australia, Bangladesh, India, Myanmar, Sri Lanka and Thailand (10), and WorldVeg mungbean advanced breeding line (3) are being tested under elevated

				(700 ppm) and ambient CO_2 conditions (400ppm) in CO_2 and Temperature Gradient Tunnels (CTGT) at controlled environment facility of ICRISAT. The major objective of the study is to understand the response of genotypes and assess genotypic variability for growth, yield, and nutritional quality traits under elevated CO_2 conditions. The trial was planted on 17th September 2021 with two replications at two different CO_2 levels (Figure 1). The trial is at the flowering stage and the data recording is in progress. The experiment would be useful in understanding the most responsive traits and genotypes under elevated CO_2 conditions that could be used in breeding future climate-smart cultivars.
2.7	Effect of elevated CO_2 on host-pathogen interactions, dry root rot disease severity and on expression of defence response genes in mungbean	Data collected will be analysed and a manuscript prepared for submission to an open access journal	October 2021	An experiment was carried out in open top chambers under elevated CO_2, the mungbean accessions (VI001400 AG, IPM99-125, EC693369, VI001244 AG, VC 3960-88 and EC693361) were used to study the host-pathogen interaction, disease severity and the expression of defence response genes. The elevated CO_2 concentrations with the disease pressure of *Macrophomina phaseolina* altered germination percentage, shoot and rot length and disease severity. The molecular analysis of root samples collected at vegetative and reproductive stages to understand the host-pathogen interaction and defence gene expression is undergoing. Hence, the experimental findings decipher the resistance mechanisms and growth dynamics operating behind the response of mungbean to elevated CO2 for addressing the challenges in future breeding programmes.
2.8	Development of Quantitative PCR assay for screening of Mungbean genotypes against dry root rot caused by *Macrophomina phaseolina*	Data collected will be analysed and a manuscript prepared for submission to an open access journal	October 2021	To develop qPCR assay for screening of mungbean genotypes, 30 accessions with diverse origin were evaluated for resistance to *Macrophomina phaseolina*. Based on preliminary results it was observed that the disease pressure in inoculated pots highlights the optimum disease pressure created in the experiment. The screening of these 30 genotypes identified

				six genotypes as resistant with dry root rot disease score less than 3 at 60 DAS. Development of qPCR technique is undergoing, that provides a precise fungal load present in genomic DNA of the plant in contrast to the visual observation and scoring.

6.3 Objective 3: Develop improved mungbean germplasm and elite lines

No.	Activity	Outputs/ Milestones	Completion date	Comments
3.1	Strengthen mungbean breeding programs in the target countries	A database training program on the implementation of KDDart by Diversity Arrays Pty Ltd, Canberra was conducted in New Delhi from 8-11 November, 2016,	December 2017	A database training program on the implementation of KDDArT by Diversity Arrays Pty Ltd, Canberra and training on plant breeding methods and the application of statistical methods in plant breeding were conducted from 23-27 October 2017 at WorldVeg South Asia, Hyderabad. Principal and Senior Biometricians from DAF and a Software Developer from Diversity Arrays delivered the training.
			December 2019	Product pipeline workshops conducted in India, Bangladesh and Myanmar.
		Product pipeline workshops to be conducted by all partners Virtual Workshop Demand-led Breeding approaches	December 2020	WorldVeg in collaboration with Syngenta Foundation for Sustainable Agriculture organized a workshop on Demand-Led Breeding (DLB) through the ACIAR funded International Mungbean Improvement Network (IMIN) project on 8th and 9th December 2020. Over 80 mungbean researchers from 20 countries of Asia and Africa came together virtually for brainstorming on DLB approaches for market segmentation and designing mungbean product profiles for some of the major mungbean growing countries.

3.2	Provide technical and scientific support to the national breeding programs of network members	Orientation and training in the Diversity Arrays KDDArT plant breeding software suite was conducted in Delhi in November 2017 concurrent to annual project meeting.	December 2017	Samsung Tabs were provided to participants from Bangladesh, India and Myanmar (two each). Software has been distributed to partners. Myanmar researchers are using KDSMArt android-based electronic data collection. Further training, with IMIN project data and roll-out of database is planned during mid-September 2017.
		Orientation and training in the Diversity Arrays KDDArT plant breeding software suite was conducted in Delhi in November 2017 concurrent to annual project meeting.	December 2017	Orientation and training in the Diversity Arrays KDDArT plant breeding software suite was conducted in Delhi in November 2017 concurrent to the annual project meeting. To follow up, Samsung tablets were provided to participants from Bangladesh, India and Myanmar (two each). Software has been distributed to partners. Myanmar researchers are using KDSMArt android-based electronic data collection. A follow up training on the use of KDSMArt by network partners with IMIN project data and the roll-out of the database was conducted in October 2017. During the mid-term review it was decided to conduct a three-day follow-up training program in India, Bangladesh and Myanmar. Dr. Aditya Pratap from ICAR-IIPR joined the molecular breeding group at WorldVeg to work on genome-wide association mapping in mungbean during November 2017. A training plan for 2018/19 involving scientists from BARI, ICAR-IIPR, DAR, and WorldVeg on marker-assisted selection, virus diagnosis and genebank curation was developed.
		Training conducted for partners on	June 2019	A workshop on “Enhancing farmers’ access to improved mungbean varieties and good agricultural practices in Southeast Asia” Kampaeng Saen, Thailand, 23-24 April 2019
		Orientation and training in the database management	June 2019	Follow up trainings on KDDart conducted in India, Bangladesh and Myanmar.
			October 2021	Virtual workshop on updates in KDDart Database management system conducted with participants from Asia and Africa on 27 November 2020.

No.	Activity	Outputs/ Milestones	Completion date	Comments
		Support for viral diagnostics	June 2019	In order to elucidate the diversity of the begomovirus infected legumes in the partner countries, samples from each country were selected and subjected to full-length DNA-A and DNA-B sequence analysis. Results indicated that most samples were infected with mungbean yellow mosaic India virus (MYMIV; Begomovirus), while only very few test samples were infected with mungbean yellow mosaic virus (MYMV; Begomovirus). Although the diversity was discovered in the test samples, it suggests that MYMIV was the major constraint in the production of legumes in the 4 countries.
			October 2021	All the samples collected in Africa tested negative for Begomovirus and for Soybean mosaic virus (SMV), suggesting that they were not the constraint for mungbean production in the target countries. Results indicated that Potyvirus was predominant in Benin, Tanzania and Uganda, while Cucumber mosaic virus (CMV) was prevalent in Kenya. Most samples which tested positive for Potyvirus were also positive for Bean common mosaic virus (BCMV), indicating that BCMV was the major potyvirus in the target countries; however, several samples were infected with unknown Potyvirus.

No.	Activity	Outputs/ Milestones	Completion date	Comments
3.3	Broaden the genetic base of mungbean	30 introgression crosses to black gram and other *secondary genepool* donors completed Desired traits back-crossed into adapted backgrounds 30 introgression crosses to black gram and other secondary genepool donors completed Desired traits back-crossed into adapted backgrounds	June 2018 October 2021	Thirty four successful crosses between mungbean and related *Vigna* species such as *V. mungo*, *V. umbellata* and *V. trilobata* were developed. Backcrosses are currently in progress. At WorldVeg, crosses derived from mungbean with *V. mungo* and *V. mungo* sp. *sylvestris* have been advanced. In total, 27 mungbean crosses were produced at WorldVeg during the reporting period aiming to combine disease resistance in the offspring. In addition, 6 interspecific crosses between *V. radiata* and *V. mungo* and *V mungo* ssp. *sylvester*is were performed. Hybrid status of the F1 was confirmed based on morphological parameters. Fertile offspring was detected and the hybrids were advanced by selfing. From twenty successful crosses two fertile interspecific populations between *Vigna radiata* and *Vigna mungo* have been recovered by DAF. Potential heat tolerance and resistance to bacterial and fungal diseases will be screened in single cross material and in introgression crosses made to Australian commercial varieties and elite breeding lines from 2022 onwards. AT IIPR Kanpur, 11 crosses were developed and advanced with *Vigna mungo* and other *Vigna* species as the donors and elite mungbean lines as the recipients.

3.4	Provide network member breeders including partners from Kenya, Tanzania and Uganda improved mungbean lines with desirable traits (at least 10 lines per tier)	Tier 1: Mungbean lines with MYMV resistance genes pyramided, lines with synchronised maturity, high yield and short duration lines for mechanical harvest	July 2016	Fifty-nine AVMU breeding lines (AVMU prefix) are being multiplied by the partner countries (except India).
		Tier 2: Lines with improved tolerance to terminal heat stress	September 2017	Heat stress tolerant mungbean lines (EC693357, EC693358, EC693369, Harsha and ML1299) were identified, will be shared with the partner countries.
		Tier 1: Mungbean lines with MYMV resistance genes pyramided, lines with synchronised maturity, high yield and short duration lines for mechanical harvest	May 2018	Tier 1: AVMU lines from WorldVeg were supplied to ICAR-IIPR (65 lines). BARI (59 lines), DAR (59 lines) and DAF (59 lines) for initial seed multiplication and further testing. 27 breeding lines including ones with resistance to all the three major species/strains of MYMD have been shared with ICAR-IIPR and will soon be shared with other partners.
		Tier 2: Lines with improved tolerance to terminal heat stress	September 2017	Tier 2: Heat stress tolerant mungbean lines (EC693357, EC693358, EC693369, Harsha and ML1299) were identified and shared with the partner countries.
		Tier 3: interspecific hybrids of mungbean with black gram and rice bean	April 2018	Tier 3: Thirty two successful crosses between mungbean and black gram & mungbean and rice bean were developed. At WorldVeg, successful crosses have been developed between popular Myanmar sprouting varieties Bhakti (VI001255 AG) and CES-14 (VI000414 AG) with a MYMD resistant parent. In addition, crosses were made between V02818 A-G (a black gram line, with resistance to bacterial foliar diseases-tan spot and halo bight) and the Australian commercial varieties; Crystal, Jade-AU, Celera II-AU and Satin II. At IIPR, 11 successful crosses have been developed using mungbean lines as the recipients and blackgram, *V. sylvestris* and *V. umbellata* as the donors
			June 2019	Tier 1: Evaluation of AVMU lines is in progress by all partners.
			June 2019	Tier 2: Evaluation of the lines in progress by the partner countries.

No.	Activity	Outputs/ Milestones	Completion date	Comments
			June 2019	Tier 3: Crosses derived from mungbean with *V. mungo* and *V. mungo* sp. *sylvestris* have been advanced.
3.5	Test improved mungbean lines	At least 5 elite mungbean lines identified in the materials from tier 1, 2 and 3 for scaling out to farmers in each country Multi-locational testing of lines will be conducted in Kenya, Tanzania and Uganda in a farmer participatory mode. A socio-economic analysis of the results will be done	October 2021	**India:** IIPR 20-1 (AVMU 1683) and IIPR 20-2 (AVMU 1690) are under multi-location evaluation in All India Coordinated Research project on MULLaRP. Currently these lines are at AVT 1 stage and have shown excellent promise for release as varieties. **Bangladesh:** Three AVMU lines (AVMU 1602, AVMU 1606 and AVMU 1608) with higher yields compared to BARImung 6 have been identified in Bangladesh for further testing (Regional Yield Trial) before potential release. **Myanmar:** Seven AVMU lines (AVMU 1631, AVMU 1632, AVMU 1642, AVMU 1643, AVMU 1659, AVMU 1688 and AVMU 1690) and two high yielding mini-core accessions (VI000559 AG and VI004934 AG) will undergo further testing. **Tanzania:** Two AVMU lines (AVMU 1601 and AVMU 1693) preferred by Mungbean farmers in Tanzania were submitted for official release requisition by Tanzania Official Seed Certification Institute (TOSCI). **Kenya:** Early maturing, high yielding mungbean lines with high iron content (AVMU 2014 and AVMU 2023) were preferred by farmers in Participatory Variety Selection. Sequeros T, Ochieng J, Schreinemachers P, Binagwa, PH. Huelgas ZM. Hapsari R, Juma, Maurice O, Kangile, JR, Karimi R, Khaririyatun N, Mbeyagala EK, Mvungi H, Nair RM, Sanya L, Nasirumbi N, Thi TL, Phommalath S, Pinn T, Simfukwe E, Suebpongsang P.2021. Mungbean in Southeast Asia and East Africa: varieties, practices and constraints. Agriculture & Food Security 10, 2 https://doi.org/10.1186/s40066-020-00273-7

7 Key results and discussion

7.1 Establish and coordinate an International Mungbean Improvement Network

The International Mungbean Improvement Network led by World Vegetable Center (WorldVeg) was initially established with partners from Bangladesh, India, Myanmar and Australia. In 2020, Kenya, Tanzania and Uganda joined the network. Annual meetings were held in the partner countries. Fortnightly meetings (online) are being conducted with the partners to monitor the project activities. The network also developed a newsletter called "Mung Central". So far eight editions have been released.

A plant breeding data management system - KDDArt - has been implemented within the network and the data collected have been shared among the partners.

The KDDart database management system is being implemented by the network. The current status of the implementation is outlined in Table 3 below. An illustration of the pedigree information maintained in the database is presented in Figure 2.

Table 3. KDDart Database Implementation: Current status

Center	Data collection (KDSmart)	Data upload (KDManage)	Pedigree information
Myanmar(DAR)	☑	☑	☑
Bangladesh(BARI)	☑	☑	☑
India(IIPR)	☑	☑	☑
Australia(DAF)	*	☑	☑
WorldVeg	☑	☑	☑

*Collecting electronic data through another platform

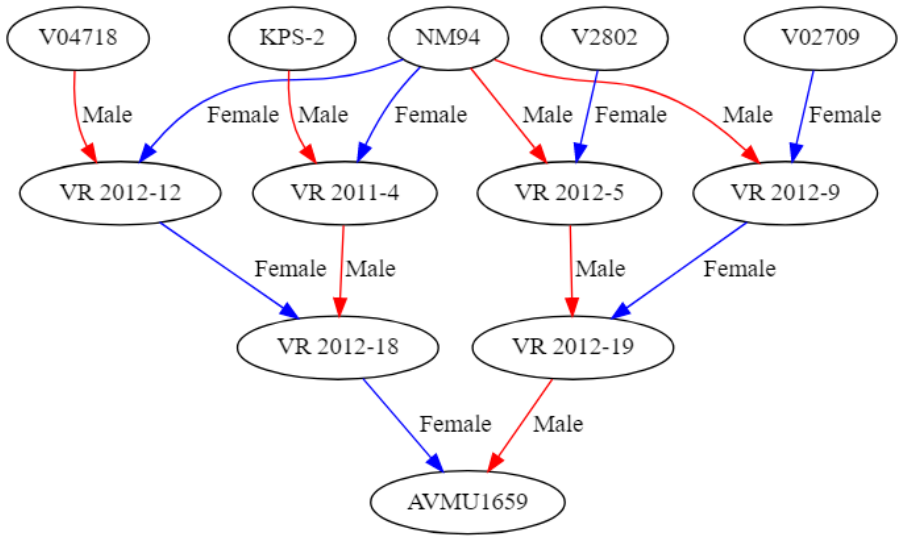


Figure 2. Pedigree information of the breeding line AVMU 1659

7.2 Improve access to mungbean genetic diversity for breeders to source traits required for future elite varieties

The mungbean mini-core was shared with partners (within and outside of the network) and evaluated with a major objective to strengthen NARS breeding programs with diverse germplasm and to identify the promising accessions with better agronomic traits, diseases and pest resistance, and nutritional quality compared to local varieties that could be used as parents for the development of varieties to meet the requirements of the regions.

7.2.1 Evaluation of Mungbean Mini-core Collection in Asia and Australia

A set of 296 accessions of mungbean mini-core collection developed by the World Vegetable Center, Taiwan was shared with IMIN partners in Asia and Australia. The evaluation of mungbean mini-core collection was done across multiple sites/environments in Australia (17), Bangladesh (11), India (12), and Myanmar (2) during 2016-2021 (Table 1). The field evaluation was done in Alpha Lattice Design with two replications in most of the locations for entire mini-core set whereas randomized complete block design was used for few trials where subset of mini-core was evaluated. The trial in Australia were conducted in Optimal Designs. The data were recorded on major agronomic, yield, and disease/pest resistance traits under natural field conditions across the sites. The combined analysis of variance for common traits across locations revealed significant genotypic, environment, and genotype × environment interaction variance for MYMD, days to 50% flowering, days to maturity, seed yield per plant, and 100 seed weight. The trait-specific genotype identified for different target traits which could be useful for the breeding program across partner countries are listed in Table 4. The GGE biplot analysis for seed yield per plant and days to maturity across the locations in Asia is presented in Figures 23 and 24, respectively (In Appendix). The term “GGE” emphasizes the understanding that G (Genotype) and GE (Genotype x Environment) are the two sources of variation that are relevant to genotype evaluation and must be considered simultaneously for appropriate genotype and test environment evaluation. The data analysis for trials conducted in Australia is in progress.

Table 4. Trait-specific accession identified based on the combined mean performance of mungbean mini-core across different locations in Asia during 2016-2021

Trait	Accessions	Trait Value
Mungbean Yellow Mosaic Disease (score)	VI004973B-BLM, VI004968AG, VI004957AG, VI002190BG, VI005066A-GM, VI004931AG, VI004965BG, VI005041AG, VI005022BG, VI004933AG, VI003252BG, VI000170B-BR, VI002487AG, VI004956AG and VI001628AG	<2.5
Days to 50% Flowering	VI002860AG, VI004734AG, VI003364AG, VI004694BG, VI002176AG, VI004954BG, VI002009BG, VI002437BG, VI002872BG, VI000618AG, VI002239AG, VI004871BG, VI002173BG, VI004666AG and VI004351AG	≤43
Days to Maturity	VI002860AG, VI002872BG, VI003364AG, VI002176AG, VI003785BG, VI004915BG, VI003734B-DG, VI002456AG, VI004694BG, VI004307AG, VI003242AG, VI003929A-BL, VI002877BG, VI002173BG and VI004871BG	≤66

Trait	Accessions	Trait Value
Seed Yield per Plant (g)	VI000815BG, VI005041AG, VI004965BG, VI002190BG, VI001282AG, VI000852AG, VI000532BG, VI004877AG, VI000319AG, VI001756BG, VI003734B-BR, VI004937AG, VI003957AG, VI004933AG and VI000470AG	≥6.7 g
100 Seed Weight (g)	VI005041AG, VI000470AG, VI002432AG, VI002456AG, VI000380AG, VI001339AG, VI001096AG, VI001124AG, VI002739AG, VI002672AG, VI004958BG, VI002195AG, VI002206AG, VI002523AG and VI002611AG	>3.8 g

7.2.2 Evaluation of Mungbean Mini-core Collection in Sub-Saharan Africa

A set of 293 accessions of mungbean mini-core collection developed by the World Vegetable Center, Taiwan was shared with National Agriculture Research System (NARS) partners across seven countries in Sub-Saharan Africa that includes Tanzania, Kenya, Uganda, Benin, Ghana, Mali and Nigeria for evaluation during 2018 and 2019 (Table 2). The evaluation across seven countries was done in Alpha Lattice Design with two replications. The data were recorded on major agronomic, yield, and disease/pest resistance traits under natural field conditions across seven locations.

The combined analysis of variance for common traits across locations revealed significant genotypic, environment and genotype × environment interaction variance for days to 50% flowering, days to maturity, plant vigor, plant height, pod yield per plant, seed yield per plant, pod length, number of pods per plant, number of seed per pod, and 100 seed weight. The trait-specific genotype identified for different target traits useful for the breeding program across partner countries are listed in Table 5.

Table 5. Trait-specific mini-core accessions identified based on the combined mean performance of mungbean mini-core accessions across 7 countries in Sub-Saharan Africa during 2018 & 19.

Trait	Accessions	Trait Value
Days to maturity	VI002802 A-BR, VI004302 AG, VI004307 AG, VI000625 B-BR, VI004145 B-BL, VI004432 B-BR, VI004347 B-BLM, VI004423 AG, VI004691 AG, VI004351 AG, VI002176 AG, VI004244 B-BR, VI002860 AG, VI004184 AG, VI004734 AG, VI002239 AG, VI002176 BG, VI003181 B-GM, VI003332 AG, VI003948 B-BR, VI000105 BG, VI003954 BG, VI003886 B-BR, VI003907 AG, VI001698 BG, VI004871 BG, VI003785 BG, VI001974 BG,	<60 days to maturity
Hundred Seed Weight (g)	VI000380 AG, VI001244 AG, VI000953 AG, VI001339 AG, VI002739 AG, VI000470 AG, VI000020 AY, VI001096 AG, VI001124 AG, VI000736 AG, VI005041 AG, VI002587 AG, VI002647 AG, VI002523 AG, VI002195 AG, VI002456 AG, VI002432 AG, VI002672 AG,	>6 g 100 seed weight
Number of seeds per pod	VI002063 BG, VI003801 BG, VI0035534 BG, VI003951 AG, VI003785 BG, VI002646 AG, VI000735 BG, VI005030 BY, VI003958 B-BLM, VI002487 AG, VI001126 BG,	12-14 Seeds per Plod

Number of pods per plant	VI004877 AG, VI004129 A-BLM, VI003159 AG, VI003255 AG, VI003407 AG, VI001282 AG, VI004853 BG, VI003925 B-BLM, VI004138 BG, VI003135 B-BL, VI001419 BG, VI003251 A-BL, VI000559 AG, VI003942 AG, VI002859 BG, VI003337 BG, VI003181 B-GM, VI001535 BG, VI000625 B-BR, VI002009 BG,	>25 pods per plant
Seed Yield Per Plant (g)	VI002532 AG, VI001339 AG, VI005041 AG, VI001096 AG, VI002569 BG, VI000736 AG, VI000735 BG, VI000942 AG, VI002611 AG, VI000316 AG, VI000537 BG, VI004942 BG, VI003642 AG, VI002206 AG, VI001023 BG, VI000805 BG, VIOO1221 AG, VI003379 BG, VI002063 BG, VI002195 AG, VI002587 AG, V1002469 AG, VI002523 AG and VI004965 BG	>8.5 g yield per plant

7.2.3 Screening for biotic stress

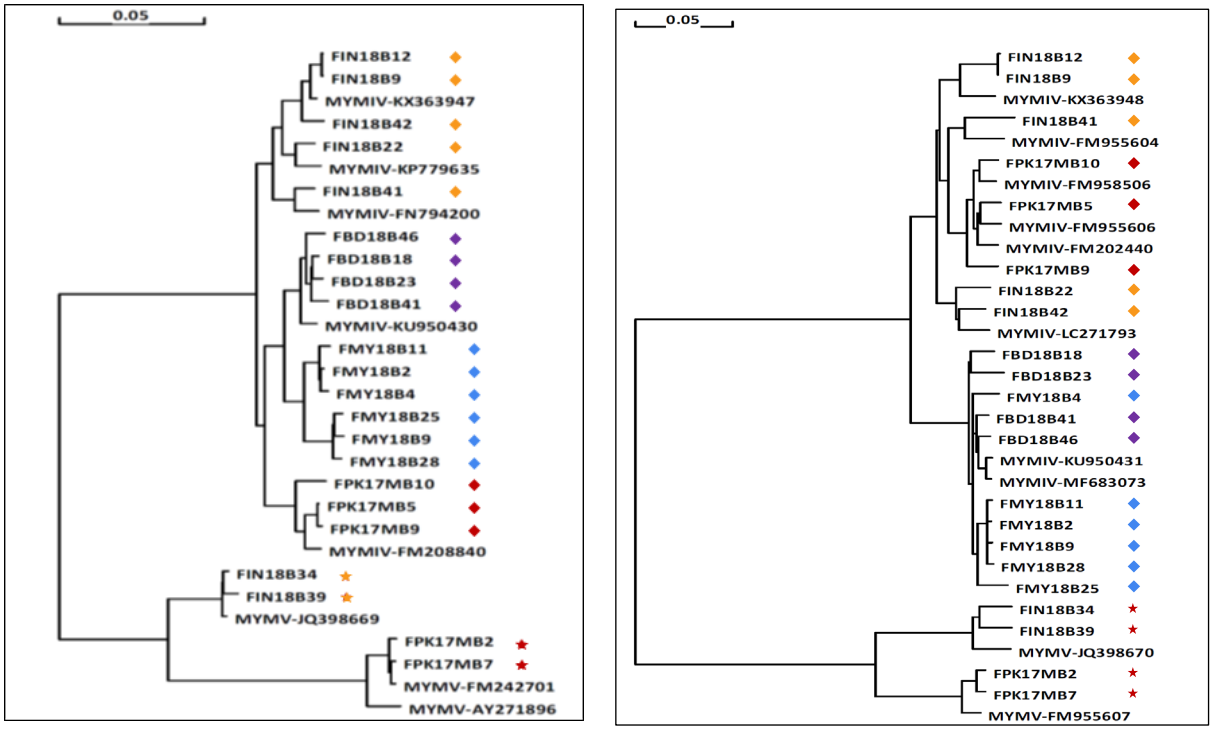
Mungbean Yellow Mosaic Disease (MYMD)

Identification of new resistant sources for yellow mosaic disease in India

Mungbean Yellow mosaic disease (MYMD) is caused by three species of viruses viz., *Mungbean yellow mosaic India virus* (MYMIV), *Mungbean yellow mosaic virus* (MYMV) and *Horsegram yellow mosaic virus* (HgYMV) in a number of pulse crops, particularly of *Vigna* group. The disease is transmitted by whiteflies. Deployment of host plant resistance is accepted as the best option for the management of YMD. For the last five years, intensive efforts have been made to develop and screen a large number of mungbean advanced breeding materials, germplasm lines and mini core collection of World Vegetable Center (AVRDC) against yellow mosaic disease. Among >450 genotypes that were screened against yellow mosaic disease for the last 5 years, three advanced breeding lines (IPM 526-11, IPM 08-1 and IPM 312-17) and seven germplasm lines (IC616147, IC616220, IC616116, EC862645, IC616208, IC16266, and IC616194) have been found resistant. These genotypes recorded 0 to 3.1% YMD incidence and <1% disease severity during all the years (2017-2021) and multiple seasons (*Kharif* and Spring/Summer) as against 61.1 to 100% YMD incidence and >70% disease severity in the susceptible check (DGGV 2) under field conditions. All these genotypes recorded 1 or 2 on YMD rating scale (1-9) which is considered as resistant category. The identity of the YMD causing virus was ascertained by PCR assays using specific primers as *Mungbean yellow mosaic India virus.* The identified YMD resistant genotypes may be used further as a donor in breeding programme to develop resistant superior cultivars of mungbean besides development of mapping populations to map genomic regions conferring the resistance to MYMIV.

Diversity of begomoviruses on mungbean in South Asia

The analysis of samples from South Asia revealed (Figure 3) the prevalence of *Mungbean yellow mosaic India virus* (MYMIV) and *Mungbean yellow mosaic virus* (MYMV).



(A) (B)

(C)

Figure 3. Phylogenetic tree of (A) DNA-A and (B) DNA-B of begomoviruses on (C) selected mungbean samples; each color represent one country, ◆ represents Mungbean yellow mosaic India virus (MYMIV) while ★ shows Mungbean yellow mosaic virus (MYMV).

Virus diseases on mungbean in Africa

All the collected samples were tested by PCR with universal begomovirus primers and by RT-PCR with universal potyvirus primers or specific primers for *Bean common mosaic virus* (BCMV; Potyvirus) and *Cucumber mosaic virus* (CMV; Cucumovirus), and by ELISA with antiserum specifically against *Soybean mosaic virus* (SMV; Potyvirus). All the samples tested negative for begomovirus and SMV, suggesting that these viruses were not the constraint for mungbean production in the target countries. Results indicated that potyvirus was predominate in Benin, Tanzania and Uganda, while CMV was prevalent in Kenya. Most samples which tested positive for potyvirus were also positive for BCMV, indicating that BCMV was the major potyvirus in the target countries; however, several samples were infected with unknown potyvirus (Table 6).

Table 6. Virus diseases on mungbean in Africa

Country	Location	Begomovirus	CMV	Potyvirus	BCMV	SMV
Benin		0	1	11	11	0
Kenya	KALRO Katumani field station	0	0	1	0	0
	Ithookwe	0	14	3	1	0
	Katumani	0	11	0	0	0
	Kampi Mawe	0	15	2	0	0
Tanzania	Fekadu Fufa Dinssa	0	6	11	8	0
Uganda	Lira District	0	0	6	5	0
	Kitgum District	0	0	4	2	0
	Arua District	0	0	0	0	0
	Serere District	0	1	9	8	0
	Mayuge District	0	0	0	0	0
Total		0	48	47	35	0

Application of Nanopore sequencing technology on virus diagnosis of mungbean samples in Uganda

In 2019, 103 mungbean leaf samples were collected from the field trials in Lira, Kitgum, Arua, Serere and Mayuge districts in Uganda. In each district, 3 pooled samples containing 5 samples with various virus-like symptoms in each were subjected to RNA extraction with Quick-RNA Plant Miniprep kit (ZYMO Research). The 3 RNA samples from each district were then mixed and subjected to double-strand cDNA synthesis, barcoding and library preparation. The library was prepared with SQK-LSK109 kit and sequencing was conducted using Flow Cell and MinION Mk1c sequencing device (Oxford Nanopore Technologies). The raw data

obtained by Nanopore sequencing is further processed by Guppy basecalling software to convert the electrical signals into the base sequence. The data set of sequence was then analyzed by EPI2ME platform to obtain preliminary taxonomic classification. Further data analysis for some individual sequences was conducted by BLASTn at National Center for Biotechnology Information.

As for the detection of begomoviruses, the same sample preparation described above was applied and the pooled samples were subjected to DNA extraction with Quick-DNA Plant /Seed Miniprep Kit (ZYMO Research). The 3 DNA samples from each location were then mixed and subjected to Rolling Circle Amplification (RCA) in order to increase the proportion of virus-derived reads for circular DNA viruses, such as begomoviruses.

The results with Nanopore sequencing approach indicated that *Bean common mosaic virus* (BCMV), *Cucumber mosaic virus* (CMV) and *Cowpea polerovirus* 2 were detected on mungbean in Uganda. BCMV and CMV were detected in all districts, while *Cowpea polerovirus 2* was detected only in Lira. However, the begomoviruses such as *Mungbean yellow mosaic virus* and *Mungbean yellow mosaic India virus* which are prevalent on mungbean in Asia were not detected in Uganda by Nanopore sequencing.

As comparing the results from Nanopore sequencing approach to the results from traditional detection systems, ELISA/RT-PCR, it is found that the former provides more virus information than the latter. In addition, the virus sequences obtained by using Nanopore sequencing technology can be used to develop new primer sets for RT-PCR, thereby improving the diagnostic efficiency of mungbean viruses (Table 7).

Table 7. Nanopore-based detection and characterization of mungbean viruses in Uganda

Location	ELISA/RT-PCR	**Nanopore Sequencing**
Northern/ Lira District *	BCMV	BCMV, CMV, *Cowpea polerovirus 2*
Northern/ Kitgum District	BCMV	BCMV, CMV
West Nile/ Arua District	-	BCMV, CMV
Eastern/ Serere District	BCMV, CMV	BCMV, CMV
Eastern/ Mayuge District	-	BCMV, CMV

*Strategies of pooling and barcoding samples for each location were adopted

Dry root rot disease

Mungbean mini-core accessions were screened against Dry Root Rot (DRR) resistance using the paper towel at World Vegetable Center South Asia, Hyderabad (India). Twenty-nine resistant accessions identified in the preliminary test were re-evaluated by the paper towel method to see the consistent resistance response. Eighteen accessions consistent with resistance response in the repeated paper towel experiment were further evaluated for DRR resistance in a glasshouse in Hyderabad through the sick pot method. A subset of 30 accessions showing resistant (27) and susceptible (3) reactions in the preliminary paper towel

experiment in Hyderabad was selected from 296 mini-core accessions. These accessions were evaluated for DRR resistance in the field at Food Legume Research Section, Department of Agricultural Research (DAR), Yezin, Myanmar. All the experiments were conducted from 2017 to 2019.

Evaluation of the 296 mungbean mini-core accessions by paper towel method identified 29 accessions with DRR resistance (disease scores: ≤ 3). In a repeated paper towel experiment with 29 resistant accessions, 18 accessions were identified as resistant, six moderately resistant, and five were moderately susceptible, and the ANOVA exhibited a significant ($P<0.0001$) variation in disease scores (Table 29; please see Appendix).

Data of the repeated glasshouse experiments revealed that accessions VI000766BG, VI001244AG, VI001268BG, VI001282AG, VI001400AG, VI001490AG, VI001509AG, VI001535BG, and VI003699B-BR performed consistent resistance in sick pot 1 and 2. These accessions had lower DRR incidence (≤10.0%) than the susceptible check (VC6930-88), which showed 91.36% disease incidence in sick pot 1 and 96.20% in sick pot 2. The disease reaction of resistant and susceptible accessions is shown in Figure 4. During 2018 and 2019 in Yezin, Myanmar, out of the 30 accessions, ten accessions were found DRR resistance with ≤10% disease incidence in both years of evaluations. Pooled analysis of percent disease incidence data of 15 accessions common in both glasshouse and field revealed the stability of accessions VI001509AG, VI001244AG, and VI001400AG for DRR resistance across years and locations (Table 30; please see Appendix).

