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Bacterial Pustule- an important disease in Soybean: A review

TOTADE S. P.^{1,2}, GUPTA S. K.^{1,2*}, MANJAYA J. G.^{1,2}

¹Homi Bhabha National Institute, Mumbai-400085 India,

²Nuclear Agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Mumbai-400085, India

Email: skgupta@barc.gov.in

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ABSTRACT

Soybean is an economically important crop known for its high protein and oil content. Production of soybean is consistently threatened by many biotic factors. Among them, bacterial pustule caused by bacteria *Xanthomonas citri* pv. *glycines* (Xcg) is a very destructive disease threatening the soybean production worldwide. This review article provides an overview on bacterial pustule disease of soybean including biology of the Xcg pathogen, disease symptoms, detection, screening methodologies, the global distribution and genetic variability of Xcg. The article also summarizes the management strategies and details of resistance sources available in soybean against bacterial pustule. In addition, it highlights recent advances in identifying resistance loci and QTLs against Xcg through genetic linkage analysis as well as genome-wide association studies (GWAS).

Keywords: Soybean, Bacterial pustule, *Xanthomonas citri* pv. *glycines*, disease resistance, Xcg

Soybean (*Glycine max* (L.) Merr.), often referred to as the *miracle crop*, *wonder crop*, or *golden bean*, is an annual, self-pollinating diploid species (2n = 40) with a genome size of 1.1 giga base (Schmutz et al., 2010; Carey and Lal, 2021). It belongs to the genus *Glycine* Willd., within the family Fabaceae, subfamily Papilionoideae, and tribe Phaseoleae (Hymowitz et al., 1998; Dupare et al., 2008). The genus *Glycine* is divided into two subgenera: *Glycine* and *Soja*. The cultivated soybean (*Glycine max* (L.) Merr.) and its wild annual progenitor *Glycine soja* Sieb. & Zucc. are members of the subgenus *Soja* (Kollipara et al., 1997). In contrast, the sub genus *Glycine* comprises 16 wild perennial species

that inhabit diverse geographical regions and a broad range of climatic conditions (Singh et al., 1988, 1992; Tindale and Craven, 1988, 1993; Kollipara et al., 1997; Dupare et al., 2008). Like other legumes, soybean can fix atmospheric nitrogen through symbiotic association with *Rhizobium* species, thereby enhancing soil fertility (Kebede, 2021).

Soybean is highly valued for its exceptional nutritional profile, containing approximately 40% protein and 20% oil, along with important vitamins and minerals (Liu, 1997). It serves as a primary source of oil and protein and is widely used in animal feed and the production of various soy-

based food products (Hartman et al., 2011). Soybean is an affordable source of high-quality protein, comparable to animal protein, making it a vital food to help meet the nutritional demands of the growing global population (Messina, 2022). Additionally, it is rich in essential fatty acids, isoflavones, folic acid, carbohydrates, minerals, and vitamins (Dukariya et al., 2020).

Globally, soybean is cultivated in about 116 countries, with Brazil, USA, Argentina, China, and India being the top producers, contributing 41%, 30.5%, 6.74%, 5.25%, and 4.03%, respectively (FAO STAT 2023). Currently, soybean ranks as the leading oilseed crop in both India and the world (Chandra et al., 2022). In India, it is grown on approximately 12.06 million hectares, yielding about 13.58 million tons with an average productivity of 1,126 kg/ha (Soni et al., 2021). Soybean world productivity has increased substantially from 1,128 kg/ha in 1960 to 2,711 kg/ha in 2023 (FAO STAT 2023).

Although breeding efforts have led to significant yield improvements, inconsistent production levels remain a major concern for soybean and the continuous expansion of soybean cultivation has increased the crop's susceptibility to a variety of diseases (Sharma et al., 2014). Soybean productivity is threatened by many biotic factors and major soybean diseases include bacterial pustule, rust, yellow mosaic disease, charcoal rot, and anthracnose (Sharma et al., 2014). Among these, bacterial pustule is one of the most destructive diseases of

soybean, occurring worldwide and causing significant yield losses. The disease is caused by *Xanthomonas citri* pv. *glycines* (*Xcg*). It is a foliar disease of soybean, with its development strongly favoured by a combination of high temperature, high humidity, and sporadic rainfall (Bernard & Weiss, 1973). Infected soybean leaves typically exhibit yellow-green spots accompanied by raised pustules, which eventually enlarge into necrotic lesions. These lesions can lead to premature defoliation, ultimately causing significant yield losses (Groth & Braun, 1986; Sain & Gour, 2013).

This review article aims at updating the present state of knowledge about different aspects of bacterial pustule disease and is organized into different sections that provide a comprehensive overview of the pathogen, covering its biology, disease symptoms, detection methods, screening techniques, disease cycle, genetic variability, economic impact, management strategies, and the genetic and genomics resources available in soybean to combat the disease.

Causal organism

Hedges (1922) first observed the characteristic symptoms such as water soaking and raised centres at the infection sites, which led him to refer to the disease as "bacterial pustule" and named the causal organism as *Bacterium phaseoli* var. *sojense*. Later, Hedges (1924) provided a more detailed description of the symptoms, isolated the pathogen from infected plants, and successfully reproduced the disease by inoculating healthy plants.

The pathogen underwent several taxonomic re-classifications over time. Initially, it was identified as *Xanthomonas campestris* pv. *glycines* (Nakano, 1919; Dye, 1978) and later renamed *Xanthomonas axonopodis* pv. *glycines* by Vauterin et al. (1995). Most recently, Constantin et al. (2016) reclassified the organism as *Xanthomonas citri* pv. *glycines*. This species belongs to the family *Lysobacteraceae* within the class Gamma proteobacteria.

Morphology and detection of *Xcg*

Xcg is an aerobic, gram-negative, motile, encapsulated bacterium that exhibits a rod-shaped morphology with dimensions of $0.9 \times 1.6 \mu\text{m}$ (Sain and Gour, 2013). When cultivated on semi-solid media, *Xcg* produces colonies with variable morphology ranging from circular to irregular shapes. These colonies appear as flattened, glistening structures with convex profiles and display the characteristic yellow to bright yellow coloration (Kumar and Jahagirdar, 2017). This distinctive pigmentation results from the production of xanthomonadin, a unique yellow pigment that serves as a diagnostic marker for the entire *Xanthomonas* genus (Starr and Stephens, 1964; Schaad and Stall, 1988).

The *Xcg* has specific environmental preferences, with optimal growth occurring at 25-30°C and neutral pH conditions (pH 7.0). Growth is severely compromised outside these parameters, and the organism cannot survive extreme temperature conditions of 10°C or 45°C (Sain and Gour 2013,

Kumar and Jahagirdar, 2017). The *Xcg* produces several biologically active compounds like bacteriocin, auxin, extracellular polysaccharide and toxins (Fett et al., 1987; Thowthampitak et al., 2008; Sain and Gour, 2013) that contribute to its pathogenic lifestyle. *Xcg* exhibits characteristically slow growth rates on standard culture media, which can complicate isolation and identification procedures in laboratory conditions. Modern molecular biology techniques have revolutionized *Xcg* detection and quantification capabilities. Specific PCR primers have been developed targeting the glycinecinA gene and PstI fragment containing the open reading frame of the TAL gene, enabling direct *Xcg* pathogen detection from infected plant samples without requiring culture-based methods (Oh et al., 1999; Khaeruni et al., 2007). Further, Real-time PCR assays based on the rpoD gene has been developed for quantitative assessment to determine contamination levels in seed samples with high precision and sensitivity (Watanabe and Sawada, 2013).

Distribution and economic importance

Bacterial pustule (BP) disease causes significant yield losses in soybean, with severity varying based on agro-climatic conditions, infection levels, plant development stages, and varietal susceptibility. BP disease occurrence has been reported from several countries, including USA (Wolf and Foster, 1917), India (Patel and Kulkarni, 1954), Ukraine (Muras, 1964), Brazil (Hedgedorn et al., 1969),

Thailand (Prathuangwong, 1983), China (Qui-en-Chen and Jinkai Bai, 1987), Korea (Hwang and Lim, 1998), and North Dakota (Heitkamp et al., 2014). Yield losses due to the BP disease in soybean has been reported upto 15% in the USA (Hartwig and Johnson, 1953), 30 to 95% in Ukraine (Klykov, 1963), 40% in Thailand (Prathuangwong and Amnuaykit, 1987) and 16 to 19% in Korea (Hong et al., 2011; Kang et al., 2021). In India, the disease is prevalent in almost all of the soybean growing regions like Madhya Pradesh, the North Eastern States, Rajasthan, Himachal Pradesh, and Uttarakhand, with potential yield losses ranging from 15% to 53% (Madhavi et al., 2011; Sain and Gour, 2013).

Disease symptom

The causative bacterium enters the plant through stomata and subsequently induces abnormal cellular proliferation within the leaf mesophyll (Wolf, 1924; Hedges, 1924). The infection triggers both hyperplasia (increased cell division) and hypertrophy (cellular enlargement), leading to the development of intumescences that eventually rupture to form the disease's characteristic pustular lesions. Initial symptoms of the disease include the appearance of minute, pale green spots with distinct elevated centers, predominantly occurring in the inter-venial regions on either leaf surface (Wolf, 1924; Groth and Braun, 1986; Sain and Gour, 2013). Later a small raised, light-colored pustule forms in the central portion of the original spots, usually on the abaxial surface (Jones and Fett, 1987). Individual lesions

demonstrate considerable variability in size, ranging from minute specks to extensive, irregular patches (Wolf, 1924). Coalescence of adjacent lesions creates larger, mottled brown areas that compromise leaf integrity. As infected tissue undergoes necrosis, mechanical stress from wind can tear away the damaged zones, resulting in characteristic ragged leaf. Severe infections cause rapid defoliation within 8-10 days of symptom onset and infection may extend beyond foliar tissue, with pods developing small, reddish-brown, slightly elevated lesions (Sain and Gour, 2013).

Disease cycle

The pathogen overwinters in crop debris, seeds, or in the rhizosphere (Diachun & Valeau, 1944). The pathogen is known to survive in crop residues and seeds (Lehmann, 1931; Graham, 1953; Fett, 1979). *Xcg* naturally infects *Dolichos biflorus* in India and redvine in the United States (Jones, 1961). Additionally, other legumes like common bean, lima bean, horse gram and *Vigna* species including cowpea can also be the hosts of *Xcg* (Elliot, 1951). Entry into the host occurs through natural openings or wounds, after which the bacterium multiplies intercellularly (Wolf, 1924; Nyval, 1979), leading to localized leaf spots. The soil- and seed-borne inoculum must be disseminated under warm and humid conditions, which accelerate bacterial multiplication and increases the severity of disease (Kang et al. 2021). The Disease incidence is influenced by the susceptibility of the soybean genotype, the virulence of the

pathogen, and favourable weather conditions. The disease manifests throughout all stages of plant development, with younger leaves being more prone to infection than older ones (Jones and Fett 1987). It may also spread systemically through the plant's vascular system. Plant to plant and field-to-field transmission

can occur via rain splashes and wind-driven rain (Khare et al., 2003). Recent epidemiological data (Tchemadon et al. 2021) indicated that while the disease can occur throughout the plant's growth cycle, it reaches maximum severity during flowering (37.4%) and pod development stages (44.6%).

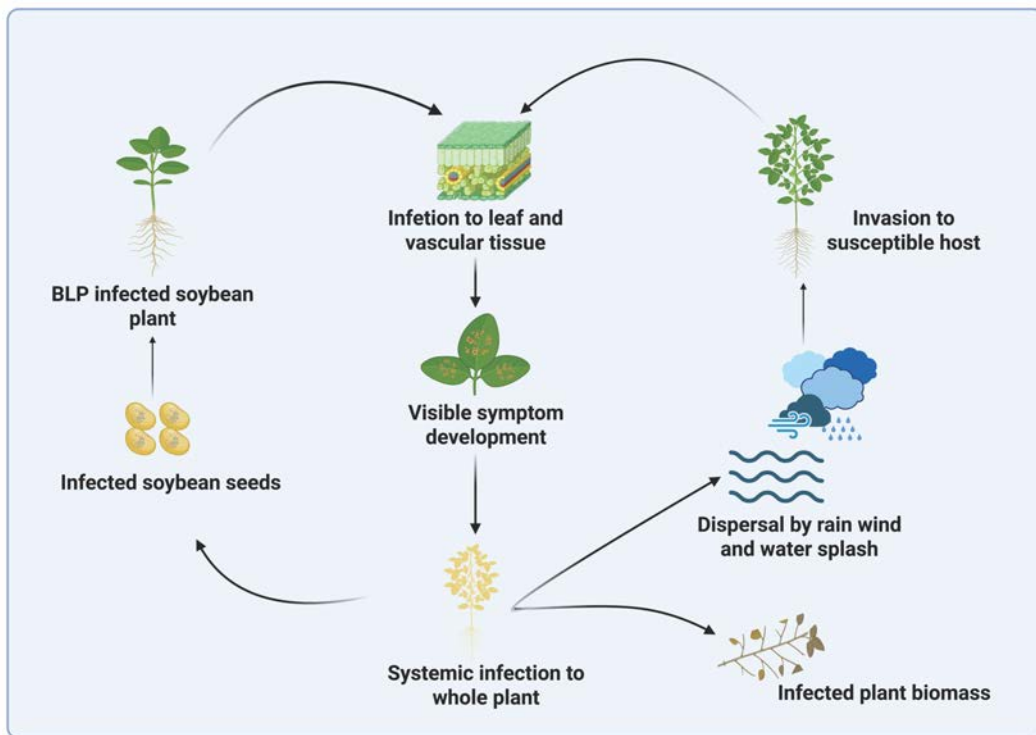


Fig. 1. The life cycle of *Xanthomonas citri* pv. *glycines*. The figure was created with BioRender.com.

Pathogenic variability of *Xcg*

The bacterium *Xcg* is known to have pathogenic variability i.e., it consists of a different pathogenic race. Prathuangwong and Choethana (1998) isolated 100 *Xcg* isolates and classified them into 10 different pathotypes based on their reaction to three different soybean cultivars with varying

resistance level to BP disease. Significant pathogenic diversity within *Xcg* populations was observed and most aggressive isolate produced larger leaf lesion and less aggressive isolate produced smaller leaf lesions. Hwang and Lim (1998) isolated 63 *Xcg* isolates and evaluated for pathogenic variability on 11 soybean genotypes.

On the basis of differential reaction, the *Xcg* isolates were divided into five different races. Kaewnum et al. (2005) provided unique insights into *Xcg*'s broader host interactions by testing hypersensitive response (HR) induction on multiple plant species like tobacco, tomato, cucumber, pea, and sesame. The identification of isolate KU-P-34017 as capable of inducing HR across all tested species, with tomato showing highest sensitivity, suggests some *Xcg* isolates may have broader host interaction capabilities than previously recognized. Park et al. (2008) used *avrBs3*-homologous patterns to classify 155 *Xcg* Korean strains and classified them into six different types of strains. This molecular approach revealed the potential role of *avrBs3* homologs in both pathogenicity mechanisms and host recognition specificity. Similarly, Kang et al., (2021) collected 106 *Xcg* isolates and grouped them into 11 classes on the basis of *avrBs3* banding patterns. They also observed increase in diversity and emergence of new dominant strains suggesting ongoing evolutionary pressure and adaptation within *Xcg* populations.

Screening methods

The BP disease screening can be carried out under natural field conditions or artificial conditions. However, due to lack of uniform distribution of pathogen in the natural environment, an artificial inoculation method in controlled environmental conditions is highly preferred for consistent results. Different artificial screening techniques are available to

evaluate the soybean genotypes for BP resistance. In excised leaf technique, leaves excised from the plants are arranged in plastic trays containing water and an inoculum was deposited at the injury spot made with the help of sterile tooth pick (Sharma et al., 1993; Manjaya and Pawar, 1999; Totade et al., 2022, 2023). In detached leaf assay, the petiole of excised leaves was wrapped with moist cotton and inoculation was done either by swabbing the leaf surface with inoculum-laden cotton bud or by pricking the leaf surface with the grid of 16 pins embedded in cork base (Surin et al., 1993). Similarly, in cotyledon assay, cotyledon from 10-14 days old seedling were wounded and inoculated with the bacterial inoculum (Hwang et al., 1992). In artificial screening, BP symptom development time varies depending on the inoculation method and generally symptom develop with 10-14 days post-inoculation (dpi).

Disease management

The control of bacterial pustules has been difficult due to the high variability of the pathogen, its ability to survive in diverse environments, and its vast host range (Shankar et al., 2018). The control measures for BP disease includes deployment of cultural practices, physical, chemical and biological measures to reduce the *Xcg* inoculum to least possible level.

Cultural practices

Removal of alternative host and the soil solarization in summer is necessary to eradicate the pathogen

from the soil and crop debris (Khare et al., 2003). Hong et al., (2011) suggested that delayed sowing of susceptible cultivars could minimize the *Xcg* severity and yield losses.

Seed disinfection by physical and chemical method

Bacterial pustule disease can be easily transmitted through infected seeds. Therefore, preventing the *Xcg* infection from seed is very important to avoid disease spread. Dry heat treatment (DHT) can be effective in eliminating *Xcg* from soybean seeds, but the temperature and duration of the treatment are critical to minimize negative effects on seed viability. Savitri et al. (2023) found a temperature treatment of 25°C for 12 hours optimal for both eliminating the bacteria and maintaining seed viability in soybean seeds. Similarly, treatment of seeds in hot water at 52-53 °C for 25 minutes was found optimal to controls the seed borne infection of *Xcg* in soybean (Khare 2003).