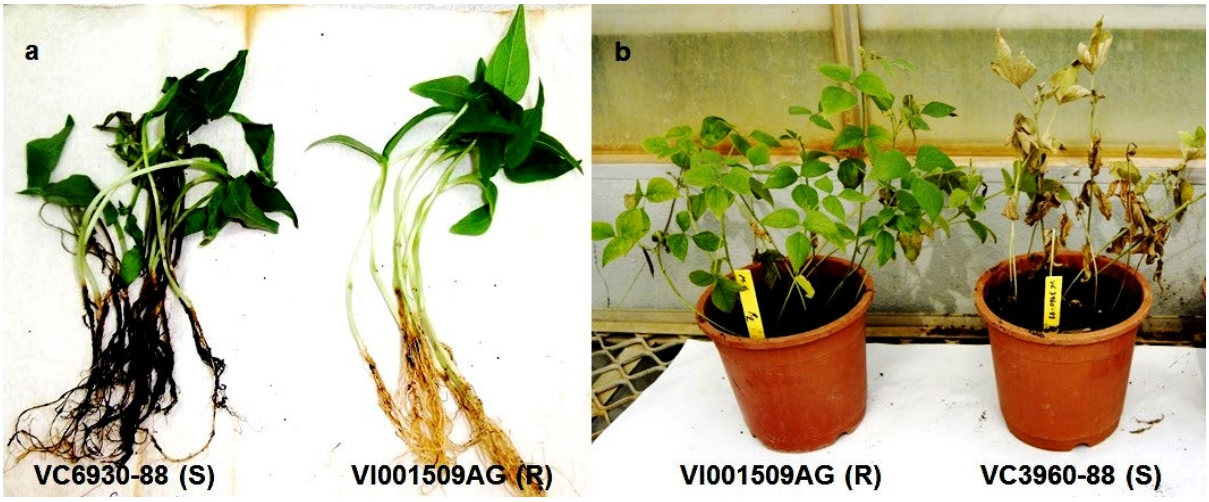


Figure 4. Mungbean accessions showing susceptible (S) and resistant (R) reactions against DRR in paper towel (a) and sick pot (b) experiments at the WorldVeg South Asia, Hyderabad, India

Anthracnose disease

The 296 mungbean mini-core accessions were evaluated under natural disease pressure for anthracnose resistance from July to September (kharif season) at the World Vegetable Center, South Asia, Hyderabad, India, in 2016, 2017, and 2018. A subset of 74 accessions was selected from 296 mungbean mini-core accessions based on their anthracnose resistance and agronomic performance in Hyderabad were evaluated at the experimental farm of the Department of Plant Pathology, CSK Agricultural University, Palampur, Himachal Pradesh, India, in 2018 and 2019, to determine the variation in anthracnose resistance at different locations. Disease severity score of each accession was recorded on five randomly selected plants within a row using a 1-to-9point rating scale. The accessions with disease severity

scores of '1' were considered immune (I: no infection), and those with scores 9.0 were considered highly susceptible (HS: above 51% foliage affected).

Based on disease severity scores, twenty-two accessions were consistently anthracnose resistant under the categories of immune, highly resistant, and resistant with scores ranged from ≥1.0 to ≤ 3.0 during the period of study. Out of the 74 accessions evaluated in Palampur, two accessions were resistant in 2018, and in 2019, one was immune, nine were highly resistant, and 15 were resistant. Combined analysis of variance of 65 accessions common in Hyderabad and Palampur revealed highly significant effects of environment, genotype (accessions), and genotype × environment interaction on the disease severity. The combined GGE biplot analysis of data across years and locations confirmed that the seven accessions VI000559AG, VI001162AG, VI001520A-BLM, VI002529B-B, VI003699B-BG, VI003720BG and VI005024B-BL were resistant during 2016 to 2018 in Hyderabad, and only in 2019 in Palampur, and the same accessions were moderately resistant in 2018 in Palampur (Table 31; please see Appendix).The seven resistant accessions identified from both test locations could be used as potential donors in the anthracnose resistance breeding program.

Powdery mildew disease

Screening of 296 mini-core accessions for powdery mildew disease was carried out during the 2016, 2017, and 2018 at WorldVeg South Asia, Hyderabad and in 2019 at Palampur, under field conditions. During 2016, out of 296 accessions, 46 were highly resistant, 102 were resistant, 95 were moderately resistant, 46 were moderately susceptible, 7 were susceptible and none of them were highly susceptible (Table 8).

Table 8. Resistant reaction of mungbean mini-core accessions for powdery mildew (*Podosphaera fusca*) disease at Worldveg South Asia, Hyderabad, India during 2016

Number of accessions	Resistant reaction	Disease score range
46	Highly Resistant	0
102	Resistant	0.1-1.0
95	Moderately resistant	1.1-2.0
46	Moderately susceptible	2.1-3.0
7	Susceptible	3.1-4.0
0	Highly susceptible	4.0-5.0

Powdery mildew disease was rated on 0-5 rating scale where 1= Highly resistant and 5= Highly susceptible, $p>0.05$.

During 2017, Out of 296 accessions, 9 were highly resistant, 71 were resistant, 171 were moderately resistant, 38 were moderately susceptible, 95 were susceptible and 02 were highly susceptible (Table 9, Figure 5).

Table 9. Resistant reaction of mungbean mini-core accessions for powdery mildew (*Podosphaera fusca*) disease at WorldVeg South Asia, Hyderabad, India during 2017

Number of accessions	Resistant reaction	Disease score range
9 (VI000470 AG, VI000852 AG , VI001162 AG, VI003019 A-BLM , VI003019 BG , VI003720 BG , VI003744 AG , VI005030 BY, VI005041 AG)	Highly Resistant	0
71	Resistant	0.1-1.0
171	Moderately resistant	1.1-2.0
38	Moderately susceptible	2.1-3.0
95	Susceptible	3.1-4.0
2 (VI001514 AG VI003563 A-BR)	Highly susceptible	4.0-5.0

Powdery mildew disease was rated on 0-5 rating scale where 1= Highly resistant and 5= Highly susceptible, p>0.05.

Figure 5. Mungbean mini-core accessions showing resistant reaction against powdery mildew disease in field in the 2017 *kharif* season at WorldVeg South Asia, Hyderabad, India

Out of 296 accessions, 14 were highly resistant, 68 were resistant, 98 were moderately resistant, 73 were moderately susceptible, 38 were susceptible and 05 were highly susceptible (Table 10, Figure 6). Accession VI003720 BG was found resistant at WorldVeg, Hyderabad, during 2016, 2017, 2018 and 2019. Accessions VI001162 AG and VI005030 BY were found resistant in WorldVeg, Hyderabad during 2016, 2017, 2019 and Palampur during 2019. The three resistant accessions identified from these test locations could be used as potential donors in the powdery mildew resistance breeding program.

Table 10. Resistant reaction of mungbean mini-core accessions for powdery mildew (*Podosphaera fusca*) disease at WorldVeg South Asia, Hyderabad, India during 2018

Number of accessions	Resistant reaction	Disease score range
14 (VI000551 AG, VI001533 BG , VI001548 AG , VI001556 BG, VI002274 B-BL , VI003276 BG, VI003534 AG , VI003534 BG , VI003658 BG , VI003678 BG , VI003699 B-BR , VI003720 BG , VI003734 B-BR VI003744 AG)	HR	0
68	R	0.1-1.0
98	MR	1.1-2.0
73	MS	2.0-3.0
38	S	3.0-4.0
5 (VI001562 AG, VI003364 AG, VI004351 AG, VI004480 AG, VI004666 AG)	HS	4.0-5.0

HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S- Susceptible, HS- Highly susceptible, powdery mildew disease was rated on 0-5 rating scale where 0-Highly resistant and 5= Highly susceptible, F value: 7.48, p<0.0001.

VI002456 AG (S) **VI001533 BG (R)**

Figure 6. Mungbean mini-core accessions showing a resistance reaction against powdery mildew (*Podosphaera fusca*) in field in kharif season-2018 at WorldVeg South Asia, Hyderabad, India

Screening experiments for powdery mildew were sown under field conditions in Australia in 2018 (Table 11), 2019 and 2020 (Table 12). Visual disease ratings are made on a 1-9 scale where 1 = no disease and 9 = dead plants. By way of comparison in 2020, seventy-three mini core lines performed better than Opal-AU, the Australian variety with best available powdery mildew protection. Poor infection and low discrimination between genotypes was encountered in the 2019 trial which was subject to extreme drought.

Table 11. Summary of Australian powdery mildew scoring in 2018

Number of accessions	Resistant reaction	Disease score range
19 (VI000170 B-BR, VI001162 AG, VI001411 AG VI001509 AG, VI003255 AG, VI003337 BG VI003382 BG, VI003407 AG, VI003534 AG VI003534 BG, VI003560 BG, VI003678 BG VI003699 BG, VI003894 B-BLM, VI003929 A-BL VI003958 B-BLM, VI004010 AG, VI005022 BG VI005024 B-BL)	R	1.1 – 2.0
29	MR	2.1 – 3.0
14	MR	3.1 – 4.0
21	MR-MS	4.1 – 5.0
72	MS	5.1 – 6.0
96	MS	6.1 – 7.0
36	S	7.1 – 8.0
0	HS	8.1 – 9.0

F value = 0.28, p<0.001, cv = 12.35%; R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS- Highly susceptible

Table 12. Summary of Australian powdery mildew screening in 2020

Number of accessions	Resistant reaction	Disease score range
23 (VI000238 AG., VI000542 BY, VI000938 AG VI001385 AG, VI001403 BR, VI001411 AG VI002173 BG, VI003159 AG, VI003181 B-GM VI003251 A-BL, VI003251 A-BLM, VI003255 AG VI003337 BG, VI003382 BG, VI003407 AG VI003514 BG, VI003642 AG, VI003678 BG VI003929 A-BL, VI003958 B-BLM, VI004048 A-GM, VI005022 BG, VI005024 B-BL)	R	1.1 – 2.0
9	MR	2.1 – 3.0
28	MR	3.1 – 4.0
62	MR-MS	4.1 – 5.0
137	MS	5.1 – 6.0
35	MS	6.1 – 7.0
2 (VI002860 AG, VI004694 BG)	S	7.1 – 8.0
0	HS	8.1 – 9.0

R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S- Susceptible, HS- Highly susceptible

Cercospora leaf spot disease

Based on the other desirable traits, 74 mini-core accessions selected from 296 mini-core accessions were evaluated at CSK Agriculture University Palampur during *kharif* 2018, against Cercospora leaf spot disease caused by *Cercospora canescens* under field conditions. Out of 74 accessions, 13 were resistant, 45 were moderately resistant, 7 were moderately susceptible, and 9 were susceptible (Table 13, Figure 7).

Table 13. Resistant reaction of mungbean mini-core accessions for Cercospora leaf spot (*Cercospora canescens*) disease at CSK Himanchal Pradesh Agricultural University, Palampur (India)

Number of accessions	Resistant reaction	Disease score range
-	HR	0
VI000020 AY, VI000380AG, VI000589 B-BR, VI000852 AG , VI001221AG, VI001268BG, VI001482 BG, VI001509 AG, VI001535 BG, VI003019 A-BLM, VI003720 BG, VI003785BG, VI004743 AG (13)	R	0.1-1.0
45	MR	1.1-2.0
VI000212 A-BLM, VI001284AG, VI001419 BG, VI001490 AG, VI001548 AG, VI001576 BG, VI002012BG (7)	MS	2.1-3.0
VI000818 BG, VI001244 AG, VI001411 AG, VI003235AG, VI003251A-BL-M, VI003407AG, VI003894B-BLM, VI004822BG, VI005024 B-BL (9)	S	3.1-4.0
-	HS	4.1-5.0

R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S- Susceptible, Cercospora leaf spot disease was rated on 0-5 rating scale where 0-Highly resistant and 5= Highly susceptible, F value: 3.8, p<0.088

VI003407AG (S) **VI000589 B-BR (R)**

Figure 7. Mungbean mini-core accessions showing a resistance reaction against Cercospora leaf spot disease in field in *kharif* season-2018 at CSK Himanchal Pradesh Agricultural University, Palampur (India)

Halo blight disease

Halo blight is a seed-borne bacterial disease caused by the pathogen *Pseudomonas savastanoi* pv. *phaseolicola.* There are no in-crop control options for halo blight and genetic resistance is recognised as the most effective means of crop protection. Screening experiments for halo blight were sown under field conditions in Australia in 2018 and 2020 (Table 14 & 15). Predicted scores for disease ratings are presented in tables below. In Australia visual disease ratings are made on a 1-9 scale where 1 = no disease and 9 = dead plants. Poor infection and low discrimination between genotypes was encountered in the 2018 trial, the highest resistance was in VI005024 B-BL a black gram accession which reflects other screening in Australia that some of the best sources of bacterial resistance are in *Vigna mungo.*

Table 14. Summary of Australian halo blight screening in 2018

Number of accessions	Resistant reaction	Disease score range
1 (VI005024 B-BL)	R	1.1 – 2.0
45	MR	2.1 – 3.0
162	MR	3.1 – 4.0
66	MR-MS	4.1 – 5.0
19	MS	5.1 – 6.0
3	MS	6.1 – 7.0
0	S	7.1 – 8.0
	VS	8.1 – 9.0

F value = 0.593, p<0.001, cv = 17.58; HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S- Susceptible, HS- Highly susceptible

Table 15. Summary of Australian halo blight screening in 2020

Number of accessions	Resistant reaction	Disease score range
2 (VI003514 BG and VI003699 BG)	R	1.1 – 2.0
20	MR	2.1 – 3.0
39	MR	3.1 – 4.0
77	MR-MS	4.1 – 5.0
82	MS	5.1 – 6.0
70	MS	6.1 – 7.0
6	S	7.1 – 8.0
0	HS	8.1 – 9.0

HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S- Susceptible, HS- Highly susceptible

Mungbean in Australia requires multiple foliar resistances, the following figure represents the halo blight and powdery mildew reactions from 2020 screening of the World Vegetable Center Mini Core Collection (296 genotypes) as well as the Australian Diversity Panel (450 genotypes) for halo blight and powdery mildew. Australian commercial varieties, are plotted for comparison in Figure 8. That halo blight has been a major focus of Australian breeding (releases Celera II-AU and Opal-AU) is represented in the few germplasm accessions are available with superior halo blight resistance. There is however considerable scope for genetic

improvement in powdery mildew. Note also that the majority of genetic diversity is in the small seeded type (blue data points) and presents a significant breeding challenge for the export markets for large green shiny beans that are served by Australian and Burmese breeding programs.

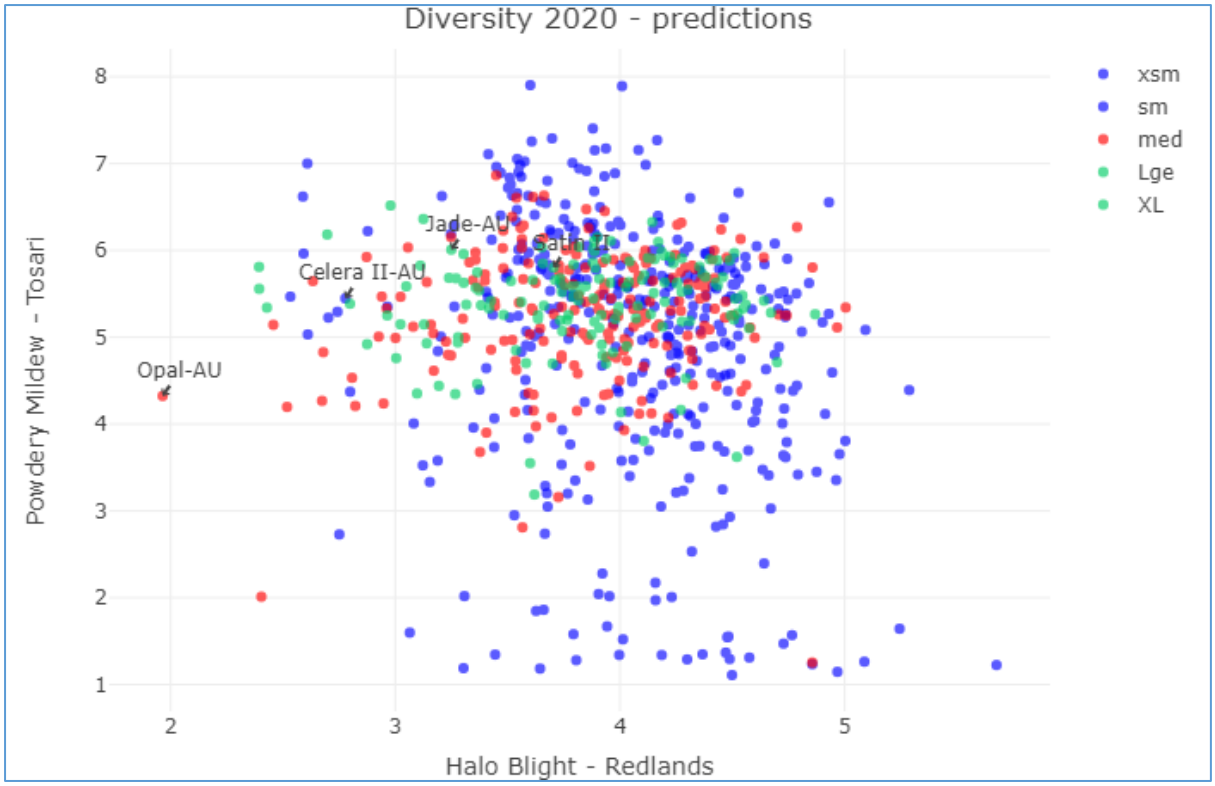


Figure 8. Plot showing halo blight and powdery mildew reactions of mini core and Australian Diversity Panel mungbean germplasm

Cowpea aphid

The mini-core accessions were evaluated for the resistance to cowpea aphids during the post-rainy season, 2017-2018. The cowpea aphid damage on the plants was assessed based on the population density on the plant parts and plant vigour. The rating scale of (1 to 5) where (1 = highly resistant, 2 = moderately resistant/tolerant, 3 = moderately susceptible, 4 = susceptible, 5 = highly susceptible was used to record the aphid infestation on different genotypes) (Figure 27; Please see Appendix). The visual damage scores were recorded at 20, 40, and 60 days after sowing. Among 296 mini-core accessions, 97 were resistant, while, 78 accessions were moderately resistant to cowpea aphids (Table 16; Figure 9).

Table 16. Summary of the field evaluation of mungbean mini-core accessions against cowpea aphids 2017-18 at WorldVeg South Asia, Hyderabad, India

Response to Aphid infestation	Damage rating (1-5)	No. of accessions
Resistant	1	97
Moderately resistant	2	78
Susceptible accessions	3-5	121

F = 2.15, *p* = <0.0001, CV (%) = 41.09

Resistant (VI003181 B-GM) **Susceptible (VI002239 AG)**

Figure 9. Screening of mungbean mini-core accessions against cowpea aphid *(Aphis craccivora)* at WorldVeg South Asia, Hyderabad, India during 2017-18

Screening of Advanced Breeding Lines

The AVMU lines were screened against the cowpea aphids at WorldVeg South Asia, Hyderabad, India during 2016-2017. Based on the plant vigour and population density of cowpea aphids, plants were scored with 1-5 rating scale at 20, 40, and 60 days after sowing. In the field evaluation during 2017, two lines (AVMU1692 and AVMU1633) were found to be resistant, while 34 lines were found tolerant to cowpea aphids.

Thrips

The mini-core accessions were field evaluated for the resistance against thrips during 2017-2019. Plants were scored based on the plant vigour and the visual damage symptoms caused due to thrips incidence, with 1-5 rating scale (1 = highly resistant, 2 = moderately resistant, 3 = moderately susceptible, 4 = susceptible, 5 = highly susceptible) (Figure 28, see Appendix). The damage scores were recorded at 20, 40, and 60 days after sowing. During 2017, out of 296 accessions, 56 were resistant to thrips with a damage score of 1, while, 155 accessions showed moderate resistance against thrips damage, and 85 accessions were susceptible to thrips damage (Table 17; Figure 10). It is also notable that seven accessions *viz;* VI001419 BG, VI003251 A-BL, VI003914 AG, VI003957 AG, VI004743 AG, VI003235 AG, and VI003548 AG were resistant to both thrips and cowpea aphids.

Table 17. Field evaluation of mungbean mini-core collection against thrips during 2017-2018 at WorldVeg South Asia, Hyderabad, India

Response to thrips infestation	Damage rating (1-5)	No of accessions
Resistant	1	56
Moderately resistant	2	155
Susceptible	3-5	85

F = 2.09, *p* = <0.0001, CV (%) = 56.8

Resistant (VI005024 B BL)

Susceptible (VI004942 BG)

Figure 10. Mini-core accessions VI005024 B-BL showing resistance to thrips damage during screening of mini-core accessions against thrips at WorldVeg South Asia, Hyderabad, India

All the mini-core collection (296 accessions) was re-evaluated for resistance response to thrips under field conditions at WorldVeg South Asia, Hyderabad, India, during 2018-19. Among 296 accessions, seven accessions showed resistance to thrips with a damage score of 1 and 60 accessions showed moderate resistance/tolerance with a scoring of 2 whereas 229 accessions were susceptible to thrips with damage rating scoring ranging from 3-5 (Table 18). Among the resistant accessions, five (VI001096 AG, VI001419 BG, VI001514 AG, VI003548 AG, VI003914 AG) were consistently resistant to thrips in the trials conducted during 2017-2019.

Table 18. Field evaluation of mungbean mini-core collection against thrips during 2018-2019 at WorldVeg South Asia, Hyderabad, India

Response to thrips infestation	Damage rating (1-5)	Number of accessions
Resistant	1	7 (VI003548 AG, VI003914 AG VI001419 BG, VI004743 AG, VI001514 AG, VI001268 BG, VI001096 AG)
Moderately resistant/tolerant	2	60
Susceptible accessions	3-5	229

F = 3.07, *p* = <0.0001, CV (%) = 17.23

Molecular characterization of thrips collected from mungbean at World Vegetable Center, South Asia field was carried out through sequencing. Two species of thrips were identified

from the mungbean as; Yellow thrips - *Thrips palmi* and Black thrips - *Caliothrips indicus* (Figure 11).

Yellow thrips- *Thrips palmi*

Black thrips- *Caliothrips indicus*

Figure 11. Identification of thrips species in mungbean

The AVMU lines were screened against the thrips at WorldVeg South Asia, Hyderabad, India during 2018-2019. Based on the plant vigour and the visual damage symptoms due to thrips incidence, plants were scored with 1-5 rating scale **(**1 = highly resistant, 2 = moderately resistant/tolerant, 3 = moderately susceptible, 4 = susceptible, 5 = highly susceptible. The densities of the thrips from three randomly selected plants were counted at 20 and 40 days after germination. The damage scores were recorded at 20, 40, and 60 days after sowing. In this field evaluation during 2018-19, five lines (AVMU 16101, AVMU 1658, AVMU 1678, AVMU 16105, and AVMU 1618) out of 87 AVMU lines were resistant to thrips, while 17 lines showed moderate resistance to thrips attack (Table 19; Figure 12)

Table 19. Screening of mungbean AVMU lines against thrips during 2018-2019 at WorldVeg South Asia, Hyderabad, India

Number of AVMU lines	Damage rating (1-5)	Remarks
5 (AVMU16101, AVMU1658, AVMU1678, AVMU16105, AVMU1618)	1	Highly Resistant
17	2	Moderately Resistant/Tolerant
65	3-5	Susceptible

F = 5.89, *p* = <0.0001, CV (%) = 13.2

During 2018-19 field evaluation, the thrips densities were recorded at 20 and 40 days after sowing (DAS). The lowest thrips density was observed in AVMU1643, AVMU1685 and AVMU1695 (1.34-1.71/3 plants) at 20 DAS whereas AVMU16101, AVMU16105, AVMU1618, AVMU1620, AVMU1685 and AVMU1695 (1.41-1.62 thrips/3 plants) had lowest thrips density at 40 DAS (Table 20a and 20b)

Table 20a. Thrips density in improved mungbean lines at 20 days after germination

Mungbean advanced breeding lines	Thrips count/3 plants
AVMU1643, AVMU1685, AVMU1695	1.34-1.71
AVMU1611, AVMU1615, AVMU1627, AVMU1633, AVMU1638, AVMU1641	7.5-9.0

F = 4.40; *p* = <.0001

Table 20b. Thrips density in improved mungbean lines at 40 days after germination

Mungbean advanced breeding lines	Thrips count/3 plants
AVMU 16101, AVMU16105, AVMU1618, AVMU1620, AVMU1685, AVMU1695	1.41-1.62
AVMU1607, AVMU16102, AVMU1616, AVMU1617, AVMU1627, AVMU1639, AVMU1643, AVMU1646, AVMU1654, AVMU1656, AVMU1678, NM94	8.3-11.53

F = 3.85; *p* = <.0001

Figure 12. Thrips susceptible line-AVMU1686 (left) and resistant line-AVMU16101 (right)

Bruchids

The mini-core accessions (296) were screened against the bruchids infestation (*Callosobruchus maculatus*) under laboratory conditions at WorldVeg South Asia, Hyderabad, India during 2019-2020. A total of 150 seeds from each accession were divided into 3 replicates of 50 seeds and were kept in closed boxes/vials. Five pairs of 1- to 3-days old adults were released into the vial and allowed lay eggs for a week. On the 8th day, adults were removed and number of eggs laid on the seeds was counted. After 3 weeks from the date of adult removal, the number of emerging F1 adults were recorded every day until last adult emerges from each box. Simultaneously, the number of undamaged as well as bruchid-

damaged seeds were recorded. The susceptibility Index scale was used to determine the resistance of seeds against the bruchids (SI < 2.0 as highly resistant; 2.1 – 3.0 as moderately resistant; 3.1 – 5.0 as moderately susceptible; >5 as highly susceptible)

Four (VI001628 AG, VI001412 AG, VI004297 AG, VI004710 AG) out of 296 mini-core accessions were found to be resistant to *C. maculatus,* while 3 accessions (VI001762 A-GM, VI000942 AG, and VI000232 AG) showed moderate resistance to bruchids infestation. However, 290 accessions were susceptible to *C. maculatus*); (Table 21)

Table 21. Summary of laboratory screening of mungbean mini-core collection against bruchids during 2019-20 at WorldVeg South Asia, Hyderabad, India

Response to bruchid infestation	Damage rating (1-5)	Number of accessions
Resistant	1	4 (VI001628 AG, VI001412 AG, VI004297 AG, VI004710 AG)
Moderately resistant/tolerant	2	3 (VI001762 A-GM, VI000942 AG, VI000232 AG)
Susceptible	3-7	290

F=0.44; *p* <<0.0001; SE= 0.042; CV=10.63%

Forty-two advanced breeding lines were evaluated against bruchids infestation in the laboratory during 2018-19. A total of 150 seeds from each accession were divided into 3 replicates of 50 seeds and were kept in closed boxes/vials. Five pairs of 1- to 3-day-old adults were released into the vial and allowed lay eggs for a week. On the 8th day adults were removed and number of eggs laid on the seeds were counted. After 3 weeks of adult removal, the number of emerging F1 adults were recorded every day until last adult emerges from each box. Simultaneously, the number of undamaged as well as bruchid-damaged seeds were recorded; the Susceptibility Index Scale was used to determine the resistance against bruchids infestation (SI < 2.0 as highly resistant; 2.1 – 3.0 as moderately resistant; 3.1 – 5.0 as moderately susceptible; >5 as highly susceptible)

A set of 42 advanced breeding lines with two checks V2802 and NM 94 were evaluated for resistance to bruchids (*Callosobruchus maculatus*) infestation at WorldVeg South Asia, Hyderabad, India under laboratory conditions. Lines that showed resistance to bruchids included shiny green (AVMU1601, AVMU1605, AVMU1606), dull green (AVMU 1603, AVMU 1604, AVMU 1609, AVMU 1612, AVMU 1613, AVMU 1618, AVMU 1620, AVMU 1621, AVMU 1622, AVMU 1623, AVMU 1624, AVMU 1625, AVMU 1626 and AVMU 1628), and brownish (AVMU1602, AVMU1610, AVMU1611, AVMU1614, AVMU1616, AVMU1617, AVMU1619) seeds (Table 32; please see Appendix), Figure 13).

Figure 13. Bruchid resistant-AVMU 1601 (left) and susceptible check-NM94 (right)

Whitefly and Jassids

Thirteen (13) improved mungbean lines along with selected urdbean lines along with local checks were screened under field conditions against sucking insect pests, viz. whitefly and jassid during post rainy season, 2018 at Punjab Agricultural University, Ludhiana, Punjab, India. The trial was subjected to a natural infestation of the pests in the field. The population of whitefly, *Bemisia tabaci*, and jassid, *Empoasca* sp. was recorded from three spots/ replication/entry with the help of Kooner Cage (Ht. 60 cm, dia 45 cm) as well as from each trifoliate leaf. The incidence of jassids (in a cage) on different test entries ranged from 4.50-14.33 per cage as compared to 4.50-4.67 per cage on checks. Incidence of whitefly (in a cage) on different test entries ranged from 4.17-45.67 per cage as compared to 3.33-10.50 per cage on checks (Table 34; please see Appendix).

Stem fly

A subset of 39 mini-core accessions and 33 AVMU lines along with the checks (ML1628, NM94, V2802) were field evaluated for the resistance sources against the stem fly (*Ophiomyia phaseoli*). Stem fly incidence was assessed on the 15 old seedlings by destructive sampling method. About 10 plants from each genotype was removed from the soil; roots and the stem were examined for presence of immature (maggots/pupae) stages and the entry holes made of the stem fly maggots. Numbers of damaged plants were converted into percentage damage by stem fly. The damage of 0-10% was considered as resistant genotype. Two out of 39 mini-core accessions and one out of 33 AVMU lines were resistant to stem fly attack during 2019 (Table 22).

Table 22. Summary of screening of subset of mungbean mini-core and AVMU lines against stem fly during 2019-20 at WorldVeg South Asia, Hyderabad, India

Resistance level	List of Mini-core accessions	No. of AVMU lines
10-30% damage (Resistant)	2 accessions (VI001509AG, VI001520A-BLM)	1 line (AVMU 1643)
10-20 % damage (Moderately resistant)	2 accessions (VI003720BG, VI005024B-BL)	0
50-70; >70 (Susceptible)	34	31

F=15.19; $p<<0.0001$; SE=0.001; CV=12.91%

7.2.4 Screening for abiotic stress

Salt tolerance

Forty mungbean lines were screened and contrasting lines were identified based on Salinity Induction Response (SIR) technique at the seedling level. As tolerance is a developmental stage specific, we further subjected the identified nine tolerant and nine susceptible lines for physiology based whole plant growth and yield phenotyping assay under 150 and 300 mM NaCl stress in pots. The results shown a considerable reduction in growth and yield performances of both tolerant and susceptible lines, but a few lines displayed relatively a better biomass and pod yield on par with non-stressed control plants. Based on seedling and whole plant level tolerance, a few tolerant (EC 693357, 58, 66, 71 and ML 1299) lines were identified for further investigation. Efforts are underway to use these identified tolerant lines as donor source for salinity breeding program to introgress with high yielding popular varieties (Manasa et al., 2017).

Heat tolerance

A study was conducted by WorldVeg, Hyderabad in collaboration with the Department of Botany, Panjab University, Chandigarh, India to evaluate high temperature effect on different mungbean lines for their vegetative and reproductive performances. Forty-one mungbean lines were grown in containers under full irrigation condition in outdoors; screened for growth and yield traits at two sowing dates: (1) the normal sowing time (NS) in March, so that day/night temperatures during the reproductive stage were <40/28 ◦C, and (2) late-sown (LS) in April so that temperatures during the reproductive stage were higher (>40/28 ◦C). In LS plants, leaves showed symptoms of leaf rolling and scorching and chlorosis compared to NS plants. Adding to that, the phenology was accelerated, leading to a sizable reduction in leaf area, biomass, flowers and pods. Interestingly, shortening of flowering time and podding duration was evident that decreased pod and seed yields. Further, in LS plants, reproductive function was distinctly condensed in most of the lines, causing increased flower and pod abortions, implying, heat stress during the reproductive phase of late sown plants of mungbean was found to be injurious. A few promising heat-tolerant lines (EC693357, EC693358, EC693369, Harsha and ML1299) have been identified, which would not only serve as useful donor/s for breeding programs, also act suitable base plant source to gain more insights on heat stress induced effects in cell metabolism (Sharma et al, 2016).

The HT-tolerant lines grown under elevated CO_2 levels (550 and 700 µL L−1) showed a considerable improvement in growth rates (13.5%, 67.8%, and 46.5% in plant height, leaf area, and total dry matter, respectively) and pod and seed yield (48.7% and 31.7%, respectively), compared to local checks under the same environments. Interestingly, the symptoms of accelerated pod maturity were also observed in most of these lines. The outcome of the study would undoubtedly open up opportunities for increased yield potentials of legumes under the conditions of the warming climate and elevated levels of carbon dioxide (Bindumadhava et al, 2018).

Drought adaptation

Twenty-four elite mungbean genotypes were grown with and without water stress for 25 days in a controlled environment. Top view and side view (two) images of all genotypes captured by a high-resolution camera installed in the high-throughput phenomics were analyzed to extract the pertinent parameters associated with plant features. We tested eight different multivariate models employing machine learning algorithms to predict fresh biomass from different features extracted from the images of diverse genotypes in the presence and absence of soil moisture stress. Based on the mean absolute error (MAE), root mean square error (RMSE), and R squared (R2) values, which are used to assess the precision of a model, the partial least square (PLS) method among the eight models was selected for the prediction of biomass. The predicted biomass was used to compute the plant growth rates and water-use indices, which were found to be highly promising surrogate traits as they could differentiate the response of genotypes to soil moisture stress more effectively. To the best of our knowledge, this is perhaps the first report stating the use of a phenomics method as a promising tool for assessing growth rates and also the productive use of water in mungbean crop (Rane et al., 2021).

LysiField: Drought stress imposition was done at early reproductive stage (30 days after sowing) to capture genetic variability in water-use and agronomic traits. Interesting genotypes with high seed yield, high TE and low water demand: AVMU 1640; EC 693360 (VC6486-10-51); EC 693368 (PUSA9072); KPS 1 and VI004958 BG. (Krithika Anbazhagan, ICRISAT, unpublished).

Root parameters

The mini-core collection was screened under modified semi-hydroponic screening conditions to determine the variation for fourteen root-related traits. The collection displayed wide variations for the primary root length, total surface area, and total root length, and based on agglomerative hierarchical clustering eight homogeneous groups displaying different root traits could be identified. Germplasm with potentially favorable root traits has been identified for further studies to identify the donor genotypes for breeding cultivars with enhanced adaptation to water-deficit stress and other stress conditions (Aski et al., 2021).

Phosphorus deficiency

Phosphorus deficiency mainly affects the growth and development of plants along with changes in root morphology and increase in root-to-shoot ratio. Deciphering the genetic basis of phosphorus use efficiency (PUE) traits can benefit our understanding of mungbean tolerance to low-phosphorus condition. To address this issue, 144 diverse mungbean genotypes were evaluated for 12 PUE traits under hydroponics with optimum- and low-phosphorus levels. The broad sense heritability of traits ranged from 0.63 to 0.92 and 0.58 to 0.92 under optimum- and low-phosphorus conditions, respectively. This study reports for the first time such a large number of genome wide Single nucleotide polymorphisms (SNPs) (76,160) in mungbean. Further, genome wide association study was conducted using 55,634 SNPs obtained by genotyping-by-sequencing method. The genome-wide SNP genotyping information of mungbean AM panel was integrated with PUE trait phenotyping data, ancestry coefficient (Q matrix), and relative kinship matrix (K) data using general linear model (GLM) (Q model) and mixed linear model (MLM) approach. The results indicated that total 136 SNPs shared by both GLM and MLM models were associated with tested PUE traits under different phosphorus regimes. We have identified SNPs with highest p value (–log10(p)) for some traits like, TLA and RDW with p value (–log10(p)) of more than 6.0 at LP/OP and OP condition. We have identified nine SNPs (three for TLA and six for RDW trait) which was found to be present in chromosomes 8, 4, and 7. One SNP present in Vradi07g06230 gene contains zinc finger CCCH domain. In total, 71 protein coding genes were identified, of which 13 genes were found to be putative candidate genes controlling PUE by regulating nutrient uptake and root architectural development pathways in mungbean. Moreover, we identified three potential candidate genes VRADI11G08340, VRADI01G05520, and VRADI04G10750 with missense SNPs in coding sequence region, which results in significant variation in protein structure at tertiary level. The identified SNPs and candidate genes provide the essential information for genetic studies and marker-assisted breeding program for improving low-phosphorus tolerance in mungbean (Reddy et al., 2020).

Root architectural traits in response to phosphorus deficiency

In a study conducted at the Indian Agricultural Research Institute (IARI), root architectural traits of 153 mungbean genotypes were compared under optimum and low phosphorus (P) conditions. Significant variations and medium to high heritability were observed for the root traits. Total root length was positively and significantly correlated with total root surface area, total root volume, total root tips and root forks under both optimum P ($r = 0.95$, $r = 0.85$, $r = 0.68$ and $r = 0.82$ respectively) and low P ($r = 0.95$, $r = 0.82$, $r = 0.71$ and $r = 0.81$ respectively). The magnitudes of the coefficient of variations were relatively higher for root forks, total root tips and total root volume. Total root length, total root surface area and total root volume were major contributors of variation and can be utilized for screening of P efficiency at the seedling stage. Released Indian mungbean varieties were found to be superior for root traits than other genotypic groups. Based on comprehensive P efficiency measurement, IPM-288, TM 96–25, TM 96–2, M 1477, PUSA 1342 were found to be the best highly efficient genotypes, whereas M 1131, PS-16, Pusa Vishal, M 831, IC 325828 were highly inefficient. Highly efficient

genotypes identified would be valuable genetic resources for P efficiency for utilizing in the mungbean breeding programme (Reddy et al., 2020).

Mungbean physiology

A single physiology experiment was conducted in Australia in the southern summer of 2016 to investigate the relationship between phenology, vegetative and reproductive growth and also the architecture and components of grain yield in small and large seeded mungbean germplasm. The mungbean parents of the nested association mapping populations were selected for inclusion since the mini core collection was still in the initial stage of being shared. Using the NAM parents fitted with a preliminary physiology experiment that had been conducted in an earlier ACIAR small research activity and allowed any useful variation to be further explored through the NAM populations themselves. Thirty genotypes were sown in destructive and non-destructive plots. Plants were dissected at physiological maturity and hierarchical data recorded on number of fruiting sites, number of pods per cluster, pod length, number of seeds per pod and weight of seeds per pod.

7.2.5 Nutritional quality

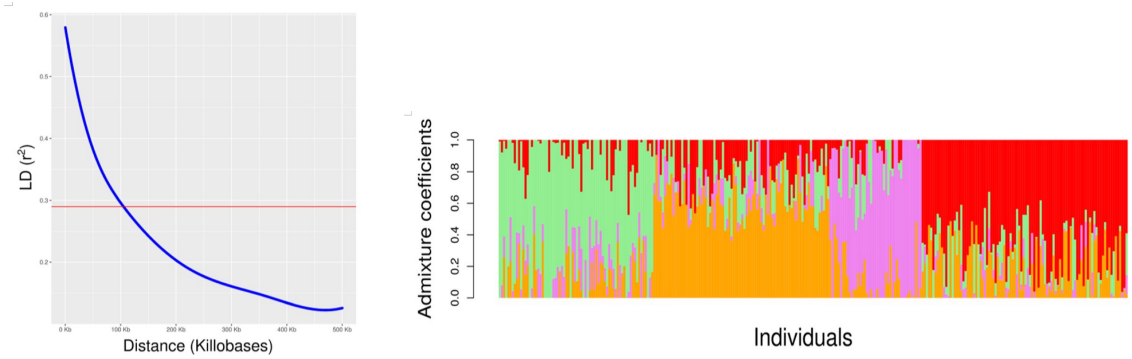
Improved iron content

We aimed at understanding how iron is taken up in mungbean and how increasing its availability in the soil changes the iron distribution within three popular mungbean varieties, NM-94, CN9-5 and Harsha. We could show that mungbean secretes phenolic compounds to support its iron acquisition and observed significant quantitative variations in the phenolic release, and root-surface ferric reductase activity among the three varieties. We found that in terms of iron distribution between organs, plants react differently when grown on soils with significantly different Fe content. In standard soils, the CN9-5 and Harsha varieties tended to achieve better iron distribution towards the seed, and higher iron content than NM-94. On the contrary, on iron-rich soil iron distribution towards the seed in NM-94 was strongly enhanced and led to the highest content among the three varieties (Nair et al., 2020).

Fifty-one high yielding mungbean lines (Table 1) were selected at WorldVeg from populations: NM 94 x CN 9-5, CN 9-5 x NM 94 and Harsha x NM94 and were distributed (50 seeds of each line) to partners in National Agricultural Research Organization (NARO), National Semi-Arid Resources Research Institute (NaSARRI), Soroti, Uganda; Tanzanian Agricultural Research Institute, Arusha, Tanzania and Kenya Agricultural and Livestock Research Organization (KALRO), Katumani, Kenya. Testing of these lines is in progress by the partners at multi-locations and the best line(s) selected will be submitted for varietal release.

7.3 Genetic characterization of the mungbean mini-core collection

A total of 24,870 raw SNPs were obtained through GBS from DArTSeq. SNPs that were not physically mapped to chromosomes or unmapped scaffolds were removed, resulting in 22,844 SNPs, which corresponds to a marker density of in average one SNP per 20 kb. A set of 5,041polymorphic markers evenly distributed over the genome and with a minimum allele frequency of 5% was assembled for linkage disequilibrium and structure analysis. Linkage disequilibrium decay distance was estimated as the physical distance over which the linkage between pair of loci declines to 50% of the maximum and amounted to 105kb (Figure 14a), suggesting that roughly 4,000 evenly distributed markers should be sufficient for genome-wide association analysis. Population structure analysis resulted in four subpopulations (orange: subpopulation 1, purple: 2, green: 3 and red: 4 in figure 14.b)). 70% of the accessions were attributed to one of the four populations, the remaining 30% were admixed (Figure 14b). Sub-populations 1 and 4 were the most closely related (F_{ST} =0.08) and populations 2, 3 and 4 show considerable degree of differentiation (F_{ST} =0.42, 0.43, 0.37 respectively).



a) b)

Figure 14. a) Linkage disequilibrium decay and b) population structure of the mungbean mini-core collection.

Genome-wide association mapping of loci conditioning morphologic and developmental traits, as well as resistances to diseases

Genome-wide association studies were tried for all available phenotypic data. Pilot experiments were performed on traits with high heritability such as plant or seed colour and lustre or seed size. Strong association with seed coat lustre was found on a locus on chromosome 5 and for hypocotyl colour on chromosome 2. Candidate loci for seed size were identified on chromosomes 1, 4, 6, 8 and 9. Days to flowering showed strong genotype by environment interaction and association with different loci was found at different locations (Figure 15).

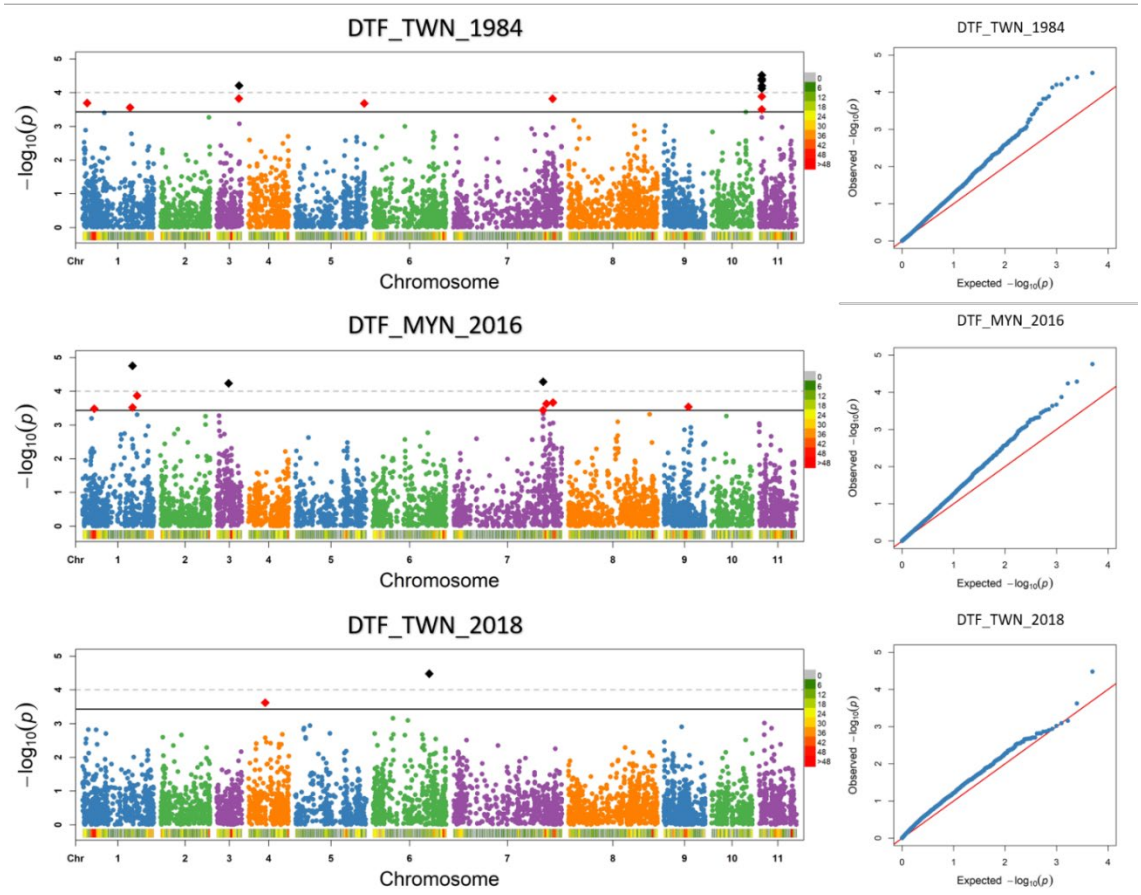


Figure 15. Manhattan plots and q-q- plots depicting the association between the variation of time to 50% flowering in three environments, Taiwan 1984, Taiwan 2018 and Myanmar 2016.

GWAS for disease resistances produced putative associations. Genotype by Environment (GxE) interaction and the low significance of the associations detected required additional validation of the associations in segregating populations. Populations to map powdery mildew and MYMV resistance have been produced and phenotyping has been initiated in several environments.

7.4 Develop improved mungbean germplasm and elite lines

During the final year of IMIN1, partner organisations conducted meeting of major stakeholders to define the product profile(s) in each country. The stakeholder meetings involved both men and women participants. Seed quality traits (seed size, seed colour, seed lustre) were selected based on the domestic as well as the international market demand. The different market segments (grain and sprout) were also considered. Traits such as tall plant habit and synchronous maturity were selected for ease of manual harvesting (major workload shared by women). The above traits will also aid in the mechanical harvesting of the crop, which will reduce the drudgery of harvesting. In the final IMIN1 workshop, a separate brainstorming session was conducted involving all the partners to review and agree on the product profiles developed and in the selection of parents for developing populations. The project will support partners to review product profiles annually to check that they remain current and appropriate over time. The mungbean product profile of the partner countries is presented in Figure 16.

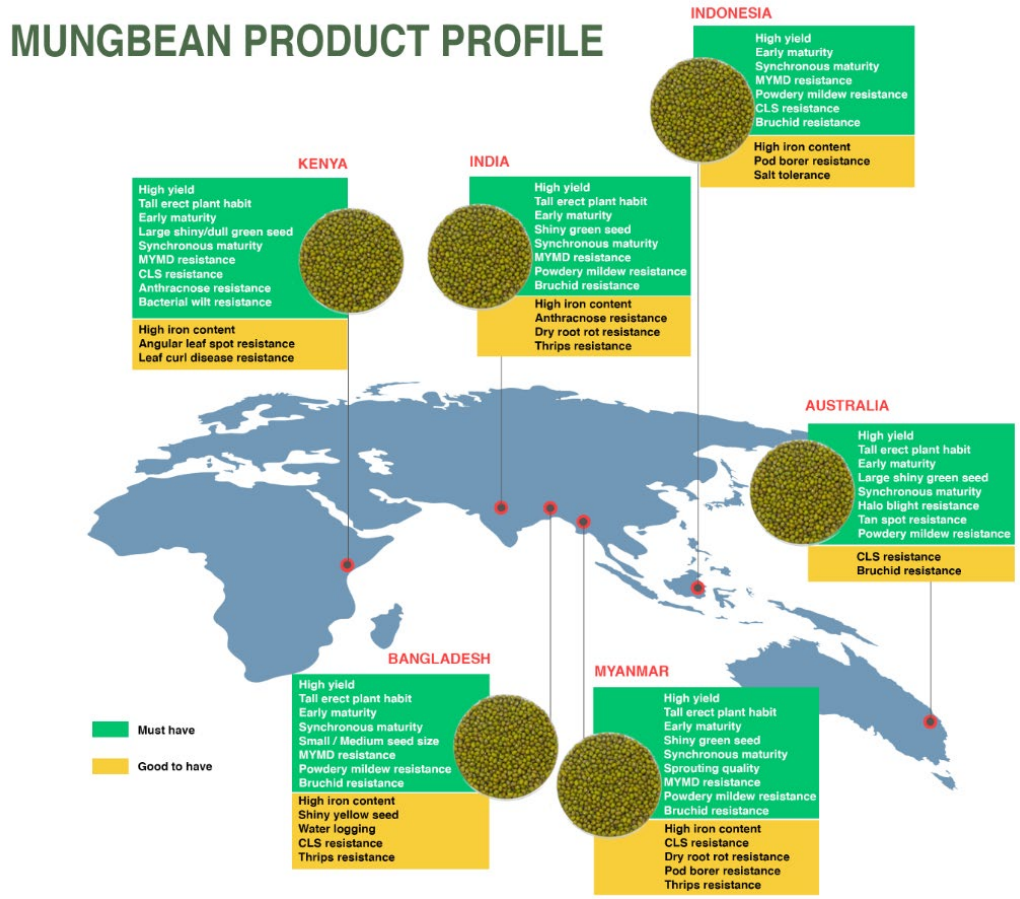


Figure 16. Product profiles for mungbean across production regions

Targeted crosses have been developed for country specific needs. For example, Breeding lines were developed by crossing the best commercial sprouting variety in Myanmar with MYMD resistant donor parents.

Interspecific crosses: Breeding lines were developed by WorldVeg by crossing Australian commercial mungbean varieties (Celera II-AU (VI064210), Crystal (VI064208), Jade-AU (VI064209), Satin II (VI064211) with a multiple bacterial disease resistant black gram (*Vigna mungo*) donor (VO2818) – Figure 17. Confirmation of hybridity of interspecific crosses: We tested 27 SSR markers for polymorphism, after checking 3 SSR markers are available: MB340, MB94, and VR040. Generation advancement of 188 lines is in progress from the above crosses.

Crosses were made between AVMU1647 (early and synchronous maturing Multi-disease resistant breeding line) with *Vigna mungo* sub sp. *sylvestris;* VI031914: VI064738 and VI031415. Twenty F3 lines from these crosses are currently in generation advancement.

Figure 17. Interspecific mungbean cross

VRVM2019-7- (VI064208 x VO2818) confirmed hybrid with SSR markers.

In Australia 17 mungbean accessions from the mini-core collection were used to make 40 new and unique crosses as part of the Australian breeding program. Segregating materials were advanced to the F_3 generation in 2019. This second round of crossing with the accessions from the collection was on the basis of unreplicated observations of adaptation and putative resistance to foliar disease and water logging. In particular, two mini core accessions identified in field trials in 2018 have been used to further extend the mungbean nested association mapping resource; these are VI003699 (putative multiple foliar resistance) and VI002173 (putative waterlogging tolerance). Respectively, 133 and 80 F_2-derived-F_3 F_6 single plant progeny have been produced to date through single seed descent and field increase.

In Australia two successful inter-specific crosses have been between mini core line VI000020 AY and the multiple disease resistant *Vigna mungo* donor V02818 AG with eighty-two of the single cross progeny have been seed increased and will be shared with the network. The Australian National Mungbean Improvement Program (funded and managed by DAF and the Australian Grains R&D Corporation DAF/GRDC) has already begun introgression of this material to elite locally adapted breeding lines. Two hundred and eighteen derived introgression lines were evaluated in the 2020/21 season. These and F_4 single cross interspecific will be available for bacterial and fungal disease screening from 2022 onwards.

Figure 18. F_1 progeny of single cross inter-specific MAUS17-020 (V02818 AG x VI000020 AY)

7.4.1 Evaluation of mungbean Advanced Breeding Lines in Asia

Around 90 advanced breeding lines with location-specific checks were evaluated across different sites in IMIN partner countries in Asia from 2016 to 2021. A total of 26 trials were conducted with 11 to 90 advanced breeding lines for their evaluation for yield and agronomic traits and/or for resistance to disease and pest infestation (Table 23). The field evaluation was done in Randomized Complete Block Design (RCBD) with two-three replications. The data were recorded on major agronomic, yield, and disease/pest resistance traits under natural field conditions across the sites. Based on initial testing, seven advanced breeding lines were selected and tested further across the location in Myanmar. The advanced breeding line, AVMU 1659 (449 kg/ha) recorded superior over best check Yezin 11 (403 kg/ha). However, three advanced breeding *viz.,* AVMU 1642 (367 kg/ha), AVMU 1645 (400 kg/ha), AVMU 1659 (450 kg/ha) recorded superior for seed yield per ha over Yezin 14 (320 kg/ha). The biplot analysis for seed yield per ha and days to maturity is presented in Figures 23 & 24 (See Appendix). Two principal components of scattered biplot explained 85.28% (PC1- 62.42%, PC2- 22.86%) of total variation due to genotype and genotype × environment interaction for seed yield per plant. In this biplot analysis, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the polygon. The genotype AVMU 1631, AVMU 1632, Yezin 9 AVMU 1642 and Yezin 14 are farthest from the origin of biplot, which indicates that these genotypes are either superior or poor performer in some or all the environments for seed yield per plant (Figure 33). The ABLs AVMU 1645, and AVMU 1659 along with check variety Yezin 11 and Yezin 14 were reported with highest mean seed yield per plant (plotted on right side of the biplot) and least distance from the average environment axis indicates their stable performance across locations for seed yield per plant (Figure 33). Two principal components of scattered biplot explained 86.94% (PC1- 59.96%, PC2- 26.98%) of total variation due to genotype and genotype × environment interaction for days to maturity. In this biplot analysis, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the polygon. The genotype Yezin 11, AVMU 1642, AVMU 1643, Yezin 9, AVMU 1657 and AVMU 1632 are farthest from the origin of biplot indicates that these genotypes are either superior or poor performer in some or all the environments for seed yield per plant (Figure 34). The ABLs AVMU 1642 and AVMU 1643 plotted farthest left side of the biplot indicates lower mean for

days to maturity with greater length from AEA indicates higher GEI of these two genotypes for maturity across locations (Figure 34).

In India, two advanced breeding lines i.e. AVMU 1683 (IIPM 20-1) and AVMU 1690 (IIPM 20-2) were proposed for national-level testing in All India Coordinated Research Project (AICRP) trials. Based on their superior performance for seed yield per ha over checks in Initial Varietal Trial (IVT), these two entries are promoted to Advanced Varietal Trials (AVT) which are under progress. The performance of these two advanced breeding lines during IVT is presented in Table 24.

Table 23. Details of trials conducted with mungbean advanced breeding lines evaluated across locations during 2016-21

S. No	Country	Site	Year	Season	Trial Type	Lines#
1	Myanmar	Yezin	2020	Monsoon	ABLs Evaluation	11
2	Myanmar	Magway	2020	Monsoon	ABLs Evaluation	11
3	Myanmar	Latpadan	2020	Monsoon	ABLs Evaluation	11
4	Myanmar	Hmawbi	2020	Monsoon	ABLs Evaluation	11
5	Myanmar	Thonekhwa	2020	Monsoon	ABLs Evaluation	11
6	Myanmar	Yezin	2021	Monsoon	ABLs Evaluation	26
7	Myanmar	Yezin	2021	Pre-Monsoon	ABLs Evaluation	26
8	Bangladesh	Gazipur	2018	*Kharif_1*	ABLs Evaluation	59
9	Bangladesh	Gazipur	2017	*Kharif_1*	ABLs Evaluation	59
10	Bangladesh	Madaripur	2020	*Kharif_1*	ABLs Evaluation	38
11	Bangladesh	Gazipur	2021	*Kharif_1*	ABLs Evaluation	52
12	Bangladesh	Rangpur	2021	*Kharif_1*	ABLs Evaluation	52
13	Bangladesh	Madaripur	2021	*Kharif_1*	ABLs Evaluation	52
14	Bangladesh	Gazipur	2021	*Kharif_1*	ABLs Evaluation	48
15	Bangladesh	Rangpur	2021	*Kharif_1*	ABLs Evaluation	48
16	Bangladesh	Madaripur	2021	*Kharif_1*	ABLs Evaluation	48
17	India	Kanpur	2018	*Kharif*	ABLs Evaluation	90
18	India	Kanpur	2021	Summer	ABLs Evaluation	90
19	India	Hyderabad	2016	Post-Rainy	ABLs Screening for Powdery Mildew	42
20	India	Hyderabad	2017	Rainy	ABLs Evaluation	90
21	India	Hyderabad	2017	Post-rainy	ABLs Evaluation	90
22	India	Hyderabad	2017	Post-rainy	ABLs Screening against Aphid Infestation	87
23	India	Hyderabad	2019	Spring	ABLs Screening against Thrips Infestation	87
24	India	Hyderabad	2019	laboratory	ABLs Screening against Bruchids Infestation	42
25	India	Hyderabad	2021	Spring	ABLs Screening against Thrips Infestation	72
26	India	Hyderabad	2021	Spring	ABLs Screening against Thrips Infestation	72

Table 24. Performance of two advanced breeding lines for seed yield per ha (kg) in Initial Varietal Trials in North Eastern Plain Zone (NEPZ) under AICRP trials in India

Crop: Mungbean			Locations						
S.No.	**Varieties**	**Code No.**	**Ayodhya**	**Ranchi**	**Shillongani**	**Mohanpur**	**CSA Kanpur**	**Varanasi**	**Mean**
1.	Pant M 4 (Ch)	KM 20-96	1292	1069	1372	713	1222	208	1112
2.	IIPM 20-2	KM 20-101	1319	1041	1229	1541	1433	532	1283
3.	IPM 2-3 (Ch)	KM 20-103	986	937	924	1123	1250	776	993
4.	Varsha (Ch)	KM 20-115	1146	986	1389	890	1089	521	1103
5.	IIPM 20-1	KM 20-118	1165	876	1483	1323	897	602	1211
	CV %		7.27	9.43	7.27	12.02	2.52	23.25	
	CD at 5%		134.96	153.81	142.91	181.51	46.97	189.29	
	Grand mean		1142	996	1203	925	1141	498	
	State Av. Yield		335	793	535	848	335	335	

7.4.2 Evaluation of mungbean Advanced Breeding Lines in Africa

A set of 63 unique advanced breeding lines (AVMU) of mungbean developed at the World Vegetable Center, Taiwan was shared with NARS (National Agriculture Research System) partners across eight African countries that includes Tanzania (57 lines), Kenya (52 lines), Uganda (54 lines), Côte d'Ivoire (15 lines), Ghana (15 lines), Nigeria (15 lines), Benin (15 lines) and Burkina Faso (15 lines) for evaluation during 2018 and 2019. The ABLs were shared and evaluated with a major objective to strengthen NARS breeding programs with improved genotypes and to identify the promising lines with better agronomic and yield performance along with higher diseases/pest resistance and nutritional quality compared to local varieties that could be released in the region for commercial cultivation.

Kenya: A set of 60 lines that includes 52 ABLs and eight local check cultivars were evaluated across three locations *i.e.,* KampiMawe, Katumani, and Ithookwe in Kenya during 2018 & 2019. The combined analysis across locations for days to maturity revealed that the ABLs AVMU 1633, AVMU 1643, AVMU 1635, AVMU 1692, AVMU 1641, AVMU 1625, AVMU 1626, AVMU 1602, and AVMU 1630 matured earlier (≤73 days) compared to local check NDENGU TOSHA (76 days) and KAT N26 (86 days). The ABLs AVMU 1608 (13.05 g/plant) followed by AVMU 1612 (10.46 g/plant) and AVMU 1631 (10.03 g/plant) recorded superior for seed yield per plant compared to NDENGU TOSHA (9.52 g/plant) and BIASHARA (8.13 g/plant). The biplot analysis for seed yield per plant is presented in Figure 35; see Appendix). Promising entries with stable performance across locations will be proposed for national-level yield testing to identify potential lines for release in the country. Two principal components of scattered biplot explained 77.26% (PC1- 54.72%, PC2- 22.54%) of total variation due to genotype and genotype × environment interaction for seed yield per plant. In this biplot analysis, a polygon was formed by connecting the vertex genotypes with straight lines and the

rest of the genotypes placed within the polygon. The genotype 8 (AVMU 1608), 55 (KAT N26), 20 (AVMU 1620), 19 (AVMU 1619), 51 (AVMU 1692), 37 (AVMU 1639), 12 (AVMU 1612), and 8 (AVMU 1608), are farthest from the origin of biplot indicates that these genotypes are either superior or poor performer in some or all the environments for seed yield per plant (Figure 35). The ABLs 1 (AVMU 1601), 15 (AVMU 1615) and 14 (AVMU 1614), along with check 53 (BIASHARA) were reported with highest mean seed yield per plant (plotted on right side of the biplot) and least distance from the average environment axis indicates their stable performance across locations for seed yield per plant (Figure 35).

Tanzania: A set of 57 lines and three local checks were evaluated at Tanzania Agriculture Research Institute (TARI), Selian, Arusha and World Vegetable Center, Eastern and Southern Africa Regional headquarters, Duluti, Arusha, Tanzania using alpha lattice design (12 × 5) with three replications during 2018. Based on the performance at both the locations, 10 superior lines (AVMU 1601, AVMU 1608, AVMU 1624, AVMU 1625, AVMU 1628, AVMU 1640, AVMU 1653, AVVMU 1691, AVMU 1692, and AVMU 1693) were selected and evaluated along with two local checks *i.e.* Nuru and Imara using randomized complete block design with three replications. Based on combined analysis across two locations in 2019, four ABLs i.e. AVMUs 1625 (13.22 g/plant), 1692 (11.00 g/plant), 1693 (10.78 g/plant) and 1624 (9.65 g/plant) recorded superior seed yield per plant over a local variety (8.1 g/plant) and Nuru (7.71 g/plant). These lines were at par with the local variety for maturity duration. These four lines along with AVMU 1601 were proposed for evaluation across different agro-ecological zones for two more seasons at TARI Ukiriguru center in Mwanza regions, (Misungwi and Magu), TARI Ilonga in Morogoro region, TARI Selian Center in the Arusha region where trials were conducted at WorldVeg, at Tengeru and at Miwaleni in Kilimanjaro region. Two genotypes *viz.,* AVMU 1601 and AVMU 1693 were identified as superior over check varieties Nuru and a local cultivar across the tested regions and were preferred by the farmers during farmer's participatory varietal selection (FPVS). Therefore, these two varieties were proposed for national performance trials for further release by TOSCI upon meeting the required standard as per the seed act and its regulations. The GGE biplot analysis of seed yield per plant is present in Figure 36; see Appendix). The environment centred biplot reported advanced breeding lines 10 (AVMU 1693) with highest mean seed yield per plant (plotted on right side of the biplot) and stable performance across both the locations (Figure 36).

Uganda: Fifty-four advanced breeding lines of mungbean were evaluated at two locations i.e. Serere and Arua districts of Uganda during the second season of 2018 (2018B). In 2019, six additional entries were included and the second-year evaluation was conducted across five different locations *viz.,* Serere, Lira, Kitgum, Mayuge, and Arua. The data on agronomic and morphological traits and response to diseases such as Mungbean Yellow Mosaic Disease, Powderly Mildew, Halo Blight, Cercospora Leaf Spot, and Anthracnose were recorded from all trial sites. The combined analysis across sites revealed that all the ABLs matured in ≤65 days in Uganda. The advanced breeding lines i.e. AVMUs 1610, 1627, 1612, 1620, 1631, 1607, and 1608 recorded higher yield (≥8.4 g/plant) across locations. The biplot analysis seed yield per ha is presented in Figure 37; see Appendix). Promising entries with stable performance across locations will be proposed for national-level yield testing to further identify potential lines for releases in the country for commercial cultivation. Two principal components

of scattered biplot explained 58.87% (PC1- 46.00%, PC2- 12.87%) of total variation due to genotype and genotype × environment interaction for seed yield per plant. In this biplot analysis, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the polygon. The genotype 17 (AVMU1617), 54 (AVMU1693), 12 (AVMU1612), 10 (AVMU1610), 59 (NAROGRAM1), 38 (AVMU1638), and 53 (AVMU1692), are farthest from the origin of biplot indicates that these genotypes are either superior or poor performer in some or all the environments for seed yield per plant (Figure 37). The ABLs 10 (AVMU1610), 11 (AVMU1611), 3 (AVMU1603), 13 (AVMU1613), and 4 (AVMU1604) along with check variety 56 (KAT00308) were reported with highest mean seed yield per plant (plotted on right side of the biplot) and least distance from the average environment axis indicates their stable performance across locations for seed yield per plant (Figure 37).

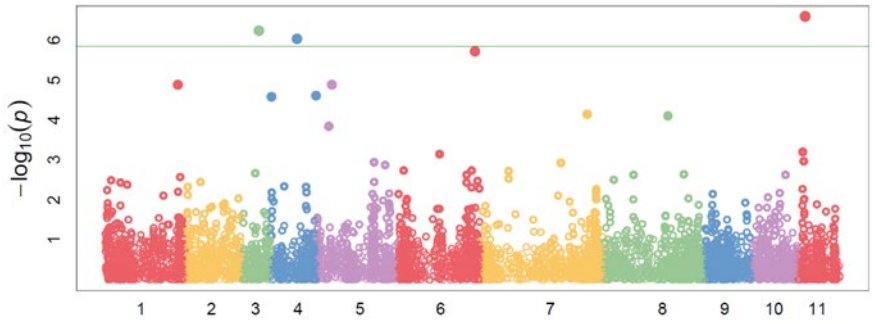
8 Impacts

8.1 Scientific impacts – now and in 5 years

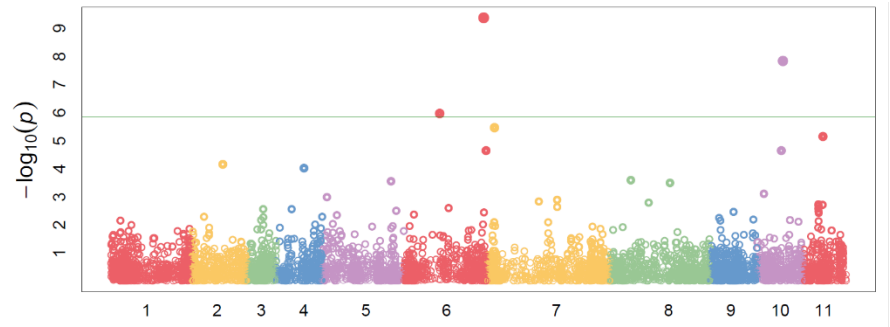
8.1.1 GWAS – Marker-trait associations

The current information generated through GWAS is limited. Some associations with high heritability traits were obtained, other traits such as time to flowering showed strong genotype by environment (GxE) effect, consequently different markers are associated with flowering time variation at different locations. Associations for disease resistances also varied across regions, for example, loci associated with powdery mildew resistance (Figure 19). This is not surprising, as different strains of the pathogen may interact with different host genes and different climatic conditions may elicit different responses to powdery mildew infection in the host. Nevertheless, these results need further validation. For other resistance genes, the obtained associations were around the significance threshold, which is due to the small population size and low frequency of the resistance allele in the population. Development of segregating populations and testing the response of their offspring at multiple locations will provide validation for responses under high GxE and will help overcoming the problem of low significance for several disease resistance loci. These efforts will facilitate the development of marker-assisted selection methods for mungbean breeding.

Re-analysis of the raw reads of the genotyping by sequencing together with sequencing reads obtained from other biodiverse mungbean materials by mapping the reads to multiple reference sequences that became available recently will improve the SNP set available for mungbean.



a)



b)

Figure 19. Manhattan plot of GWAS on powdery mildew resistance. a) Shanhua, Tainan, b) Hyderabad, India, average over 2 seasons

The phenotypic and genotypic data produced by the project, together with available climate data open the path towards modeling variation of traits in different climate scenarios. Time to 50% flowering has been used as trait to pilot such analysis. Times to flowering is of particular interest, as it partly controls earlyness of the crop, which is an important trait for fitting mungbean as a rotation crop in the often very short interval between two main crops. A new mathematical model was developed that described the dynamic control of time to flowering in mungbean by daily values of maximal and minimal temperature, precipitation, day length and solar radiation. The models were cross-validated and demonstrated that the phenology of adaptive traits, like flowering time, is strongly predicted not only by local environmental factors but also by plant geographic origin and genotype. The model has been deleloped further, and models were constructed using approximate Bayesian computation highlighting genetic factors regulating flowering time.