The seed treatment with thiram combined with streptocycline or Agrimycin-100 (Srivastava and Bais, 1985) and combination of an antibiotic (streptomycin) with copper fungicide (Blitox 50 copper oxychloride) also have been suggested to reduce the seed born spread of bacterial pustule disease in the soybean (Thapliyal and Dubey, 1986; Prathuangwong and Choochoa, 1989; Singh et al., 1990). Laboratory test determined that Streptocycline (750 ppm) and bordeaux mixture at 1% concentration would be effective in controlling *Xcg* (Kumar and Jahagirdar,

2017). Kumari et al., (2018) reported that the treatment of soybean seeds with thymol nano-emulsion for 4 h not only reduce the microbial load but also can increase the plant height, seeds/pod, 100 seed weight, root length, and the number of nodules of soybean plants. Unfortunately, there is no information regarding the inhibitory efficacies in fields after application of the above-mentioned bactericides.

Biological control

Biological control is an environment-friendly and cost-effective approach to control BP disease. Bacterial antagonist of *Xcg* has received significant attention as a control agent. Salerno and Sagardoy, (2003) reported that treatment of soybean leaves with *Bacillus subtilis* 210, 72h before the inoculation of *Xcg* could reduce the lesions on soybean plants. *Bacillus subtilis* functions as a biological control agent by inducing plant defence mechanisms and enhancing physiological responses, thereby increasing tolerance to the pathogen and decreasing disease severity. Similarly, application of lipopeptide- a surfactin produced by *Bacillus amyloliquefaciens*, reduced the disease severity and enhanced the plant growth (Preecha et al., 2010). Single spray (10⁸cfu/ml) of fluorescent *Pseudomonas* (pf18) at the time of first appearance of BP lesion on soybean plants, could reduce the further spread of the disease (Shankar et al., 2018; Sain, 2010). Similarly, Wijayanto et al. (2017) reported that the application of bio-fertilizer bio-fresh in combination with

soybean litter can reduce the BP disease severity in susceptible cultivars.

Genetic resources for resistance to bacterial pustule

Breeding for disease resistance is the most effective and eco-friendly strategy to reduce yield losses. Developing soybean varieties with durable BP disease resistance requires knowledge of genetics of the BP resistance. Genetics of BP resistance in soybean has been investigated in several studies. Classical genetics analysis suggested that the BP resistance in CNS variety is controlled by single recessive gene designated as *Rxp* (Hartwig and Lehman, 1951; Narvel et al., 2001). The resistance in another soybean genotype PI96188, exhibiting novel symptoms of BP (showing no chlorotic haloes) was also governed by a single recessive gene (Kim et al., 2011). In India, Sharma et al., (1993) reported new resistance sources, P-4-2 and P-169-3 showing immune reactions under artificial conditions. Manjaya and Pawar (1999) reported that resistance in genotype P-4-2 is controlled by duplicate recessive genes. Similarly, Totade et al., (2022) Identified four *Xcg* resistant soybean genotypes (TS-3, P-4-2, Hara Soya and Himso 1685) among 136 soybean germplasm. Totade et al., (2023) also reported that duplicate recessive genes govern the BP resistance in Indian soybean genotypes TS-3.

Genomic resources for resistance to bacterial pustule

Advancements in molecular biology have enabled the identification of DNA

markers linked to BP resistance in soybean, aiding in faster and more accurate breeding through marker-assisted selection (Table 1). Palmer et al. (1992) identified a malate dehydrogenase isozyme genetically linked to *Rxp* locus, which is involved in susceptibility to bacterial pustule. Narvel et al. (2001) mapped the BP resistance locus *Rxp* in cultivar ‘CNS’ on linkage group D2 (Chromosome 17) using SSR markers Satt372 and Satt014. Later on, Kim et al. (2004) found an AFLP marker ‘McctEact97’, that was more tightly linked to the BP resistance locus than SSR marker Satt372. The *Rxp* locus was further fine-mapped to 33 kb region between SSR marker SNUSSR_17_09 and SNP marker SNUSNP_17_12 using 227 recombinant inbred lines and identified two potential candidate genes (Glyma17g09780 and Glyma17g09790) for BP resistance in the region (Kim et al. (2010). Another BP resistance locus in the genotype PI96188 was genetically mapped on chr 10 using SSR marker Sat_108 (Kim et al. 2011). Recently, in an Indian soybean genotype ‘TS-3’, Totade et al. (2023) mapped two BP resistance loci, r1 and r2 on chromosomes 2 and 6, respectively, indicating new resistance loci for BP, different from the traditional *Rxp* gene located on chromosome 17.

In addition, several quantitative trait loci (QTLs) associated with BP resistance also have been reported (Table 2). In a study, Van et al. (2004) reported a major QTL (Satt372) on LG D2 (chr. 17) associated with resistance

to all six isolates of *Xcg* used under greenhouse and field conditions. In addition, several minor QTLs on LG A1 (chr 5), C1 (chr. 4), O (chr. 10), F (chr. 13) and L (chr19) were also found showing resistance to various isolates. Seo et al., (2009) identified four QTLs located on LG B2 (Chr.14), D2 (chr 17), I (Chr 20) and K (Chr. 9) using a RIL population, accounting for 36.4% of total phenotypic variation. Similarly, Zhao et al., (2022) identified one major QTL (*qrxp-17-2*) and two minor QTLs (*qrxp-05-1* and *qrxp-17-1*) accounting for 74.33%, 7.26% and 22.26% phenotypic variations, respectively. In addition, 11 stable BP resistance QTNs that were significantly associated with BP resistance were also identified by combining linkage mapping and GWAS analysis. The gene Glyma.17G086300, which was located in *qrxp-17-2* QTL region, was identified as a potential candidate gene for BP resistance (Zhao et al., 2022). Cardoso-Sichieri et al. (2024) identified a resistance region on chromosome 6 through QTL mapping using a cross between genotype Williams 82 (resistant) and PI 416937 (susceptible), suggesting that Williams 82 carries an additional recessive resistance gene to bacterial pustule beyond the well-known *Rxp* gene.

Most studies on bacterial pustule resistance relied on QTL mapping in biparental populations, which limits mapping resolution due to restricted genetic diversity and fewer recombination events. In contrast, genome-wide association studies (GWAS) offer higher resolution by

capturing historical recombination event across natural populations, making them more effective for accurately identifying resistance loci (Oraguzie et al. 2007; Korte and Farlow 2013). GWAS have significantly contributed to identifying genomic regions associated with resistance to bacterial pustule in soybean (Table 3). Using GWAS, Chang et al. (2016) identified three significant SNPs on chromosomes 1 (SNP s715580342), 11 (SNP s715609404), and 17 (SNP ss715628133) associated with BP resistance. The SNP (ss715628133) which was present within the coding region of an RLK gene (Glyma17g09801) was located between marker SNUSNP17_2 &_12 and Satt372, two candidate resistance genes (Glyma17g09780 and Glyma17g09790) previously reported by Kim et al. (2010), indicating that candidate gene Glyma17g09801 along with Glyma17g09780 and Glyma17g09790 may contribute to resistance for BP. Similarly, Cardoso-Sichieri et al. (2024) performed a GWAS by screening a panel of 212 diverse soybean genotypes of Brazilian, American and Asian origin, against two Brazilian *Xcg* isolates (IBS 333 and IBS 327) and identified two new genomic regions associated with BP resistance on chr 6 and 18. Cardoso-Sichieri et al. (2024) also reported two candidate resistance genes (Glyma.06g311000 and Glyma.18g025100) for bacterial pustule on chromosomes 6 and 18, respectively.

Kim et al. (2011) used RNA-Seq to compare gene expression between BP resistant and BP susceptible soybean near-isogenic lines and found that 134 defense related genes exhibited significant differential expression at 0, 6, and 12 hours after inoculation with the bacterial pustule pathogen. Study also showed that pathogen-associated molecular pattern (PAMP) and damage-associated molecular pattern (DAMP) receptors and the genes induced by these receptors were highly expressed at 0 hai in resistant plants, indicating that bacterial pustule resistance in soybean is associated with strong basal defense, including early recognition of pathogens and activation of JA-mediated defence and PR genes, contributing to effective disease resistance. Further, Kang et al. (2012) analysed RNA-Seq data from BP resistant and BP susceptible soybean NILs treated with *Xcg* and observed a significant fold-change in nucleotide-binding site and leucine-rich repeat (NBS-LRR) genes expression between the two NILs. These findings imply that NBS-LRR-mediated effector-triggered immunity (ETI) may contribute to bacterial pustule resistance, functioning in coordination with basal defences like PAMP/DAMP recognition and JA/PR gene pathways. Further, the location of these NBS-LRR genes within the disease resistance QTL regions strengthens

their candidacy as resistance-related genes.

Future Prospects

High pathotype variability in *Xcg* indicate that new strains can quickly overcome existing resistance genes in soybean. Therefore, large-scale germplasm screening is needed to identify new resistance genes or QTLs against *Xcg*. Wild soybean species, which remain largely unexplored for *Xcg* resistance, could offer novel resistance sources and help broaden the genetic base of cultivated soybean. Despite the availability of molecular markers linked to *Xcg* resistance loci/QTLs, their use in transferring these resistance traits to susceptible soybean genotypes remains limited. Therefore, there is a need to accelerate bacterial pustule resistance breeding in soybean through marker-assisted selection (MAS). Additionally, pyramiding multiple resistance loci/QTLs is crucial to enhance resistance against emerging *Xcg* strains to provide durable, broad-spectrum resistance. Since, no resistance gene for bacterial pustule has been identified or cloned till date, the potential for precise genetic improvement, including transgenic or genome-editing approaches (e.g., CRISPR), remains limited. Hence, efforts should focus on fine mapping, positional cloning and gene expression analysis to pinpoint the causal resistance genes.

Table 1. List of molecular markers linked with resistance to bacterial pustule (*Xcg*) in soybean

Mapping Population (size)	Resistance (R) & susceptible (S) Parents of mapping population	Locus	Flanking/linked markers	Genetic distance	LG/Chr.	Reference
F ₂ (650)	Clark 63 × PI 437477B	<i>Rxp</i>	Malate isozyme	15.18 (% recombination)	-	Palmer et al. 1992
F ₄ derived lines (116)	Young (R) and PI416937 (S)	<i>Rxp</i>	Satt372 and Satt014	3.9 cM and 12.4 cM	17 (D2)	Narvel et al., 2001
RILs (130)	SS2-2 (R) and Jangyeobkong (S)	<i>Rxp</i>	Satt372 and MectEact97	-	17 (D2)	Kim et al., 2004
RILs (227)	Taekwangkong (S) and Danbaekkong (R)	<i>Rxp</i>	SNUSSR17_9 and SNUSNP17_12	-	17 (D2)	Kim et al., 2010
RILs (88)	PI 96188 (R) and Jinjool (S)	<i>Nov1 symptom</i>	Sat_108	21.5 cM	10 (O)	Kim et al., 2011
F ₂ (196)	TS3 (R) and PK472 (S)	<i>r1</i>	Sat_183 and BARCSOYSSR_02_1613	0.9 cM and 2.1 cM	2 (D1b)	Totade et al., 2023
		<i>r2</i>	BARCSOYSSR_06_0024 and BARCSOYSSR_06_0013	1.5 cM and 2.1 cM	6 (C2)	

Table 2. List of QTLs associated with resistance to bacterial pustule (*Xcg*) in soybean

S. No.	Mapping Population	Resistance susceptible (S) of mapping population	(R) & Parents	Number of QTLs	Chr. (LG)	R ² value (%)	Flanking/linker markers	Reference
1.	RILs	Danbaekdong (R) and Suwon157 (S)		1	4 (C1)	7	Satt294	Van et al. (2004)
				1	5 (A1)	13	Satt155	
				2	10 (O)	11-19	Satt243 & Satt259	
				1	13 (F)	8	Satt269	
				1	17 (D2)	9-43	Satt372	
				2	19 (L)	6-11	Satt143 & Satt156	
				1	9 (K)	6	Satt137	
2.	RILs	Shinpaldalkong (R) and Keunolkong (S)		1	14 (B2)	7	Satt556	Seo et al., (2009)
				1	17 (D2)	11-21	Satt135 and Satt397	
				1	20 (I)	3	Satt496	
3.	RILs	Meng8206 (R) and Zhengyang (S)		1	5 (A1)	7.26	Gm05_7667820 and Gm05_7668047	Zhao et al., 2022
				2	17 (D2)	22.26-74.33	Gm17_5628119 and Gm17_7603802	
				2	6 (C2)	31.44 & 31.60	Chr06:48,718,599 and Chr06:49,937,209	
4.	F ₂	Williams 82 (R) and PI 416937 (S)		2	6 (C2)	31.44 & 31.60	Chr06:48,718,599 and Chr06:49,937,209	Cardoso-Sichieri et al. (2024)

Table 3. List of genomic regions associated with *Xcg* resistance identified by GWAS analysis in soybean

S. No.	Plant Material	<i>Xcg</i> strain used for screening	Significantly SNPs	associated	Physical Position (bp)	Chr. (LG)	R ² (%)	References
1.	USDA Germplasm	-	ss715580342		52,249,479	1 (D1a)	-	Chang et al. (2016)
			ss715609404		16,992,622	11 (B1)		
			ss715628133		7,307,486	17 (D2)		
2.	118 genotypes	Strain 2440	Gm03_36438792_G_T		36,438,792	3 (N)	13-16	Capobianco da Fonseca et al. 2021
			Gm03_36634361_G_A		36,634,361			
			Gm03_38069022_A_G		38,069,022			
			Gm03_46055685_C_T		46,055,685			
			Gm03_46214163_C_T		46,214,163			
			Gm05_682648_A_G		682,648	5 (A1)	14	
			Gm08_42793022_A_G		42,793,022	8 (A2)	15	
			Gm10_2437001_A_G		2,437,001	10 (O)	14	
			Gm13_27665585_A_G		27,665,585	13 (F)	14	
			Gm13_29677928_G_T		29,677,928			
			Gm13_32875289_C_A		32,875,289			
		Strain 2447	Gm06_9442481_T_C		9,442,481	6 (C2)	94	
			Gm15_5097389_T_C		5,097,389	15 (E)	94	
			Gm15_5363077_C_T		5,363,077			
			Gm15_5438610_G_A		5,438,610			
			Gm17_7280661_C_T		7,280,661	17 (D2)	94	
3.			Gm05_7667820		7,667,820	5 (A1)	3.30-3.42	Zhao et al., 2022
			Gm05_7668047		7,668,047			
			Gm17_5628119		5,628,119	17 (D2)	3.30-7.88	
			Gm17_5628133		5,628,133			
			Gm17_7603802		7,603,802			
			Gm17_7604008		7,604,008			

Continue Table 3

4.	212 genotypes	IBS 327	Gm17_7603992 Gm17_7712768 Gm17_7721556 Gm17_7736150 Gm17_7754016 Gm17_7754048 6 SNPs	7,603,992 7,712,768 7,721,556 7,736,150 7,754,016 7,754,048 7,549,194 1,564,029 42,076,334 5,884,688 1,872,108 1,872,252 40,793,724 39,054,333 32,140,407 49,886,965 50,029,391 50,048,102 25,379,321 6,791,972 7,274,359 41,078,868 37,084,674 16,111,543 16,926,588 37,488,371	-	Cardoso- Sichieri et al. (2024)
		IBS 333	14 SNPs	6 (C2)	6 (C2)	
				11 (B1)	11 (B1)	
				13 (F)	13 (F)	
				14 (B2)	14 (B2)	
				18 (G)	18 (G)	
				18 (G)	18 (G)	
				2 (D1b)	2 (D1b)	
				3 (N)	3 (N)	
				5 (A1)	5 (A1)	
				6 (C2)	6 (C2)	
				6 (C2)	6 (C2)	
				6 (C2)	6 (C2)	
				7 (M)	7 (M)	
				11 (B1)	11 (B1)	
				11 (B1)	11 (B1)	
				13 (F)	13 (F)	
				17 (D2)	17 (D2)	
				18 (G)	18 (G)	
				18 (G)	18 (G)	
				18 (G)	18 (G)	

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Evaluation of Soybean Genotypes for Antixenosis against *Spodoptera litura*: Identifying Potential Donors for Resistance Breeding

***VANGALA RAJESH, LOKESH KUMAR MEENA, SANJAY GUPTA,
SHIVAKUMAR M, V NATARAJ, GIRIRAJ KUMAWAT,
MRINAL KUCHLAN, MILIND B. RATNAPARKHE,
GYANESH K. SATPUTE**

ICAR-National Soybean Research Institute, Indore, MP-452001.

Email: vangala.rajesh@icar.org.in

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ABSTRACT

Soybean (Glycine max L. Merrill) is an important legume crop valued for its protein and oil, yet its yield is often limited by insect pests, particularly the tobacco caterpillar, Spodoptera litura. In this study, 100 soybean genotypes including popular cultivars, pre-breeding lines and resistant and susceptible checks, were evaluated for antixenosis resistance under controlled laboratory conditions. Antixenosis was assessed using the Preference Index (C) in a free choice assay and genotypes were classified into strong, moderate, slight antixenosis, and preferred host categories. Among the tested genotypes, F4P21, F3P18, CAT 2503, Hara Soya, Hardee, G5P22, JS 20-69, along with resistant checks AGS 155 (CAT 47) and AKSS 67 (CAT 146) exhibited strong antixenosis. Twelve genotypes showed moderate antixenosis, 37 displayed slight antixenosis, and 42 were identified as preferred hosts. Data visualization using violin plots and hierarchical clustering with dendrograms illustrated the variation and grouped genotypes according to resistance levels. The identified resistant genotypes provide valuable donor lines for breeding programs targeting S. litura resistance. These results reinforce the role of host plant resistance as a sustainable strategy to reduce insecticide use and promote environmentally friendly soybean production.