The pilot experiment using crop models to predict changes in flowering time under different temperature regimes indicates that based on the phenotype and genotype data collected by the project, phenotype prediction for specific climates is becoming possible.

8.1.2 Physiology – empowering future gains in mungbean productivity and resilience

Analysis of agronomic, phenological, biomass and pod dissection of mungbean physiology carried out by DAF has started to reveal the inter-relationships between phenology, plant architecture, yield components and that these differ markedly between small-seeded, large-seeded mungbean and black gram. PCA plot shown in Figure 20 below represents genotypes as data points and traits as vectors. Genotypes are colour coded into groupings of phenology and grain size.

In this single experiment under optimal rainfed conditions crop duration strongly influenced grain yield. Greater genetic diversity in small-seeded genotypes is represented in both early and late maturity. In terms of plant architecture small-seeded and in particular black gram genotypes had an alternative yield strategy with more fruiting sites per plant than large-seeded genotypes . In mungbean pod length was very strongly associated with grain size and grain number per pod. Black gram such as the legacy Australian variety Regur is very much the outgroup in these regards; its indeterminate nature produces many flowering sites from close to the ground and sets fewer pods at each of these sites. These finding have implications for future mungbean improvement and in particular recovering high yielding progeny when making crosses between large and small seeded mungbean germplasm groups and inter-specific crosses. This experiment informed the need for a greater focus on understanding mungbean physiology that will be undertaken at World Vegetable Center and University of Queensland in IMIN2.

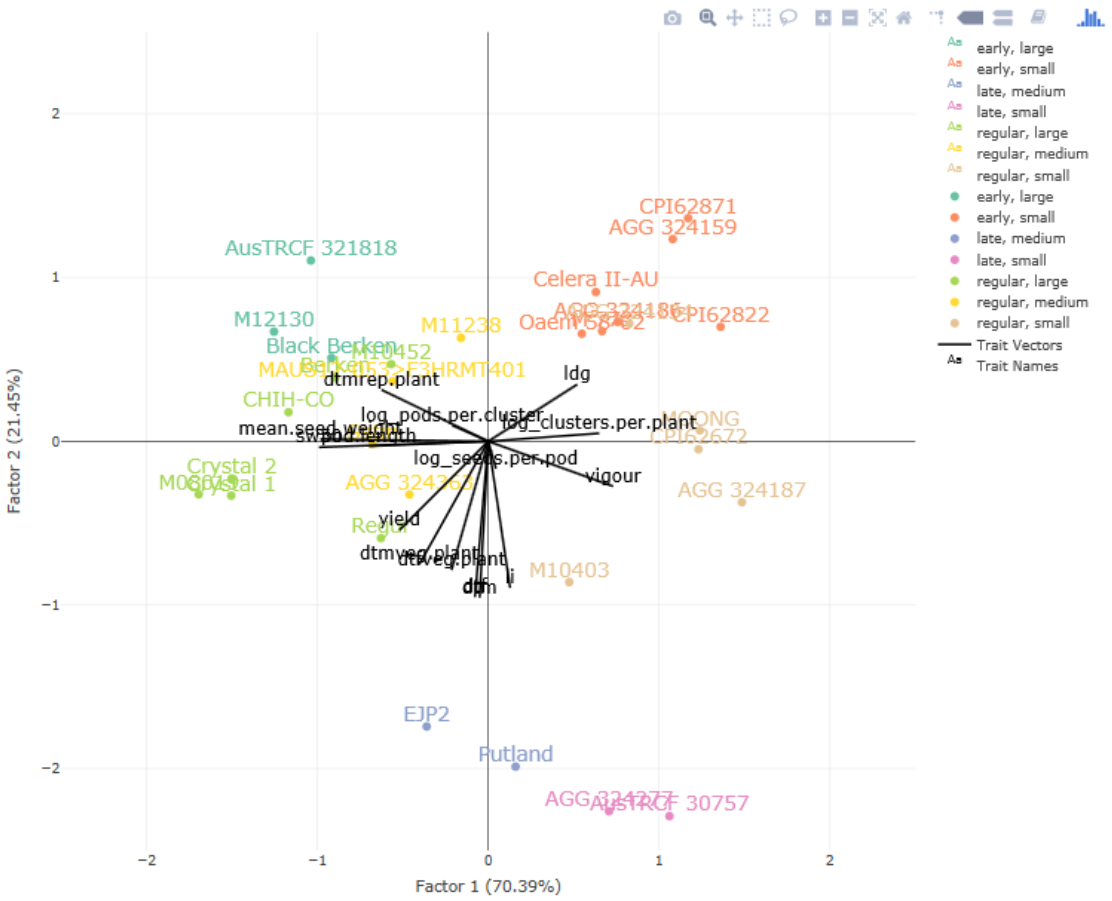


Figure 20. Factor Analysis representing genotypes and traits in mungbean and black gram (key to trait abbreviations dtf – days to flowering, dtm – days to marurity, ldg – lodging)

8.1.3 Mungbean Nested Association Mapping (NAM) populations, a resource for trait dissection and genomics in mungbean

The mungbean NAM populations were developed under a Queensland Government investment with the Queensland University of Technology. The NAM consists of 2060 genotypes with the recurrent parent 'Crystal' and 26 cultivated mungbean donors (single cross F_2 derived populations) and four wild Australian *Vigna radiata* var. *sublobata* donors (single backcross populations). Development of fixed lines and genotyping with DArTseq markers was carried out prior to 2016. Screening and preliminary genomic analysis conducted with the DAF/GRDC National Mungbean Improvement Program has revealed a putative QTL marker for halo blight (halo blight scores hb or 15 families are shown on Figure 21 and the allele effect in Table 25).

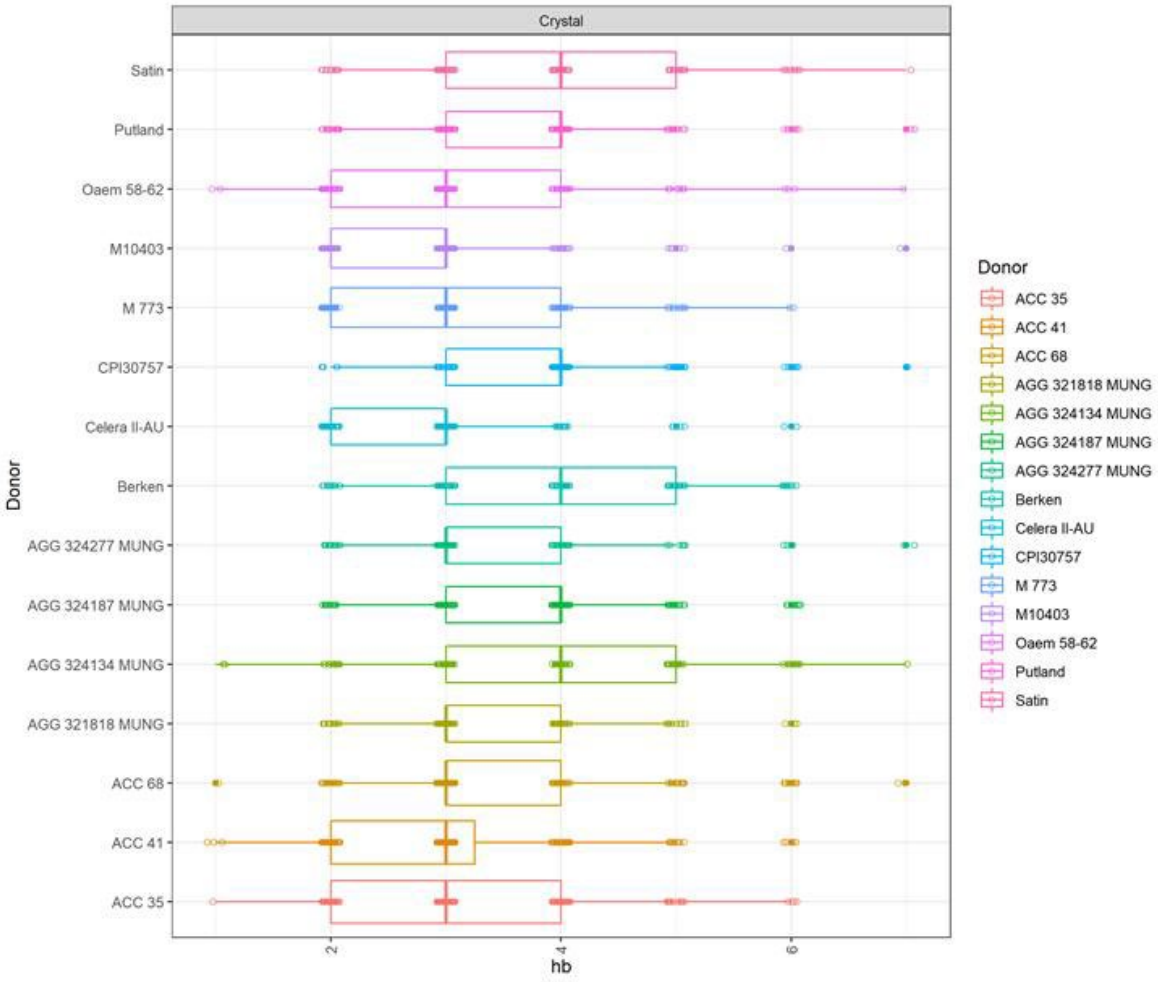


Figure 21. Raw halo blight disease scores for fifteen families in the mungbean NAM. Disease scored 1-9 where 1- no disease and 9 = dead plants. The recurrent parent Crystal had a score of 4

Table 25. Allele effects and probabilities for halo blight resistance in the mungbean NAM

Genotype	Allele effect	Allele probability
AGG 324187 MUNG	0.181	0.148
ACC 41	-0.177	0.066
ACC 35	-0.016	0.451
CPI30757	0.252	0.073
AGG 321818 MUNG	-0.036	0.418
AGG 324277 MUNG	-0.005	0.487
Berken	0.212	0.111
Celera II-AU	-0.238	0.086

Crystal	0.09	0.196
M 773	-0.155	0.183
M10403	-0.238	0.065
Oaem 58-62	-0.13	0.228
Putland	0.26	0.056

Green shading represents alleles effects contributing to resistance, yellow and orange shading represents allele effects contributing to susceptibility

8.2 Capacity impacts – now and in 5 years

All partners in the network have commenced collection of data using the KDSmart application. The KDManage database had been populated with pedigree of the recently shared advanced lines. It is expected that this systematic collection and storage of data will become a routine activity of the breeding programs and this would lead to sharing of data among the partners.

IMIN1 has trained young researchers in breeding and pathogen detection, and has raised awareness of the opportunities provided by genomics assisted breeding.

IMIN1 supported the partners in building facilities for improving the efficiency of the breeding programs. In Myanmar, a glasshouse facility (50m2) was built within the Yezin campus of DAR for raising of plants under controlled conditions. This facility will allow breeders to conduct artificial hybridisation. A net house facility (18.94 m x 6.83 m) was installed at the IIPR campus in Dharwad to enable artificial hybridisation as well as seed multiplication with protection from insect vectors.

8.3 Community impacts – now and in 5 years

8.3.1 Economic impacts

Economic impacts are not expected in the time of the project. The impact pathway is based on adoption by farmers of improved varieties. This would result in economic benefits: increased production, increased productivity, reduced costs and increased profitability.

Development of Android based application for Farmers in India: Mung Advisor

Keeping in view the soaring numbers of farmers using smartphones in India in recent times, a need and justification was felt for providing an ICT based platform to them which could act as a one-stop solution to all their queries related to mungbean cultivation. Thus, the ICAR-Indian Institute of Pulses Research, Kanpur developed an interactive application tool, “Mung Advisor” which is now available on android smartphones through Google playstore https://play.google.com/store/apps/details?id=com.mungadvisor&hl=en). This app is currently bilingual in English and Hindi and downloadable free of cost. Mungbean is grown in three seasons across India viz., Spring/Summer, *Kharif* (Monsoon season) and rabi (winters)/rice fallow (Figure 22). This app covers all the three seasons and provides region- and season-specific information on improved varieties, cultural practices, insect-pest and disease management, post-harvest technology, marketing, etc. in mungbean. An automatic seed calculator is an integral part of the app which calculates the seed required per given area to obtain optimum plant stand. The app also provides information on plant architecture,

weather advisories, latest statistics and nutritional profile of mungbean besides having a dedicated section on mungbean recipes. The section on 'FAQs' provides answers to all commonly asked questions which may occur to a farmer's mind. Further, the farmers can also ask questions on the problems faced by them in real situation in mungbean cultivation and they can also use it as a diagnostic tool and upload their concerns in the form of text and pictures which will be answered by experts on the real-time basis. Supported by ACIAR through International Mungbean Improvement Network (IMIN), such an app is also being developed for other partner countries.

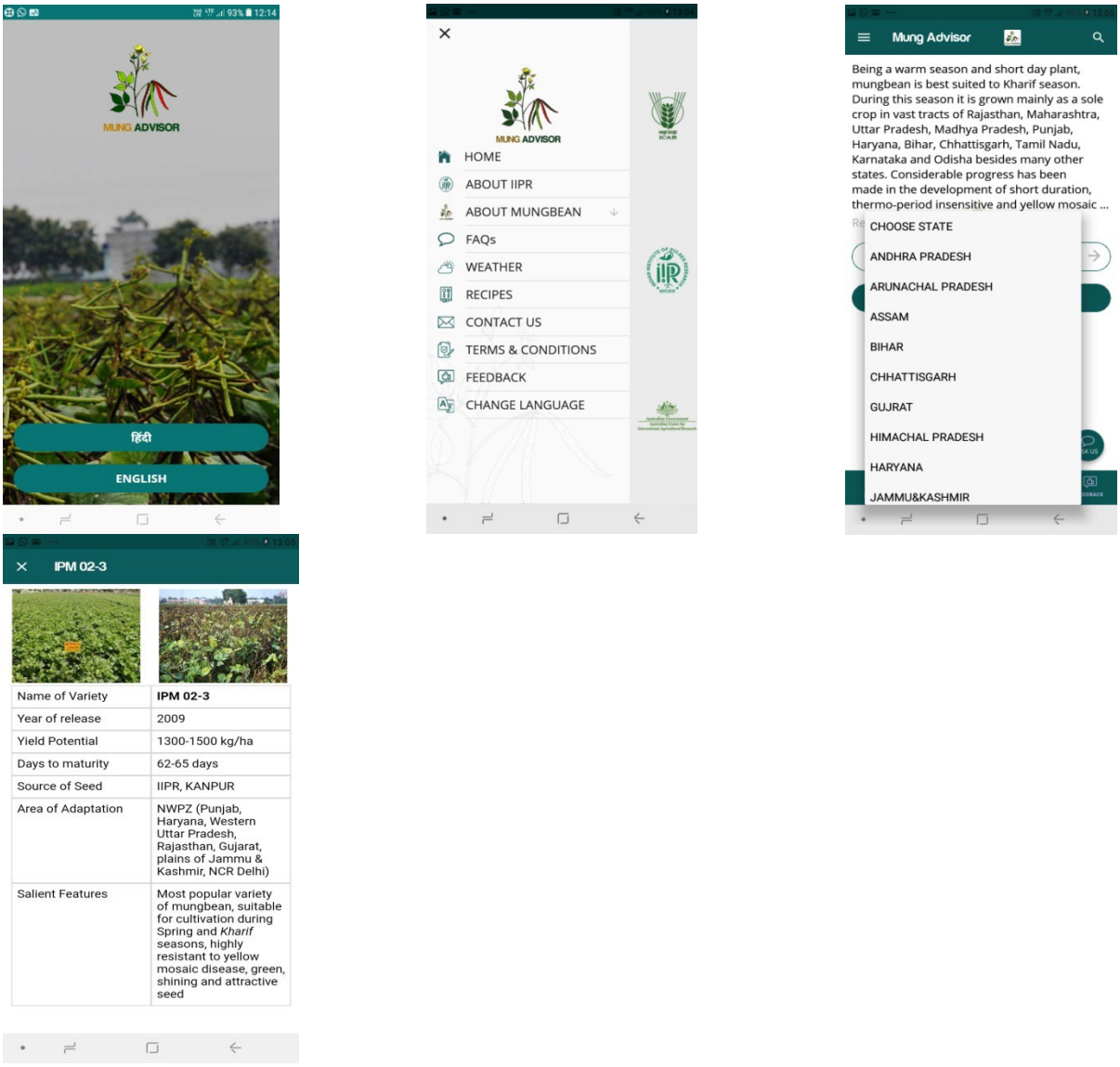


Figure 22. Android based application for Farmers in India: Mung Advisor

8.3.2 Social impacts

Social impacts are not expected in the time of the project. The impact pathway is based on the adoption by farmers of improved varieties, providing a range of social impacts. Mungbean with resistance to disease reduces farmer's risks and incentivise their investment in the crop. Mungbean with higher yield can increase productivity and profitability. Increased availability of

mungbean, with higher nutritional value, can contribute to improved nutrition, when the crop is used by those in need.

8.3.3 Environmental impacts

Not expected in the time of the project. The impact pathway is based on improved mungbean as a component of diversified cereal-based systems in many regions, with the corresponding potential benefits on disease management (rotation and break crop) and soil quality (N fixation). In Myanmar mungbean can be a sole cash crop so the system's diversification benefits would be less compelling. Variation in grain yield, fodder quality and animal intake observed in mungbean lines (Nair et al., 2021) is promising in the usefulness of the crop as a dual purpose one.

8.4 Communication and dissemination activities

The Network is in regular communication through fortnightly zoom meetings as well as emails involving all of the partners. A WhatsApp group has been created to disseminate quick messages. The "Mung Central" newsletter has been launched with eight editions disseminated to date. New stories are being contributed by the Network regularly.

The Mungbean Stakeholders Workshop was held at the ICAR-Indian Institute of Pulses Research, Kanpur from 10th – 11th February 2019. Fifty stakeholders attended the workshop which consisted of progressive mungbean farmers, representatives from Dal Millers Association, leading industrialists dealing with pulse products, equipment manufacturers and renowned mungbean researchers from India.

The number of farmers using smartphones in India is soaring. It is evident that there was a need for information and communication technology (ICT) based platform for farmers, which could act as a one-stop solution to all their queries related to mungbean cultivation. The ICAR-Indian Institute of Pulses Research, Kanpur, developed an interactive bilingual application tool, "Mung Advisor" which is now available on Android smartphones through Google play store, described in section 8.3.1 above. Mung Advisor was launched by the Hon'ble Vice-President of India, Shri M Venkaiah Naidu on 19 May, 2019 during the 24th Annual Group Meet of All India Coordinated Research Project on Mungbean, Urdbean and Arid Legumes held at Acharya NG Ranga Agricultural University (ANGRAU), Lam, Guntur, Andhra Pradesh, India, and was aired on a number of national electronic and print media. Supported by the ACIAR through International Mungbean Improvement Network (IMIN), this app will soon be upgraded to cover all the IMIN partner countries and be multi-lingual for each region.

As part of ACIAR-IMIN project, a workshop was held in Yangon, Myanmar on 7-8 February 2019, organized by Department of Agricultural Research (DAR), Myanmar. Participants in the workshop included representatives from DAR, Yezin Agricultural University (YAU), Myanmar Pulses, Beans & Sesame Merchants Association, Myanmar Awba Group, ICCO and farmers from Yangon region.

12 August 2020 - Virtual meeting - Release of book - Nair, RM, Schafleitner R, Lee S-H. (Eds.), The Mungbean Genome. Springer International Publishing, Cham, by Dr. Eric Huttner, Research Program Manager, Crops, ACIAR.

12 October 2020 - "The Billion-dollar Bean" gave top billing to mungbean during a World Food Prize side event webinar.

9 Conclusions and recommendations

9.1 Conclusions

Declining crop yields, increased agricultural risks, diminishing soil fertility and environmental degradation are some of the main challenges which continue to threaten societal goals of improving food, income and nutrition security especially in smallholder farming. Sustainable intensification is a viable climate smart agriculture practice that significantly enhances system productivity and consequently resilience in rural smallholder farming systems (Makate et al., 2016).

There is large demand for options for sustainable intensification of tropical cropping systems of Africa, South Asia and Australia. As a short duration legume crop, mungbean has already demonstrated great value as the best warm-season rotation crop that fits between the major crops of wheat, rice, sorghum and sugarcane. The further global potential for development of mungbean is demonstrated in Australia: Supported by improved varieties, best management practice and increasing global demand for pulses, it has transitioned from an opportunity crop to a central part of dryland tropical farming enterprises. Continued, coordinated research and breeding is required for paradigm change of mungbean on a global scale and it is necessary to address current and emerging constraints for sustainable and profitable mungbean cultivation.

The International Mungbean Improvement Network (ACIAR project CIM-2014-079, 'IMIN1') has addressed the needs of the estimated 10 million smallholder farmers growing mungbean on 7 million ha in Asia and Africa through the supply of improved varieties. The project has increased the efficacy of mungbean breeding programs in three partner countries (Bangladesh, Myanmar and India) by providing new germplasm for multi-location evaluation and sourcing favourable traits for breeding, building the capacity of plant breeders and deploying modern breeding methods supported by IT tools for data capture, sharing and analysis. Elite breeding lines developed during IMIN1 are at early stages of testing for variety release. In the final year of IMIN1, the project has also engaged with mungbean breeding programs in Kenya, Uganda and Tanzania.

The partner countries are committed to improving mungbean production. India has prioritised pulses in directing its research resources and is becoming a key technology partner in this regional project. In Bangladesh, needs for sustainable cropping system intensification require continuous supply of improved pulse crops. Short duration mungbean is ideally suited to the narrow window between two rice crops or between a dry season crop and the monsoon rice, as shown by several ACIAR projects (CIM-2014-076, CSE-2011-077, etc.). In Myanmar, mungbean improvement is fully aligned with the government focus on growing export crops and the country's mungbean breeding program offers the best opportunity for rapid progress in this value chain. In Indonesia, a partner in follow-on project IMIN2, mungbean is an important cash crop and has potential to be developed in marginal areas, especially in areas with limited water. Indonesia's mungbean production area reduced from about 300,000 ha in 2008 to about 250,000 ha in 2017 because of low yields and high production costs (Sequeros et al., 2021). The mungbean breeding program aims for high productivity, early maturity, synchronous maturity, and resistance to major pests and diseases in both small and large seed types. The main production constraints include lack of access to good quality seed of improved varieties as well as low-intensive cultivation methods. In East Africa, Kenya, another partner in IMIN2, has the largest area (about 300,000 ha) under mungbean, either as a mono crop, in rotation or as an intercrop with maize, sorghum and other legumes. Despite increased mungbean area and production, Kenya is not able to meet its growing domestic demand. Climate change resulting in erratic rainy season patterns necessitates determinate, early-

maturing varieties (Karimi et al. 2019). New varieties must have high and stable yields, resistance to major pests and diseases and possess farmer-desired agronomic traits, including synchronous maturity.

In **Australia**, the project has demonstrated that current mungbean genetic and genomic resources contribute to a better understanding of the physiological architecture of grain yield and the exploiting of genotype x environment x management interactions. The DAF/GRDC/IMIN2's focus on physiology, or 'how mungbeans work' and on bacterial diseases will contribute significantly to delivering improved productivity, reliability and resilience of mungbean through developing and releasing varieties with superior yield, multiple disease resistance and large green shiny grain for export markets. Genomics, breeding tools, new adaptive traits and international breeding efforts in IMIN are an essential part of a dynamic and efficient Australian mungbean breeding program. The outcomes of the IMIN2 are aligned to the Queensland Government Priority "Create jobs in a strong economy: grow rural exports and add value to primary production…".

Research opportunities: IMIN1 showed that bacterial diseases are the most significant upcoming biotic stresses affecting mungbean. They are reported as prevalent in Africa and should be considered as future risks in Asia (Nair et al*.,* 2019). Halo blight and tan spot are seed-transmitted diseases. Planting infected seed results in widespread distribution of the disease within the crop and an increased number of initial infection sites from which the disease can spread. Both bacterial diseases have no means of control once established in-crop and can account for crop losses over 30%; bacterial diseases have already had a major impact on industry confidence and future growth of mungbean production in Australia and worldwide. Developing resistant varieties therefore should be a priority not only in Australia but globally. Australia's National Mungbean Improvement Program (NMIP) is deploying major gene resistance in the next suite of Australian variety releases, but a strategic approach to resistance is required and could be extended to impact throughout the network. IMIN2 proposes to address bacterial diseases through collaboration with international pulse pathologists, breeders and industry. An understanding is required of pathogen diversity and virulence. The multi-partner network proposed will be ideal for screening genetic diversity and recombinant (Nested Association Mapping; NAM) populations using field and high-throughput phenotyping of germplasm and breeding lines to identify the multiple sources of major and minor genes required to breed varieties with durable resistance.

The Australian project team will bring on a new partner for IMIN2. Researchers from the University of Queensland will collaborate with the project partners to dissect the physiological and genetic basis of flowering behaviour and canopy development by studying the NAM populations in field phenotyping experiments in Australia and Myanmar, and Phenospex platform in Taiwan. Novel breeding approaches will be applied to enable rapid stacking of multiple traits with the objective of designing new high yielding mungbean germplasm with determinate synchronous flowering.
In IMIN2 the Australian project team will explore a collaboration with the North American pulse industry. Dry beans are sown to 800,000 hectares in the USA, in particular *Phaseolus vulgaris* production in the mid-west is constrained by four seed-borne bacterial diseases including halo blight (*Pseudomonas savastanoi*), bacterial wilt (tan spot, *Curtobacterium flaccumfaciens*) and bacterial blight (*Pseudomonas syringae*). Research and industry collaboration would provide vital bacteriology experience and breeding strategies to develop resistant mungbean cultivars for the Network as well as model seed production systems and for the development of integrated disease management practices.

Germplasm exchange and breeding modernisation: In its final year IMIN1 completed the export from Australia to the partners of a genetic diversity panel of 466 accessions (Noble et al., 2018) and the 2060 inbred lines of the World's first mungbean Nested Association Mapping (NAM) populations. In combination with the mini-core collection analysed in IMIN1, this is a

powerful and coordinated mungbean resource which has been fully genotyped on the DArTseq platform. Genomic resources generated for mungbean during the last years together with a large volume of phenotypic data and capacity building performed during the 1st phase of IMIN have paved the path for modern mungbean breeding. Genomics-assisted breeding has already accelerated the introgression of bruchid resistance (War et al*.,* 2017) into elite lines and is likely to achieve the same effect with disease and pest resistances identified in the mini core collection during IMIN1 (Nair et al*.,* 2019). More complex disease resistances (Pandey et al*.,* 2020), abiotic stress tolerances (HanumanthaRao et al*.,* 2016) implicating multiple traits and genes and agronomic traits including yield components now are main research targets for improving the mungbean crop. IMIN1 won the Agricultural Greater Good Award 2020 (USD 250k) sponsored by Illumina, which provides 20 tera base pair sequence information to the project, bringing genomics research on mungbean to a completely new level.

9.2 Recommendations

The successful International Mungbean Improvement Network (IMIN1) will be extended to the second phase (IMIN2) and will tackle newly emerging challenges. It will follow a multidisciplinary and farmer-participatory approach to mobilize mungbean biodiversity to deliver improved high yielding, short duration, pest and disease resistant mungbean lines to improve the livelihood of smallholder farmers in mungbean growing regions in Asia and Africa. The crop improvement and evaluation activities, and also partly pre-breeding will predominantly be performed in the target countries, while molecular breeding and genomic and phenomic research will be done mostly in Australia, India and Taiwan, but in tight collaboration with the other national project partners. Training in molecular breeding will be embedded as much as possible in the regional programs, focusing on the productive analysis of data. Complementary funding opportunities will be explored to extend the training activities related to mungbean technologies beyond the scope of this proposal. Abiotic stress tolerance traits required to adapt the crop to new ecosystems and to prepare mungbean for impacts of climate change will be identified in the mini-core and NAM population using state of the art approaches including high throughput automatized phenotyping and pan-genomic analyses.

Genetic and molecular resources mobilised and characterised in IMIN1 will be applied to the identification of key genes and the corresponding markers. Resistance to newly emerging constraints (such as bacterial and fungal diseases as well as insect pests) available in the mungbean mini-core collection will be introgressed into elite varieties. Improved lines carrying resistance to major diseases and pests will be tested in the target regions and scaled to reach farmers as soon as possible. Available integrated pest management strategies will be tested as a second row of defence against pathogens and pests where genetic resistance is not found. Variation of iron content in mungbean grains will be identified and bioavailability from different food matrices will be measured. The project will attempt a natural biofortification of the crop by transferring the high iron traits to elite lines.

9.2.1 Using genetic and genomic resources for mungbean research and breeding

Whole-genome sequencing reads of 150 mini-core accessions and 30 Australian NAM parent lines are available. The Illumina Greater Agricultural Good Award provided the resources for expanding sequencing to the full mini-core collection, newly accessible accessions from central and north Asia, breeding lines and the NAM population parents became available, allowing the production of a pangenome based on short sequencing reads representing at least 500 mungbean materials. The mungbean pan-genome would give insight in gene copy number variations and short indels and rearrangements. Additional high-quality whole genome reference sequences will be produced using Oxford Nanopore long read sequencing

for key lines important for mungbean breeding would provide additional insight into larger genomic rearrangements and would allow to study the effects of structural variation on phenotypes in biodiverse mungbean materials. It is also recommended to include identified *V. mungo* lines for sequencing. *V. mungo* is a potential donor for various traits for mungbean breeding and genomic information on this species would facilitate molecular breeding approaches in interspecific population(s). The gene content of the mini-core accessions NAM parents and breeding lines could be analysed and compared. Associations between sequence and gene copy number polymorphisms, indels and traits of interest (transpiration rate, biomass under drought/heat/control/waterlogging, flower number, flowering time and HI) could be analysed using QTL studies and k-mer mapping (Voichek and Weigel, 2020). Found associations could be validated in the NAM and mini-core collection or in breeding populations. These studies should be a collaboration between the IMIN project team with science partners like the Australian and Taiwanese Universities with expertise in bioinformatics and genomics. The results of these studies such as information on alleles and haplotypes conferring certain traits will be used by breeders and make breeding more effective.

Yield and grain (size, colour and lustre) quality are the most market-sensitive traits for mungbean breeders to address, and both yield and grain size are heavily influenced by the environment. In addition to yield, phenology and harvest index should be chosen as important component traits and phenotyped at the WorldVeg and ICRISAT high throughput phenotyping systems to measure the development of different plant organs including pods over time. High throughput analysis of time to flowering and harvest index among accessions and in segregating populations (NAM population) in two environments will identify interactions between these traits and with the environment, which then are validated in further selected testing environments of IMIN. Multilocation trials in IMIN I and II provide a unique opportunity to investigate gene by environment by management interactions. These data will be used by science partners to parametrize crop models, which will be used by breeders to find materials that are well adapted to new environments. For measuring grain quality criteria, Near Infrared Spectroscopy assays will be developed. Quality traits are of paramount importance particularly for the high premium sprout market segment.

Understanding of key pathogens of mungbean and strategic breeding for genetic resistance requires three aspects i) development of reliable high throughput screening protocols (lab and glasshouse), ii) assessment of mungbean diversity panels and NAM progeny for susceptibility to bacterial diseases, iii) phenotypic disease characterisation and virulence surveillance in mungbean farming regions (local, national or international).

Diseases of mungbean can have significant implications for acceptance and expansion of the crop. In particular, the foliar bacterial diseases of halo blight, caused by *Pseudomonas savastanoi phaseolicola* and tan spot, caused by *Curtobacterium flaccumfaciens flaccumfaciens*, are ubiquitous to many mungbean growing regions. In Australia, yield loss to these diseases can be up 40% when conditions are conducive affecting the reliability of the crop (Noble et al., 2018). There are currently no chemicals registered for management of either disease further discouraging farmers growing the crop. Therefore, if mungbean is to become a stable and reliable crop, genetic resistance to problem diseases is imperative.

The current approach to developing genetic resistance to halo blight and tan spot involves screening for resistance in large-scale field trials. This approach can be (i) inefficient as natural infection is sporadic making reliable selection infrequent (ii) misleading especially when knowledge of pathogen diversity and virulence within the target pathogens are lacking. There are examples in cereals where selection for resistance to one disease shifts the dynamics to favour one or more untargeted disease or pathotype. For example, certain alleles of the Mlo gene are widely used for resistance to powdery mildew in barley. Lines carrying this allele are known to be susceptible to other diseases such as *Ramularia* leaf spot (McGrann et al., 2014; Wolter et al., 1993). Ramularia leaf spot has become a significant barley disease in Europe over the period of Mlo deployment.

9.2.2 Essential steps to tackle diseases of mungbean

1) Conducting annual surveys to understand disease prevalence and epidemiology and identify novel sources virulence in regions where mungbean is grown. This component can take a regional, national or international focus and employ a DNA based methodology to identify bacterial biomass. Fortunately, qPCR primers for major bacterial diseases of mungbean are readily available (e.g. see Cho et al., 2010). The project will enable (i) better understanding of disease prevalence and conditions that promote infection (ii) identify sources of virulence in pathogen population which can then be used to challenge new breeding lines.

2) Comprehensive screening of genotype by pathotype interaction in the glasshouse and field then incorporation of these superior sources of resistance into adapted material. This component will require fine-tuning of inoculation techniques and improving disease-scoring protocols to ensure reliable differentiation in levels of resistance in the host. Fine-tuning of techniques and infection protocols is undergoing. Establishing the relationship between seedling screening in the glasshouse and field responses should also be undertaken. The project will provide a benchmark assessment of current mungbean varieties and breeding lines and identify sources of resistance for future breeding.

3) There is opportunity for improving in-field disease control whether through better agronomy and crop management practices to minimise disease pressure (e.g. planting time, management of crop stubble and crop rotation) or through evaluation of chemicals and modes of action for efficacy against major mungbean diseases. Some success stories exist from old research (see J. D Taylor 1972); little progress towards spray products have been made however.

Exchange of germplasm, leaf & DNA samples and samples of pests & pathogens will be undertaken between the project partners.

Improved germplasm/breeding lines including those derived from inter-specific hybridisation, targeting biotic and abiotic stresses shared with partners in the first phase will be evaluated in multi-environment trials. This includes 320 inbred lines from four interspecific crosses of adapted high yielding Australian varieties to the green-seeded *Vigna mungo* (black gram) accession V02818AG that was identified as a dual resistance donor for bacterial diseases halo blight and tan spot. Crosses made to Australian varieties: Crystal, Jade-AU (large green shiny), Celera II-AU (small green shiny) and Satin II (large green dull) represent key market types for all of the network partner countries. In addition, one hundred inter-specific progenies between this same black gram disease resistance donor V02818AG and mini-core accession VI000020AY were developed in IMIN1 and will be available for disease screening in IMIN2.

A number of important pest and disease resistances were identified during IMIN1 in the mungbean mini-core collection. Some of these resistance genes are already tagged with molecular markers. IMIN2 will introgress these resistances into elite lines by marker-assisted selection (MAS), and validate the resistant phenotype in the selected progenies.

Resistance genes to other important pests and diseases will be mapped by combining phenotypic data continuously obtained in IMIN1 with available and newly generated genomics data for marker-assisted breeding of improved lines. For more complex traits including multigenic disease resistance and nutritional traits pan-genomics tools and k-mer mapping (Voichek and Weigel, 2019) will be applied to elucidate the genetic basis of these traits and prepare their introgression from unadapted materials into elite varieties. In addition, genomic selection will be tested for predicting crop performance, especially for low heritability traits.

New NAM populations will be developed based on parents selected for traits prioritized during the annual meeting of the IMIN1 held during 8-11 September 2019 in Kanpur, India.

Phenotypic data for resistances to viral, bacterial and fungal diseases are available for the mini-core collection and for some improved lines. Available and partly newly generated genotype data will be used to map resistance genes against these diseases at WorldVeg HQ. Priority diseases are MYMD (multiple strains/species), Cercospora leaf spot (CLS), powdery mildew, Anthracnose, dry root rot, bacterial blight, halo blight and tan spot. Associations between markers and resistance traits will be validated in a set of lines with known resistance phenotype by the IMIN partners. Validated markers will be handed over to breeders of the IMIN project for MAS.

The lines identified by screening for disease and pest resistance and for abiotic stresses will be utilized by hybridisation with elite mungbean lines to develop improved lines with multiple traits as per the product pipelines developed by project partners.

10 References

10.1 References cited in report

Afzal MA, Bakr MA, Hamid A, Haque MM, Aktar MS. 2006. Adoption and seed production mechanisms of modern varieties of mungbean in Bangladesh. In Improving income and nutrition by incorporating mungbean in cereal fallows in the Indo-Gangetic Plains of South Asia, DFID Mungbean Project for 2002–2004. AVRDC Publication No. 06-682. Shanhua, Taiwan: The World Vegetable Center (AVRDC).

Bradbury PJ, Zhang Z, Kroon DE, Casstevens TM, Ramdoss Y, Buckler ES. 2007. TASSEL: software for association mapping of complex traits in diverse samples. *Bioinformatics*. Jun 22; 23 (19):2633-5. doi.org/10.1093/bioinformatics/btm308

Cho MS, Jeon YH, Kang MJ, Ahn HI, Baek HJ, Na YW, Choi YM, Kim TS, Park DS. 2010. Sensitive and specific detection of phaseolotoxigenic and nontoxigenic strains of *Pseudomonas syringae* pv*. phaseolicola* by TaqMan real-time PCR using site-specific recombinase gene sequences. *Microbiological Research*, 165(7), 565-572. doi.org/10.1016/j.micres.2009.11.001

Indian Institute of Pulses Research 2011. Vision 2030, Ed. Gupta S, Indian Institute of Pulses Research (ICAR): Kanpur. https://iipr.icar.gov.in/pdf/vision_250715.pdf

John AT, Makkar S, Swaminathan S, Minocha S, Webb P, Kurpad AV, Thomas T. 2021. Factors influencing household pulse consumption in India: A multilevel model analysis. 2021. *Global Food Security.* Jun 1;29:100534. doi.org/10.1016/j.gfs.2021.100534

Kusmec A, Schnable PS. 2018. Farm CPU pp: Efficient large-scale genome-wide association studies. *Plant Direct.* Apr; 2 (4):e00053. doi.org/10.1002/pld3.53

Lipka AE, Tian F, Wang Q, Peiffer J, Li M, Bradbury PJ, Gore MA, Buckler ES, *Zhang Z. 2012. GAPIT: genome association and prediction integrated tool. *Bioinformatics*, 28:2397–2399. doi.org/10.1093/bioinformatics/bts444

Makate C, Wang R, Makate M, Mango N. 2016. Crop diversification and livelihoods of smallholder farmers in Zimbabwe: adaptive management for environmental change. *SpringerPlus*, *5*(1),1135. doi:10.1186/s40064-016-2802-4.

McGrann GRD, Stavrinides A, Russell J, Corbitt MM, Booth A, Chartrain, L,Thomas WTB, Brown JK. 2014. A trade off between mlo resistance to powdery mildew and increased susceptibility of barley to a newly important disease, Ramularia leaf spot. *Journal of Experimental Botany,* 65(4), 1025-1037. doi.org/10.1093/biosci/biy039

Nair RM, Giri RR, Boddepalli VN, Prasad KVSV, Devulapalli R, Blümmel M. 2021. Variation in grain yield, fodder quality and animal intake parameters in two dual purpose legume crops: Mungbean and Vegetable soybean grown in semi-arid tropical India. *Legume Research* (44):207-214. doi.org/10.18805/LR-4078

Nair RM, HanumanthaRao B, Anil Kumar V, Rathore A, Brumbarova T, Ivanov R. 2020. Availability of soil iron determines the distribution strategy and seed iron content in mungbean (*Vigna radiata*) plants. *Plant and Soil*, 446,413–423. Doi.org/ 10.1007/s11104-019-04360-y

Nair RM, Pandey AK, War AR, Hanumantharao B, Shwe T, Alam AKMM, Pratap A, Malik SR, Karimi R, Mbeyagala EK, Douglas CA. 2019. Biotic and abiotic constraints in mungbean production—progress in genetic improvement. *Frontiers in Plant Science*, 10, p.1340. doi.org/10.3389/fpls.2019.01340

Noble TJ, Young AJ, Douglas CA, Williams B, Mundree S. 2019. Diagnosis and management of halo blight in Australian mungbeans: a review. *Crop and Pasture Science*, 70(3), 195-203. doi.org/10.1071/CP18541

Pandey AK, Basandrai AK, Bansandrai D, Boddepalli VN, Rathore A, Adapala G, Nair RM. 2021b. Field-relevant New Sources of Resistance to Anthracnose caused by *Colletotrichum truncatum* in a Mungbean Mini-core Collection. *Plant Disease*, Jul;105(7):2001-2010. doi.org/10.1094/PDIS-12-20-2722-RE

Pandey AK, Burlakoti RR, Rathore A, Nair RM. 2020. Morphological and molecular characterization of *Macrophomina phaseolina* isolated from three legume crops and evaluation of mungbean genotypes for resistance to dry root rot. *Crop Protection* 127: 104962. doi.org/10.1016/j.cropro.2019.104962

Pandey AK, Yee M, Win MM, Lwin HMM, Adapala G, Rathore A, Sheu ZM, Nair RM. 2021a. Identification of new sources of resistance to dry root rot caused by *Macrophomina phaseolina* isolates from India and Myanmar in a mungbean mini-core collection. *Crop Protection*, *143*, p.105569. doi.org/10.1016/j.cropro.2021.105569

Rane J, Raina SK, Venkadasamy G, HanumanthaRao B, Hanjagi PK, Giri R, Jangid KK, Kumar M, Nair RM. 2021. Use of Phenomics for Differentiation of Mungbean (*Vigna radiata* L. Wilczek) Genotypes Varying in Growth Rates Per Unit of Water *Frontiers in Plant Science*, doi.org/10.3389/fpls.2021.692564

Sekhon HS, Bains TS, Kooner BS, Sharma P. 2007. Grow summer mungbean for improving crop sustainability, farm income, and malnutrition. *Acta Horticulturae* 752: 459–464. doi.org/ 10.17660/ActaHortic.2007.752.83

Sequeros T, Ochieng J, Schreinemachers P, Binagwa, PH. Huelgas ZM. Hapsari R, Juma, Maurice O, Kangile, JR, Karimi R, Khaririyatun N, Mbeyagala EK, Mvungi H, Nair RM, Sanya L, Nasirumbi N, Thi TL, Phommalath S, Pinn T, Simfukwe E, Suebpongsang P.2021. Mungbean in Southeast Asia and East Africa: varieties, practices and constraints. *Agriculture & Food Security* 10, 2. doi.org/10.1186/s40066-020-00273-7

Shanmugasundaram S, Keatinge JDH, Hughes Jd'A. 2009. The mungbean transformation, diversifying crops, defeating malnutrition. *IFPRI Discussion Paper* 00922 [Online]. Available: https://ebrary.ifpri.org/utils/getfile/collection/p15738coll2/id/30176/filename/30177.pdf Accessed [24 April 2012].

Taylor JD. 1972. Field studies on halo-blight of beans (*Pseudomonas phaseolicola*) and its control by foliar sprays. *Annals of Applied Biology*, 70(3), 191-197. doi/10.1111/j.1744-7348.1972.tb04704.x

United States Department of Agriculture (USDA) 2021. GAIN Grain and Feed Annual Report Number: BG2021-0014.

Voichek Y, Weigel D. 2020. Identifying genetic variants underlying phenotypic variation in plants without complete genomes. Nat Genet 52, 534–540. doi.org/10.1038/s41588-020-0612-7.

War AR, Murugesan S, Boddepalli VN, Srinivasan R, Nair RM. 2017. Mechanism of Resistance in Mungbean [*Vigna radiata* (L.) R. Wilczek var*. radiata*] to bruchids, *Callosobruchus spp*.(Coleoptera: Bruchidae). *Frontiers in Plant Science*, 8, p.1031. doi.org/ doi.org/10.3389/fpls.2017.01031

War AR, Taggar GK, Hussain B, Taggar MS, Nair RM, Sharma HC. 2018. Plant defence against herbivory and insect adaptations. *AoB Plants*, 10(4), p.ply037. doi.org/10.1093/aobpla/ply037

Wolter M, Hollricher K, Salamini F, Schulze-Lefert, P. 1993. The mlo resistance alleles to powdery mildew infection in barley trigger a developmentally controlled defence mimic phenotype. Molecular and General Genetics 239, 122-128. doi.org/10.1007/BF00281610

10.2 List of publications produced by project

1. Aski MS, Rai N, Reddy VRP, Gayacharan, Dikshit HK, Mishra GP, Singh D, Kumar A, Pandey R, Singh MP, Pratap A, Nair RM, Schafleitner R. 2021. Assessment of root phenotypes in mungbean mini-core collection (MMC) from the World Vegetable Center (AVRDC) Taiwan. *PLOS One* 16(3): e0247810. doi.org/10.1371/journal.pone.0247810
2. Bhandari K, Sharma KD, Bindumadhava H, Siddique KHM, Gaur P, Agrawal SK, Nair R M, Nayyar H. 2017. Temperature sensitivity of food legumes: a physiological insight, *Acta Physiologiae Plantarum* 39:68. DOI 10.1007/s11738-017-2361-5.
3. Bindumadhava H, Nair RM, Nayyar H, Riley JJ, Easdown W. 2017. Mungbean Production under a Changing Climate - Insights from Growth Physiology. *Mysore Journal of Agricultural Sciences* 51 (1): 21-26.
4. Bindumadhava H, Sharma L, Nair RM, Nayyar H, Riley JJ, Easdown W. 2018. High-temperature-tolerant mungbean (*Vigna radiata* L.) lines produce better yields when exposed to higher CO_2 levels. *Journal of Crop Improvement.*doi.org/10.1080/15427528.2018.1439132.
5. Breria CM, Hsieh CH, Yen JY, Nair R, Lin CY, Huang SM, Noble TJ, Schafleitner R. 2019. Population structure of the World Vegetable Center mungbean mini-core collection and genome-wide association mapping of loci associated with variation of seed coat luster. *Tropical Plant Biology* 1-2.doi.org/10.1007/s12042-019-09236-0.
6. Dasgupta U, Mishra GP, Dikshit HK, Mishra DC, Bosamia T, Roy A, Jyotika B, Priti, Aski M, Kumar RR, Singh AK, Kumar A, Sinha SK, Chaurasia S, Praveen S, Nair RM. 2021. Comparative RNA-Seq analysis unfolds a complex regulatory network imparting yellow mosaic disease resistance in mungbean [*Vigna radiata* (L.) R. Wilczek]. *PLOS One* 16(1): e0244593. doi.org/10.1371/journal.pone.0244593
7. HanumanthaRao B, Nair RM, Nayyar H. 2016. Salinity and High Temperature Tolerance in Mungbean [*Vigna radiata* (L.) Wilczek] from a Physiological Perspective. *Frontiers in Plant Science 7*:957. doi: 10.3389/fpls.2016.00957.
8. Karimi R, Nair RM, Ledesma D, Mutisya DL, Muthoni L. 2019. Performance and participatory evaluation of green gram genotypes in the semi-arid environments of Eastern Kenya *East African Agricultural and Forestry Journal* 83 (2):119–136. 10.1080/00128325.2019.1599491
9. Kelly LA, Vaghefi N, Bransgrove K, Fechner NA, Stuart K, Pandey AK, Sharma M, Nemeth MZ, Liu S-Y, Tang S-R, Nair RM, Douglas CA, Kiss L. 2021. One crop disease, how many pathogens? *Podosphaera xanthii* and *Erysiphe vignae* sp. *nov.* identified as the two species that cause powdery mildew of mungbean (*Vigna radiata*) and black gram (*V. mungo*) in Australia *Phytopathology*.doi:org/ 10.1094/PHYTO-12-20-0554-R.
10. Kumar N, Bharat D, Amaresh N, Shivakumar H, Shivakumar R, Arshad, P, Subramanian, R, Easdown W, Bindumadhava H, Nair RM. 2018. Science-based horticultural interventions for improving vegetable productivity in the state of Karnataka, India. *Cogent Food & Agriculture*.doi.org/10.1080/23311932.2018.146173.
11. Kumawat KC, Sharma P, Nagpal S, Gupta RK, Sirari A, Nair RM, Bindumadhava H, Singh S. 2021. Dual Microbial Inoculation, a Game Changer? – Bacterial Biostimulants With Multifunctional Growth Promoting Traits to Mitigate Salinity Stress in Spring Mungbean *Frontiers in Microbiology* 11 3491.doi.org/10.3389/fmicb.2020.600576
12. Manasa R, Reddy R, Bindumadhava H, Nair RM, Prasad TG, Shankar AG. 2017. Screening mungbean (*Vigna radiata* L.) lines for salinity tolerance using salinity induction response technique at seedling and physiological growth assay at whole plant level.

International Journal of Plant, Animal and Environmental Sciences. 7 (4). 11-16. doi.org/10.13140/RG.2.2.15958.24642

13. Mishra GP, Dikshit HK, S. V. R, Tripathi K, Kumar RR, Aski M, Singh A, Roy A, Priti, Kumari N, Dasgupta U, Kumar A, Praveen S, Nair RM. 2020. Yellow Mosaic Disease (YMD) of Mungbean (*Vigna radiata* (L.) Wilczek): Current Status and Management Opportunities. *Frontiers in Plant Science.* 11:918. doi: 10.3389/fpls.2020.00918
14. Mmbando F, Mbeyagala E, Binagwa P, Karimi R, Opie H, Ochieng J, Mutuoki T, Nair RM. 2021. Adoption of improved mungbean production technologies in East Africa, *Agriculture* 11 (6), 528; doi.org/10.3390/agriculture11060528
15. Nair RM, Giri RR, Boddepalli VN, Prasad KVSV, Devulapalli R, Blümmel M. 2021. Variation in grain yield, fodder quality and animal intake parameters in two dual purpose legume crops: Mungbean and Vegetable soybean grown in semi-arid tropical India *Legume research* (44):207-214. doi.org/ 10.18805/LR-4078
16. Nair, R.M., HanumanthaRao, B., Anil Kumar, V., Rathore, A., Brumbarova, T., and Ivanov, R. (2020) Availability of soil iron determines the distribution strategy and seed iron content in mungbean (*Vigna radiata*) plants, Plant and Soil, 446,413–423. doi.org/10.1007/s11104-019-04360-y
17. Nair RM, Götz M, Winter S, Giri RR, Boddepalli VN, Sirari A, Bains TS, Taggar GK, Dikshit HK, Aski M, Boopathi M, Swain D, Rathore A, Anil Kumar V, Lii E C, Kenyon L. 2017. Identification of mungbean lines with tolerance or resistance to yellow mosaic in fields in India where different begomovirus species and different *Bemisia tabaci* cryptic species predominate. *European Journal of Plant Pathology* doi.org/10.1007/s10658-017-1187-8.
18. Nair RM, Leelapriya T, Dhilip KS, Boddepalli VN, Ledesma DR. 2018. Beneficial effects of Extremely Low Frequency (ELF) Sinusoidal Magnetic Field (SMF) exposure on mineral and protein content of mungbean seeds and sprouts*. Indian Journal of Agricultural Research*, 52 (2): 126-132.
19. Nair RM, Pandey AK, War AR, HanumanthaRao B, Shwe T, Alam AKMM, Pratap A, Malik SR, Karimi R, Mbeyagala EK, Douglas CA, Rane J, Schafleitner, R. 2019. Biotic and Abiotic Constraints in Mungbean Production—Progress in Genetic Improvement. *Frontiers in Plant Science* 10:1340. doi: 10.3389/fpls.2019.01340
20. Pandey AK, Basandrai AK, Bansandrai D, Boddepalli VN, Rathore A, Adapala G, Nair RM. 2021. Field-relevant New Sources of Resistance to Anthracnose caused by *Colletotrichum truncatum* in a Mungbean Mini-core Collection *Plant Disease* doi.org/10.1094/PDIS-12-20-2722-RE
21. Pandey AK, Burlakoti RR, Kenyon L, Nair RM. 2018. Perspectives and Challenges for Sustainable Management of Fungal Diseases of Mungbean [*Vigna radiata* (L.) R. Wilczek var. *radiata*]: A Review. *Frontiers in Environmental Science* 6:53. doi.org/10.3389/fenvs.2018.00053
22. Pandey AK, Burlakoti RR, Rathore A, Nair RM. 2020. Morphological and molecular characterization of *Macrophomina phaseolina* isolated from three legume crops and evaluation of mungbean genotypes for resistance to dry root rot. *Crop Protection* 127: 104962. doi.org/ 10.1016/j.cropro.2019.104962
23. Pandey AK, Yee M, Win MM, Lwin HMM, Adapala G, Rathore A, Sheu Z-M, Nair RM. 2021. Identification of new sources of resistance to dry root rot caused by *Macrophomina phaseolina* isolates from India and Myanmar in a mungbean mini-core collection, *Crop Protection*, 143,105569, doi.org/10.1016/j.cropro.2021.105569.

24. Pataczek L, Zahir ZA, Ahmad M, Rani S, Nair R, Schafleitner R, Cadisch G, Hilger T. 2018. Beans with Benefits—The Role of Mungbean (*Vigna radiata*) in a Changing Environment. *American Journal of Plant Sciences*, 9, 1577-1600. doi.org/ 10.4236/ajps.2018.97115
25. Pratap A, Gupta S, Nair RM, Gupta SK, Schafleitner R, Basu PS, Singh CM, Prajapati U, Gupta AK, Nayyar H, Mishra AK. 2019. Using plant phenomics to exploit the gains of genomics. *Agronomy* 9:126. doi.org/10.3390/agronomy9030126
26. Priti, Mishra GP, Dikshit H K, Vinutha T, Tontang MT, Stobdan T, Sangwan S, Aski M, Singh A, Kumar RR, Tripathi K, Kumar S, Nair RM, Praveen S. 2021. Diversity in Phytochemical Composition, Antioxidant Capacities, and Nutrient Contents Among Mungbean and Lentil Microgreens When Grown at Plain-Altitude Region (Delhi) and High-Altitude Region (Leh-Ladakh), India *Frontiers in Plant Science,* 12, P.1485 doi.org/10.3389/fpls.2021.710812
27. Priya M, Dhanker OP, Siddique KHM, Bindumadhava H, Nair RM, Pandey S, Singh S, Varshney RK, Prasad PVV, Nayyar H. 2019. Drought and heat stress-related proteins: an update about their functional relevance in imparting stress tolerance in agricultural crops. *Theoretical and Applied Genetics* 132, 1607–1638. doi.org/10.1007/s00122-019-03331-2
28. Priya M, Sharma L, Kaur R, Bindumadhava H, Nair RM, Siddique KHM, Nayyar H. 2019. GABA (γ-aminobutyric acid), as a thermo-protectant, to improve the reproductive function of heat-stressed mungbean plants. *Scientific Reports* 9, 7788. https://doi.org/10.1038/s41598-019-44163-w.
29. Priya M, Sharma L, Singh I, Bains TS, Siddique KHM, Bindumadhava H, Nair RM, Nayyar H. 2019. Securing reproductive function in mungbean grown under high temperature environment with exogenous application of proline*. Plant Physiology and Biochemistry*, 140:136–150. doi.org/10.1016/j.plaphy.2019.05.009
30. Priya M, Siddique KHM, Dhankhar OP, Prasad PVV, Bindumadhava H, Nair RM, Nayyar H. 2018. Molecular breeding approaches involving physiological and reproductive traits for heat tolerance in food crops. *Indian Journal of Plant Physiology*. 23, 697–720. doi.org/10.1007/s40502-018-0427-z
31. Rane J, Raina SK, Venkadasamy G, HanumanthaRao B, Hanjagi PK, Giri R, Jangid KK, Kumar M, Nair RM. 2021. Use of Phenomics for Differentiation of Mungbean (*Vigna radiata* L. Wilczek) Genotypes Varying in Growth Rates Per Unit of Water *Frontiers in Plant Science*, doi.org/10.3389/fpls.2021.692564
32. Reddy V RP, Aski MS, Mishra GP, Dikshit HK, Singh A, Pandey R, Singh, Gayacharan, Ramtekey V, Priti, Rai N, Nair RM. 2020. Genetic variation for root architectural traits in response to phosphorus deficiency in mungbean at the seedling stage *PLOS One* 15(6): e0221008. doi.org/10.1371/journal.pone.0221008.
33. Reddy VRP, Das S, Dikshit HK, Mishra GP, Aski M, Meena SK, Singh A, Pandey R, Singh MP, Tripathi K, Gore PG, Priti, Bhagat TK, Kumar S, Nair RM, Sharma TR. 2020. Genome-Wide Association Analysis for Phosphorus Use Efficiency Traits in Mungbean (*Vigna radiata* L. Wilczek) Using Genotyping by Sequencing Approach *Frontiers in Plant Science* 11:537766. doi.org/10.3389/fpls.2020.537766
34. Reddy VRP, Das S, Dikshit HK, Mishra GP, Aski MS, Singh A, Tripathi K, Pandey R, Bansal R, Pal Singh M, Gore PG, P. B. M, Kothari D, Rai N, M. Nair R. 2021. Genetic Dissection of Phosphorous Uptake and Utilization Efficiency Traits Using GWAS in Mungbean. *Agronomy*. 11(7):1401. doi.org/10.3390/agronomy11071401

35. Reddy VRP, Dikshit HK, Mishra GP, Aski M, Singh A, Bansal R, Pandey R, Nair RM. 2021. Comparison of different selection traits for identification of phosphorus use efficient lines in mungbean. *PeerJ* 9:e12156. doi.org/10.7717/peerj.12156 https://agricultureandfoodsecurity.biomedcentral.com/articles/10.1186/s40066-020-00260-y
36. Schafleitner R, Huang SM, Chu SH, Yen JY, Lin CY, Yan MR, Krishnan B, Liu MS, Lo HF, Chen CY, Chen LF, Wu DC, Bui TGT, Ramasamy S, Tung CW, Nair RM. 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 Biology*, 16:159. doi.org/ 10.1186/s12870-016-0847-8
37. Schreinemachers P, Sequeros T, Rani S, Rashid MA, Gowdru NV, Rahman MS, Ahmed MR, Nair RM. 2019. Counting the beans: quantifying the adoption of improved mungbean varieties in South Asia and Myanmar. *Food Security* 11, 623-634. doi,org/10.1007/s12571-019-00926-x.
38. Sehgal A, Sita K, Siddique KHM, Kumar R, Bhogireddy S, Varshney RK, HanumanthaRao B, Nair RM, Prasad PVV, Nayyar H. 2018. Drought or/and Heat-Stress Effects on Seed Filling in Food Crops: Impacts on Functional Biochemistry, Seed Yields, and Nutritional Quality *Frontiers in Plant Science* 9, doi.org/10.3389/fpls.2018.01705.
39. Sequeros T, Ochieng J, Schreinemachers P, Binagwa, PH. Huelgas ZM. Hapsari R, Juma, Maurice O, Kangile, JR, Karimi R, Khaririyatun N, Mbeyagala EK, Mvungi H, Nair RM, Sanya L, Nasirumbi N, Thi TL, Phommalath S, Pinn T, Simfukwe E, Suebpongsang P.2021. Mungbean in Southeast Asia and East Africa: varieties, practices and constraints. *Agriculture & Food Security* 10, 2. doi.org/10.1186/s40066-020-00273-7
40. Sequeros T, Schreinemachers P, Depenbusch L, Shwe T, Nair RM. 2020. Impact and returns on investment of mungbean research and development in Myanmar. *Agriculture & Food Security* 9(1) 5. doi.org/10.1186/s40066-020-00260-y
41. Sharma L, Priya M, Bindumadhava H, Nair RM, Nayyar H. 2016. Influence of high temperature stress on growth, phenology and yield performance of mungbean [*Vigna radiata* (L.) Wilczek] undermanaged growth conditions, *Scientia Horticulturae* 213:379–391.doi.org/10.1186/s12870-016-0847-8.
42. Sita K, Sehgal A, Bindumadhava H, Nair RM, Prasad PVV, Kumar S, Gaur P, Farooq M, Siddique KHM, Varshney RK, Nayyar H. 2017. Food Legumes and Rising Temperatures: Effects, Adaptive functional mechanisms, specific to Reproductive phase, and Strategies to improve Heat tolerance. *Frontiers in Plant Science.* 8, 1-30. doi.org/10.3389/fpls.2017.01658/full.
43. Sokolkova A, Burlyaeva M, Valiannikova T, Vishnyakova M, Schafleitner R, Lee C_R, Ting C-T, Nair RM, Nuzhdin S, Samsonova M, von Wettberg E. 2020. Genome-wide association study in accessions of the mini-core collection of mungbean (*Vigna radiata*) from the World Vegetable Gene Bank (Taiwan). *BMC Plant Biology* 20, 363. doi.org/10.1186/s12870-020-02579-x
44. Swehla A, Pandey AK, Nair RM. 2020. Bioactivity of *Trichoderma harzianum* isolates against the fungal root rot pathogens with special reference to *Macrophomina phaseolina* causing dry root rot of mungbean. *Indian Phytopathology* 73, 787–792. doi.org/10.1007/s42360-020-00288-x
45. van Zonneveld M, Rakha M, Tan SY, Chou YY, Chang CH, Yen JY, Schafleitner R, Nair R, Naito K, Solberg SØ. 2020. Mapping patterns of abiotic and biotic stress resilience

uncovers conservation gaps and breeding potential of Vigna wild relatives. *Scientific Reports* 10:1-1. doi.org/10.1038/s41598-020-58646-8

46. War AR, Murugesan S, Boddepalli VN, Srinivasan R, Nair RM. 2017. Mechanism of Resistance in Mungbean [*Vigna radiata* (L.) R. Wilczek var. *radiata*] to Bruchids, *Callosobruchus* spp. (Coleoptera: Bruchidae). *Frontiers in Plant Science*.doi.org/10.3389/fpls.2017.01031.
47. War AR, Taggar GK, Hussain B, Taggar MS, Nair RM, Sharma HC. 2018. Plant defence against herbivory and insect adaptations. *AoB PLANTS* 10: ply037; doi: 10.1093/aobpla/ply037.

Book Chapters

1. Dikshit HK, Mishra GP, Somta P, Shwe T, Alam AKMM, Bains TS, Nair RM. 2020. Classical Genetics and Traditional Breeding in Mungbean. In: Nair R, Schafleitner R, Lee SH. (eds) The Mungbean Genome. Compendium of Plant Genomes. Springer, Cham. https://doi.org/10.1007/978-3-030-20008-4_4
2. Douglas C, Pratap A, Hanumantha Rao H, Manu B, S Dubey S, Singh P, Tomar R. 2020. Breeding Progress and Future Challenges: Abiotic Stresses. In: Nair R, Schafleitner R, Lee SH. (eds) The Mungbean Genome. Compendium of Plant Genomes. Springer, Cham. https://doi.org/10.1007/978-3-030-20008-4_6
3. Ebert AW, Dubois T, Tenkouano A, Mavlyanova R, Wang J-F, Bindumadhava H, Srinivasan R, Kumar S, Beed FD, Pottorff M, Chen W-Y, Nair RM, Nayyar H, Riley JJ. 2018. Chapter 14. Sustainable Vegetable Production to Sustain Food Security under Climate Change at Global Level, Food Security and Climate Change Ed(s) Shyam Singh Yadav, Robert Redden, ISBN: 978-1-119-18065-4, Wiley-Blackwell, 536 pp.
4. Nair R. 2020. Breeding Progress and Future Challenges—Nutritional Quality. In: Nair R, Schafleitner R, Lee SH. (eds) The Mungbean Genome. Compendium of Plant Genomes. Springer, Cham. https://doi.org/10.1007/978-3-030-20008-4_7
5. Pratap A, Douglas C, Prajapati U, Kumari G, War AR, Tomar R, Pandey AK, Dubey S. 2020. Breeding Progress and Future Challenges: Biotic Stresses. In: Nair R, Schafleitner R, Lee SH. (eds) The Mungbean Genome. Compendium of Plant Genomes. Springer, Cham. https://doi.org/10.1007/978-3-030-20008-4_5
6. Schafleitner R. 2020. Molecular Marker Resources and Their Application. In: Nair R, Schafleitner R, Lee SH. (eds) The Mungbean Genome. Compendium of Plant Genomes. Springer, Cham. https://doi.org/10.1007/978-3-030-20008-4_8
7. Schafleitner R, Nair RM. 2020. Future Prospects and Challenges. In: Nair R, Schafleitner R, Lee SH. (eds) The Mungbean Genome. Compendium of Plant Genomes. Springer, Cham. https://doi.org/10.1007/978-3-030-20008-4_12

Conference papers

1. Aski MS, Rai N, Dikshit HK, Mishra GP, Singh D, Prachi, Gayacharan, Kumar A, Pandey R, Singh MP, Pratap A, Nair RM, Schafleitner R. 2021. Ideal root phenotypes for combating abiotic stresses in mungbean Abstracts: National Web Conference on

Sustaining Pulse Production for Self-sufficiency and Nutritional Security, Feb. 9-11, ICAR-Indian Institute of Pulses Research, Kanpur, U.P., India, pp-376.