Keywords: Soybean, host preference, violin plots, hierachial clustering, dendrogram

Soybean (*Glycine max* L. Merrill) is one of the most important grain legumes serves as a vital source of both protein and oil for human diets and livestock feed, making it a key contributor to global food and nutritional security. Compared to other legumes, soybean protein is recognized for its superior quality and higher digestibility. In addition, the crop is

rich in bioactive compounds such as isoflavones, phytosterols, and essential minerals, which further enhance its nutritional importance in the human diet (Zongbiao *et al*, 2025; Usman *et al*, 2025). India is one of the leading soybean-producing nations, with Madhya Pradesh, Maharashtra, and Rajasthan accounting for the largest share of cultivation. The crop has

gained prominence not only for its economic and nutritional value but also for its role in sustainable agriculture. As a legume, soybean contributes to soil fertility through biological nitrogen fixation, reducing the need for synthetic fertilizers. In addition, its inclusion in crop rotations improves soil health and helps suppress pest and disease incidence in subsequent cereal and other crops (Amar singh, 2025). Soybean productivity is strongly influenced by both biotic and abiotic factors. Insect pests are a major constraint to soybean production, causing 15–20% yield loss annually (Biswas, 2013). The tobacco caterpillar, *Spodoptera litura* (Fabricius), is a destructive defoliator across soybean-growing regions during the kharif season (Lokesh and Rajesh, 2023). Early instars feed gregariously, skeletonizing leaves, while third instars feed individually, leaving only veins (Ashutosh and Neeta Gaur, 2023). Larvae also attack tender pods causing 30–50% pod loss (Harish et al., 2009), and untreated fields can suffer up to 68% yield reduction compared with protected plots (Bayu et al., 2018). *Spodoptera litura* is known to rapidly develop resistance to chemical insecticides due to its short life cycle and the intensive use of these products. To reduce chemical residues and promote sustainable crop protection, the cultivation of resistant soybean genotypes is a practical and cost-effective strategy within integrated pest management (IPM) (Ashutosh and Neeta Gaur, 2023).

Host plant resistance is widely recognized as one of the most effective approaches to combat phytophagous insects. Antixenosis, a plant resistance mechanism in which specific traits deter insect feeding, oviposition, or sheltering, plays a crucial role in reducing pest damage (Kogan & Ortman, 1978). The use of resistant genotypes not only lowers dependence on chemical insecticides but also minimizes environmental pollution, delays the development of insecticide-resistant pest populations, and protects natural enemies (Bayu et al., 2018). The present study aims to evaluate the antixenotic resistance of soybean germplasm using a no-choice laboratory assay against *S. litura*.

MATERIALS AND METHODS

The study was carried out during *kharif* 2019 at ICAR–National Soybean Research Institute, Indore, Madhya Pradesh, India. A total of 100 soybean genotypes were evaluated, including popular cultivars, pre-breeding lines derived from *Glycine max* and *Glycine soja* (PB), advance breeding lines along with two resistant checks (AGS 155/CAT 47 and AKSS 67/CAT 146) and two susceptible checks (JS 335 and JS 93-05) presented in Table 1.

The antixenosis response of soybean genotypes against *Spodoptera litura* larvae was evaluated using the Preference Index (C) (Kogan and Goeden, 1970).

The Preference Index was calculated using the formula:

$C = 2A / M + A$, where:

- **A** = Dry weight of leaves of the test genotype consumed by larvae
- **M** = Dry weight of leaves of the susceptible check consumed by larvae

Egg masses of *S. litura* were obtained from the National Bureau of Agricultural Insect Resources (NBAIR), Bengaluru. For the assay, pre-weighed leaf samples of all genotypes were arranged in a circular pattern on a Petri plate lined with a thin thermocol sheet. Leaves were fixed with pins to prevent displacement or contact. Ten third-instar larvae of *S. litura* were released at the centre of each plate. After 8 hours, remaining leaves were collected, oven-dried at 50 °C for 15 minutes, and weighed. The weight of leaves consumed by larvae was determined using the relationship between fresh and dry weight. The experiment was conducted in three replications. Based on the calculated Preference Index (C), genotypes were classified as follows (AICRP on soybean, 2024).

C value	Antixenosis response
0.10 to 0.25	Extreme antixenosis
0.26 to 0.50	Strong antixenosis
0.51 to 0.75	Moderate antixenosis
0.76 to 0.99	Slight antixenosis
1.00 or > 1.00	Preferred host

The Statistical analyses included classification of genotypes, hierarchical clustering with dendrograms, and

visualization using violin plots, performed in RStudio 2025.09.0 with the packages dplyr, ggplot2, and gg dendro.

RESULTS AND DISCUSSION

The assessment of 100 soybean genotypes for antixenosis against *Spodoptera litura* showed considerable variation in non-preference traits (Table 2). Based on the Preference Index (C), genotypes were grouped into four categories viz., strong antixenosis, moderate antixenosis, slight antixenosis, and preferred host. Among the evaluated genotypes, 9 displayed strong antixenosis (Fig 3) viz., F4P21, F3P18, CAT 2503, Hara soya, Hardee, G5P22, JS 20-69 along with 2 resistant checks AGS 155 (CAT 47), AKSS 67 (CAT 146), 12 exhibited viz., AGS 25, MACS 1460, PS 1613, PK 472, PS 1611, RVS 2001-4, TAMS 98-21, MAUS 47, PB 197 (522P4), NRC 86, MACS 1520, RSC 10- 46 moderate antixenosis, 37 were categorized as slight antixenosis, and 42 were identified as preferred hosts (Table 3). This wide range of responses indicates substantial genetic variability for antixenosis among the tested lines.

Genotypes exhibiting strong and moderate antixenosis are valuable as potential donor lines for breeding programs aimed at enhancing resistance in susceptible soybean varieties against *S. litura*. The high number of preferred host genotypes suggests that most genotypes remains vulnerable to this

pest, highlighting the need to incorporate resistant lines into breeding programs. The use of resistant genotypes can reduce reliance on chemical insecticides, minimize environmental impacts, and contribute to sustainable crop management. Similar results were observed by Ashutosh and Neeta Gaur, 2023; De Queiroz et al., 2020 and Boica Junior et al., 2015

Visualization of the data using violin plots illustrated the distribution of Preference Index values across genotypes, enabling clear differentiation between resistant and susceptible lines (Fig 1). Hierarchical clustering and dendrogram analysis grouped genotypes based on similarity in antixenosis response, facilitating the identification of clusters with high resistance (Fig 2). These results provide a practical basis for selecting donor genotypes for breeding programs targeting *S. litura* resistance.

Overall, the study demonstrates significant variability in antixenosis among soybean germplasm, emphasizing its importance as a host plant resistance mechanism and its potential contribution to integrated pest management strategies. Incorporating genotypes with strong or moderate antixenosis into breeding programs can support environmentally sustainable

soybean production by reducing pesticide use and enhancing durable resistance to defoliator pests.

CONCLUSION

The evaluation of 100 soybean genotypes for antixenosis against *Spodoptera litura* demonstrated significant variation in non-preference responses. Notably, F4P21, F3P18, CAT 2503, Hara Soya, Hardee, G5P22, JS 20-69, along with resistant checks AGS 155 (CAT 47) and AKSS 67 (CAT 146), exhibited strong antixenosis. These genotypes, together with lines showing moderate antixenosis, represent promising donor material for breeding programs aimed at enhancing pest resistance in susceptible soybean varieties. Incorporating these genotypes into breeding strategies can reduce dependence on chemical insecticides, promote sustainable production, and support integrated pest management. Systematic screening for antixenosis provides a practical foundation for developing soybean varieties with durable resistance to defoliator pests.

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Table 1: Evaluated genotypes in the study for antixenosis

Genotype	Accession	Genotype	Accession	Genotype	Accession
G1	JS 20-34	G36	H2P2	G71	F4P21
G2	JS 95-60	G37	CAT 2503	G72	CAT 1477
G3	NRC 131	G38	PB 152(362)	G73	CAT 1483
G4	CAT 2911	G39	PB 28 (124P1)	G74	CAT 1847
G5	AGS FARM ACC	G40	PB 111 (230)	G75	CAT 488
G6	KARUNE	G41	PB 202 (532)	G76	CAT 349
G7	PB 115(259)	G42	PB 187D	G77	F3P18
G8	JS 20-38	G43	PB 219	G78	AGS 25
G9	NRC 130	G44	PB 197 (522P4)	G79	Bragg
G10	SREL 56A	G45	PB 53 (141P1)	G80	Hardee
G11	NRC 7	G46	PB 117(334)	G81	NRC 86
G12	VLS 65	G47	PB 183D	G82	JS 97-52
G13	RVS 2001-4	G48	PB 16(122P3)	G83	PK 472
G14	SL 958	G49	PB 190 (Q515)	G84	Dsb 21
G15	Dsb 32	G50	PB 220	G85	Kalitur
G16	RKS 24	G51	PB 216 D	G86	Young
G17	JS 20-98	G52	PB 157 (367P2)	G87	UPSM 534
G18	GAURAV	G53	PB 41(31)	G88	RSC 10-46
G19	JS 20-29	G54	PB 432 (P1)	G89	TAMS 98-21
G20	AMS-MBS-18	G55	PB 194 (516)	G90	Dsb 23
G21	NRC 128	G56	PB 7A 109-1A	G91	Hara soya
G22	JS 20-69	G57	NRC 37	G92	MACS 1460
G23	RVS 2001 -18	G58	RKS 18	G93	MACS 1520
G24	Birsa soya 1	G59	Shivalik	G94	G5P22
G25	RKS 45	G60	EC 396065	G95	PS 1611
G26	MAUS 47	G61	EC 391181	G96	PS 1613
G27	TG X 302-2A	G62	EC 241412	Susceptible check 1	JS 335
G28	Monetta	G63	SL E 1	Susceptible check 2	JS 93-05
G29	VP 1165	G64	SHILAJEET	Resistant check 1	AGS 155 (CAT 47)
G30	NRC 154	G65	JS 20-94	Resistant check 2	AKSS 67 (CAT 146)
G31	RAUS-5	G66	JS 20-116		
G32	JS 90-41	G67	Punjab		
G33	SL 1104	G68	Ankur		
G34	PS 1572	G69	Alankar		
G35	SPEC 56A	G70	Lee		

Table 2 : C Values of soybean genotypes

Genotype	C value	Genotype	C value	Genotype	C value
G1	1.18	G36	1.16	G71	0.33
G2	1.16	G37	0.35	G72	0.87
G3	0.87	G38	1.01	G73	1.27
G4	0.81	G39	1.02	G74	1.46
G5	1.15	G40	1.24	G75	1.25
G6	1.19	G41	1.24	G76	1.21
G7	1.08	G42	1.56	G77	0.27
G8	0.78	G43	1	G78	0.52
G9	0.87	G44	0.73	G79	0.79
G10	0.83	G45	1.19	G80	0.44
G11	0.83	G46	1.18	G81	0.73
G12	1.29	G47	1.21	G82	1.23
G13	0.68	G48	1.19	G83	0.64
G14	0.79	G49	1.22	G84	1.22
G15	0.82	G50	0.88	G85	1.22
G16	0.85	G51	0.76	G86	1.23
G17	0.83	G52	1.18	G87	0.85
G18	1.19	G53	0.86	G88	0.74
G19	1.16	G54	1.22	G89	0.68
G20	0.89	G55	0.79	G90	1.16
G21	0.78	G56	0.88	G91	0.37
G22	0.49	G57	0.85	G92	0.61
G23	0.87	G58	0.88	G93	0.73
G24	1.21	G59	0.86	G94	0.44
G25	0.89	G60	0.96	G95	0.65
G26	0.65	G61	0.88	G96	0.68
G27	0.85	G62	0.82	Susceptible check 1	1.5
G28	0.89	G63	1.19	Susceptible check 2	1.5
G29	0.82	G64	0.84	Resistant check 1	0.47
G30	0.89	G65	1.18	Resistant check 2	0.47
G31	0.86	G66	1.18		
G32	1.28	G67	1.22		
G33	0.87	G68	1.28		
G34	0.82	G69	1.22		
G35	0.8	G70	1.23		

Table 3. Classification of soybean genotypes based on antixenosis (c-value)

Category	Number of genotypes	Genotypes (Accession / Genotype)
Strong antixenosis (0.26-0.50)	9	F4P21 (G71), F3P18 (G77), CAT 2503 (G37), Hara soya (G91), Hardee (G80), G5P22 (G94), AGS 155 (CAT 47, Resistant 1), AKSS 67 (CAT 146, Resistant 2), JS 20-69 (G22)
Moderate antixenosis (0.51-0.75)	12	AGS 25 (G78), MACS 1460 (G92), PS 1613 (G96), PK 472 (G83), PS 1611 (G95), RVS 2001-4 (G13), TAMS 98-21 (G89), MAUS 47 (G26), PB 197 (522P4, G44), NRC 86 (G81), MACS 1520 (G93), RSC 1046 (G88)
Slight antixenosis (0.76-0.99)	37	PB 216 D (G51), JS 20-38 (G8), NRC 128 (G21), SL 958 (G14), PB 194 (516, G55), Bragg (G79), PS 1572 (G34), SREL 56A (G10), NRC 7 (G11), RKS 24 (G16), TG X 302-2A (G27), UPSM 534 (G87), PB 41(31, G53), Shivalik (G59), NRC 130 (G9), RVS2001-18 (G23), CAT 1477 (G72), PB 220 (G50), PB 7A 109-1A (G56), RKS 18 (G58), EC 391181 (G61), AMS-MBS-18 (G20), RKS 45 (G25), Monetta (G28), NRC 154 (G30), SPEC 56A (G35), NRC 37 (G57), CAT 2911 (G4), Dsb 32 (G15), VP 1165 (G29), EC 241412 (G62), JS 2098 (G17), RAUS-5 (G31), EC 396065 (G60), NRC 131 (G3), SL 1104 (G33), SHILAJEET (G64)
Preferred host (1.00 or >1.00)	42	PB 219 (G43), Dsb 21 (G84), JS 335 (Susceptible 1), JS 20-29 (G19), Birsra Soya 1 (G24), PB 152(362, G38), PB 28 (124P1, G39), PB 190 (Q515, G49), PB 432 (P1, G54), Kalitaur (G85), Young (G86), Lee (G70), JS 9752 (G82), H2P2 (G36), PB 115(259, G7), PB 117(334, G46), Ankur (G68), KARUNEE (G6), PB 53 (141P1, G45), CAT 349 (G76), Alankar (G69), Punjab (G67), JS 93-05 (Susceptible 2), JS 9560 (G2), AGS FARM ACC (G5), PB 157 (367P2, G52), JS 20-94 (G65), JS 20-116 (G66), Dsb 23 (G90), JS 20-34 (G1), GAURAV (G18), PB 16(122P3, G48), PB 183D (G47), PB 111 (230, G40), PB 202 (532, G41), CAT 488 (G75), CAT 1483 (G73), JS 90-41 (G32), VLS 65 (G12), SL E 1 (G63), CAT 1847 (G74), PB 187D (G42)

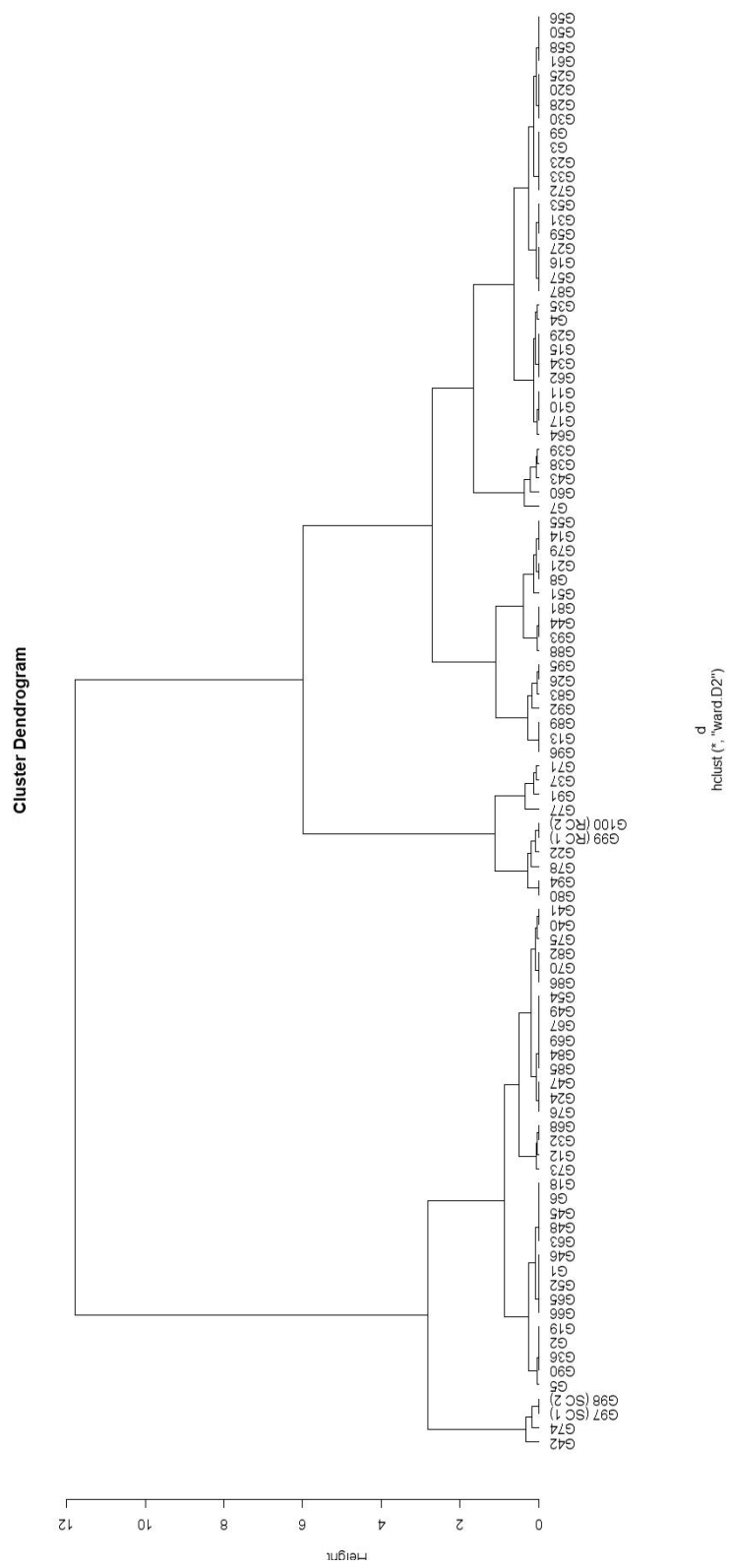


Fig 1. Cluster Dendrogram (Hierarchical cluster) for antixenosis of soybean genotypes under study.