2. Boddepalli VN, War AR, Pandey AK, Shivanna A, Gowda A, Chaudhari S, Nair RM. 2021. Development of black gram varieties with improved protein quality, and resistance to bruchids and mungbean yellow mosaic disease. Abstracts: National Web Conference on Sustaining Pulse Production for Self-sufficiency and Nutritional Security, Feb. 9-11, ICAR-Indian Institute of Pulses Research, Kanpur, U.P., India, pp-97.
3. Chang CH, Shen CY, Chen WY, Yen JY, Nair RM, Solberg SO. 2016. Salt tolerance screening of the AVRDC mungbean (*Vigna radiata*) collection. *20th EUCARPIA General Congress*, At ETH Zurich, Switzerland, Volume: Book of Abstracts (Eds. Roland Kölliker and Beat Boller), Agroscape, Institute for Sustainability Sciences ISS, p 297.
4. Chaudhary S, Priya M, Sharma I, Nair RM, Bindumadhava H, Nayyar H.2021. Assessment of mungbean [*Vigna radiata* (L.) Wilczek] genotypes for heat tolerance Abstracts: National Web Conference on Sustaining Pulse Production for Self-sufficiency and Nutritional Security, Feb. 9-11, ICAR-Indian Institute of Pulses Research, Kanpur, U.P., India, pp-361.
5. Douglas CA, Paccapelo V, Nair RM, Schafleitner R, Shwe T, Alam AKMM, Pratap A, Huttner E. 2018. The shiny green revolution - dissecting grain yield components in genetically diverse germplasm of green gram and black gram *Seventh International Food Legumes Research Conference*, Marrakesh, Morocco, May 06-08, 44-45.
6. Gowda A, Kumar D, Wankhede D, Pradhan H, Boddepalli VN, Archak S, Singh N, Singh K, Chaudhari S, Nair RM. 2021. Identification of sources of resistance against *Colletotrichum lindemuthianum* responsible for anthracnose disease in black gram. Abstracts: National Web Conference on Sustaining Pulse Production for Self-sufficiency and Nutritional Security, Feb. 9-11, ICAR-Indian Institute of Pulses Research, Kanpur, U.P., India, pp-316.
7. Kumawat KC, Sharma P, Nair RM, Bindumadhava H, Sirari A. 2018. Amelioration of salinity stress with 1-aminocyclopropane -1- carboxylate (ACC) deaminase containing bacteria in summer mungbean *Seventh International Food Legumes Research Conference*, Marrakesh, Morocco, May 06-08, 225.
8. Nair RM. 2019. Developing mungbeans for the sprout market segment *KSBS and SABRAO 14th International Conference on Plant Breeding for Sustainable Development* from 2-5 July, in South Korea
9. Nair RM. 2016. Use of genetic resources for legume improvement at AVRDC- The World Vegetable Center, *National Symposium on Vegetable Legumes for Soil and Human Health*, Eds Singh et al, Feb 12-14, 241.6.
10. Nair RM, Pandey AK, Bindumadhava H, Shwe T, Alam AKMM, Pratap A, Malik SR, Karimi R, Mbeyagala EK, Douglas C, Schafleitner R. 2020. Breeding Better Mungbeans through the International Mungbean Improvement Network, Theme: International conference on “Pulses as the Climate Smart crops: Challenges and Opportunities” (ICPulse2020) (February 10-12, ICAR-Central Institute of Agricultural Engineering, Bhopal, Madhya Pradesh, India).
11. Nair RM, Schafleitner R, Douglas C, Alam AKM, Pratap A, Shwe T, Huttner E. 2016. An International network to improve mungbean breeding and production In: Legumes for a Sustainable World – *ILS2 Second International Legume Society Conference*, Portugal, 11-14 October, 267.
12. Nair RM, Schafleitner R, Douglas C, Shwe T, Alam AKMM, Pratap A, Gupta S, Huttner E. 2017. International networking for mungbean improvement In National *Symposium on Pulses for nutritional security and agricultural sustainability*, IIPR, Kanpur, 2-4 December, 53-54.
13. Nair RM, Schafleitner R, Yang R-Y, Kenyon L, Srinivasan R, Hanson P, Ebert A, Easdown W, Hughes J.d’A, Keatinge JDH. 2014. Enhancing mungbean production and consumption, paper presented at the *VI International food Legume research*

Conference (IFLRC) and VII International Conference on Legume Genetics and Genomics (ICLGG) July 7-11, Saskatoon.
14. Nair RM, War AR, Pandey A, Schafleitner R, Douglas C, Shwe T, Alam AKMM, Pratap A, Gupta S. Huttner E. 2018. Mungbean mini-core collection: A treasure trove for resistance to pests and diseases *Seventh International Food Legumes Research Conference*, Marrakesh, Morocco, May 06-08, 59-60.
15. Nair RM, Yan MR, Srinivasan R, Schafleitner R. 2015. Developing bruchid resistant mungbean varieties SABRAO 13th Congress and International conference IPB International Convention Center, Bogor, Indonesia 14th – 16th September, 52.
16. Nayyar H, Gaur P, Kumar S, Bindumadhava H, Nair RM, Kumar J, Siddique KHM, Vara Prasad PV, Singh S. 2018. Evaluation of heat sensitivity in food legumes and approaches for heat tolerance *Seventh International Food Legumes Research Conference*, Marrakesh, Morocco, May 06-08, 22.
17. Nayyar H, Gaur P, Kumar S, Singh S, Bindumadhava H, Nair RM, Prasad PVV, Siddique KHM. 2016. How heat stress affects the physiology of summer and winter - season food legume crops? In: Legumes for a Sustainable World – *ILS2 Second International Legume Society Conference*, Portugal, 11-14 October, 71.
18. Pandey AK, Yee M, Win MM, Lwin HMM, Boddepalli VN, Gowda A, Chaudhari S, Nair RM. 2021. Identification of sources of resistance against dry root rot caused by *Macrophomina phaseolina* in a mungbean mini-core collection. Abstracts: National Web Conference on Sustaining Pulse Production for Self-sufficiency and Nutritional Security, Feb. 9-11, ICAR-Indian Institute of Pulses Research, Kanpur, U.P., India, pp-330.
19. Schafleitner R, Douglas C, Shwe T, Alam AKMM, Prata, A, Gupta S, Yen JY, Breria CA, Boddepalli VN, Huang SM, Lin JY, Nair RM. 2018. Diversity of Mungbean yellow mosaic virus resistance genes in mungbean (*Vigna radiata*) *Seventh International Food Legumes Research Conference*, Marrakesh, Morocco, May 06-08, 197-198.
20. Schafleitner R, Nair RM, Khan S, Kuziev B, Schreinemachers P, Hilger T, Solberg SO. 2016. Beans with Benefits: Integrating improved mungbean as a catch crop into the dryland systems of South and Central Asia. *20th EUCARPIA General Congress*, At ETH Zurich, Switzerland, Volume: Book of Abstracts (Eds. Roland Kölliker and Beat Boller), Agroscape, Institute for Sustainability Sciences ISS, p 145.
21. Singh D, Kumari G, Prajapati U, Singh Y, Tiwari P, Nair RM, Gupta S, Singh NP, Pratap A. 2021. Morphological evaluation of mungbean mini-core set for resistance against Mungbean Yellow Mosaic India virus (MYMIV). Abstracts: National Web Conference on Sustaining Pulse Production for Self-sufficiency and Nutritional Security, Feb. 9-11, ICAR-Indian Institute of Pulses Research, Kanpur, U.P., India, pp-357.

Crop manuals

1. Mbeyagala KE, Amayo R, Obuo J.P, Pandey A K, War AR, Nair RM. 2017. A manual for mungbean (greengram) production in Uganda. National Agricultural Research Organization (NARO), 32 pages.
2. Mbeyagala KE, Amayo R, Obuo. JP, War AR, Nair RM, Ugen MA. 2017. Bruchids in stored greengram/mungbean. A NaSARRI-AVDRC- World Vegetable Center Publication. Pages 4
3. Nair RM, War AR, Pandey AK. 2017. How to grow Mungbeans in Odisha. World Vegetable Center Publication. Pages 7.

11 Appendixes

11.1 Table 26. Capacity building activities conducted in IMIN

S. No.	Capacity Building Activity	Participants	Country	Year
1	Introduction and Demonstration on KDDart Database management in mungbean breeding	Researchers from IMIN Partner countries	India	10 November 2016
2	Training Program on Plant Breeding Database Management and Statistics	Researchers from IMIN Partner countries	India	23-27 October 2017
3	Training program on KDDart Database management	Researchers from India and Taiwan	India	1-3 August 2018
4	Training program on KDDart Database management	Researchers from BARI	Bangladesh	6-8 August 2018
5	Training program on KDDart Database management	Researchers from DAR	Myanmar	10-14 August 2018
6	Hands on training on recent updates in KDDart Database management	Researchers from IIPR, Kanpur	India	15-16 May 2019
7	Hands on training on recent updates in KDDart Database management	Researchers from BARI	Bangladesh	10-11 July 2019
8	Hands on training on recent updates in KDDart Database management	Researchers from DAR	Myanmar	7-8 August 2019
9	Hands on training on recent updates in KDDart Database management	Researchers from IIPR, Dharwad	India	28 August 2019
10	Virtual workshop on Digital Tools and Data Management in Breeding	IMIN Partners	Virtual	12 August 2020
11	Virtual workshop on updates in KDDart Database management system	WorldVeg researchers	Virtual	27 November 2020
12	Virtual workshop on Demand-led Breeding Approaches for market segmentation and designing mungbean product profiles	Mungbean Researchers from Asia and Africa	Virtual	8-9 December 2020

11.2 Table 27. List of countries with which WorldVeg mini-core collection was shared

Country	2015	2016	2017	2018	2019	2020	2021
Australia	296	15			10		
Bangladesh	296	122	111	61			
Benin				293			
Canada					293		
France					10		
Germany		5	16				
Ghana				293			
India		321					
Indonesia							296
Kenya				293			
Mali				293			
Mozambique		7		7			
Myanmar	296	67	79	57			
Nigeria				293			
Pakistan	296						
Paraguay		12					
PNG							293
Russia Federal				296			
South Korea						293	
Taiwan				54	5	116	50
Tajikistan					7		
Tanzania		7		293			
Thailand				293			
Uganda				293		3	
Uzbekistan	296	2	12				
total	**1480**	**854**	**218**	**2819**	**325**	**412**	**639**

11.3 Table 28. Details of mungbean mini-core lines distributed from WorldVeg, Hyderabad, India

S. No	Center	No. of Accessions	Research for
1.	ICAR-Indian Institute of Pulses Research (ICAR-IIPR)	296	Agronomic traits, biotic and abiotic stress
2.	ICAR-Indian Agricultural Research Institute (ICAR-IARI)	296	Agronomic traits, biotic and abiotic stress
3.	ICAR-National Institute for Abiotic Stress Management (ICAR-NIASM)	296	Heat and drought tolerance
4.	CSK Himachal Pradesh Agricultural University (CSKHPAU)	74	Anthracnose resistance

11.4 Evaluation of Mungbean Mini-core Collection in Asia and Australia

Seed yield per plant (g)

Two principal components of scattered biplot explained 31.04% (PC1- 17.89%, PC2- 13.15%) of total variation due to genotype and genotype × environment interaction for seed yield per plant. In this biplot analysis, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the polygon. The genotype 644 (VI000815BG), 850 (VI004024AG), 874 (VI004691AG), 735 (VI002532AG), 724 (VI002239AG), 686 (VI001556BG), 857 (VI004129A-BLM), 649 (VI000953AG), 652 (VI001066BG), 695 (VI001652BG), 623 (VI000470AG), 619 (VI000319AG) and 906 (VI005041AG), are farthest from the origin of biplot indicates that these genotypes are either superior or poor performer in some or all the environments for seed yield per plant (Figure 23). The polygon view of biplot analysis showed that the genotypes fell in 8 sections and the test environments fell in three sections. The environments ISH_18 (Ishwardi 2018), KAN_18 (Kanpur 2018), HYD_R16 (Hyderabad rainy 2016), HYD_R17 (Hyderabad rainy 2017), HYD_PR17 (Hyderabad post-rainy 2017), HYD_R18 (Hyderabad rainy 2018), HYD_PR18 (Hyderabad post-rainy 2018) and GAZ_19 (Gazipur 2019) are plotted together in one sector with acute angles between their respective environmental vectors indicates positive correlation among the environments (Figure 23). The second vector comprised of GAZ_17 (Gazipur 2017), GAZ_18 (Gazipur 2018), MAD_20 (Madaripur 2020) whereas third sector consist of BAR_18 (BARI 2018) and DHA_21 (Dharwad 2021). All the environments in same sector forming a mega-environment indicating that these locations share common environmental conditions. The genotypes 624 (VI000532BG), 898 (VI004958BG), 887 (VI004877AG), 720 (VI002190BG), 829 (VI003886B-BR), 663 (VI001284AG), 777 (VI003251A-BL), 785 (VI003364AG), 647 (VI000938AG), 645 (VI000818BG), are some of the genotypes reported with highest mean seed yield per plant (plotted on right side of the biplot) and least distance from the average environment axis indicates their stable performance across locations for seed yield per plant (Figure 23).

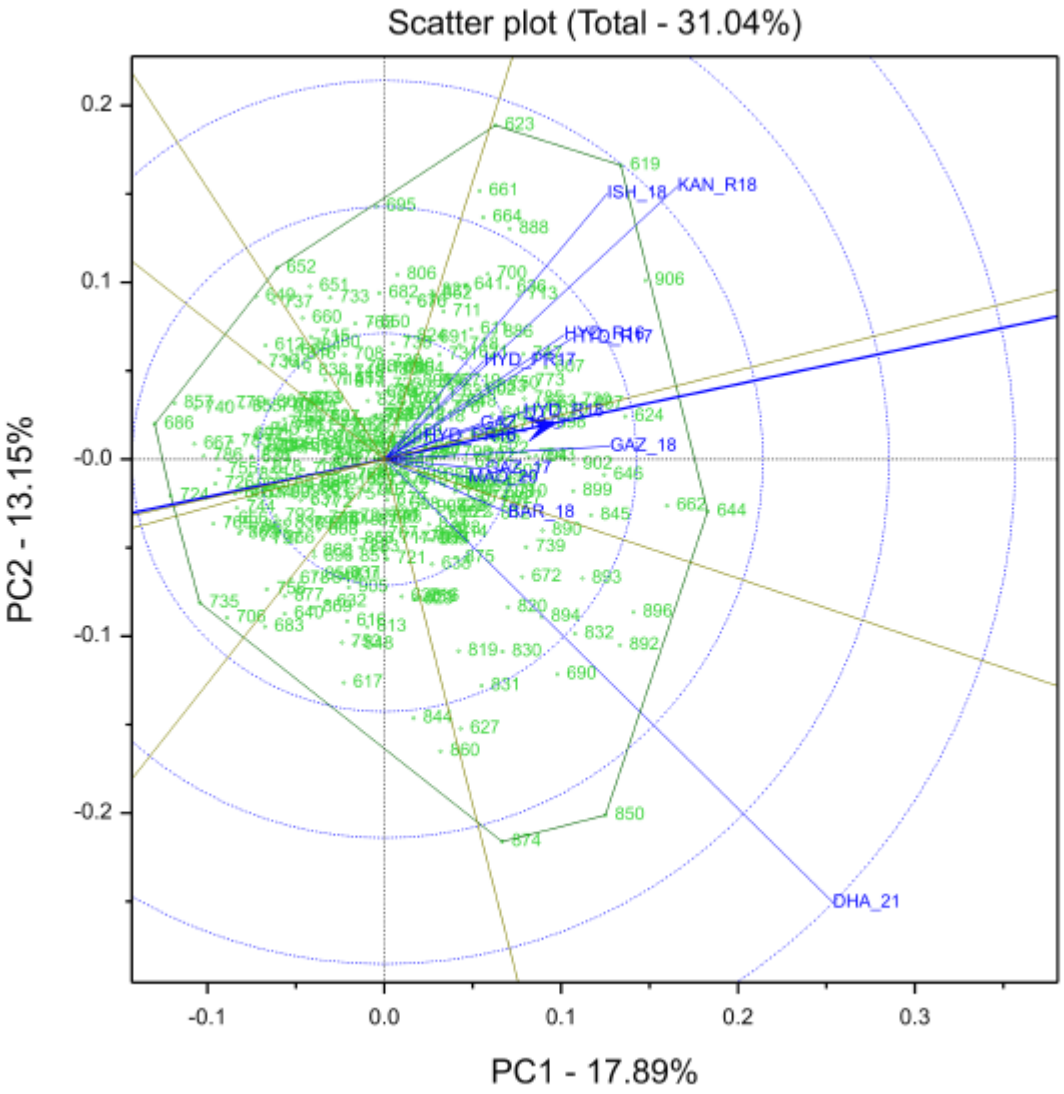


Figure 23. GGE biplot analysis for seed yield per plant of mungbean mini-core evaluated across locations in Asia during 2016-21.

Days to maturity

Two principal components of scattered biplot explained 44.26% (PC1- 26.11%, PC2-18.15%) of total variation due to genotype and genotype × environment interaction for days to maturity plant. In this biplot analysis, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the polygon. The genotype 729 (VI002437BG), 894 (VI004954BG), 901 (VI004969AG), 747 (VI002872BG), 746 (VI002860AG), 888 (VI004915BG), 861 (VI004243B-BR), 608 (VI000164BG), 855 (VI004096AG), 903 (VI005022BG), and 806 (VI003563A-BR) are farthest from the origin of biplot indicates that these genotypes are either superior or poor performer in some or all the environments (Figure 24). The polygon view of biplot analysis showed that the genotypes fell in 12 sections and the test environments fell in three sections. All the environments except Dharwad_21 (DHA_21) and Hyderabad rainy 2017 (HYD_R17) are plotted together with acute angles between their respective environmental vectors indicates positive correlation among the environments (Figure 24). All the environments in same sector forming a mega-

environment indicating that these locations share common environmental conditions. The genotypes 746 (VI002860AG), 747 (VI002872BG), 888 (VI004915BG), 821 (VI003734B-DG), 730 (VI002456AG), 875 (VI004694BG), 865 (VI004307AG), and 776 (VI003242AG) are some of the genotypes reported with lowest mean (65-66 days) for days to maturity (plotted on left side of the biplot) and least distance from the average environment axis indicates their stable performance across locations for days to maturity (Figure 24).

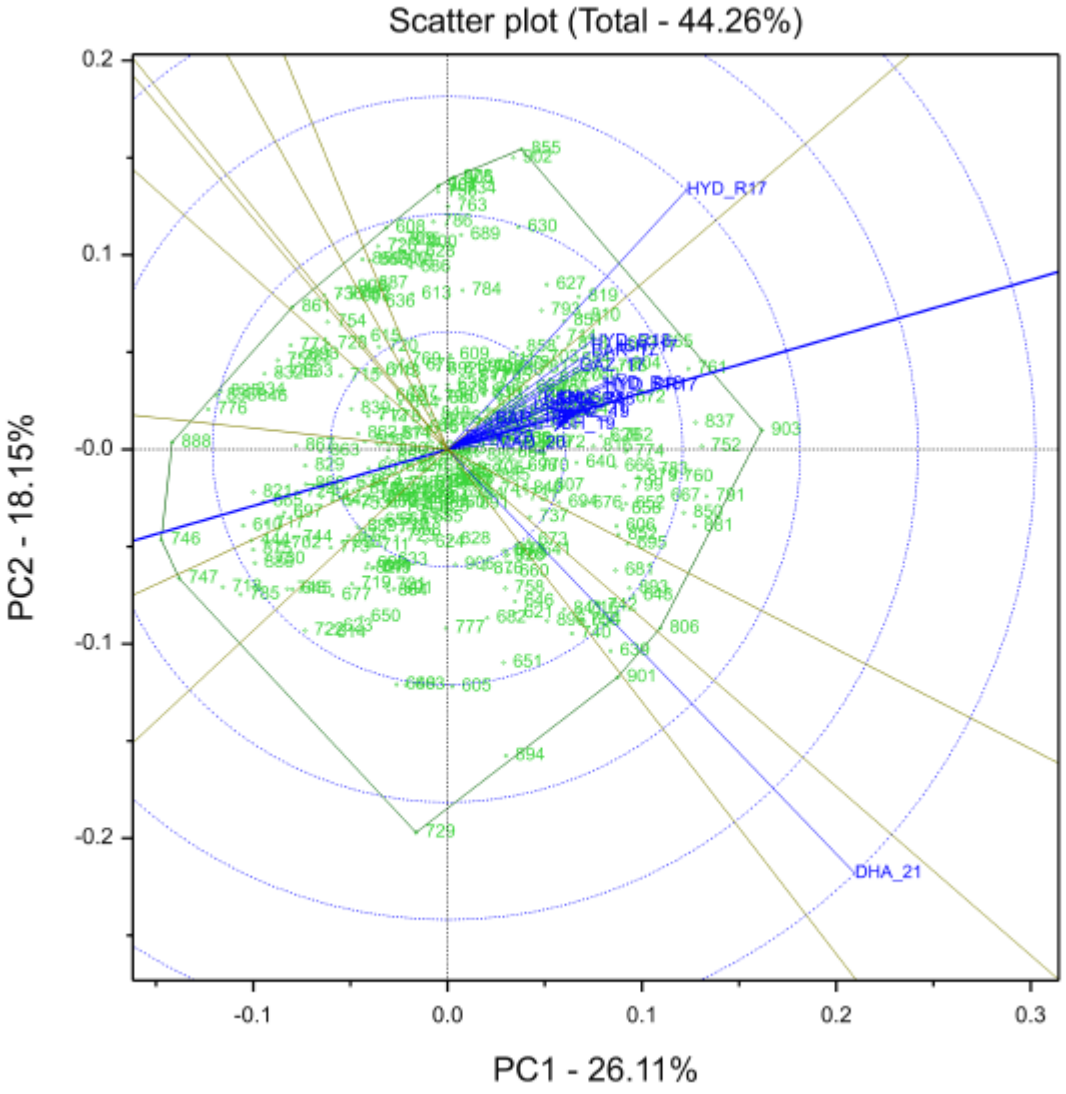


Figure 24. GGE biplot analysis for days to maturity of mungbean mini-core evaluated across different location in Asia during 2016-2021.

11.5 Evaluation of Mungbean Mini-core Collection in Sub-Saharan Africa

Seed Yield per Plant (g)

Two principal components of scattered biplot explained 43.37% (PC1- 25.75%, PC2- 17.62%) of total variation due to genotype and genotype x environment interaction for seed yield per plant. In this biplot analysis, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the polygon. The vertex genotypes in the biplot for seed yield per plant are 20 (VI000537 BG), 126 (VI002523 AG), 128 (VI002532 AG), 54 (VI001221 AG), 6 (VI000175 BY), 118 (VI002274 B-BL), 264 (VI004694 BG), 246 (VI004129 A-BLM), 9 (VI000212 A-BLM), 99 (VI001806 AG), 133 (VI002646 AG), and 39 (VI000815 BG) are the farthest from the origin of biplot indicates that these genotypes are either superior or poor performer in some or all the environments (Figure 25). The polygon view of biplot analysis showed that the genotypes fell in 12 sections and the test environments fell in three sections. All the environments except Ghana_2019 are plotted together with acute angles between their respective environmental vectors indicates positive correlation among the environments (Figure 25). All the environments except Benin_2019 and Ghana_2019 are plotted in the same section forming a mega-environment.

The genotypes 285 (VI004957 AG), 190 (VI003514 BG), 13 (VI000316 AG), 66 (VI001412 AG), 53 (VI001211 AG), 52 (VI001191 BG), 81 (VI001557 BG), 32 (VI000732 AG), 280 (VI004934 AG), and 176 (VI003337 BG) are some of the genotypes reported with higher mean and least distance from the average environment axis indicates their stable performance across locations. The genotypes 20 (VI000537 BG), 43 (VI000942 AG), 59 (VI001339 AG), 126 (VI002523 AG), 38 (VI000805 BG), 128 (VI002532 AG) and 48 (VI001096 AG) are plotted farthest on the right side with greater length from average environment axis indicates their high mean performance with higher genotype × environment interaction for seed yield per plant.

Days to maturity

Two principal components of scattered biplot explained 69.93% (PC1- 58.38%, PC2- 11.57%) of total variation due to genotype and genotype × environment interaction for days to maturity. The vertex genotypes in the biplot *viz.,* 293 (VI005030 BY), 290 (VI004973 B-BLM), 220 (VI003886 BY), 135 (VI002672 AG), 30 (VI000680 AG) and 21 (VI000542 BY) are the farthest from the origin of biplot indicates that these genotypes are either earliest or late maturing in some or all the environments (Figure 26). The polygon view of biplot analysis showed that the genotypes fell in 7 sections and the test environments fell in two sections. All the environments except Benin_2019 are plotted in one section with acute angles between their respective environmental vectors indicates positive correlation among the environments (Figure 26). All the environments except Benin_2019 are plotted in the same section forming a mega-environment.

The genotypes plotted left side of the perpendicular line are desirable for days to maturity as they are early maturing than the population mean across environments. The genotypes 135 (VI002672 AG), 251 (VI004244 B-BR), 59 (VI001339 AG), 25 (VI000578 AG), 256 (VI004347 B-BLM), 29 (VI000625 B-BR), 229 (VI003944 B-BR), 159 (VI003159 AG), 257 (VI004351 AG), and 261 (VI004639 AG) reported with earliest maturity as they are plotted farthest on left side of the biplot with least distance from the average environment axis indicates their stable performance across locations (Figure 26).

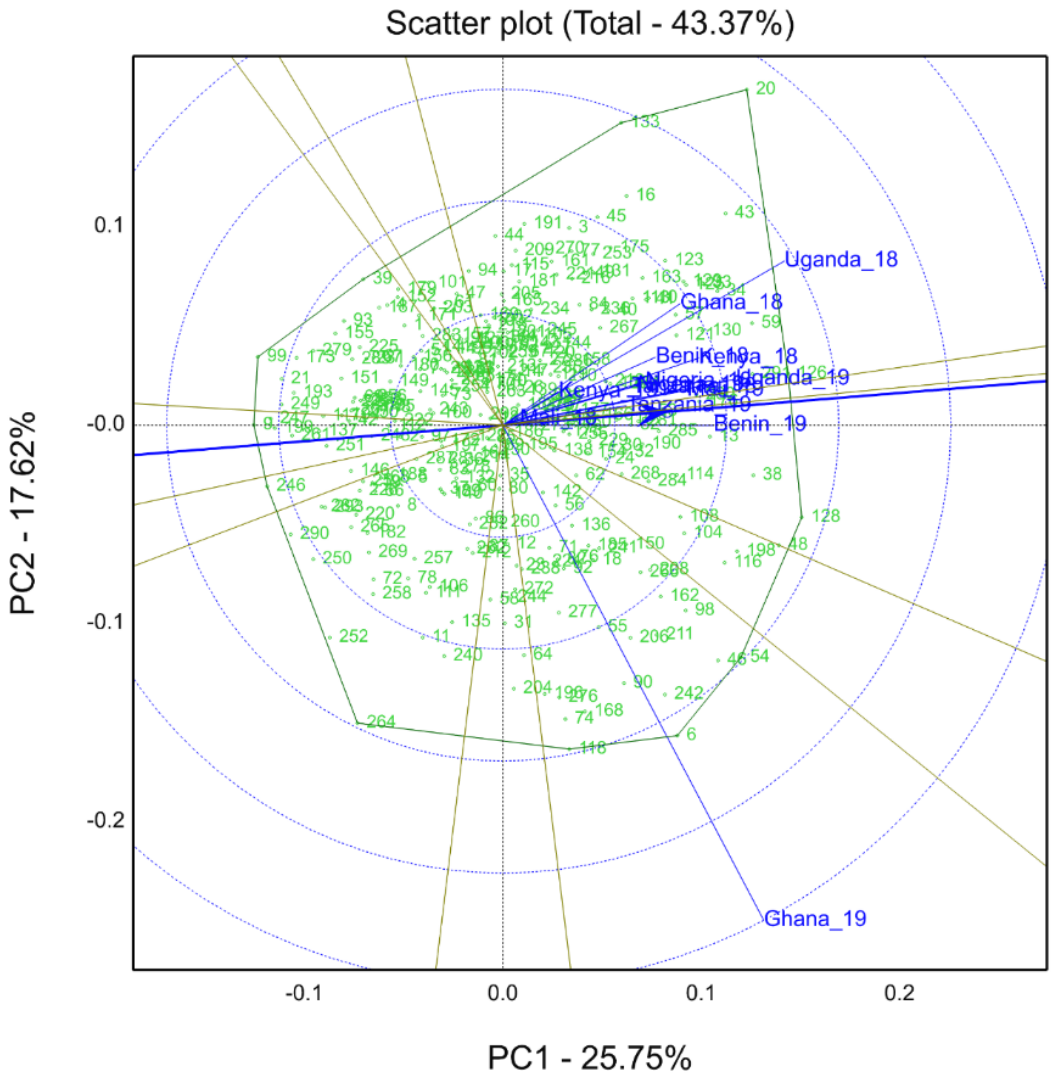


Figure 25. GGE biplot analysis for seed yield per plant of mungbean mini-core evaluated across seven countries in Africa during 2018-19.

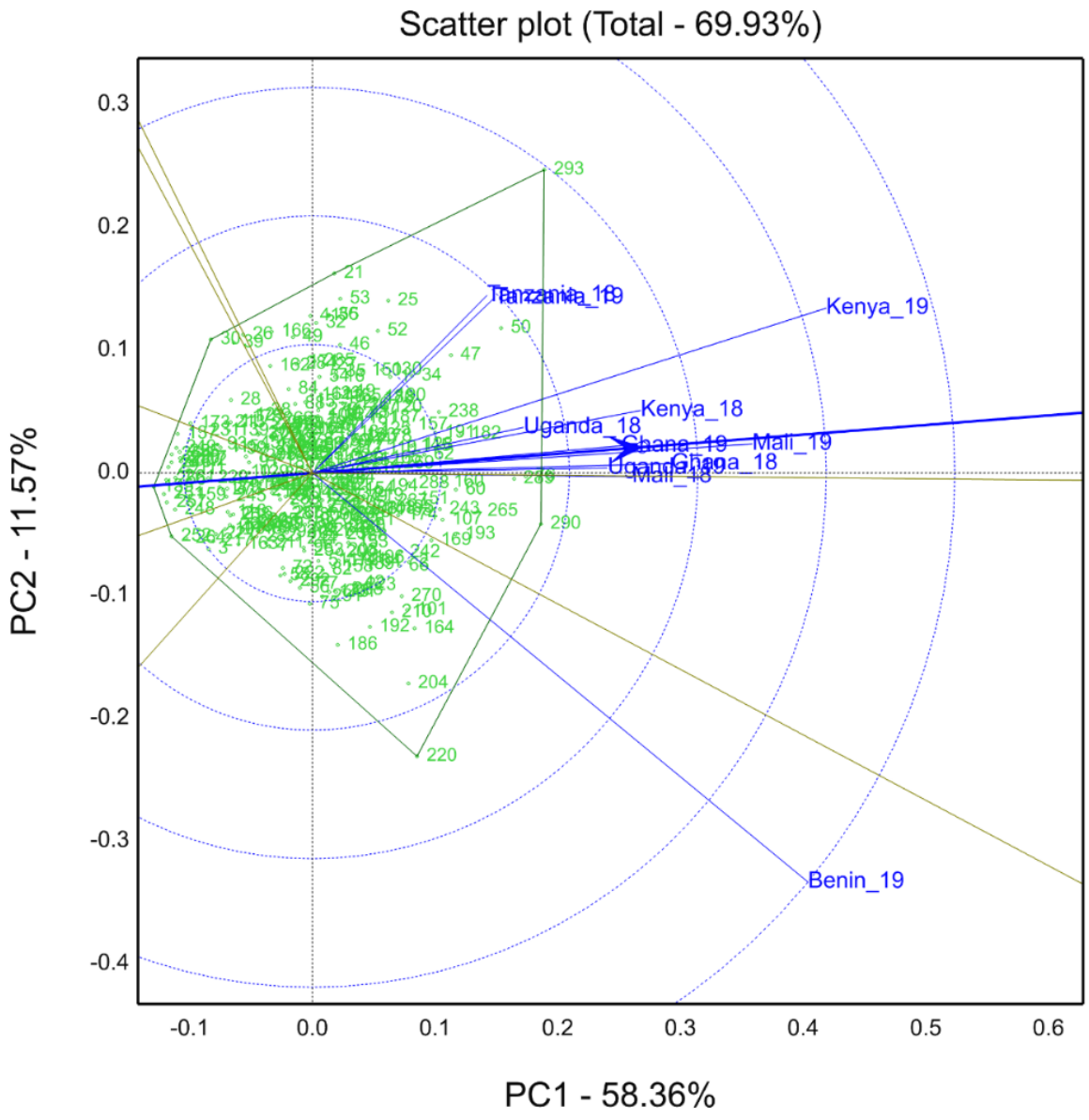


Figure 26. GGE biplot analysis for days to maturity of mungbean mini-core evaluated across seven countries in Africa during 2018-19.