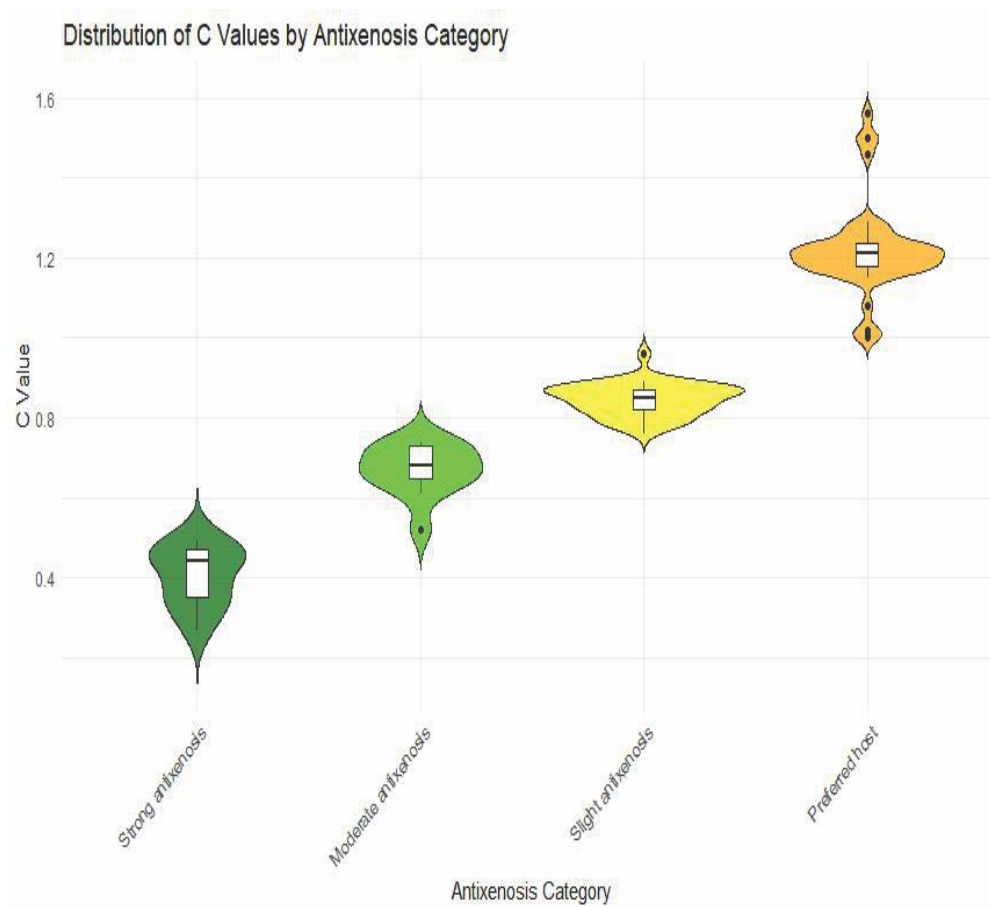


Fig 2: Violin plots for antixenosis of soybean genotypes

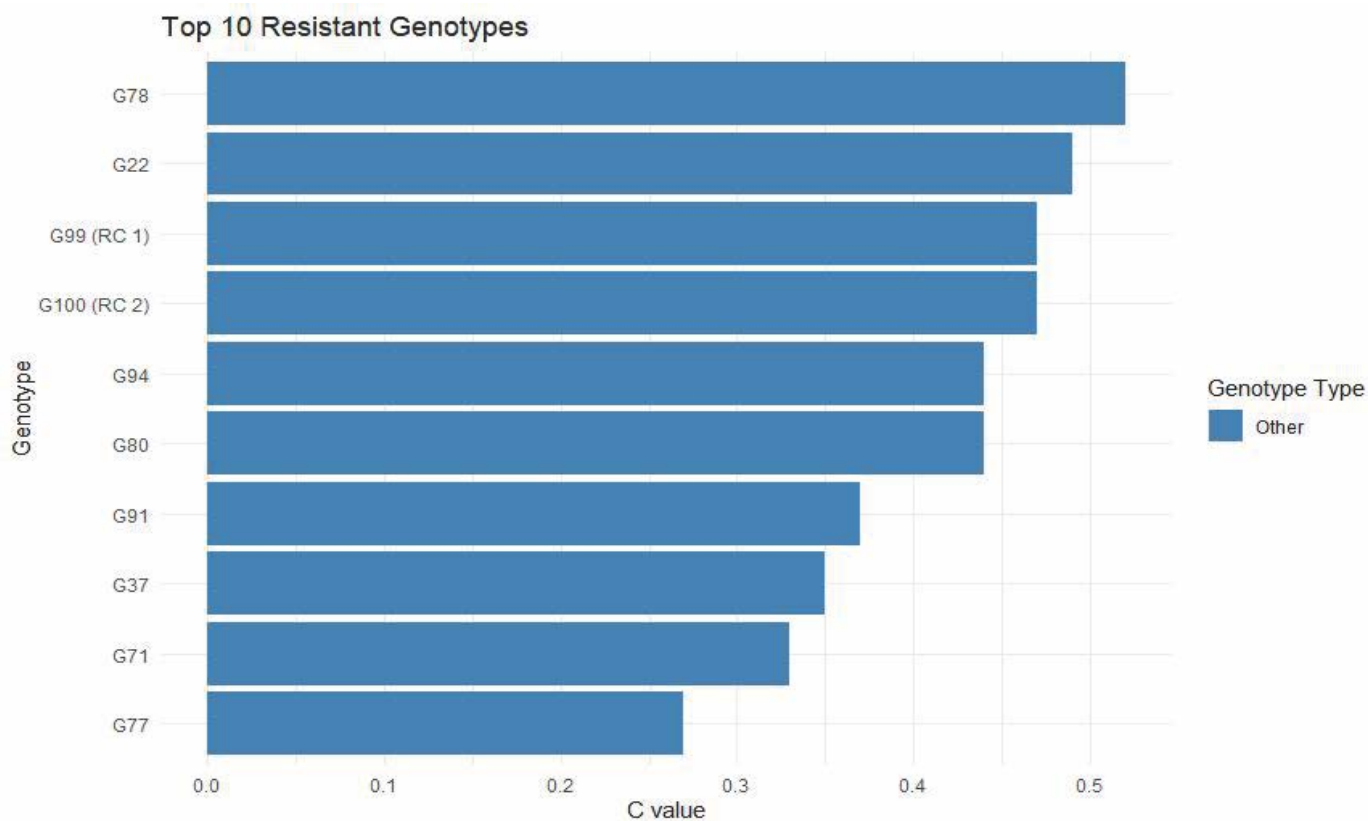


Fig 3. List of the top 10 resistant soybean genotypes for antixenosis

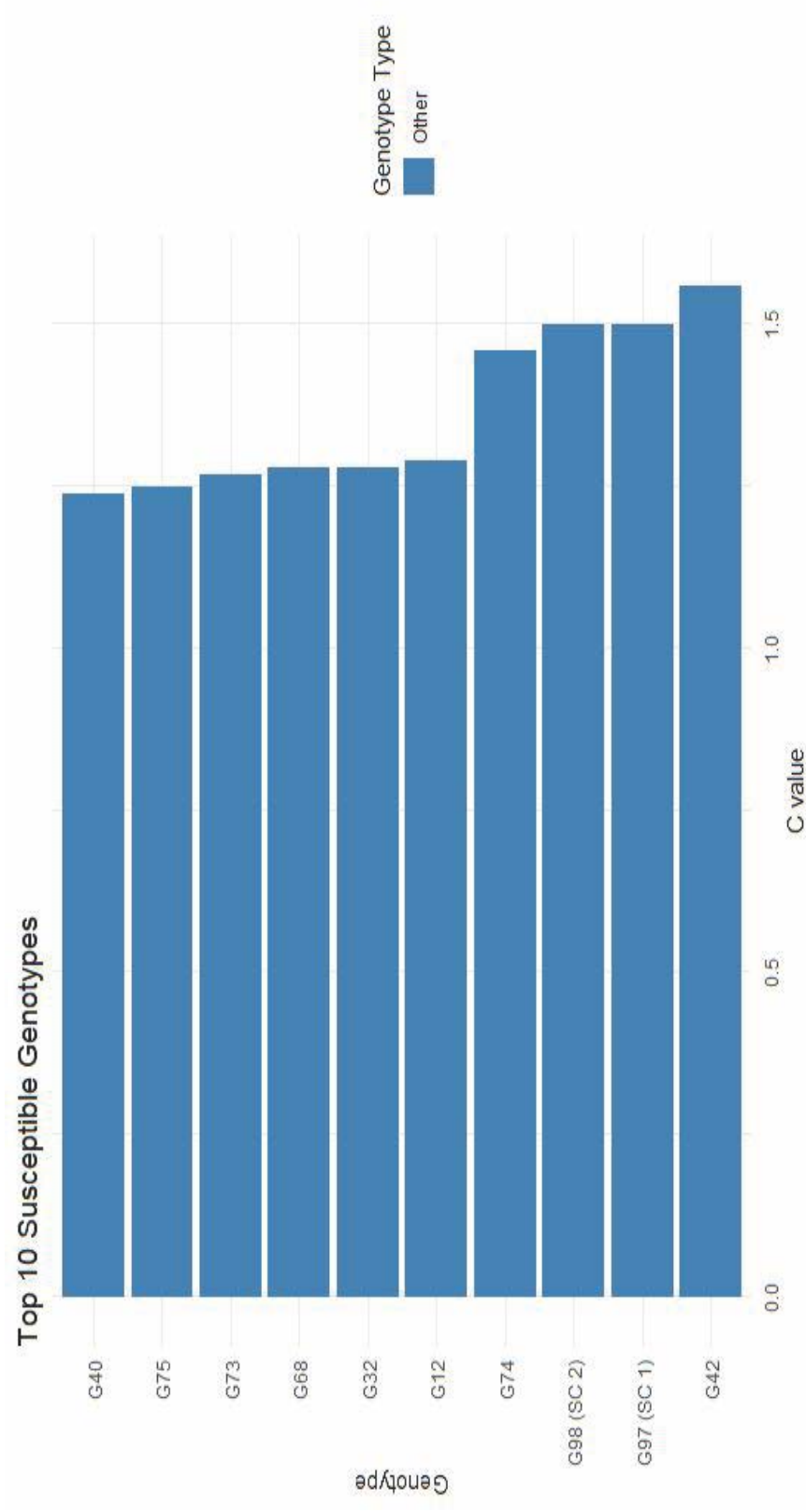


Fig 4. List of the top 10 susceptible soybean genotypes for antixenosis

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Screening of Soybean Genotypes Against Stem fly and Girdle beetle

P. V. BHAGAT, F. S. KHAN, R. S. JADHAV, P. R. PURI,
Q. D. R. KSHIRSAGAR

*Department of Entomology, Vasantrao Naik Marathwada Krishi
Vidyapeeth, Parbhani*

Email: bhagatpratiksha46@gmail.com

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ABSTRACT

Field trial was conducted in kharif 2024-25 at AICRP on Soybean, VNMKV, Parbhani (M.S.). Total 20 genotypes were screened against stem borers viz., stem fly and girdle beetle. Against girdle beetle, overall infestation was ranged from 8.53% to 29.65%. Among 20 genotypes, lowest of 8.53% infestation was recorded in genotype JS 95-60 and was categorized as resistant (R) against girdle beetle. Twelve genotypes showed moderate resistance (MR) including JS 21-72 (11.09%), MACS 1520 (11.15%), KDS 726 (12.10%), DLSb 1 (12.60%), DS 3108 (12.58%), RVSM 2011-35 (12.69%), MAUS 612 (13.80%) and DSb 23 (13.90%). Four genotypes were low resistant (LR), two susceptible (S) and maximum infestation was recorded in RVS 13-20 (29.65%) and was found highly susceptible (HS) against girdle beetle. Stem fly infestation was ranged from 15.36% to 44.87%. Among 20 genotypes, JS 95-60 (15.36%) and JS 21-72 (17.16%) were recorded lowest infestation and found resistant (R) against stem fly. Six genotypes viz., DS 3108 (27.46%), MAUS 731 (28.31%), NRC 130 (22.98%), RVS 13-20 (28.82%), SKF-SPS-11 (27.28%) and MAUS 158 (18.36%) were moderately resistant (MR). Twelve genotypes were low resistant (LR). Highest infestation was recorded in genotype RVS 2007-06 (44.87%) and found low resistant (LR) against stem fly.

Key words: Soybean, Screening, Girdle beetle, Stem fly.

Soybean (*Glycine max* L. Merrill), a major leguminous crop of the Fabaceae family, is globally recognized for its high nutritional value, containing approximately 40% protein and 20% oil. It serves as an essential source of plant-based protein, particularly in vegetarian diets, contributing significantly to addressing protein-calorie malnutrition in India, where a majority of the population depends on pulses for protein intake. (Dhore *et al.*, 2024).

The crop originated in China and was introduced to India during the 1970 (Andole, 1984). Currently, major soybean-producing countries include the USA, Brazil, Argentina, China, and India. For the 2024–25 season, global soybean production was projected at 420.78 million metric tons (USDA, 2024). In India, soybean is cultivated over 129.35 lakh hectares, producing 133.60 lakh metric tons with an average productivity of 1033 kg/ha. Maharashtra

is a key contributor, with 84.38 lakh metric tons harvested from 51.59 lakh hectares (productivity: 1636 kg/ha), while the Marathwada region alone accounts for 42.535 lakh metric tons from 26.193 lakh hectares (productivity: 1623 kg/ha). (Annual Report, 2024).

Despite its economic and nutritional importance, soybean production is constrained by a wide array of insect pests. In India, over 273 insect species have been reported on soybean, with key pests including defoliators (*Spodoptera litura*, *Chrysodeixis acuta*, *Helicoverpa armigera*), sap feeders (*Aphis glycines*, *Bemisia tabaci*, *Empoasca kerri*), stem borers (*Melanagromyza sojae*, *Obereopsis brevis*), and others (Patil *et al.*, 2014; Chaudhari *et al.*, 2020). Yield losses due to these pests range from 20% to 100% depending on pest severity and crop stage (Sharma *et al.*, 2014). In particular, stem fly *M. sojae* infestation may reduce grain weight by over 85% (Dhore *et al.*, 2024). The girdle beetle, *Obereopsis brevis* (Swedenborg) is one of the significant hidden pests of soybean in Marathwada region of Maharashtra (Bhamare *et al.*, 2018). In case of heavy incidences yield may reduce by up to 40 per cent (Thipse, 2012).

Host plant resistance is considered an eco-friendly and economically viable approach to manage insect pests. According to Kogan (1982), insect resistance was an inheritable trait that allows plants to inhibit pest development or recover from pest-induced injury through biochemical or morphological mechanisms. Identifying resistant genotypes through systematic

screening not only aids in sustainable pest management but also reduces reliance on chemical pesticides and associated environmental hazards. Hence, in present study screening of different genotypes was carried out.

MATERIAL AND METHODS

An experiment was conducted during *kharif* 2024-25 to screen soybean genotypes against major insect pests using twenty genotypes, including 18 test entries and 2 local checks MAUS 2 (susceptible check) and MAUS 158 (resistant check). The trial was laid out in a randomized block design (RBD) with two replications. Each gross plot consisted of three rows of 5-meter length, spaced at 45 cm × 5 cm. The sowing was carried out on 12th July 2024 at the Experimental farm of AICRP on Soybean, VNMKV Parbhani. (M.S) under uniform agronomic conditions. The genotypes used included DLSb 1, DSb 23, DS 3108, JS 21-72, JS 95-60, KDS 726, MACS 1520, MAUS 2, MAUS 158, MAUS 612, MAUS 725, MAUS 731, MAUS 780, NRC 130, NRC 152, RSC 10-52, RVS 13-20, RVS 2007-06, RVSM 2011-35 and SKF-SPS-11.

To determine the level of resistance or susceptibility, the AICRP method of classification was followed, which categorizes genotypes based on their deviation from the mean pest incidence using critical difference (CD) at 1% and 5% levels.