11.6 Pest and Disease reactions

Table 29. DRR disease reaction of identified resistant mungbean accessions in the repeated paper towel methods (Pandey et al., 2021a)

Mungbean accessions	Origin	Paper towel 1		Paper towel 2	
		Disease score	Reaction category	Disease score	Reaction category
VI000203B-BR	Afghanistan	2.8	R	1.3	R
VI000319AG	Pakistan	1.6	R	1.9	R
VI000732AG	India	2.6	R	1.8	R
VI000764AG	India	2.5	R	2.6	R
VI000766BG	India	2.1	R	2.4	R
VI000805BG	India	3.0	R	4.4	MR
VI000815BG	India	2.2	R	3.6	MR
VI000818BG	India	2.5	R	1.7	R
VI000981BG	Philippines	1.4	R	4.5	MR
VI001244AG	Philippines	1.6	R	1.7	R
VI001268BG	India	1.6	R	2.2	R
VI001282AG	India	1.5	R	2.1	R
VI001284AG	India	2.6	R	1.7	R
VI001400AG	India	2.0	R	3.0	R
VI001403BR	India	1.6	R	5.3	MS
VI001412AG	India	3.0	R	3.9	MR
VI001419BG	India	1.9	R	2.7	R
VI001482BG	India	2.7	R	5.1	MS
VI001490AG	Iran	3.0	R	3.0	R
VI001509AG	Pakistan	1.0	I	1.1	R
VI001535BG	India	2.4	R	2.4	R
VI001548AG	India	2.9	R	2.5	R
VI001576BG	India	1.7	R	5.5	MS
VI002529B-BL	Thailand	2.4	R	2.7	R
VI002587AG	Australia	2.8	R	3.1	MR
VI003070AG	India	2.5	R	4.4	MS
VI003699B-BR	India	2.5	R	3.0	R
VI004024AG	Australia	1.3	R	6.4	MS
VI004811BG	India	2.9	R	3.5	MR
VI002589BG	Unknown	8.2	S	7.6	S
CV%		14.89		6.12	
LSD		1.23		0.18	
R-Square		0.87		0.96	
MSS		7.10**		0.53**	

Significant at 1% probability level, CV: Coefficient of variation, LSD: Least significant difference, MSS: Mean sum of square, DRR disease score was rated on a 1-to-9 rating scale, where 1 = Immune and 9 = Highly susceptible, I= Immune, R: Resistant, MR: Moderately resistant, MS: Moderately susceptible, S: Susceptible, HS: Highly susceptible

Table 30. DRR disease reaction of identified resistant mungbean accessions in the glasshouse and in the field

Mungbean accessions	Sick pot-Hyderabad		Field-Yezin, Myanmar	
	Sick pot 1 (2018)	Sick pot 2 (2018)	2018	2019
	PDI (Reaction category)	PDI (Reaction category)	PDI (Reaction category)	PDI (Reaction category)
VI000203B-BR	13.01(MR)	13.01 (MR)	×	0.00 (HR)
VI000319AG	16.35 (MR)	16.35 (MR)	81.41 (HS)	4.23 (R)
VI000732AG	16.35 (MR)	10.00 (R)	13.29 (MR)	0.00 (HR)
VI000764AG	13.01 (MR)	13.01 (MR)	16.6 (MR)	1.12 (R)
VI000766BG	10.0 (R)	10 (R)	88.04 (HS)	9.78 (R)
VI000805BG	×	×	×	2.21 (R)
VI000815BG	×	×	0.00 (HR)	2.40 (R)
VI000818BG	20.0 (MR)	13.01 (MR)	65.83 (HS)	31.00 (S)
VI000981BG	×	×	86.52 (HS)	3.79 (R)
VI001244AG	6.67 (R)	6.67 (R)	3.77 (R)	2.31 (R)
VI001268BG	10 (R)	6.67 (R)	99.99 (HS)	16.16 (MR)
VI001282AG	6.76 (R)	6.67 (R)	43.06 (S)	8.85 (R)
VI001284AG	4.58 (R)	13.01 (MR)	28.48 (MS)	27.41 (MS)
VI001400AG	10.00 (R)	10.00 (R)	3.88 (R)	0.00 (HR)
VI001403BR	×	×	×	0.92 (R)
VI001406BG	×	×	23.70 (MS)	×
VI001412AG	×	×	62.21 (HS)	2.57 (R)
VI001419BG	13.01(MR)	10.00 (R)	73.43 (HS)	0.39 (R)
VI001482BG	×	×	9.74 (R)	0.03 (R)
VI001490AG	10.0 (R)	4.58 (R)	0.92 (R)	×
VI001509AG	4.58 (R)	4.58 (R)	2.60 (R)	0.17 (R)
VI001535BG	6.76 (R)	4.58 (R)	49.80 (S)	7.31 (R)
VI001548AG	13.01 (MR)	13.01 (R)	95.68 (HS)	0.32 (R)
VI001576BG	×	×	40.18 (S)	0.30 (R)
VI002529B-BL	20.00 (MR)	1.20 (R)	0.33 (R)	2.69 (R)
VI002587AG	×	×	0.00 (HR)	0.59 (R)
VI002589AG	×	×	6.51 (R)	3.66 (R)
VI003070AG	×	×	73.25 (HS)	1.66 (R)
VI003220AG	×	×	55.37 (HS)	×
VI003456AG	×	×	94.25 (HS)	×
VI003699B-BR	10.00 (R)	10.00 (R)	31.57 (S)	×
VI004024AG	×	×	7.98 (R)	0.00 (HR)
VI004811AG	×	×	0.63 (R)	0.23 (R)
VC6930-88	91.36 (HS)	96.20 (HS)	×	×
Yezin 11	×	×	82.5 (HS)	1.3 (R)
Yezin 14	×	×	29.2 (MS)	0.3 (R)
SE	0.0037	0.004	0.02	0.002
Probability (F>0.05)	<0.0001*	<0.0001*	>0.003*	>0.0006*
Chi-square value	×	×	0.60	0.70
F-Value	22.56	22.75	5.67	2.88

*Significant, ×: not performed, SE: Standard error, PDI: Percent disease incidence, HR: Highly Resistant, R: Resistant, MR: Moderately resistant, MS: Moderately susceptible, S: Susceptible, HS: Highly susceptible

Table 31. Disease severity scores on selected accessions from a multiyear and multi-location evaluation of a mungbean mini-core collection for anthracnose resistance in India and their agronomic characteristics. (Pandey et al., 2021b)

MC No.	Accession name	Mean Disease Severity Scores[a]					Agronomic characteristics		
		Hyderabad			Palampur		Days to 50% flowering[d]	Days to maturity[cd]	Yield per plant (g)[d]
		2016[b]	2017[b]	2018[b]	2018[b]	2019[b]			
1	VI000020AY	1.0[b]	1.4[ef]	3.0[abcdefghijklmno]	4.3[abcd]	8.1[ab]	39	64	7.9
8	VI000203B-BR	2.3[ab]	3.3[abcdef]	7.5[abcdef]	5.9[abcd]	3.0[ab]	42	74	7.4
9	VI000212A-BLM	7.3[ab]	8.5[a]	2.6[bcdefghijklmnop]	4.0[d]	$	40	71	5.8
15	VI000319AG	1.5[ab]	2.9[bcdef]	3.2[bcdefghijklmnop]	5.5[abcd]	3.0[ab]	35	65	7.5
16	VI000380AG	2.0[ab]	2.1[bcdef]	3.0[bcdefghijklmnop]	5.7[abcd]	$	37	66	10.1
18	VI000470AG	2.2[ab]	2.9[bcdef]	2.2[ghijklmnop]	6.0[abc]	8.5[a]	36	63	13.0
20	VI000537BG	1.8[ab]	2.1[bcdef]	3.6[abcdefghijklmno]	*	*	42	65	9.7
24	VI000559AG	2.5[ab]	2.5[bcdef]	2.5[efghijklmnop]	5.0[abcd]	2.5[ab]	39	69	7.0
26	VI000589B-BR	3.5[ab]	2.0[cdef]	4.3[abcdefghijklmno]	6.0[abc]	$	40	72	6.2
32	VI000732AG	1.9[ab]	4.3[abcdef]	3.0[bcdefghijklmnop]	3.1[cd]	4.9[ab]	38	69	7.3
36	VI000764AG	1.5[ab]	2.3[bcdef]	2.9[bcdefghijklmnop]	3.0[abcd]	$	38	66	9.1
37	VI000766BG	2.4[ab]	4.6[abcdef]	4.5[abcdefghijklmno]	5.9[abc]	$	36	67	9.4
38	VI000805BG	8.5[ab]	5.1[abcdef]	4.9[abcdefghijklmno]	4.3[abcd]	6.3[ab]	35	64	10.0
39	VI000815BG	1.4[ab]	4.2[abcdef]	6.8[abcdefghijk]	5.9[abcd]	3.4[ab]	37	65	12.8
40	VI000818BG	1.5[ab]	6.9[abcdef]	7.9[a]	6.6[a]	8.2[a]	35	63	8.6
41	VI000852AG	2.2[ab]	3.1[abcdef]	3.6[abcdefghijklmno]	5.0[abcd]	$	37	64	11.1
45	VI000981BG	1.4[ab]	2.4[bcdef]	5.7[abcdefghijklmn]	5.0[abcd]	4.1[ab]	36	63	10.1
50	VI001126BG	1.9[ab]	5.2[abcdef]	2.5[cdefghijklmnop]	5.7[abcd]	1.1[b]	45	68	11.2
51	VI001162AG	1.9[ab]	3.0[abcdef]	2.6[bcdefghijklmnop]	4.3[abcd]	2.9[ab]	41	73	5.0
53	VI001211AG	2.5[ab]	2.5[bcdef]	3.6[abcdefghijklmno]	4.9[abcd]	8.2[a]	40	71	10.2
54	VI001221AG	6.3[ab]	2.7[bcdef]	3.1[bcdefghijklmnop]	5.6[abcd]	8.2[a]	37	65	8.5
55	VI001244AG	1.8[ab]	3.7[abcdef]	5.5[abcdefghijklmn]	6.5[ab]	7.4[ab]	37	66	8.8
56	VI001268BG	2.8[ab]	3.1[abcdef]	3.8[abcdefghijklmno]	6.6[a]	$	37	69	9.5
57	VI001282AG	3.7[ab]	6.6[abcdef]	3.0[bcdefghijklmnop]	6.0[abc]	8.1[ab]	36	66	10.2
58	VI001284AG	5.6[ab]	4.9[abcdef]	3.5[abcdefghijklmno]	5.9[abcd]	6.9[ab]	37	64	8.5
61	VI001400AG	1.1[b]	2.2[bcdef]	3.5[abcdefghijklmno]	4.0[abcd]	2.3[ab]	43	70	9.7
62	VI001403BR	3.0[ab]	6.2[abcdef]	3.9[abcdefghijklmno]	5.9[abcd]	5.5[ab]	42	71	7.6
65	VI001411AG	3.6[ab]	2.1[bcdef]	3.9[abcdefghijklmno]	3.9[abcd]	2.6[ab]	41	68	8.5
66	VI001412AG	1.4[ab]	4.6[abcdef]	7.0[abcdefghi]	5.9[abcd]	2.9[ab]	41	66	11.3
67	VI001419BG	2.6[ab]	2.4[bcdef]	5.2[abcdefghijklmno]	4.7[abcd]	1.9[ab]	42	74	7.4
71	VI001482BG	2.0[ab]	5.8[abcdef]	4.3[abcdefghijklmno]	5.2[abcd]	3.7[ab]	38	72	10.6
72	VI001490AG	3.2[ab]	3.8[abcdef]	4.3[abcdefghijklmno]	5.6[abcd]	1.9[ab]	34	63	9.4

MC No.	Accession name	Mean Disease Severity Scores[a]					Agronomic characteristics		
		Hyderabad			Palampur		Days to 50% flowering[d]	Days to maturity[cd]	Yield per plant (g)[d]
		2016[b]	2017[b]	2018[b]	2018[b]	2019[b]			
73	VI001509AG	3.5^{ab}	4.9^{abcdef}	2.9^{bcdefghijklmnop}	6.2^{ab}	3.4^{ab}	37	66	6.6
74	VI001514AG	3.7^{ab}	3.0^{abcdef}	2.9^{bcdefghijklmnop}	5.0^{abcd}	2.9^{ab}	40	72	6.7
75	VI001520A-BLM	1.3^{ab}	1.7^{def}	1.9^{lmnop}	5.7^{abcd}	1.8^{ab}	39	73	9.4
77	VI001535BG	1.9^{ab}	5.1^{abcdef}	4.2^{abcdefghijklmno}	3.7^{bcd}	3.9^{ab}	38	64	8.8
79	VI001548AG	2.8^{ab}	2.5^{bcdef}	2.5^{efghijklmnop}	6.3^{ab}	4.3^{ab}	42	66	8.9
83	VI001576BG	2.3^{ab}	2.7^{bcdef}	4.5^{abcdefghijklmno}	6.7^{a}	5.9^{ab}	37	68	8.9
88	VI001651BG	2.5^{ab}	3.0^{abcdef}	2.0^{lmnop}	*	*	39	66	10.8
89	VI001652BG	2.4^{ab}	2.8^{bcdef}	3.0^{bcdefghijklmnop}	*	*	41	66	10.0
92	VI001692AG	5.6^{ab}	4.6^{abcdef}	4.8^{abcdefghijklmno}	6.0^{abc}	4.5^{ab}	37	64	11.0
94	VI001728AG	1.3^{ab}	3.0^{bcdef}	2.6^{bcdefghijklmnop}	*	*	39	72	9.8
102	VI001859BG	5.8^{ab}	3.7^{abcdef}	3.8^{abcdefghijklmno}	6.4^{ab}	9.0^{a}	41	70	8.4
106	VI002012BG	1.3^{ab}	5.3^{abcdef}	3.9^{abcdefghijklmno}	6.3^{ab}	6.3^{ab}	37	65	9.7
107	VI002051BG	2.6^{ab}	7.3^{abcd}	3.6^{abcdefghijklmno}	6.1^{abc}	6.6^{ab}	40	69	9.2
125	VI002487AG	1.5^{ab}	3.1^{abcdef}	5.3^{abcdefghijklmno}	6.1^{abc}	5.9^{ab}	39	70	8.2
127	VI002529B-BL	1.5^{ab}	2.3^{bcdef}	2.9^{bcdefghijklmnop}	5.1^{abcd}	1.0^{b}	40	72	7.2
131	VI002587AG	1.5^{ab}	7.3^{abcde}	3.9^{abcdefghijklmno}	5.0^{abcd}	1.8^{ab}	37	67	9.9
146	VI002993BG	1.6^{ab}	4.1^{abcdef}	4.8^{abcdefghijklmno}	4.7^{abcd}	3.9^{ab}	37	66	9.9
148	VI003019A-BLM	1.5^{ab}	5.1^{abcdef}	2.0^{klmnop}	6.5^{ab}	5.5^{ab}	37	69	7.1
149	VI003019BG	1.0^{b}	3.8^{abcdef}	4.5^{abcdefghijklmno}	5.6^{abcd}	3.0^{ab}	39	70	5.4
154	VI003068A-BR	2.1^{ab}	2.2^{bcdef}	2.6^{bcdefghijklmnop}	*	*	44	74	9.0
155	VI003070AG	3.0^{ab}	5.8^{abcdef}	4.8^{abcdefghijklmno}	4.7^{abcd}	1.9^{ab}	38	67	8.8
158	VI003135B-BL	1.8^{ab}	3.6^{abcdef}	5.7^{abcdefghijklmn}	6.0^{abc}	2.5^{ab}	37	63	7.8
162	VI003183AG	4.2^{ab}	4.5^{abcdef}	6.3^{abcdefghijklm}	5.4^{abcd}	8.8^{a}	40	67	7.6
167	VI003235AG	1.5^{ab}	2.9^{bcdef}	3.0^{bcdefghijklmnop}	4.7^{abcd}	3.3^{ab}	44	74	10.1
169	VI003251A-BL	1.4^{ab}	4.2^{abcdef}	2.6^{bcdefghijklmnop}	6.0^{abc}	3.9^{ab}	41	72	16.1
170	VI003251A-BLM	2.1^{ab}	3.9^{abcdef}	3.9^{abcdefghijklmno}	5.7^{abcd}	3.9^{ab}	38	66	9.9
175	VI003332AG	2.1^{ab}	4.8^{abcdef}	6.7^{abcdefghijkl}	6.5^{ab}	8.8^{a}	42	74	8.0
176	VI003337BR	1.5^{ab}	2.9^{bcdef}	2.0^{jklmnop}	*	*	42	75	9.4
180	VI003407AG	1.8^{ab}	5.1^{abcdef}	4.0^{abcdefghijklmno}	5.9^{abc}	7.4^{ab}	39	68	8.3
185	VI003465BG	2.7^{ab}	2.7^{bcdef}	6.8^{abcdefghijk}	5.0^{abcd}	2.0^{ab}	40	68	8.8
190	VI003493BG	1.4^{ab}	2.4^{bcdef}	1.9^{mnop}	*	*	37	66	8.3
191	VI003517BG	1.1^{b}	1.9^{cdef}	4.0^{abcdefghijklmno}	4.3^{abcd}	4.8^{ab}	38	70	8.5
194	VI003534BG	2.2^{ab}	1.2^{abcdef}	2.9^{bcdefghijklmnop}	5.0^{abcd}	8.1^{ab}	42	79	12.8
197	VI003563A-BR	5.0^{ab}	4.2^{abcdef}	4.9^{abcdefghijklmno}	6.4^{ab}	5.0^{ab}	37	67	9.8
207	VI003699B-BG	1.0^{b}	3.0^{abcdef}	1.0^{p}	4.0^{abcd}	1.4^{ab}	37	73	19.5

MC No.	Accession name	Mean Disease Severity Scores[a]					Agronomic characteristics		
		Hyderabad			Palampur		Days to 50% flowering[d]	Days to maturity[cd]	Yield per plant (g)[d]
		2016[b]	2017[b]	2018[b]	2018[b]	2019[b]			
208	VI003720BG	2.5^{ab}	1.9^{cdef}	2.0^{klmnop}	4.3^{abcd}	2.2^{ab}	38	66	6.6
212	VI003744AG	1.6^{ab}	5.6^{abcdef}	2.3^{ghijklmnop}	5.7^{abcd}	2.5^{ab}	38	68	9.5
214	VI003760BG	1.4^{ab}	2.4^{bcdef}	2.5^{defghijklmnop}	*	*	37	70	7.0
215	VI003785BG	2.2^{ab}	3.5^{abcdef}	7.0^{abcdefghijklmno}	5.3^{abcd}	$	37	65	11.0
222	VI003894B-BLM	6.5^{ab}	2.7^{bcdef}	2.0^{klmnop}	3.6^{bcd}	1.9^{ab}	41	66	7.8
235	VI003958B-BLM	1.5^{ab}	3.2^{abcdef}	3.1^{bcdefghijklmnop}	*	*	39	69	7.6
236	VI003959BG	2.7^{ab}	2.1^{bcdef}	3.9^{abcdefghijklmno}	2.6^{bcd}	2.5^{ab}	39	71	12.5
239	VI004024AG	1.5^{ab}	5.7^{abcdef}	3.5^{abcdefghijklmnop}	4.0^{abcd}	3.0^{ab}	39	73	10.1
241	VI004045A-DGM	1.9^{ab}	2.8^{bcdef}	2.6^{bcdefghijklmnop}	*	*	40	71	9.8
251	VI004244B-BR	7.9^{ab}	8.0^{ab}	6.4^{abcdefghijklm}	6.1^{abc}	7.5^{ab}	36	62	5.0
258	VI004423AG	7.5^{ab}	7.6^{abc}	5.3^{abcdefghijklmno}	6.0^{abcd}	9.0^{a}	37	64	5.0
267	VI004743AG	2.2^{ab}	1.6^{def}	3.0^{bcdefghijklmnop}	5.0^{abcd}	3.4^{ab}	40	73	11.9
270	VI004811BG	2.6^{ab}	5.6^{abcdef}	4.4^{abcdefghijklmno}	6.3^{ab}	8.0^{ab}	37	67	8.0
271	VI004822BG	3.4^{ab}	2.7^{bcdef}	4.4^{abcdefghijklmno}	6.0^{abc}	4.9^{ab}	36	66	7.1
292	VI005024B-BL	1.4^{ab}	2.0^{cdef}	2.0^{ijklmnop}	4.6^{abcd}	3.0^{ab}	42	76	10.3
293	VI005030BY	7.1^{ab}	2.7^{bcdef}	2.6^{bcdefghijklmnop}	5.3^{abcd}	3.5^{ab}	42	71	6.9
294	VI005041AG	2.6^{ab}	6.9^{abcde}	6.0^{abcdefghijklm}	6.0^{abc}	$	37	66	10.9

Score 1= no aphids

Score 2 = few individual aphids

Score 3 = few small individual colonies

Score 4 = several small colonies

Score 5 = large continuous colonies/dead plants

Figure 27. Visual scale for the assessment of cowpea aphid damage under different categories

Figure 28. Visual 1 to 5 scale for the assessment of thrips damage: 1= Resistant (healthy leaves, no damage symptoms) 2= moderately resistant/tolerant (few leaves damaged), 3 = moderately susceptible (most of the leaves damaged), 4 = Susceptible (whole plant damaged but less curling), 5 = highly susceptible (all leaves showing curling/stunted growth)

Table 32. Screening of improved mungbean lines against *Callasobruchus maculatus*

Mungbean line	Seed colour	No. of seeds	Total no. of eggs	No. of damaged seed	No. of adults emerged	Damage (%)
AVMU 1601	Shiny Green	50	64	0	0	0
AVMU 1602	Brown	50	58	0	0	0
AVMU 1603	Dull Green	50	71.3	1.7	1.7	3.3
AVMU 1604	Dull Green	50	62	0	0	0
AVMU 1605	Shiny Green	50	75	0	0	0
AVMU 1606	Shiny Green	50	57.3	0	0	0
AVMU1607	Shiny Green	50	78.9	0	0	0
AVMU 1609	Dull Green	50	86.7	0	1	0
AVMU 1610	Brown	50	77.7	0	0	0
AVMU 1611	Brown	50	79.7	0	0	0
AVMU 1612	Dull Green	50	101.3	0.7	0.7	1.3
AVMU 1613	Dull Green	50	77.3	0.3	0.3	0.7
AVMU 1614	Brown	50	63.7	0	0	0
AVMU 1615	Brown	50	76	0	0	0

Mungbean line	Seed colour	No. of seeds	Total no. of eggs	No. of damaged seed	No. of adults emerged	Damage (%)
AVMU 1616	Brown	46	102	0	0	0
AVMU 1617	Brown	40	93.7	0	0	0
AVMU 1618	Dull Green	50	76.3	0	0	0
AVMU 1619	Brown	50	62	0	0	0
AVMU 1620	Dull Green	50	64	0	0	0
AVMU 1621	Dull Green	50	56.3	0	0	0
AVMU 1622	Dull Green	50	92	0	0	0
AVMU 1623	Dull Green	50	63.3	0	0	0
AVMU 1624	Dull Green	50	77	1	0.7	2
AVMU 1625	Dull Green	50	67	1.7	1.7	3.3
AVMU 1626	Dull Green	50	83.7	0	0	0
AVMU 1627	Dull Green	50	106.3	1.3	1	2.7
AVMU 1628	Dull Green	50	108	0	0	0
AVMU 1629	Dull Green	50	94	1	1	2
AVMU 1630	Dull Green	50	91	0.7	0.3	1.3
AVMU 1646	Dull Green	50	56.3	20.3	20.3	40.7
AVMU 1647	Shiny Green	50	94.7	12.3	19	24.7
AVMU 1648	Shiny Green	50	78.3	11.7	10.3	23.3
AVMU 1649	Shiny Green	50	77.7	8.7	8.7	17.3
AVMU 1650	Shiny Green	50	83.3	20.7	20.7	41.3
AVMU 1651	Shiny Green	50	95	32.3	31	64.7
AVMU 1652	Shiny Green	50	78	20	20	40
AVMU 1653	Dull Green	50	65.3	17	17	34
AVMU 1654	Dull Green	50	64.3	23	23	46
AVMU 1655	Shiny Green	50	88	28.3	28.3	56.7
AVMU 1656	Shiny Green	50	76.7	14.7	14	29.3
AVMU 1657	Shiny Green	50	90.3	32	32	64
AVMU 1658	Shiny Green	50	62.7	5.3	5.3	10.7
AVMU1659	Dull Green	50	95	34	32	64.0
AVMU 1660	Dull Green	50	92	24	38.7	48
NM94	Dull Green	50	107	49.3	45.3	98.7
V2802	Shiny Green	50	63.7	0	0	0
F			9.43	159.45	172.16	159.45
p			<0.001	<0.001	<0.001	<0.001
LSD (P 0.05)			13.93	2.67	2.66	5.35
CV (%)			10.9	11.6	10.6	12.6

Data shown is as mean of three replications.

Mechanism of resistance in improved mungbean lines against bruchids

The physical (seed hardness) and biochemical properties (phenol content, condensed tannins, soluble protein, starch content and sugar content) of the 42 AVMU lines were assessed in the laboratory (Table 8) to understand the biochemical basis for the resistance in the AVMU lines.

Some of the bruchid resistant lines showed higher hardness than some of the susceptible lines (Fig. 4). The highest seed hardness was observed in AVMU 1625 (54.12 N), V2802

(53.99 N), AVMU 1652 (52.71 N), AVMU 1619 (51.70) and AVMU 1630 (51.43). The lowest seed hardness was observed in AVMU 1655 (17.21 N), AVMU 1617 (16.90 N) and AVMU 1649 (15.95 N). (Fig. 8).

Phenol content of some of the AVMU lines with reduced bruchid damage was significantly higher than that of V2802 and NM 94. AVMU 1602, AVMU 1607, AVMU 1615 and AVMU 1618 showed higher levels of condensed tannins compared to the checks. Soluble protein content was significantly different between bruchid resistant and the susceptible lines. The soluble sugar and starch contents of bruchid resistant mungbean lines were significantly lower than the susceptible lines and the susceptible check, NM94. HPLC chromatogram showed differential peaks among the bruchid resistant and bruchid susceptible AVMU lines and V2802 and NM 94 (Fig. 9). Thus, the higher amounts of phenols, tannins and proteins, and the lower contents of total soluble sugars and starch can be attributed to the resistance and/or susceptibility to *C. maculatus* in mungbean. However, in-depth studies are needed to elucidate the effects of these compounds on bruchid growth and development to confirm their role in resistance/susceptibility of mungbean to bruchids.

Table 33. Seed hardness and biochemical profile of improved mungbean lines

Mungbean lines	Seed hardness (N)	Phenol content (µg GAE g^{-1} Seed)	Condensed tannins (µg CE g^{-1} seed)	Soluble protein (mg g^{-1} seed)	Starch content (µg Glu E g^{-1} seed)	Sugar content (µg Glu E g^{-1} seed)
AVMU 1601	31.3	7.40	5.63	177.45	101.00	5.87
AVMU 1602	46.0	6.03	6.03	179.10	122.20	18.97
AVMU 1603	46.3	6.91	5.41	178.05	80.30	5.75
AVMU 1604	34.7	4.24	4.56	175.05	86.00	24.97
AVMU 1605	29.2	4.76	4.73	169.95	122.70	26.50
AVMU 1606	34.4	3.78	4.07	172.05	147.80	6.45
AVMU 1607	41.8	3.05	6.28	170.70	178.90	6.32
AVMU 1609	21.9	2.37	4.64	165.45	84.20	21.44
AVMU 1610	42.3	3.42	4.43	174.75	76.50	6.76
AVMU 1611	33.9	3.49	5.09	176.25	85.40	5.89
AVMU 1612	29.6	1.75	4.06	179.40	147.00	22.08
AVMU 1613	29.7	2.98	3.91	169.35	128.80	22.09
AVMU 1614	43.1	5.39	2.34	180.90	107.50	21.81
AVMU 1615	26.0	4.45	6.32	169.95	81.90	6.40
AVMU 1616	25.6	4.11	1.42	177.90	147.40	19.63
AVMU 1617	16.9	3.34	5.09	174.75	146.30	12.42
AVMU 1618	21.9	6.27	6.15	108.80	107.50	23.82
AVMU 1619	51.7	7.29	5.37	183.90	94.20	5.57
AVMU 1620	37.2	3.24	3.10	185.70	122.00	23.71
AVMU 1621	38.6	5.68	3.96	169.20	124.00	5.61
AVMU 1622	49.0	5.37	4.11	175.35	82.10	24.05
AVMU 1623	24.8	5.57	4.04	172.20	100.60	22.12
AVMU 1624	24.3	3.38	3.10	174.30	76.50	16.71

Mungbean lines	Seed hardness (N)	Phenol content (µg GAE g^{-1} Seed)	Condensed tannins (µg CE g^{-1} seed)	Soluble protein (mg g^{-1} seed)	Starch content (µg Glu E g^{-1} seed)	Sugar content (µg Glu E g^{-1} seed)
AVMU 1625	54.2	3.41	3.45	179.85	89.00	23.25
AVMU 1626	35.2	5.26	3.08	160.95	85.50	21.98
AVMU 1627	27.8	6.31	3.25	180.45	87.50	24.08
AVMU 1628	34.2	5.17	3.44	157.35	99.00	6.66
AVMU 1629	34.0	3.79	3.39	178.50	75.20	23.52
AVMU 1630	51.4	3.01	4.24	171.90	112.70	23.44
AVMU 1646	29.3	5.01	3.52	182.55	92.60	6.09
AVMU 1647	40.7	4.92	4.02	172.95	198.10	15.86
AVMU 1648	43.5	4.32	3.31	168.60	153.20	8.41
AVMU 1649	16.0	4.65	4.55	185.40	135.00	9.11
AVMU 1650	35.7	5.22	3.74	190.20	153.50	6.98
AVMU 1651	37.1	5.00	3.74	163.35	121.90	7.21
AVMU 1652	52.7	4.37	3.30	180.30	89.80	5.95
AVMU 1653	43.2	3.43	3.53	171.90	117.40	6.25
AVMU 1654	29.7	2.84	3.06	182.10	199.40	13.99
AVMU 1655	17.2	6.00	3.91	164.40	122.30	6.09
AVMU 1656	23.7	5.49	4.56	187.65	121.70	5.82
AVMU 1657	36.6	5.31	5.73	177.30	111.20	6.32
AVMU 1658	38.7	4.64	5.82	178.65	130.30	12.93
AVMU 1659	33.0	5.68	3.38	163.50	121.00	16.75
AVMU 1660	23.2	6.12	4.69	159.30	132.20	16.03
V2802	54.0	5.22	4.80	191.40	101.00	21.79
NM94	32.5	3.04	1.32	154.50	139.00	27.80
P	<0.001	<0.01	<0.01	<0.05	<0.01	<0.05
F	26.78	79.45	54.08	99.9	83.09	44.32
LSD (P 0.05)	3.80	1.58	1.30	8.10	7.98	3.74
CV (%)	12.2	10.3	13.76	15.20	14.88	10.89

Data shown is as mean of three replications

F = 107.45, *p* = <0.001, LSD (P 0.05) = 3.80, CV (%) = 12.2

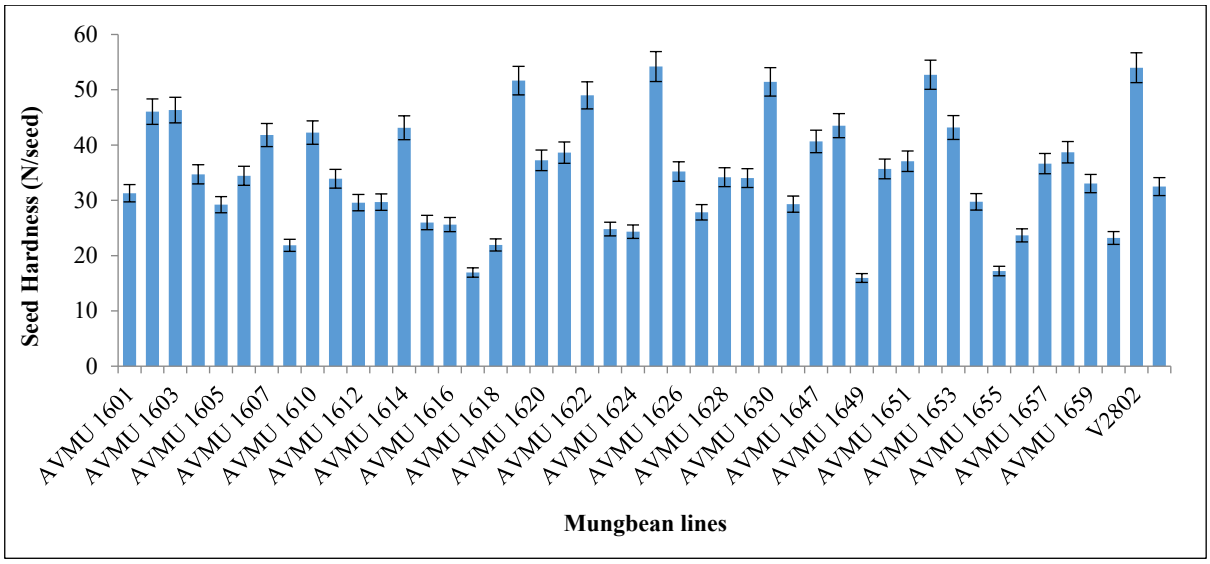


Figure 29. Seed hardness of improved mungbean lines

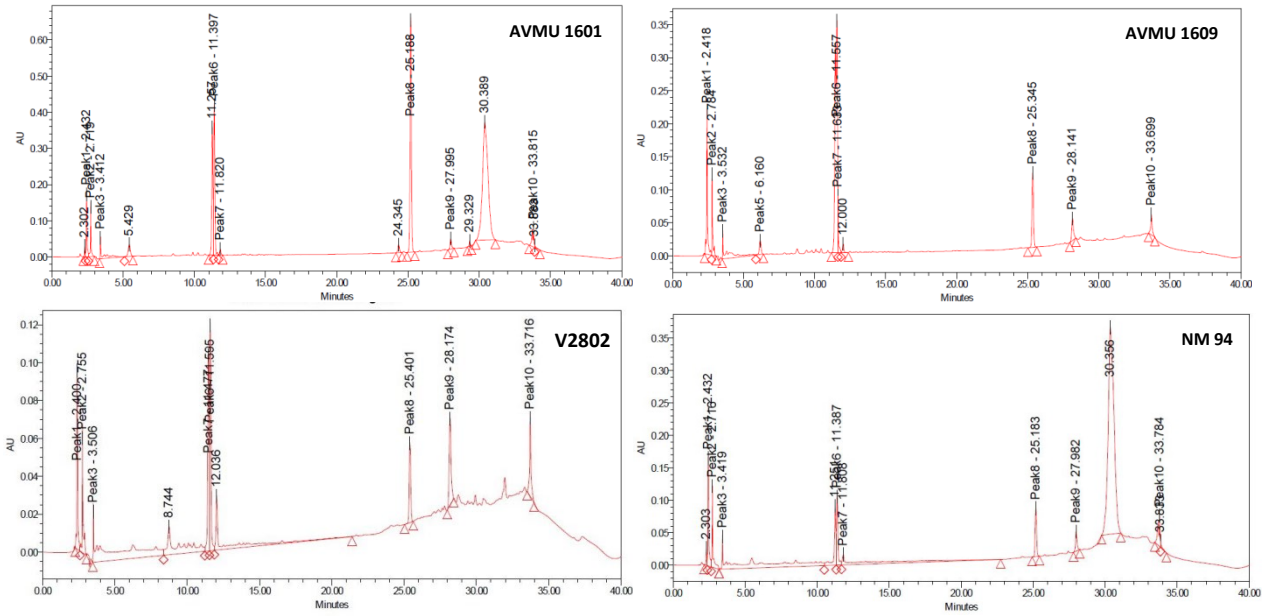


Figure 30. HPLC chromatograms of AVMU 1601, AVMU 1609, V2802 and NM94

Table 34. Incidence of whitefly, *Bemisia tabaci* and jassid in mungbean and urdbean

S.No.	Entries	Number of jassid adults		Number of whitefly adults		Yield (kg/ha)
		Per trifoliate leaf	Per cage	Per trifoliate leaf	Per cage	
1.	AVMU 1676	2.67 (1.91)	4.50 (2.30)	2.33 (1.81)	4.83 (2.36)	1493
2.	AVMU 1678	3.00 (1.98)	5.67 (2.54)	2.00 (1.73)	4.17 (2.22)	2405
3.	AVMU 1679	2.33 (1.82)	9.50 (3.21)	3.17 (2.02)	6.67 (2.73)	1079
4.	AVMU 1681	2.17 (1.77)	5.00 (2.42)	2.00 (1.73)	4.83 (2.37)	762
5.	AVMU 1682	2.50 (1.86)	5.00 (2.41)	2.83 (1.93)	5.50 (2.43)	784
6.	AVMU 1683	2.17 (1.77)	6.50 (2.70)	3.17 (2.02)	9.83 (3.16)	790
7.	AVMU 1684	2.00 (1.73)	6.67 (2.72)	2.67 (1.90)	8.33 (2.97)	1398
8.	AVMU 1685	2.67 (1.91)	5.50 (2.52)	2.33 (1.81)	7.00 (2.79)	1217
9.	AVMU 1686	2.33 (1.82)	7.17 (2.81)	2.33 (1.82)	14.67 (3.95)	385
10.	AVMU 1687	2.33 (1.82)	8.67 (3.08)	2.50 (1.86)	12.33 (3.59)	395
11.	AVMU 1688	2.83 (1.94)	7.50 (2.85)	2.67 (1.90)	5.50 (2.50)	1226
12.	AVMU 1689	2.83 (1.94)	8.83 (3.11)	2.33 (1.81)	5.67 (2.53)	1214
13.	AVMU 1690	2.50 (1.86)	4.50 (2.32)	2.50 (1.85)	8.00 (2.93)	1288
14.	ML 1628	3.00 (1.99)	8.83 (3.08)	2.50 (1.86)	6.33 (2.67)	1791
15.	NM 94	2.50 (1.86)	14.33 (3.91)	2.67 (1.89)	7.33 (2.82)	141
16.	Mash 1-1	2.00 (1.73)	11.33 (3.49)	4.83 (2.40)	28.17 (5.24)	1019
17.	VM 02164	2.00 (1.73)	12.33 (3.63)	5.00 (2.43)	26.50 (5.14)	223
18.	TV 1312	2.00 (1.73)	12.33 (3.63)	5.00 (2.40)	45.67 (6.79)	707
19.	TV 1299	2.00 (1.73)	11.00 (3.45)	5.00 (2.40)	25.17 (4.94)	*
20.	GBNO 3-1	2.00 (1.73)	12.83 (3.70)	5.00 (2.40)	23.50 (4.91)	*
21.	ML 2056 (ch)	2.50 (1.86)	4.67 (2.35)	2.17 (1.77)	3.33 (2.00)	1956
22.	Mash 338 (ch)	2.00 (1.73)	4.50 (2.33)	3.83 (2.18)	10.50 (3.36)	2432
	C.D. 5%	(0.16)	(0.44)	(0.27)	(0.86)	190

Figures in parentheses are the mean transformed square root values
**Plants died due to severe incidence of MYMV

Compatibility of insecticides with Trichoderma for seed treatment and management of sucking pests in mungbean

Trichoderma is a biocontrol agent which shows antagonistic activity towards a broad spectrum of phytopathogens. It is widely used as a pest management component in sustainable agriculture production. It can be safely used with chemical fertilizers, however, some insecticides might not show compatibility with *Trichoderma* beyond specific concentrations, and need to be identified before combining them.