The classification includes six categories:

- (1) Highly resistant (HR) : values < (mean – CD at 1%)
- (2) Resistant (R) : values between (mean – CD at 1%) and (mean – CD at 5%)
- (3) Moderately resistant (MR) : values between (mean – CD at 5%) and the mean
- (4) Low resistant (LR) : values between the mean and (mean + CD at 5%)
- (5) Susceptible (S) : values between (mean + CD at 5%) and (mean + CD at 1%)
- (6) Highly susceptible (HS) : values > (mean + CD at 1%).

This classification was used to determine the genotypic reaction to specific insect pests based on observed data and statistical significance (Proceeding and Technical Programme 2023-24)

Method of recording observations

Observations for genotype screening were recorded weekly, starting from 7 days after germination (DAG) until peak pest incidence, following the AICRP classification method to assess genotype reactions.

- 1) Stem fly:- stem tunneling was assessed at physiological maturity by measuring plant height and the length of tunneled stem in five plants, with the results expressed as a percentage.
- 2) Girdle beetle:- The number of total and girdled plants were recorded from one meter row lengths at 3 - 5 locations and percent plant infestation was calculated.

Statistical analysis

The field data collected during the course of experimentation was subjected to statistical analysis after appropriate transformation for interpretation of result. Randomized block design used in order to test level of significance among the various treatments as per Gomez and Gomez (1984).

RESULTS AND DISCUSSION

Screening of Soybean Genotypes Against Major Insect Pests

Twenty soybean genotypes along with two local checks, resistant (MAUS 158) and susceptible (MAUS 2), were evaluated under field conditions against major insect pests. Entries were categorized into six resistance groups: Highly resistant (HR), resistant (R), Moderately resistant (MR), Low resistant (LR), Susceptible (S) and Highly susceptible (HS) following the AICRP method.

(1) Girdle Beetle (*Obereopsis brevis*)

Against girdle beetle overall per cent infestation ranged from 8.53 to 29.65. Among 20 genotypes, lowest of 8.53% infestation was recorded in genotype JS 95-60 and was categorized as resistant (R) against girdle beetle. Whereas, twelve genotypes viz., DLSb 1 (12.60), DSb 23 (13.90), DS 3108 (12.58), JS 21-72 (11.09), KDS 726 (12.10), MACS 1520 (11.15), MAUS 158 (15.97), MAUS 612 (13.80), MAUS 780 (15.10), NRC 130 (14.77), NRC 152 (16.43), RVSM 2011-35 (12.69) were found moderately resistant (MR). While four genotypes MAUS 2 (24.34), MAUS 725 (24.38), RSC 10 -

52 (21.18), SKF -SPS -11 (17.56) were low resistant (LR). However genotypes MAUS 731 (29.36) and RVS 2007 - 06 (26.46) were susceptible (S) and genotype RVS 13-20 (29.65) was highly susceptible (HS).

Previous studies reported JS 93-05 as highly resistant to girdle beetle (Awasthi *et al.*, 2005), similar to JS 95-60 in present study. (Shinde *et al.*, 2018) reported RVS 2007-06 and MAUS 158 as highly resistant; however, in the present study, RVS 2007-06 showed susceptible behaviour, and MAUS 158 was moderately resistant. Khandwe and Nema (2009) classified JS 95-60 as moderately resistant (7.0 - 7.80 per cent infestation), which is in agreement with the present study where JS 95-60 showed lowest infestation (8.53%) with resistant (R) reaction.

(2) Stem Fly (*Melanagromyza sojae*)

Against stem fly overall per cent infestation ranged from 15.36 to 44.87. Among 20 genotypes, JS 95-60 (15.36)

and JS 21-72 (17.16) were recorded lowest infestation and found resistant (R) against stem fly. Whereas six genotypes DS 3108 (27.46), MAUS 158 (18.36), MAUS 731 (28.31), NRC 130 (22.98), RVS 13-20 (28.82), SKF - SPS -11 (27.28) were moderately resistant (MR). However twelve genotypes viz., DLSb 1 (36.18), DSb 23 (35.13), KDS 726 (38.53), MACS 1520 (40.27), MAUS 2 (36.77), MAUS 612 (35.93), MAUS 725 (34.76), MAUS 780 (38.52), NRC 152 (33.73), RSC 10 – 52 (35.91), RVS 2007- 06 (44.87), RVSM 2011 – 35 (31.83) were low resistant (LR).

Khandwe and Nema (2009) reported JS 95-60 as highly resistant with minimum tunnel length (1.10%) and MAUS 612 lower resistant. The current study confirms JS 95-60 resistant (15.36 % stem tunneling) and lower resistance of MAUS 612 (35.93%). Motaphale *et al.*, (2016) evaluated that MAUS 158 as moderately resistant, consistent with the present study.

Table 1: Screening of soybean genotypes against Girdle beetle, (*O. brevis*):

S.N.	Entries	Girdle beetle per cent infestation	Category
1	DLSb 1	12.60 (20.67)	MR
2	DSb 23	13.90 (21.79)	MR
3	DS 3108	12.58 (20.72)	MR
4	JS 21-72	11.09 (19.43)	MR
5	JS 95-60	8.53 (16.93)	R
6	KDS 726	12.10 (20.29)	MR
7	MACS 1520	11.15 (19.50)	MR
8	MAUS 2 (Sus.Check)	24.34 (29.50)	LR
9	MAUS 158 (Res.Check)	15.97 (23.53)	MR
10	MAUS 612	13.80 (21.61)	MR
11	MAUS 725	24.38 (29.54)	LR
12	MAUS 731	29.36 (32.79)	S
13	MAUS 780	15.10 (22.83)	MR
14	NRC 130	14.77 (22.46)	MR
15	NRC 152	16.43 (23.75)	MR
16	RSC 10 - 52	21.18 (27.33)	LR
17	RVS 13-20	29.65 (32.97)	HS
18	RVS 2007 - 06	26.46 (30.82)	S
19	RVSM 2011- 35	12.69 (20.78)	MR
20	SKF -SPS - 11	17.56 (24.72)	LR
	SE±	2.00	
	CD at 5%	5.97	
	CD at 1%	8.09	
	CV%	11.74	
	Mean	24.10	

*Figures in the parentheses are angular transformed values

Table 2: Screening of soybean genotypes against Stem fly, (*M. sojae*):

S.N.	Entries	Stem fly per cent infestation	Category
1	DLSb 1	36.18 (36.95)	LR
2	DSb 23	35.13 (36.32)	LR
3	DS 3108	27.46 (31.44)	MR
4	JS 21-72	17.16 (24.46)	R
5	JS 95-60	15.36 (23.06)	R
6	KDS 726	38.53 (38.29)	LR
7	MACS 1520	40.27 (39.37)	LR
8	MAUS2 (Sus.Check)	36.77 (37.29)	LR
9	MAUS 158 (Res.Check)	18.36 (25.24)	MR
10	MAUS 612	35.93 (36.81)	LR
11	MAUS 725	34.76 (36.10)	LR
12	MAUS 731	28.31 (32.13)	MR
13	MAUS 780	38.52 (38.34)	LR
14	NRC 130	22.98 (28.59)	MR
15	NRC 152	33.73 (35.17)	LR
16	RSC 10 - 52	35.91 (36.72)	LR
17	RVS 13-20	28.82 (32.45)	MR
18	RVS 2007 – 06	44.87 (41.93)	LR
19	RVSM 2011-35	31.83 (34.28)	LR
20	SKF -SPS -11	27.28 (31.46)	MR
	SE±	3.03	
	CD at 5%	9.04	
	CD at 1%	12.25	
	CV%	12.68	
	Mean	33.82	

*Figures in the parentheses are angular transformed values

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**Assessment of Quantitative Losses by Pulse Beetle
Callosobruchus chinensis (L.) in different Soybean Genotypes
under Laboratory Conditions**

**ARYAN RAJ, NILIMA KARAM, H. NANITA DEVI,
T. SUNANDA DEVI, L. SOPHIA DEVI AND ANUJ KUMAR**
*AICRP (Soybean), College of Agriculture, Central Agricultural University,
Imphal-795004, Manipur*

Email: nilikaram@gmail.com

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ABSTRACT

*The present study was carried out during 2024-25 at the Department of Entomology, COA, CAU, Imphal to evaluate the quantitative losses by bruchid pest, pulse beetle *Callosobruchus chinensis* (L.) on nine soybean genotypes under storage conditions over 90 days. The lowest weight loss of stored seeds was observed in genotype CAU MS-2 (3.32%), followed by CAU MS-1 (3.99%), while the highest loss incurred by JS 335 (14.39%). Similarly, seed damage ranged from minimum 4.49% in CAU MS-1 to maximum 78.68% in JS 335. Soybean genotype CAU MS-2 showed the least germination loss of 25.00% followed by CAU MS-1 (33.33%) and JS 335 recording the highest germination loss of 71.67%. These findings suggest that CAU MS-1 and CAU MS-2 exhibit highest tolerance to infestation by pulse beetle with minimum quantitative losses in storage conditions.*

Keywords: Soybean, Pulse beetle, weight loss, seed damage, germination loss, storage.

Soybean (*Glycine max* L. Merrill) is a leguminous crop originated in Asia. The crop has high quality oil approximately 20% but also contains nearly 35 to 40% protein, 9% dietary fibre and around 8.5% of moisture (Gaur and Mogalapu, 2018). In storage, soybean suffers enormous losses due to insect infestation affecting the quality, including germination, oil content and protein content, in addition to seed yield. Commonly known as bruchid, pulse beetle *Callosobruchus chinensis* (L.) (Bruchidae: Coleoptera) is an economically significant insect pest, cosmopolitan in distribution and a

serious interior feeder of seeds in many legume species. It is known to be prolific and rapid in breeding and can swiftly cause a significant quantitative drop as well as diminish the nutritional value of stored grains (Tesfu and Emana, 2013). Normally infestation starts in the field because adult beetles can easily fly and lay eggs on legume pods. Infestation is caused by grubs as well as adults. The newly hatched larva bores into the seed and starts feeding on its contents till the whole endosperm are eaten up leaving behind only the seed coat.

Bruchids cause overall seed weight loss, loss of seed viability and

altered nutritional quality due to the presence of insect frass, excrement and dead insects in and on the seed (Tuda *et al.*, 2005). The damage due to this pest affects the germinating ability and nutritive value of the seed (Sharma, 1984). The estimated post-harvest losses caused by bruchids to the pulses ranged from 30-40% within 6 months of storage and when left unattended losses could be up to 100 percent. (Govindan *et al.*, 2020). However, there is a dearth of information on soybean, indicating this beetle damage to soybean was previously deemed insignificant.

MATERIALS AND METHODS

Rearing of test insects

The initial adult culture of the test insect, pulse beetle *Callosobruchus chinensis* (L.) was started by collecting the adult beetles from infested soybean seeds from untreated godowns/grocery shops. These adult beetles were reared on insect susceptible soybean JS-335 in the laboratory conditions, Department of Entomology, College of Agriculture, Central Agricultural University, Imphal. The methodologies followed are enlisted below.

500 g of susceptible soybean seeds was cleaned, washed, dried and then sterilized at temperature of 30°C for 30 minutes to eliminate the hidden infestation, if any. The seeds was removed from the oven and placed in a glass jar (25 cm x 15 cm x 10 cm) with a muslin cloth over it for 24 hours to allow it to regain normal grain moisture without additional infestation.

5 pairs of male and female adults were released for oviposition in the glass jar containing the sample soybean seeds. The jar was covered with muslin fabric and tightly fastened with rubber bands to prevent the adults from escaping. The stock culture was maintained undisturbed at room temperature for mating and oviposition of the beetles and then newly emerged F1 progenies of the beetles were used throughout the period of experimental study. The ideal temperature and relative humidity for maintaining the culture was 32°C±20°C and 70±5%, respectively (Andrewartha, 1961).

Estimation of quantitative losses caused by pulse beetle on soybean genotypes and identify best genotype resistant against the pest under storage conditions.

Fresh, insect free and genetically pure and healthy breeder seeds of nine high yielding soybean genotypes suited in Manipur conditions free from any insect infestation were obtained from AICRP (Soybean), COA, CAU, Imphal. Moisture content for all tested genotypes was kept similar before the experiment at around 12%. Soybean variety/genotype used for the study were T1 - MACS 1460, T2 - JS 20-116, T3 - JS 335, T4 - NRC 142, T5 - MACS 1407, T6 - CAU MS-1, T7 - CAU MS-2, T8 - IC 0574366 and T9 - DSb 32

Quantitative losses caused by the pulse beetle in soybean genotypes kept for 90 days under storage condition were determined.

Weight loss due to infestation by pulse beetle *Callosobruchus chinensis* (L.)

For working out the weight loss of seeds after 90 days of infestation by pulse beetle, the beetles, frass, excreta etc. were removed from each jar and the weight of seeds was taken separately on electronic balance from each replicate. Seed weight loss was calculated from weight of damaged and undamaged seeds after 90 days of release of the beetles. Per cent weight loss was calculated by using following formula given by Boxall (1981) as follows:

% weight loss =

$$\frac{\text{Initial weight} - \text{final weight}}{\text{Initial weight}} \times 100$$

Seed damage due to infestation by pulse beetle *Callosobruchus chinensis* (L.)

The damaged seeds was separated out from the total number of seeds taken for observation in each replication. One or more holes per seed was considered as damaged ones. The following formula was used for determination of per cent seed damage as described by Mohan and Sundar babu (1999).

% seed damage =

$$\frac{\text{Number of damaged seeds}}{\text{Total numbers of seeds}} \times 100$$

Germination loss due to infestation by pulse beetle *Callosobruchus chinensis* (L.)

The viability of seeds of the different genotypes was tested after

90 days of storage. From each of the genotype, 20 seeds was taken out randomly and placed in petridish at proper distance lined with round filter paper disc wetted with water, covered by second one and folded properly and tied with rubber band. These petridishes were kept at room temperature for six days to allow sufficient time for all the seeds to germinate. Watering of seeds was done regularly to prevent drying. Each set was replicated three times. Germination success will be observed 6 days later. The number of unsprouted seeds was counted and per cent germination loss was calculated with the help of following formula modified after ISTA (1996):

% Germination loss =

$$\frac{\text{Number of unsprouted seeds}}{\text{Number of seeds used}} \times 100$$

RESULTS AND DISCUSSIONS

Percent weight loss of soybean genotypes due to pulse beetle *Callosobruchus chinensis* (L.)

The weight losses due to damage by pulse beetle infestation after 90 days of storage in different genotypes ranged in between 3.32 to 14.39 per cent. Lowest weight loss of 3.32% was observed in CAU MS-2 followed by CAU MS-1 (3.99%) which are statistically at par with each other. The maximum net weight loss was observed in variety JS-335 with a weight loss of 14.39 % which was highly infested by the pest during storage.

The result on percent weight loss of soybean genotypes due to pulse

beetle can be summarized in the order from least infestation as CAU MS-2 - 3.32%, CAU MS-1 - 3.99%, NRC 142 - 4.69%, MACS 1407- 5.09%, MACS 1460- 5.18%, DSb 32- 5.62%, IC 0574336 - 5.77%, JS 20-116- 7.22%, JS 335 - 14.39% mean weight loss inflicted after 90 days of insect infestation. Doharey *et al.* (1987) reported that weight loss caused by *C. chinensis* was 25.56 per cent after 90 days of storage period in green gram. Similar results were observed by Anandhi *et al.* (2008) who reported loss in weight was as high as 7.60% recorded at 90 days after inoculation.

The current findings are similarly consistent with those of Jat *et al* (2013), who stated that the lowest mean weight loss was reported in the instance of one adult pulse beetle pair, namely 1.81 percent.

Percent seed damage of soybean genotypes due to pulse beetle *Callosobruchus chinensis* (L.)

The percent seed damage in different varieties ranged in between 4.49 to 78.68 per cent. Least damage on seeds of 3.82% was observed in CAU MS-1 followed by CAU MS-2 with 5.28% as shown in table 1. The maximum seed loss was observed in variety JS-335 with 78.68%.

The result on percent seed damage of soybean genotypes due to pulse beetle can be summarized in the order from least infestation as CAU MS-1- 4.49%, CAU MS-2 – 5.28%, NRC-142 – 5.76%, MACS-1460- 6.16%, IC-0574336- 10.00%, DSB-32- 14.75%, JS-20-116- 31.67%, MACS-1407- 32.84% and JS-335- 78.68%

seed damage inflicted after 90 days of insect infestation, respectively.

The current findings corroborates with those of Singh *et al.* (2017), who reported that after 90 days of storage of chickpea grains, seed damage reached peak of 40.75 percent in the event of releasing one pair of adult pulse beetles. However, research by Jat *et al* (2013) stated that with the release of one pair of adult pulse beetle on chickpea, lower grain damage of 7.79 percent was reported after 90 days of storage.

Partial conformity with prior research by Babu *et al* (2021), who found that the percentage of grain damage after 90 days after insect release percent grain damage increased due to increasing exposure and insect population number, which recorded 72.72 percent in cowpea, 70.75 percent in green gram, 66.99 percent in chickpea, 54.60 percent in black gram, 29.33 percent in red gram, and 18.26 percent in soybean. Previous research by Rawat and Srivastava (2011) also indicated that the percentage of seed damage caused by *C. chinensis* was highest in cowpea (96.15 percent), followed by green gram (88.44 percent), and lowest in moth bean (74.22 percent).

Percent germination loss of different soybean genotypes due to pulse beetle

The data on germination loss as shown in table 1 depicted that there was adverse effect of insect infestation on germination percentage of soybean seeds after 90 days of storage. The screening of soybean genotypes after 90 days of infestation by pulse beetle

shows lowest per cent germination loss in JS-335 (20%) and JS-20-116 (25%). The per cent germination of the rest of the genotypes ranged from between 33.33 to 71.67 per cent after three months of storage period.