The compatibility of insecticides with *Trichoderma* for seed treatment was evaluated with poisoned food techniques by measuring the mycelial diameter of *Trichoderma*. 10 ml potato dextrose agar (PDA) medium was taken in a Petri plate and different concentrations of Thiamethoxam and Imidacloprid were added to it. After cooling, *Trichoderma* culture (6 mm)

was placed at the center of each plate. Petri plates were kept in a completely randomized design, and incubated at 28 ° C. The *Trichoderma* colony diameter was measured on days 3, 5, and 7 after treatment.

Percent Inhibition =

$$\frac{\text{Growth in untreated control} - \text{Growth in insecticide amended medium}}{\text{Growth in untreated control}} \times 100$$

Per cent inhibition of *Trichoderma* culture was increased with the raising concentration of Thiamethoxam. There are significant differences between the growth inhibition caused by 8g/L and 2g/L and 4 g/L of Imidacloprid, but other concentrations showed no significant difference (Figures 10 and 11).

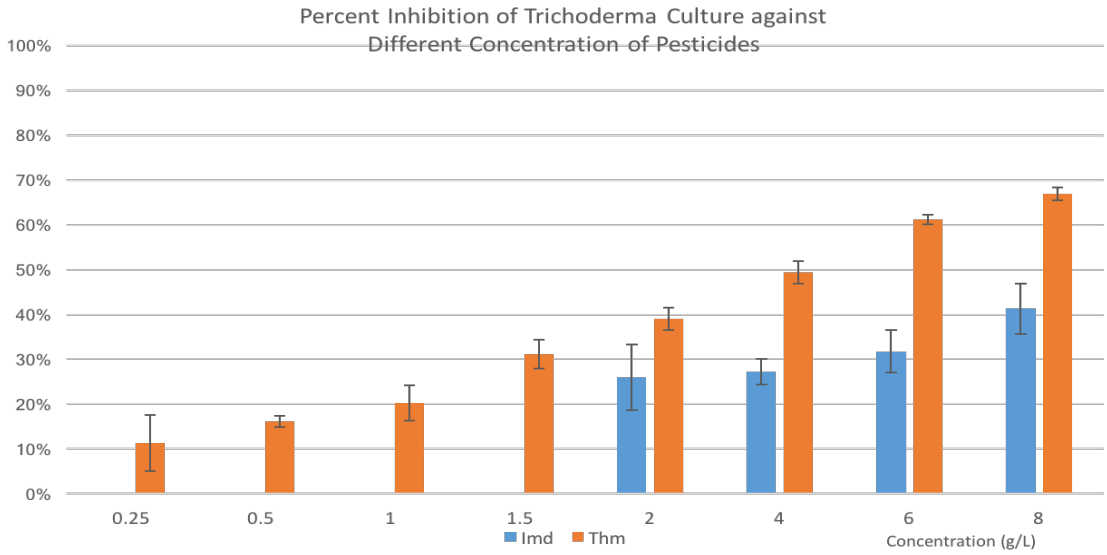


Figure 31. Percent inhibition rate of in vitro *Trichoderma* culture against different concentrations of Imidacloprid and Thiamethoxam. Data shown is Mean + SE (p = 0.006, F = 53.82, LSD = 0.12, CV (%) = 19.1; Imd = Imidacloprid, Thm = Thiamethoxam)

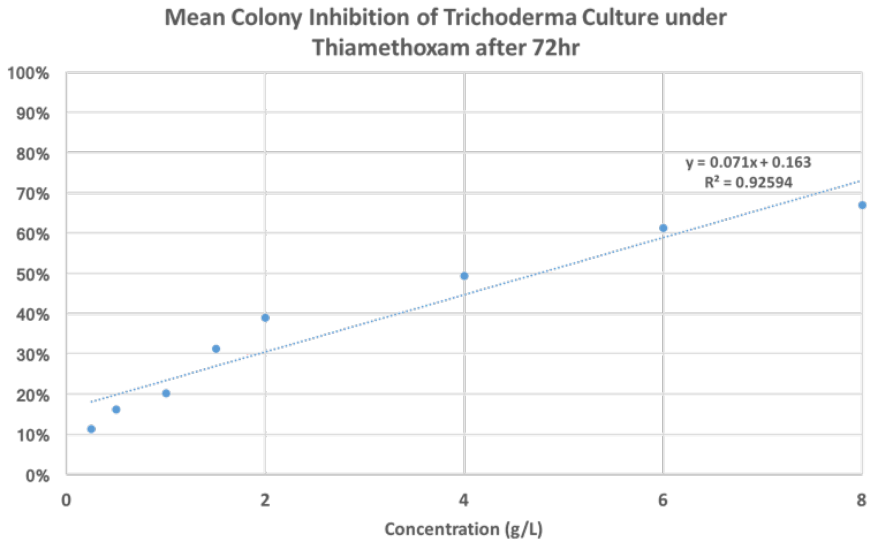


Figure 32. Mean colony inhibition rate of in vitro Trichoderma culture against different concentrations Thiamethoxam after 72 hr culture.

Effect of different seed treatment on mungbean seed germination under laboratory and field conditions

A commercial variety (NM94) was used for this study. For the germination test, 100 ml of Thiamethoxam and Imidacloprid solutions in different concentrations were prepared. The seeds were soaked in the insecticide solution for 15 mins. After shade dry, 60 µl of liquid Trichoderma culture was added into the seed container, shaken to make sure the Trichoderma is fully coated onto the seeds. After shade drying for 30 min, the seeds were kept in Petri Plates for lab germination and a separate set of seeds was sown. In laboratory experiment, thirty seeds each, 6 treatments, with 3 replications were placed onto the wet blotter paper inside the plastic containers to maintain the humidity. Seed germination (%) was recorded 72 hr after treatment/sowing. There are no significant differences between each treatment in both field and lab germination rate (Table 11).

Table 35. Effect of seed treatments in mungbean under laboratory and field conditions.

Treatment	Lab germination (%)	Field germination (%)
Imidacloprid 2 g/L + Trichoderma 13g/kg seed	63.3 ± 9.9	51.7 ± 12.0
Thiamethoxam 1 g/L + Trichoderma 13g/kg seed	55.3 ± 10.5	58.3 ± 9.7
Imidacloprid 2 g/L	58.3 ± 6.7	54.6 ± 11.2
Thiamethoxam 1 g/L	58.3 ± 11.7	55.3 ± 10.7
Trichoderma 13g/kg seed	56.7 ± 10.3	53.9 ± 14.5
Untreated Control	65.3 ± 8.9	61.7 ± 12.9
P	0.561	0.861
F	7.37	9.65
LSD (P 0.05)	10.6	9.2
CV (%)	14.5	17.8

Effect of different seed treatment on thrips damage, seedling vigor and biochemical profile of mungbean plants under field conditions

For the seed treatment for field sowing, 100 ml of Thiamethoxam and Imidacloprid solutions in different concentrations were prepared. The seeds were soaked in the insecticide solution for 15 mins. After shade dry, 60 µl of liquid Trichoderma culture was added into the seed container, shaken to make sure the Trichoderma is fully coated onto the seeds. After shade drying for 30 min, the seeds were sown. Field Experiment was done as per RBD with six treatments and three replications in each treatment. The results are shown in Table 12.

Table 36. Effect of different seed treatment on thrips damage, seedling vigor and biochemical profile of mungbean plants

Treatment	Thrips damage score*	Seedling vigor	Flavonoid content (µg cm-2)	Chlorophyll (µg cm-2)	NBI index	Soluble protein
1.	Imidacloprid 2 g/L + Trichoderma 13g/kg seed					
	2.66 ± 0.07	4.56 ± 0.12	1.120 ± 0.02	30.71 ± 3.1	25.0 ± 2.3	89.2 ± 12.4
2	Thiamethoxam 1 g/L + Trichoderma 13g/kg seed					
	2.01 ± 0.12	4.67 ± 0.11	1.214 ± 0.09	31.18 ± 5.4	23.1 ± 3.0	89.9 ± 10.2
3	Imidacloprid 2 g/L					
	2.33 ± 0.11	3.44 ± 0.09	1.282 ± 0.12	30.28 ± 3.9	26.0 ± 2.1	76.5 ± 15.7
4	Thiamethoxam 1 g/L					
	3.04 ± 0.07	4.22 ± 0.06	1.138 ± 0.04	30.73 ± 4.2	27.6 ± 2.7	84.9 ± 10.9
5	Trichoderma 13g/kg seed					
	3.33 ± 0.08	3.22 ± 0.13	1.132 ± 0.02	32.74 ± 7.0	32.7 ± 4.9	86.7 ± 12.3
Untreated Control						
	3.66 ± 0.16	3.78 ± 0.17	1.208 ± 0.04	29.68 ± 9.1	39.2 ± 3.5	87.7 ± 17.8
F	7.2	8.01	1.26	3.24	1.71	49.89
P	0.005	0.003	0.052	0.054	0.22	0.05
LSD (P 0.05)	0.74	0.661	0.179	1.822	4.81	6.8
CV (%)	14.4	9.1	8.3	3.2	9.9	12.5

Data shown is Mean +SE. *thrips damage score was given on visually rating scale of 1-5 (1= no or least damage, 5 = highest damage). Seedling vigor scoring was done at 15 days after sowing on a visual rating scale of 1-5 (1= least vigor-dead and 5 = high vigor), NBI = nitrogen basal index

11.7 Lines distributed to partners

Table 37. List of mungbean lines distributed to the partners with their Fe content

No.	Line	Fe content (mg/100g)	No.	Line	Fe content (mg/100g)
1	AVMU1677	8.08	27	AVMU 2001	15.15
2	AVMU1678	6.30	28	AVMU 2002	9.8
3	AVMU1679	7.01	29	AVMU 2003	11.48
4	AVMU1680	5.72	30	AVMU 2004	9.07
5	AVMU1681	6.47	31	AVMU 2005	8.61
6	AVMU1682	7.26	32	AVMU 2006	9.73
7	AVMU1683	4.98	33	AVMU 2007	14.02
8	AVMU1684	5.70	34	AVMU 2008	8.15
9	AVMU1685	7.77	35	AVMU 2009	8.23
10	AVMU1686	7.67	36	AVMU 2010	8.23
11	AVMU1687	5.99	37	AVMU 2011	8.03

No.	Line	Fe content (mg/100g)	No.	Line	Fe content (mg/100g)
12	AVMU1688	4.92	38	AVMU 2012	8.29
13	AVMU1689	6.98	39	AVMU 2013	8.72
14	AVMU1690	4.86	40	AVMU 2014	8.36
15	AVMU 1694	6.87	41	AVMU 2015	8.39
16	AVMU 1695	6.78	42	AVMU 2016	9.00
17	AVMU 1696	6.89	43	AVMU 2017	8.43
18	AVMU 1697	6.88	44	AVMU 2018	8.22
19	AVMU 1698	7.54	45	AVMU 2019	8.05
20	AVMU 1699	7.22	46	AVMU 2020	8.07
21	AVMU 16100	6.70	47	AVMU 2021	8.06
22	AVMU 16101	6.97	48	AVMU 2022	8.46
23	AVMU 16102	7.04	49	AVMU 2023	8.25
24	AVMU 16103	7.31	50	AVMU 2024	8.46
25	AVMU 16104	6.89	51	AVMU 2025	8.83
26	AVMU 16105	6.43			

Table 38. The project partners in IMIN1 and collaborators from other countries were provided with AVMU lines from WorldVeg:

Countries	2016	2017	2018	2019	2020	2021
Armenia		5				
Australia	59				14	163
Bangladesh	59		2		52	163
Benin			15	21		
Cambodia						115
Ghana			57			
India	183					
Indonesia					6	253
Kenya	56		52	26	25	163
Lao			4			115
Mali			15			
Mozambique	8		8			
Myanmar	59	22	9	7	52	163
Nepal	20				3	
Netherlands	26					7
Nigeria			15			
Pakistan			1			
Paraguay	1		3			
Philippines						115
PNG	5					
Republic of Ivory Coast			15			
South Africa		16				

Countries	2016	2017	2018	2019	2020	2021
Sri Lanka	12					
Taiwan				3		
Tanzania	8		57	31	25	5
Thailand				6		2
Uganda		15	39	26	25	
USA		53	9	6		
Uzbekistan	1	4				15
Vietnam		15		5		
total	**497**	**130**	**301**	**131**	**202**	**1279**

Table 39. Details of mungbean advanced breeding lines distributed in India

S. No	Center's/SAU's/Private seed company	No. of lines	Resistance/tolerance to
1.	ICAR-Indian Institute of Pulses Research (ICAR-IIPR)	90	MYMD, Bruchid and Heat stress
2.	ICAR-Indian Institute of Agricultural Research (ICAR-IARI)	87	MYMD, Bruchid
3.	Punjab Agricultural University (PAU)	205	MYMD, Bruchid and Heat stress
4.	Panjab University (PU)	45	Heat stress
6.	Odisha University of Agriculture and Technology (OUAT)	72	MYMD, Bruchid and Heat stress
7.	Tamil Nadu Agricultural University (TNAU)	15	MYMD, and Bruchid
8.	University of Agricultural Sciences-Raichur (UAS-R)	30	MYMD and Heat stress
9.	University of Agricultural Sciences-Dharwad (UAS-D)	15	MYMD, and Bruchid
10.	Bidhan Chandra Krishi Viswavidyalaya (BCKV)	15	MYMD, and Bruchid
11.	The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	55	MYMD, Bruchid and Heat stress
12.	Nirmal Seeds Pvt. Ltd.	17	MYMD, Bruchid
13.	Daftari Seeds (OPC) Pvt Ltd	20	MYMD
14.	Basant Agro Tech (I) Ltd	4	MYMD

11.8 Evaluation of Mungbean Advanced Breeding Lines

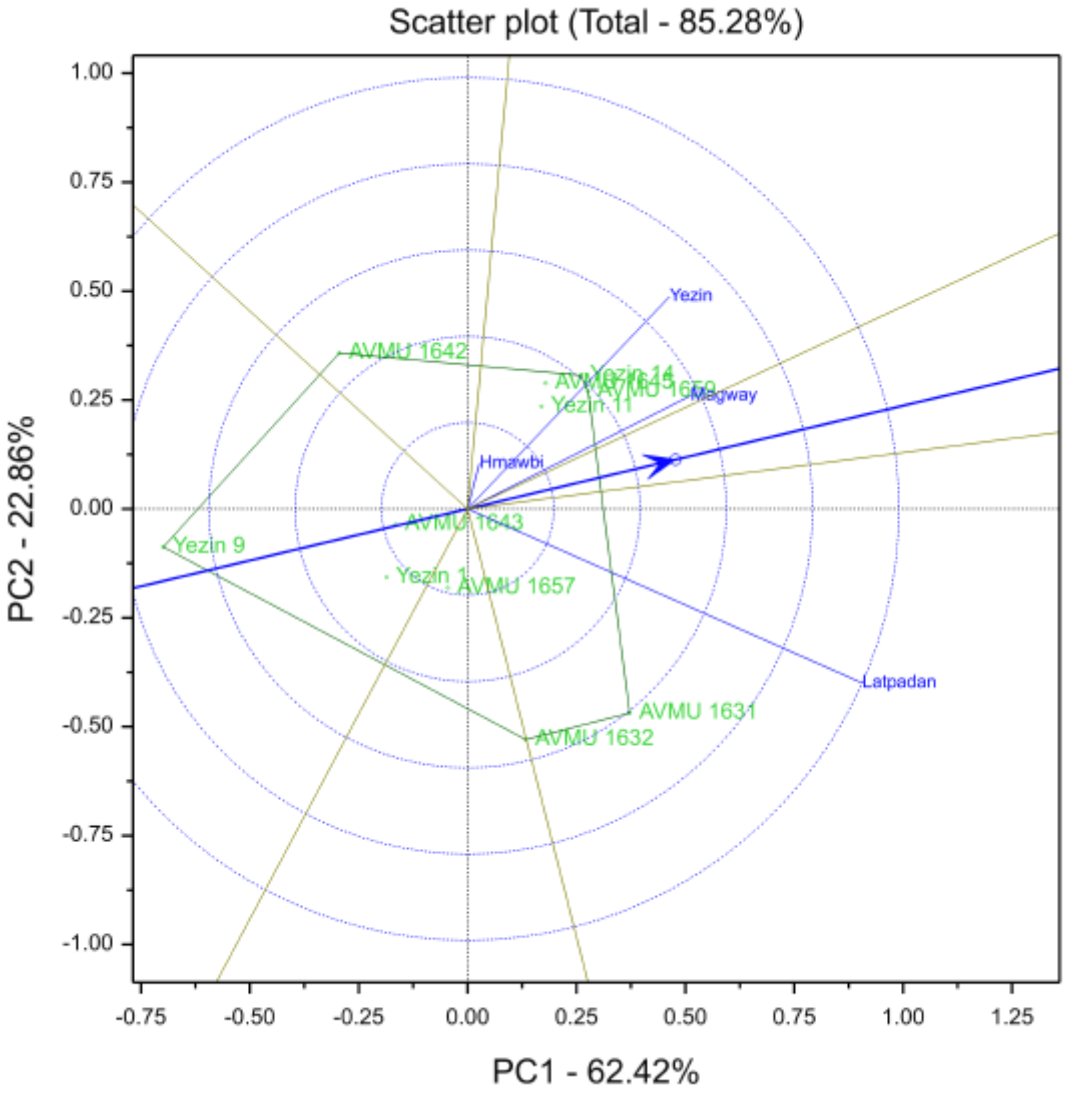


Figure 33. GGE biplot analysis for seed yield per plant of mungbean advanced breeding lines evaluated across location in Myanmar during 2020-21

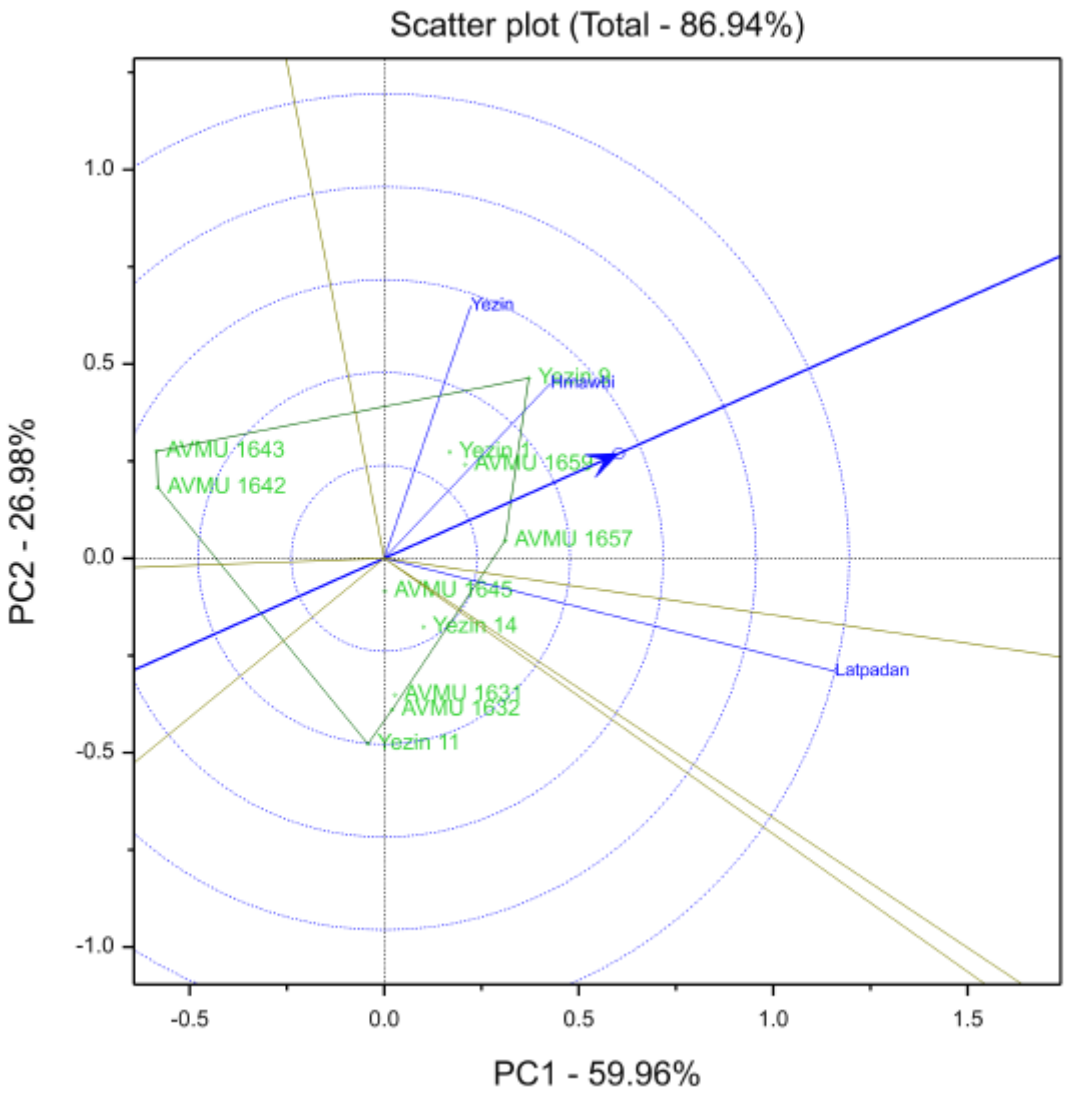


Figure 34. GGE biplot analysis for days to maturity of mungbean advanced breeding lines evaluated across the locations in Myanmar during 2020-21

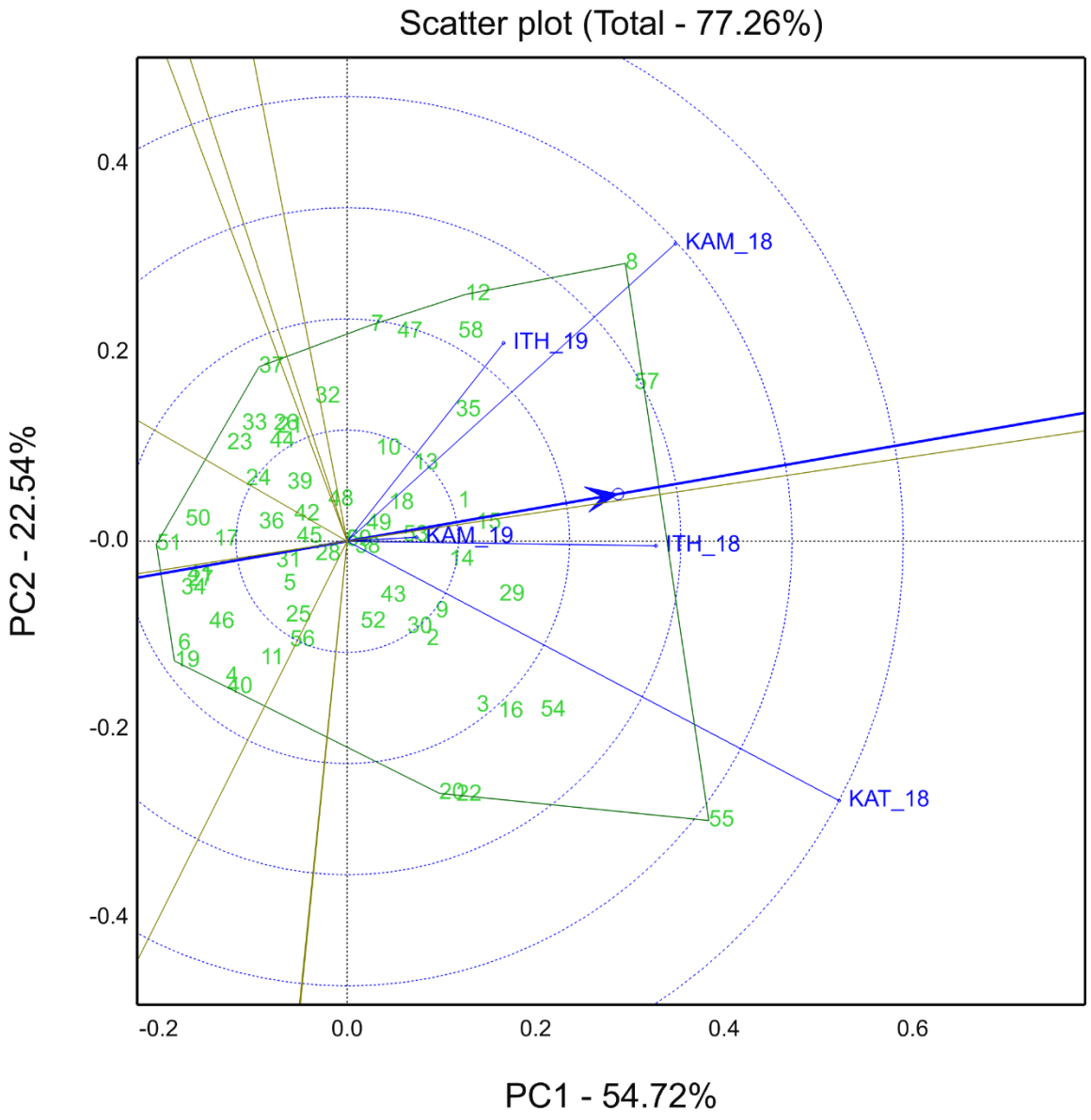


Figure 35. GGE biplot for seed yield per plant of mungbean advanced breeding lines evaluated across different locations in Kenya during 2018 and 2019.

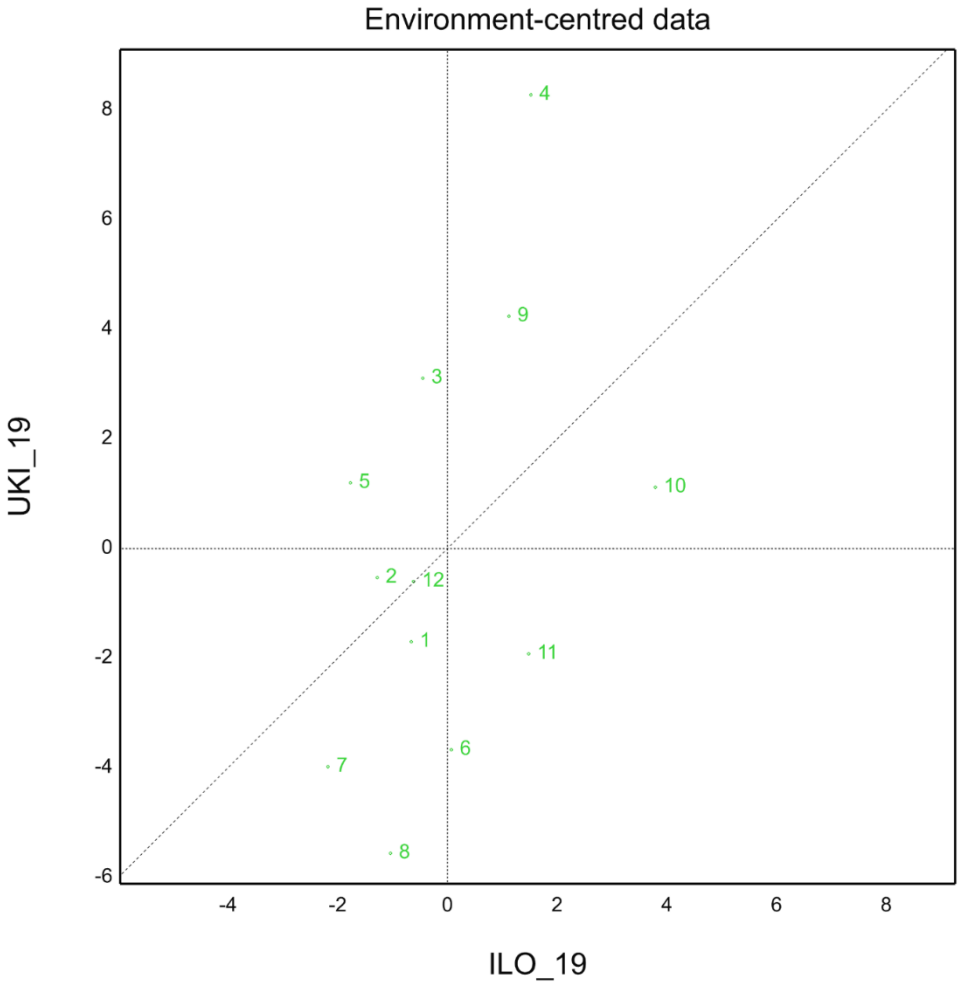


Figure 36. Environment centred biplot for seed yield per plant of selected advanced breeding lines evaluated at Ilonga and Ukiriguru, Tanzania during 2019

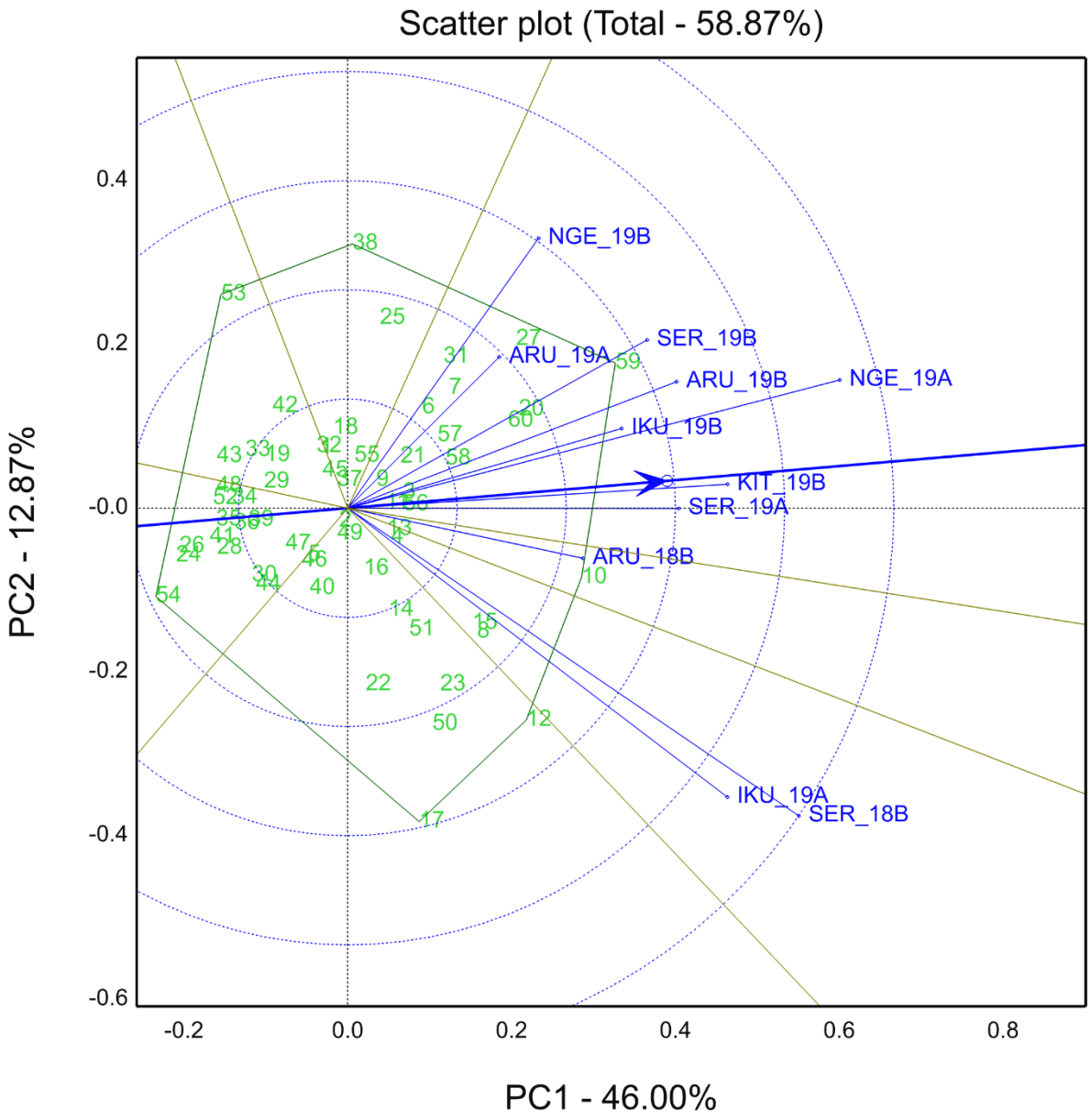


Figure 37. GGE biplot for seed yield per plant of mungbean advanced breeding lines evaluated across different locations in Uganda during 2018 and 2019.