The percent germination loss can be inferred in the order of JS 335 – 20%, JS 20-116 – 25%, MACS 1460 – 33.33%, IC 0574336 – 35%, DSb 32 – 40%, MACS 1407 - 48.33%, NRC 42 - 51.67%, CAU MS-1 - 56.67% and CAU MS-2 - 71.67% in soybean after 90 days of storage period, respectively showing a very high variation of significance. The aforementioned findings corroborate earlier research by Singh (2020), who observed germination loss of 42 and 33.6 percent, respectively in smaller and larger size of mung bean grains, respectively.

Doharey *et al.* (1987) observed 98 per cent loss in germination by *C. chinensis* in black gram seeds after 90 days of storage period. The current findings are consistent with those of Parmar and Patel (2016), who discovered mung bean susceptibility to

Callosobruchus chinensis L. during storage exhibiting 29.97-65 percent reduction in germination after six months of storage. The current findings are however contrary with those of Singh *et al* (2017), who found that one pair of adult pulse beetles caused only 28.5 percent loss in germination of mung bean and Jat *et al* (2013) who observed 29.27 percent for the release after 90 days of storage of mung bean seeds.

CONCLUSION

It can be concluded that soybean genotypes CAU MS-1 and CAU MS-2 were observed to tolerate infestation by pulse beetle (*Callosobruchus chinensis* L.) up to 90 days of storage. Genotype CAU MS-2 recorded least weight loss, least seed damage and least germination loss of 3.32%, 5.28% and 25% respectively followed by genotype CAU MS-1 with weight loss, seed damage and germination loss of 3.99 %), 4.49% and 33.33% respectively which were significantly superior to other tested genotypes.

Table 1: Screening of different soybean genotypes per cent weight loss, seed damage and germination loss after three months of storage

Treatment	Soybean Genotypes	% weight loss after 90 days of storage **	% seed damage after 90 days of storage**	% germination loss after 90 days of storage**
T1	MACS 1460	5.18 (13.50)	7.83 (16.17)	43.33
T2	JS 20-116	8.03 (16.64)	31.67 (33.67)	65.00
T3	JS 335	14.39 (23.78)	78.68 (68.20)	71.67
T4	NRC 142	4.69 (12.18)	5.76 (13.81)	36.67
T5	MACS 1407	5.09 (12.89)	12.88 (21.68)	45.00
T6	CAU MS-1	3.99 (11.70)	4.49 (12.83)	33.33
T7	CAU MS-2	3.32 (10.30)	5.28 (13.29)	25.00
T8	IC 0574336	6.67 (15.01)	14.37 (22.08)	63.33
T9	DSb 32	6.18 (14.31)	14.75 (22.30)	51.67
	SEm	0.56	2.22	2.89
	CD at 5%	1.68	6.59	8.58

**mean of the three replications; Figures in parenthesis are arc sine values

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Genetic Gain for Seed Yield and Its Components in RILs Derived from Cross of Grain Type × Edamame Soybean

**MEGHANA D P, KAMALPREET SINGH MANDAHAL,
SNEHDEEP KAUR, GAURAV KHOSLA, SHAYLA BINDRA,
INDERJIT SINGH, VIJAYA KUMAR KORABOYANA,
BALWINDER SINGH GILL**

Punjab Agricultural University, Ludhiana, Punjab, 141004

Email: gillbs@pau.edu

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ABSTRACT

The current study was formulated to evaluate 148 RILs derived from grain type (SL958) × edamame type (AGS 456) soybean for yield and component traits to identify high yielding, grain and vegetable type genotypes with YMD resistance. Significant variation in the RIL population was observed for all characters. Seed yield was found to have highest GCV, PCV, and genetic advance. Days to 50% flowering and plant height was found to be highly heritable followed by 100-seed weight. Seed yield showed significant and positive correlation with number of seeds per pod, number of pods per plant, harvest index, 100-seed weight, number of pods per plant, days to 50% flowering and plant height. The present study identified two vegetable type genotypes (RIL-122 and RIL-59) and eight grain type genotypes (RIL-105, RIL-112, RIL-31, RIL-113, RIL-141, RIL-60, RIL-36 and RIL-21) having high seed weight with resistance to yellow mosaic disease.

Keywords- Edamame, Soybean, yellow mosaic disease (YMD), genetic gains.

Soybean [*Glycine max* L. (Merrill)] belongs to family Leguminosae and subfamily Papilionoideae. It is one of the oldest crops that originated and was domesticated in the eastern half of Northern China. It is said to be a miracle crop or wonder crop due to its multiple uses *viz.* feed, fodder, biofuel, natural fertilizer, oil cakes, cleaning products, cosmetics, candle wax, and a rich protein source in form of soymilk, soy chunks, tempeh, and tofu. Being a leguminous crop, it is able to fix atmospheric nitrogen thereby replenishing soil health (Jandong et al. 2020). It is known as the

golden bean of 20th century and also entitled as “meat that grows on the plant” for having the highest amount of protein (35-40%) among all the pulses, oil content (20%), and versatile nutritional benefits (Reni and Rao 2013). Soybean is a noteworthy source of supplements of nutrients for all veggie lovers as its protein contains all the essential amino acids which are equivalent to the same amount of meat; the antioxidants present in soybean decrease the risk of cardiovascular and other diseases; its oil is free from cholesterol and contains two essential

fatty acids (linoleic and linolenic acid) that are not synthesized by the human body but are essential for growth and development. Therefore, soybean oil is gaining importance in the international market and is ranked number one among the major oil crops *viz.*, rapeseed, sunflower, groundnut cottonseed, and linseed (Mandahal et al 2025). In India, soybean secured 5th position in terms of area, production, and productivity after the Brazil, USA, Argentina, and China. The main reasons for low productivity in India are both abiotic (temperature, rainfall) and biotic (pests and diseases) stresses.

Soybeans are broadly classified into two categories *viz.*, vegetable and grain soybean. Each category has certain specific characteristics that make soybean seeds to be used as green seeds (vegetable type) or use as dry seeds (grain type). Grain soybean has small or medium-sized seeds and is low in sugar content whereas its vegetable counterpart has bold seeds with high sugar content. Efforts made to grow vegetable soybean introduced from Taiwan in Northern Plain Zone could not be succeeded because all the introduced varieties were found to be highly susceptible to yellow mosaic disease (YMD). On the other hand, grain-type soybean varieties recommended for Northern India are resistant to YMD but suffer from drawback of small seeds and late maturity. Thus, vegetable and grain-type soybeans can compensate for the shortfalls of each other. The aim of the present investigation was to evaluate RILs derived from cross of grain and vegetable soybean for yield and

component traits for identification of YMD-resistant, high yielding, vegetable and grain type soybean genotypes; and to estimate genetic parameters like the phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance, correlations and path analysis.

MATERIALS AND METHODS

The present study was conducted at the Experimental area, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Punjab. The research material consisted of a set of 148 RILs (F₇ generation) developed from the cross, SL 958 × AGS 456. SL 958 is a recommended variety for the Northern Plain Zone that is high yielding, yellow mosaic disease (YMD) resistant and small seeded (100-seed weight of 10.0g). The other parent, AGS 456 is a vegetable-type genotype introduced from AVRDC, Taiwan. It has characteristics of sweet and bold seeds (100-seed weight of 30.0g) but it is highly susceptible to YMD. Purpose of the cross was to combine YMD resistance and bold seed for vegetable type and high yield and medium seed size for grain type soybean. Original cross was attempted during *kharif* 2018 and F₁ was planted in net house in winter 2018. Since the experimental site (Ludhiana, 30°-54' North Latitude, 75°-48' East Longitude at a mean height of 240 meters above sea level) is hot spot for YMD, all the segregating generations *i.e.*, F₂ to F₇ were grown during 2019 to 2021 in net house to protect material from YMD.

For speedy development of RIL population, two generations were grown each year *i.e.*, one in winter (Feb. to May) and another during late *kharif* (mid Aug. to Nov.). From F₂ onward five seeds were harvested from each plant and planted in a hill spaced 45 x 45 cm. When the plants attained sufficient growth, only one plant was retained in a hill. The RILs along with their parents were grown in Randomized Complete Block Design using three replications during *kharif* 2022. Paired rows of three-meter length having plant to plant distance of 5 cm and row to row spacing of 45 cm was used. The crop was raised by following recommended package of practices of Punjab. The observations were recorded from five randomly tagged competitive plants in each replication and each RIL. The data on phenological traits (days to 50% flowering, days to maturity) and other metric traits (plant height, number of pods per plant, number of pods per node, number of seeds per pod, 100-seed weight, harvest index and seed yield) were recorded. Analysis of variance (ANOVA), genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2), genetic advance (GA), correlation coefficients and path analysis were computed using standard statistical procedures (R software).

RESULTS AND DISCUSSION

ANOVA and mean performance of all metric traits

Phenotypic data for all nine traits (Plant height, days to 50% flowering, days to maturity, number of pods per plant,

number of pods per node, seeds per pod, harvest index, 100-seed weight and seed yield) was subjected to analysis of variance and is presented in the table 1. All the traits showed highly significant differences among RILs. The mean and range for all the traits for parents and five best RILs are given in table 2. The mean height of entire RIL population was found to be 82.0 cm which was at par with the height of resistant parent *i.e.*, SL 958 (84.0cm) and significantly higher than the other parent, AGS 456 (40.0cm). The mean performance of days to 50% flowering was observed to be 50.5 days. The parents of RIL population *viz.*, SL 958 and AGS 456 took 56 and 40 days, respectively to flower. The results for the days to maturity showed that most of the RILs were significantly early in maturity *i.e.*, 120.2 days in comparison to SL 958 *i.e.*, 126 days whereas the other parent AGS 456 took 120 days to maturity. Data recorded on number of pods per plant showed that the average number of pods per plant was 30.6 pods and most of the RILs outperformed both the parents *viz.*, SL 958 (26.1 pods) and AGS 456 (20.0 pods). The mean for the number of pods per node was observed to be 9.0. Due to susceptibility of AGS 456 to YMD, produced fewer pods (3.0 pods per node) and the YMD resistant parent (SL 958) had 9.5 pods per node. The vegetable parent, AGS 456 recorded mean seeds per pod to be 2.0 whereas SL 958 had 2.2 seeds per pod. The mean of RIL for this trait lied in between both the parents *i.e.*, 2.5 seeds per pod. The mean harvest index (HI)

of RILs was found to be 26.4% which was higher than the HI of AGS 456 (18.3%) but lower than SL 958 (35.3%). The most important characteristic of vegetable-type soybean is 100-seed weight. The desired 100-seed weight of the vegetable soybean variety is 20.0g or more. Although the mean for this trait was found to be 11.8g, few RILs produced ~20.0g seed weight. Grain type parent SL 958 had 10.9g and AGS 456 being susceptible to YMD produced shrivelled grains having 100- seed weight of 8.0g. The 100-seed weight of RIL population ranged from 6.1-21.4g. The mean seed yield (7.4g/plant) was significantly higher than the susceptible parent (5.0g/plant) but less than SL 958(10.5g/plant). On the other hand, the values for grain yield varied from 0.4g to 23.6g/plant. The purpose of this study was to identify YMD-resistant, high yielding, vegetable and grain type soybean genotypes. Two vegetable type RILs; RIL-122 (21.4g seed weight, 10.9g seed yield) and RIL-59 (19.1g seed weight, 16.6g seed yield) having YMD (Score 2) were identified. Eight RILs *viz.*, RIL-105, RIL-112, RIL-31, RIL-113, RIL-141, RIL-60, RIL-36 and RIL-21 (table 3) having grain yield significantly higher than SL 958 with resistance to YMD (Score 1-2) have also been isolated as grain type genotypes for further testing.

Phenotypic coefficient of variance (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance (GA)

The level of varietal differences present in the soybean genotypes were estimated

on the basis of genetic parameters *viz.*, genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance for different traits; and are presented in table 4. GCV and PCV values were at par with each other portray that there is least effect of environment on the characters studied. But in contrast, few other researchers found that PCV is more than GCV (Jandong et al. 2020, Neelima et al. 2018, Jain et al. 2018, Mahbub and Shirazy 2016) depicting influence of environment on these traits. Among all the characters, seed yield has been found to had highest GCV and PCV followed by harvest index, number of seeds per pod, number of pods per node, number of pods per plant providing better scope for improvement of these characters through selection. Similar results for seed yield and number of pods per plant were also reported by Aditya et al. 2011, Akramet al. 2011, Reni and Rao 2013, Baraskar et al.2014, Goonde and Ayana 2021. Plant height and 100-seed weight showed medium GCV and PCV values whereas, days to flowering and days to maturity had low GCV and PCV. Contrary to our results, Baraskaret al.2014 reported that plant height was found to have high GCV and PCV.

It is impossible to ascertain the extent of difference which is transmitted to the progeny by analysing only GCV and PCV. Hence, knowledge of heritability is useful in predicting the genetic advance of any metric trait and also helps in selection. In present study, all the characters

showed high heritability *i.e.*, above 80% (Table 4). Desissa (2017) also reported to have more than 70% heritability for all characters studied. Among all the characters, days to 50% flowering (96.76%) was found to be highly heritable followed by plant height at maturity (96.46%), 100-seed weight (96.33%), days to maturity (95.18%), seed yield (91.93%), number of seeds per pod (90.62%), number of pods per node (89.67%) number of pods per plant (86.20%) and harvest index (82.71%). The results suggest that selection based on phenotypic expression will be helpful in advancement or improvement of traits having high heritability. The present results for high heritability were supported by several workers like for plant height (Aditya et al. 2011, Chandrawat et al. 2017), days to maturity (Mahbub and Shirazy 2016), days to 50% flowering and 100-seed weight (Aditya et al. 2011). Similar results were also reported by Chauhan and Singh (1984) and Pushpendra and Ram (1987).

Number of traits had shown high heritability coupled with high genetic advance as a percent of mean *viz.*, seed yield and its component traits (harvest index, seeds per pod, number of pods per plant, number of pods per plant and 100-seed weight) (Figure 1). These results are in agreement with the results from earlier studies (Reni and Rao 2013, Mahbub and Shirazy 2016, Chandrawat et al. 2017, Jandong et al. 2020).

CORRELATION ANALYSIS

In the present investigation, it was observed that seed yield had

positive and significant correlation with most of the characters (Table 5). Out of which number of seeds per pod (0.55) was found to have highest and significant positive correlation with seed yield followed by number of pods per plant (0.48), harvest index (0.44), 100-seed weight (0.39) and medium association with number of pods per node (0.21), days to 50% flowering (0.21) but low correlation with plant height (0.18). Aditya et al. (2011) and Mahbub et al. (2015) also observed the similar kind of results that number of pods per plant and harvest index had positive and significant correlation with grain yield. In contrast, Akramet al. (2011) reported that 100-seed weight has negative correlation with seed yield per plant. Among other traits it was observed that 100-seed weight and harvest index had high correlation (0.25) than number of pods per plant (0.13) and number of seeds per pod (0.13). Harvest index had positive correlation with the number of seeds per pod (0.33) and no correlation with days to maturity was noticed. It had negative correlation with number of pods per node (-0.13).

Number of seeds per pod exhibited crucial relation with days to 50% flowering (0.23) and significant negative correlation with number of pods per plant (-0.10) which signifies that while developing early flowering genotypes we have to sacrifice number of seeds per pod and by increasing number of seeds per pod there will be corresponding decrease in pods per plant. A remarkable correlation was noticed among number of pods per

node with number of pods per plant (0.46) and also with plant height (0.40). Thereafter significant association was recorded for number of pods per plant with plant height (0.33) which suggested that on improving plant height, number of pods per plant will also improve. Rajanna et al. (2000) reported similar results that plant height and number of pods per plant had positive and significant correlation. In the same way, days to 50% flowering had positive and significant correlation with plant height (0.32) and days to maturity (0.24). Our results for different parameters of soybean are at par with the results produced by Mahbub et al. (2015). Therefore, it is important that to increase the seed yield, emphasis should be given on correlated traits (number of pods per plant, number of pods per node, number of seeds per pod, harvest index, 100-seed weight and plant height).

Path analysis

Correlation analysis provides the degree of association between two characters studied but the association may also be due to the effect from third variable. Hence, study of direct and indirect effects of different characters on seed yield through path analysis is of high importance (Wright 1921). In the current study, dependent variable was seed yield while the remaining characters represented as the independent variables. The matrix showing direct and indirect effects of all the 8 characters on seed yield is presented in the table 6.

The traits like number of seeds per pod (0.51), number of pods per plant

(0.50), 100-seed weight (0.22) and harvest index (0.20) had positive direct effect on seed yield. The results of the present study are in agreement with the results of Chandrawat et al. (2017), Chavan et al. (2016), Silva et al. (2015) and Ramirez and Moreno (2012). In contradiction to the present results, Balla and Ibrahim (2017), Malik et al. (2007) and Showkat and Tyagi (2010) reported the negative direct effect of seed weight on seed yield. However, plant height (-0.09) and days to maturity (-0.04) were found to have negative direct effect on seed yield. Similarly, Chavan et al. (2016) also observed the negative direct effect of plant height on seed yield.

Plant height at maturity (0.17) and number of pods per node (0.23) via number of pods per plant showed positive indirect effect on seed yield. Similarly, days to 50% flowering (0.12) and harvest index (0.17) had positive direct effect on seed yield through number of seeds per pod. Similar results were also reported by Archana et al. (1999). In support of the present results, Silva et al. (2015) also reported that number of pods per plant had positive and direct effect on seed yield via number of seeds per plant. But these results are in disagreement with the results of Ganesamurthy and Seshadri (2004).

Among important traits, days to maturity had a low negative direct effect on seed yield (-0.04) and it had a low but positive indirect effect via three traits *viz.*, number of pods per plant (0.06), number of seeds per pod (0.04) and days to 50% flowering

(0.02). Number of pods per plant had a negative indirect effect on seed yield via number of seeds per pod (-0.05) and plant height (-0.03). 100-seed weight exhibited high positive direct and indirect effect via number of seeds per pod (0.07), number of pods per plant (0.06), and harvest index (0.05) on seed yield.

On the basis of above findings, it is evident that substantial genetic variability was envisaged for yield and its component traits in most of the RILs under study. Therefore, these traits governing RILs should be considered while selecting superior and desirable plants for further evolving high yielding genotypes in soybean.

Authors contribution

Conceptualization of research (Meghana DP, Gill BS); Designing of the experiments (Gill BS, Gaurav Khosla,

Shayla Bindra); Contribution of experimental materials (Gaurav Khosla, Vijaya Kumar Koraboyana, Gill BS); Execution of field/lab experiments and data collection (Meghana DP, Snehdeep Kaur, Inderjit Singh); Analysis of data and interpretation (Meghana DP, Kamalpreet Singh Mandahal); Preparation of the manuscript (Meghana DP, Kamalpreet Singh Mandahal).

Declaration

The authors declare that they do not have any conflict of interest

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Table 1: Mean squares for different traits in soybean

Source of variation	df	Plant height at maturity	Days to 50% flowering	Days to 50% maturity	Number of pods per plant	Number of pods per node
Replication	2	3085.07**	58.80**	25.97**	2829.37**	265.92**
Genotypes	147	995.97**	108.25**	97.62**	278.61**	26.76**
Error	294	12.04	1.194	1.62	14.11	0.99

Source of variation	df	Seeds per pod	Harvest index (%)	100- seed weight (g)	Seed yield (g/plant)
Replication	2	0.33*	3808.30**	61.80**	248.36**
Genotypes	147	2.32**	330.50**	21.46**	50.41**
Error	294	0.08	21.50	0.27	1.43

Table 2: Mean performance for different traits

Sr. No.	Traits	Mean performance	Mean of SL 958 (♀)	Mean of AGS 456 (♂)	Range of RILs	Five top performing RILs
1	Plant height (cm)	82.0	84.0	40.0	29.2-124.4	RIL-2 (29.2cm), RIL-15 (30.9cm), RIL-41 (34.7cm), RIL-85 (43.1cm), RIL-124 (44cm)
2	Days to 50% flowering	50.5	56	40	33-66	RIL-2 (33 days), RIL-14 (33 days), RIL-15 (34 days), RIL-117 (35 days), RIL-12 (38 days)
3	Days to maturity	120.2	126	120	95-151	RIL-128 (95 days) RIL-2 (105 days) RIL-15 (105 days) RIL-6 (105 days) RIL-3 (105 days)
4	Number of pods per plant	30.6	26.1	20.0	4.6-56.6	RIL-102 (56.6 pods) RIL-34 (56.2 pods) RIL-83 (50 pods) RIL-73 (49.9 pods) RIL-37 (49.3 pods)
5	Number of pods per node	9.0	9.5	3.0	2.4-15.6	RIL-23 (15.6 pods) RIL-1 (15.2 pods) RIL-73 (15 pods)

Continue Table 2

6	Number of seeds per pod	2.5	2.2	2.0	1.0-3.1	RIL-66 (14.9 pods)
						RIL-16 (14.6 pods)
						RIL-60 (3.1)
						RIL-93 (2.7)
						RIL-85 (2.5)
						RIL-71 (2.4)
7	Harvest index (%)	26.4	35.3	18.3	3.4-49.1	RIL-141 (2.4)
						RIL-113 (49.1 %)
						RIL-122 (48 %)
						RIL-89 (46.5 %)
						RIL-2 (46.4 %)
						RIL-86 (46.1 %)
8	100-seed weight (g)	11.8	10.9	8.0	6.1-21.4	RIL-122 (21.4g)
						RIL-59 (19.1g)
						RIL-50 (17.7g)
						RIL-105 (17.5g)
						RIL-123 (17.2g)
						RIL-73 (23.6g)
9	Seed yield (g/plant)	7.4	10.5	5.0	0.4-23.6	RIL-105 (20.4g)
						RIL-102 (20.4g)
						RIL-98 (18g)
						RIL-112 (17g)

Table 3: Promising Vegetable and Grain types genotypes identified from RIL population

Sr. No.	RIL No.	100-seed weight (g)	Seed yield (g/plant)	Harvest index (%)	YMD Score
Vegetable type genotypes					
1	RIL-122	21.4	10.9	48.0	2
2	RIL-59	19.1	16.6	30.1	2
Grain type genotypes					
3	RIL-105	17.5	20.4	26.7	2
4	RIL-112	13.1	17.0	41.0	1
5	RIL-31	12.9	16.2	39.7	1
6	RIL-113	15.4	15.3	49.1	2
7	RIL-141	14.1	14.9	30.9	2
8	RIL-60	13.8	13.5	36.1	2
9	RIL-36	13.7	13.2	24.1	2
10	RIL-21	16.3	13.1	34.0	2

Table 4: Phenotypic Coefficient of Variance (PCV), Genotypic Coefficient of Variance (GCV), heritability (h^2) and genetic advance (GA) for different traits.

Sr. No.	Traits	GCV (%)	PCV (%)	h^2 (%)	GA	GA percent of mean (%)
1	Plant height at maturity (cm)	22.09	22.50	96.46	36.64	44.70
2	Days to 50% flowering	11.99	12.19	96.76	12.11	24.30
3	Days to maturity	4.72	4.84	95.18	11.37	9.50
4	Number of pods per plant	30.72	33.09	86.20	17.96	58.76
5	Number of pods per node	32.65	34.48	89.67	5.72	63.69
6	Seeds per pod	34.98	36.75	90.62	1.70	68.60
7	Harvest index (%)	38.48	42.31	82.71	19.01	72.09
8	100- seed weight (g)	22.50	22.93	96.33	5.37	45.49
9	Seed yield (g/plant)	54.48	56.82	91.93	7.98	107.61

Table 5: Correlation coefficients among all possible pairs of traits.

Sr. No.	Character	Plant Height (cm)	Days to 50% flower	Days to maturity	Number of pods/ plant	Number of pods/ node	Number of seeds/ pod	Harvest index (%)	100-seed weight (g)	Seed yield (g/plant)
1	Days to 50% flowering	0.32**	-							
2	Days to maturity	0.07	0.24**	-						
3	Number of pods per plant	0.33**	0.07	0.12**	-					
4	Number of pods per node	0.40**	0.17**	-0.04	0.46**	-				
5	Number of seeds per pod	0.07	0.23**	0.07	-0.10*	-0.05	-			
6	Harvest index (%)	-0.03	-0.01	0.00	0.05	-0.13**	0.33**	-		
7	100-seed weight (g)	0.15**	0.05	0.04	0.13**	0.01	0.13**	0.25**	-	
8	Seed yield (g/plant)	0.18**	0.21**	0.08	0.48**	0.21**	0.55**	0.44**	0.39**	-

Table 6: Path coefficients of different traits on seed yield.

Sr. No.	Character	Plant Height (cm)	Days to 50% flower.	Days to maturity	Number of pods per plant	Number of pods per node	Number of seeds per pod	Harvest index (%)	100-seed weight (g)
1	Plant Height (cm)	-0.09	0.02	0.00	0.17	0.02	0.04	-0.01	0.03
2	Days to 50% flowering	-0.03	0.07	-0.01	0.04	0.01	0.12	0.00	0.01
3	Days to maturity	-0.01	0.02	-0.04	0.06	0.00	0.04	0.00	0.01
4	Number of pods per plant	-0.03	0.01	0.00	0.50	0.03	-0.05	0.01	0.03
5	Number of pods per node	-0.04	0.01	0.00	0.23	0.06	-0.03	-0.03	0.00
6	Number of seeds per pod	-0.01	0.02	0.00	-0.05	0.00	0.51	0.07	0.03
7	Harvest index (%)	0.00	0.00	0.00	0.02	-0.01	0.17	0.20	0.05
8	100-seed weight (g)	-0.01	0.00	0.00	0.06	0.00	0.07	0.05	0.22

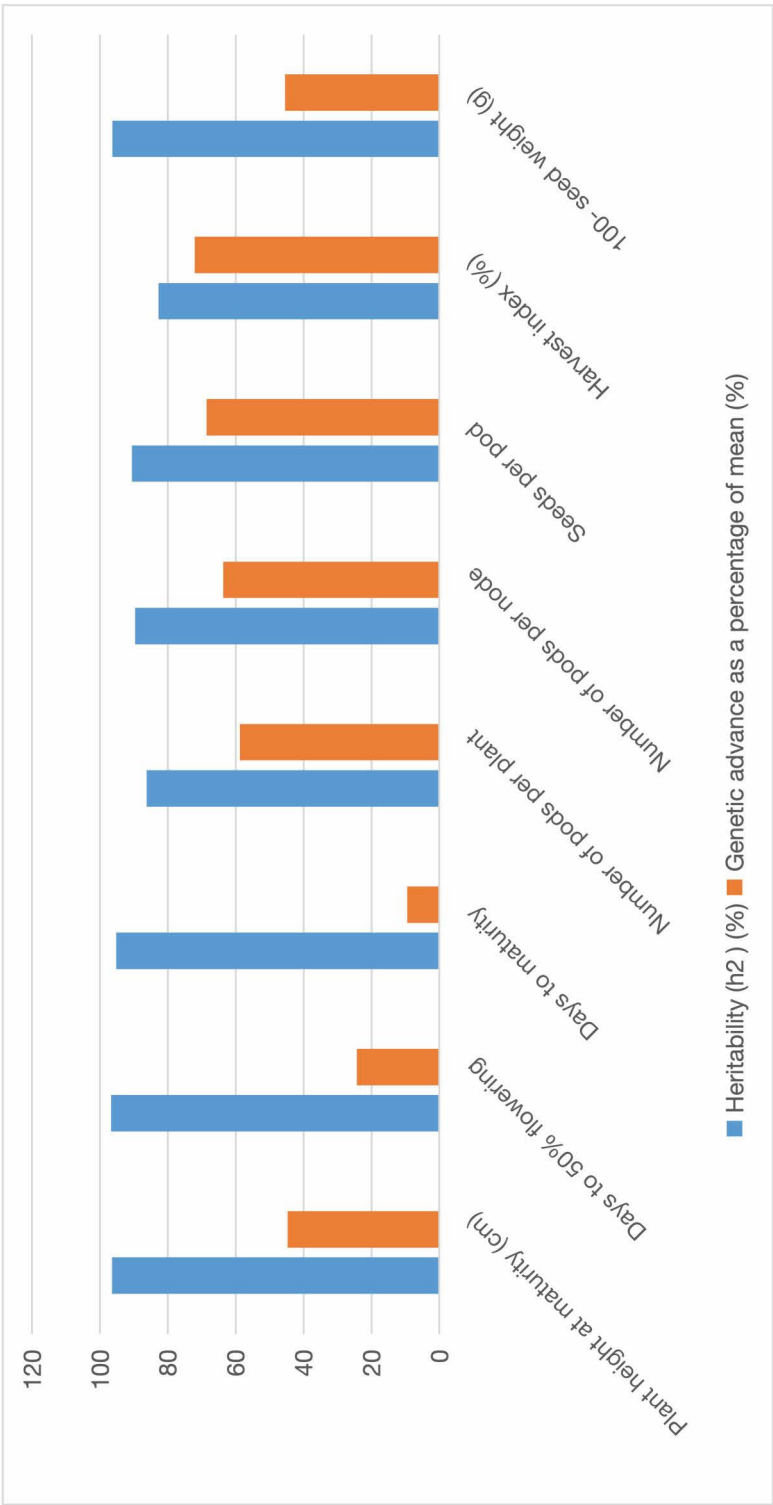


Figure 1: Heritability coupled with genetic advance as a percent of mean (%) for different traits

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Transfer Learning Approaches to Soybean Diseases Classification

SAVITA KOLHE, SANJEEV KUMAR, BU DUPARE,
MAKHAN KUMBHKAR, ANAND SAXENA

ICAR-National Soybean Research Institute, Indore, MP-452001.

Email: savitasoham@gmail.com

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ABSTRACT

Soybean diseases are a significant concern for farmers. The common diseases affecting soybean crops in this region include Alternaria Leaf Spot, Anthracnose (Pod Blight), Bacterial Blight, Cercospora Leaf Blight, Charcoal Rot, Collar Rot, and Sclerotial Blight.

Deep learning technologies have enabled the development of models for detecting plant leaf diseases. However, their application in identifying soybean diseases has been limited, with most approaches relying on traditional machine learning methods. In this work, an enhanced deep learning network model was developed to improve the accuracy of soybean leaf disease recognition. The model comprises three components: feature extraction, attention calculation, and classification.

Among the architectures evaluated LeNet, AlexNet, VGG, GoogleNet, and ResNet. The ResNet model achieved the highest classification accuracy at 87%. This performance underscores ResNet's effectiveness in capturing complex features through its deep architecture, making it a promising tool for soybean disease detection.

Implementing such advanced models can aid soybean farmers by providing timely and accurate identification of soybean diseases, thereby facilitating prompt and effective disease management strategies to safeguard crop yield and quality.

Keywords: Deep learning, CNN, LeNet, AlexNet, VGG, GoogleNet, ResNet.

Soybean is one of the most economically significant crops globally. One of the major factors limiting high-quality production of soybean crops is disease, which significantly affects both yield and plant health (Cen et al., 2020; Meng et al., 2022). Soybean diseases make significant annual losses of yields, whereby epidemiological studies showed that diseases account for about 10% of the

yield loss, while in more adverse conditions, losses can be as high as 30% (Chang et al., 2018; Guo et al., 2021). Most of the diseases affect a large proportion of soybean fields, it becomes obligatory to rapidly characterize the phenotypic traits linked to soybean diseases. This can help in early interventions, better varietal selection, right farming practices and disease

control measures. To enhance both yield as well as the quality of soybean crops, proper diagnosis of diseases in a given field in real-time is essential. Advanced methods such as remote sensing, artificial intelligence, and molecular diagnostics are increasingly being explored to enhance disease detection and management. These technologies can provide valuable insights into disease dynamics, allowing farmers to take corrective actions promptly, thereby reducing the negative impact on soybean production. Ultimately, improving disease management strategies through faster detection and real-time monitoring is critical for boosting soybean productivity and ensuring food security.

LITERATURE REVIEW

The effective disease management is vital for maximizing yield in soybean crop. Over the years, numerous research efforts have been dedicated for identifying and classifying soybean diseases using advanced computational techniques. Miao Yu (2023) used a residual neural network, leveraging transfer learning to classify four soybean diseases: Septoria Glycines Hemmi, Soybean Brown Leaf Spot, Soybean Frogeye Leaf Spot, and Soybean Phyllosticta Leaf Spot, achieving high recognition accuracy. In another study, Yu et al. (2022) built a soybean disease diagnosis model using ResNet18, focusing on the classification of Brown Leaf Spot, Frogeye Leaf Spot, and Phyllosticta Leaf Spot.

Angad Sandhu et al. (2022) introduced an innovative approach using Late-Stage Re-Training (LSRT) with the Fireworks Algorithm to enhance soybean disease prediction accuracy. Similarly, Jadhav et

al. (2021) developed a novel classification technique using the GoogleNet model, trained on 550 images of healthy and diseased leaves, including SBS, FLS, and BB. Another work by Jadhav et al. utilized Support Vector Machines (SVM) for binary classification of healthy and unhealthy leaves. Advanced deep learning methods also gained traction, as highlighted by Karlekar and Seal (2020), who employed CNN to classify 16 categories of plant diseases, including those affecting soybean.

Other studies explored a variety of models and techniques. Wu et al. (2019) applied AlexNet, GoogLeNet, and ResNet for disease classification, while Tetila et al. (2019) used a two-step approach with the SLIC algorithm for image segmentation and CNN models like Inception-v3 and ResNet-50 for classification. Araujo et al. (2019) utilized SVM for automatic identification of multiple soybean diseases, while Gui et al. (2019) employed LeNet for the recognition of soybean leaf spot diseases.

Several researchers integrated traditional image processing techniques with machine learning. Kaur et al. (2018) employed K-means clustering for the classification of Downy Mildew, Frogeye Leaf Spot, and Septoria Leaf Blight. Datta et al. (2019) used statistical and color feature extraction coupled with SVM to classify diseases affecting economically important plants, including soybeans. Pukkela and Borra (2018) highlighted precision agriculture techniques such as segmentation algorithms and clustering

for disease detection across various crops.

Furthermore, advancements in segmentation and feature extraction have contributed significantly. Patil and Lad (2021) used GLCM for feature selection and KNN and SVM for chili plant disease detection, showing the adaptability of similar techniques for soybean disease classification. Wallelign et al. (2018) utilized LeNet CNN, achieving robust results with a dataset of over 12,000 samples. The adoption of UAV images and CNNs in Tetila et al. (2019) also demonstrated the potential of aerial imagery for soybean disease identification.

Overall, the diverse methodologies employed in soybean disease detection from CNNs and residual networks to traditional SVM and clustering techniques underscore the critical role of machine learning and deep learning in modern agriculture. These approaches not only improve accuracy but also facilitate early disease detection, enabling targeted interventions and promoting sustainable farming practices.

METHODOLOGY

The proposed methodology for classifying soybean diseases involves utilizing advanced deep learning architectures, specifically LeNet, ResNet, and GoogleNet, to improve diagnostic accuracy. First, the dataset of soybean disease images is preprocessed by normalizing and augmenting the images

to increase model robustness and generalization. LeNet, a simpler model, is used as a baseline to understand performance on smaller datasets. For more complex datasets, ResNet is employed due to its deep residual learning technique, which enables the model to train very deep networks without the vanishing gradient problem, capturing intricate disease features more effectively. GoogleNet is integrated next, utilizing its inception modules that optimize computational efficiency by balancing depth and width, reducing overfitting while maintaining high accuracy.

These models are trained and validated using standard cross-validation techniques to ensure reliable performance. By combining the strengths of these architectures, the proposed methodology aims to enhance the accuracy and efficiency of soybean disease classification, ultimately supporting better accuracy as well as agricultural management decisions for soybean diseases.

Our methodology for soybean disease classification involved several stages, beginning with data collection from fields of ICAR-NSRI, Indore. We gathered a diverse dataset consisting of images representing five distinct soybean diseases: Anthracnose (300 images), Frogeye Leaf Spot (100 images), Purple Seed Stain (100 images), Rhizoctonia Aerial Blight (400 images), Yellow Mosaic (300 images), along with 300 healthy soybean images.

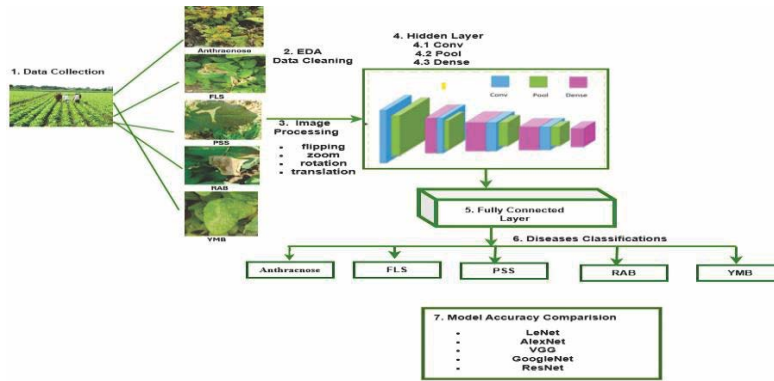


Fig 1: Architecture of Disease diagnosis using Transfer Learning

We then pre-processed the images by reshaping and normalizing the data to ensure consistency in input size and pixel value scaling. Various image augmentation techniques, such as flipping, zooming, rotating, and translation, were applied to artificially expand the dataset, thus enhancing the model's generalization ability.

For feature extraction, we employed deep learning techniques. The images were passed through convolutional layers for automatic feature extraction, followed by pooling and dense layers for further processing. The flattened output from the convolutional network was then fed into fully connected layers, allowing the model to learn complex patterns from the data. We experimented with different deep learning models, including LeNet,

AlexNet, VGG, GoogleNet, and ResNet, to classify soybean diseases. Each model's performance was evaluated based on classification accuracy, and the results were compared to determine the most effective model for soybean disease classification.

DATASET COLLECTION

The Soybean dataset is organized into 2 folders (train, test) and contains subfolders for each disease category (Anthracnose, Frogeye Leaf Spot (FLS), Purple Seed Stain, Rhizoctonia Aerial Blight, Yellow Mosaic Disease and healthy images). There is total 1400 images (JPEG) in our Soybean dataset that are collected from soybean fields of ICAR-National Soybean Research Institute, Indore as shown in Table 1.

Table 1 Details of Image Data Collection

S.No.	Diseases	Total images
1	Anthracnose	300
2	Frogeye Leaf Spot (FLS)	100
3	Purple Seed Stain	100
4	Rhizoctonia Aerial Blight	400
5	Yellow Mosaic Disease	200
6	Healthy	300
	Total	1400

Few sample images of soybean diseases from the database are shown in Fig. 2. To prepare the dataset for the training, the images originally at different resolution are resized to 128x128 pixels. Since the

images were taken in the uncontrolled environment the different lighting condition at the Soybean field of ICAR-NSRI, Indore.

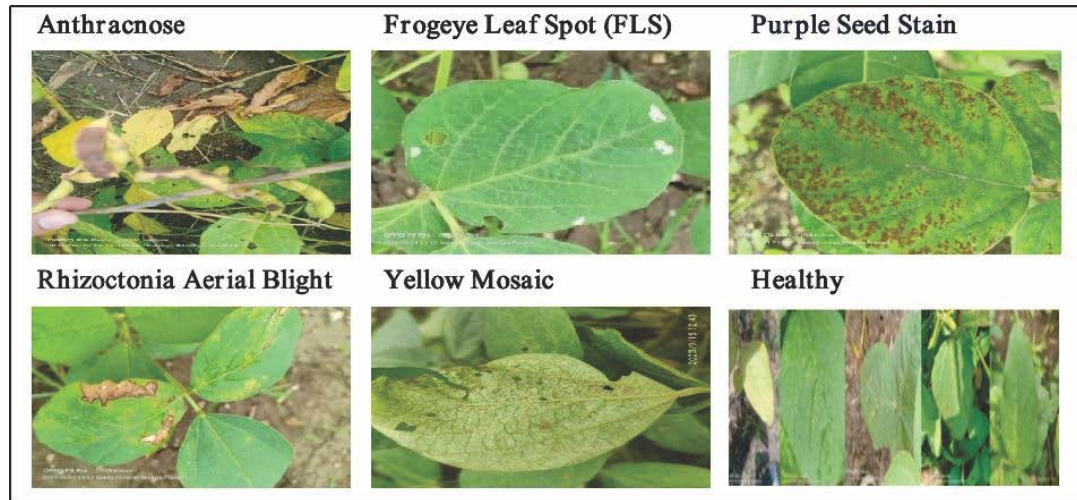


Fig. 2: Sample Pictures from Databases

DATA PREPROCESSING

In the image processing phase for the soybean disease dataset, we performed several essential data cleaning and pre-processing steps. First, we reshaped all images to a consistent size of 28x28 pixels, resulting in 784 pixels per image. This step ensured uniformity across the dataset, making it suitable for feeding into deep learning models. Next, the pixel values of the images were normalized, scaling them from the original range of 0-255 to a range of 0-1. This normalization process improved the convergence speed of the neural network during training. Additionally, the target variable, representing the different soybean disease classes, was one-hot encoded. The dataset contained a total of 10 distinct classes (0-9), with each disease or

healthy class being uniquely represented by a binary vector. These preprocessing steps were crucial in preparing the data for further analysis and model training.

TRANSFER LEARNING ARCHITECTURE

Transfer learning models like LeNet, AlexNet, VGG, GoogleNet, and ResNet are powerful tools for soybean image disease classification due to their pre-trained architectures and feature extraction capabilities. LeNet, one of the earliest convolutional neural networks (CNNs), is simple but effective for basic image classifications, making it suitable for identifying specific soybean disease patterns. AlexNet introduced deeper layers and ReLU activation, excelling in capturing

more complex features for high-resolution soybean images. VGG provides a deeper and uniform architecture with smaller filters, enhancing its ability to detect intricate patterns in disease symptoms. GoogleNet, with its Inception modules, optimizes computational efficiency while learning diverse features, making it ideal for varied disease images. ResNet solves the vanishing gradient problem through residual connections, enabling very deep networks to learn robust representations, which is crucial for accurately classifying diverse soybean diseases. Together, these models enhance precision and efficiency in plant pathology tasks.

A. LeNet was a groundbreaking Convolutional Neural Network (CNN) architecture developed by Yann LeCun, Leon Bottou, Yoshua Bengio, and Patrick Haffner in the late 1990s. Specifically designed for handwritten and machine-printed character recognition, this neural network marked a significant milestone in computer vision and deep learning. The architecture introduced innovative concepts like convolutional layers, pooling layers, and fully connected layers, which became fundamental building blocks for modern neural network designs, revolutionizing image recognition technologies.

B. AlexNet represented a significant leap forward in deep learning for image recognition. Developed by Alex Krizhevsky, Ilya Sutskever, and Geoffrey Hinton, this eight-layer neural network won the ImageNet ILSVRC-2012 competition. By leveraging two Nvidia

C. GPUs and incorporating advanced techniques like ReLU activation, max pooling, dropout, and data augmentation, AlexNet dramatically improved upon previous convolutional neural network architectures.

D. VGGNet, addressed AlexNet's complexity by introducing a more elegant solution to convolutional network design. By replacing large kernel filters with a series of smaller 3×3 convolution layers, the network simplified hyperparameter tuning while maintaining and even improving classification performance. This approach became an influential paradigm in deep learning architecture design.

E. ResNet revolutionized deep learning by introducing residual connections that solved the vanishing gradient problem plaguing increasingly deep neural networks. By implementing skip connections and batch normalization, ResNet enabled training of networks with over 100 layers, dramatically improving performance and pushing the boundaries of what was previously possible in convolutional neural network architectures.

F. GoogleNet, also known as Inception V1, marked a pivotal moment in convolutional neural network design. Proposed by Google researchers in 2014, this innovative architecture won the ILSVRC image classification challenge by introducing the inception module. By using parallel convolution operations with multiple filter sizes, GoogleNet significantly reduced classification error rates compared to its predecessors.

RESULTS AND DISCUSSION

PERFORMANCE EVALUATION OF TRANSFER LEARNING MODELS

In our study, we applied various deep learning models to classify soybean diseases, including Anthracnose, Frogeye Leaf Spot, Purple Seed Stain, Rhizoctonia Aerial Blight, Yellow Mosaic Disease, and healthy samples. Among the models tested, ResNet achieved the highest accuracy at 87.76%, followed by LeNet at 83.34%. AlexNet and VGGNet yielded similar accuracies of 78.79% and 77.57%, respectively. GoogleNet, however, demonstrated significantly lower accuracy on this dataset. These results suggest that deeper architectures like ResNet are more effective in capturing complex features necessary for accurate classification of soybean diseases. The superior performance of ResNet may be attributed to its ability to mitigate the vanishing gradient problem through residual connections, enabling the training of deeper networks. In contrast, GoogleNet's lower accuracy could be due to its architectural complexity, which may not be as well-suited for this specific soybean dataset.

Table 2: Performance evaluation of transfer learning models

S.No	Model	Accuracy
1	LeNet	83.34%
2	AlexNet	78.79%
3	VGGNet	77.57%
4	ResNet	87.76%
5	GoogleNet	72.98%

The dataset was divided into 70% for training, 10% for validation, and 20% for

testing. Various models with different architectures and learning rates were tested, with parameters like kernel size, filter size, learning rate, and activation function selected through trial and error. Table 2 shows the classification accuracy comparison of different models.

The study evaluated LeNet, AlexNet, VGGNet, ResNet, and GoogleNet algorithms for classifying soybean diseases viz. Anthracnose, Frogeye Leaf Spot, Purple Seed Stain, Rhizoctonia Aerial Blight, Yellow Mosaic, and healthy samples. ResNet achieved the highest accuracy of 87.76%, followed by LeNet (83.34%), AlexNet (78.79%), VGGNet (77.57%), and GoogleNet (72.98%). ResNet excelled at capturing complex features with its deep architecture, while LeNet proved efficient for smaller datasets. The effective combination of convolutional and pooling layers, along with the Adam optimizer, demonstrated the strong potential of CNNs in soybean disease classification.

CONCLUSIONS

We collected a comprehensive soybean dataset from ICAR-IISR, Indore, encompassing 1400 images across categories such as Anthracnose, Frogeye Leaf Spot, Purple Seed Stain, Rhizoctonia Aerial Blight, Yellow Mosaic, and healthy soybean leaves. The dataset underwent meticulous cleaning and preprocessing to ensure its suitability for model training.

Five transfer learning models were applied, including LeNet, AlexNet, VGGNet, ResNet, and GoogleNet, to

classify soybean diseases effectively. Among these, ResNet demonstrated superior performance on the dataset, achieving an accuracy of 87% in classifying soybean diseases. The classification accuracy can be further improved by running the model with more number of images.

This high-performing model effectively captured intricate features of the dataset, showcasing its potential in disease detection. The findings underline the importance of robust datasets and advanced transfer learning architectures in achieving accurate classification. This study contributes to improving soybean disease management by providing a reliable system for early diagnosis and intervention.

Future Work

To enhance the soybean dataset, we aim to expand it by including a broader range of samples, such as overlapped leaves exhibiting Anthracnose, Frogeye Leaf Spot, Purple Seed Stain, Rhizoctonia Aerial Blight, Yellow Mosaic, alongwith healthy soybean leaves. This diverse dataset will comprehensively capture various forms of

soybean leaf damage, ensuring robust model training. In the future, we plan to improve accuracy by incorporating advanced transfer learning models tailored for this expanded dataset with more number of images.

Furthermore, transitioning beyond leaf damage detection, we propose developing a sophisticated neural network capable of automatically identifying overall plant defects. This advancement will provide holistic plant

health assessment, encompassing symptoms from various plant parts. By leveraging diverse datasets and cutting-edge neural architectures, this approach has the potential to revolutionize soybean disease management, enabling timely interventions and maximizing crop productivity.

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Yield and economic insights of improved soybean (JS-9560) through cluster frontline demonstrations (CFLD) in Zunheboto district of Nagaland

**VISAKHO SHUNYU¹, RAKESH KUMAR CHAURASIA¹,
EMI DEKA SUTING², A.K. SINHA² AND A.K. MOHANTY²**

¹Krishi Vigyan Kendra, Zunheboto, Nagaland University, Lumami, Nagaland, ² ATARI, Zone VII, Barapani, Meghalaya

Email: kvkzunheboto@gmail.com

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ABSTRACT

Soybean (Glycine max) is one of the most important oilseed crops grown in the Zunheboto district of Nagaland. The productivity of local soybeans grown in the district was found to be low, 1258kg/h (Nagaland statistical handbook 2024), when compared with high-yielding varieties. Therefore, there is a need to improve the yield and also to increase the area of soybean cultivation by adopting high-yielding varieties along with an improved package of practices. Keeping this in view, cluster frontline demonstrations on improved soybean varieties with improved production practices were conducted by Krishi Vigyan Kendra, Zunheboto, during kharif 2023 and 2024, at Akuluto block of Zunheboto district, covering a total area of 30ha with 120 demonstrations across 6 villages. Improved technologies demonstrated include the use of improved soybean variety JS-9560, seed treatment with rhizobium and phosphotika @ 20g/kg, and line sowing by maintaining a distance of 35cmx10cm. The data were collected from all the selected farmers' fields and were analyzed using simple tabular analysis. The average grain yield of two years under improved technologies was found to be 1775kg/ha, which was a 58.55% increase from the average yield obtained through farmers' traditional practices of 1120kg/ha. The average technology gap and extension gap were found to be 225kg/ha and 655kg/ha, respectively, with the average technology index of 11.25%. The average net income of Rs. 74,225/ha with an average B.C ratio of 1.36 was obtained under CFLD as compared to the farmers' practice average net income of Rs. 32,250/ha with an average B.C ratio of 0.66. The results of the soybean variety JS-9560 show higher profitability at farmers' fields.

Keywords: Soybean, Cluster Front Line Demonstration, technology gap, extension gap, technology index, net income, B.C ratio.

Soybean (*Glycine max*) is a versatile crop, rich in protein and vegetable oil. Soybean is the only legume with an ample amount of essential omega-3 fatty acids and alpha-linolenic acid (Messina and Messina 2010). In addition, biotin, which is recognized as an essential nutrient factor, and is included at a

higher concentration in soybeans compared to vegetables, fruits, and most meat products (Depient *et al.* 2006). It has about 20% oil and 40% high-quality protein, compared to 20% in other legumes (Agarwal *et al.* 2013). Soybean, also known as the “Golden Bean” of the 20th century (Khader 2019), owing to its tremendous nutritional value. Soybean has good prospects in North East India due to higher productivity, but the total cultivated area in the region is very low. In the state of Nagaland, soybean is cultivated in an area of 13.76 thousand hectare with an average yield of 12.6 q/h during the year 2023-24 (Nagaland statistical hand book 2024), where in Zunheboto district of Nagaland soybean is cultivated either as a monocrop or intercropped along with jhum paddy, maize, colocasia, as well as with other pulse crops on diverse landscapes such as hill slopes, terraces, and plains, covering an area of 1931h, contributing to 14.02% of total area of the state under soybean. Locally, soybean is widely consumed as a fermented product called “Axone”. As though it is the most popular dish of the local populace, there is no large-scale cultivation of soybeans in the Zunheboto district of Nagaland. A “Cluster front-line demonstration” is a practical method used to showcase and directly demonstrate new or improved agricultural technologies, like crop varieties or improved agricultural practices, to farmers in their fields, to encourage them to adopt these advancements by visually illustrating their potential benefits in terms of increased yield and profitability compared to traditional methods. Keeping this in view, the present study was undertaken to increase the soybean production and productivity by

conducting cluster frontline demonstrations (CFLDs) in Zunheboto district of Nagaland.

MATERIALS AND METHODS

Cluster Frontline demonstrations on improved varieties of soybean were conducted in an area of 30 hectares of land involving 120 practicing farmers during the kharif season in the year 2023 & 2024, under rainfed conditions, at six villages, namely Phishumi, Litta old, Litta new, Sasthami, Ajixami, and Lumami village, under Akuluto block of Zunheboto district of Nagaland. Improved soybean variety JS-9560 was used for the demonstration. Each demonstration was conducted in an area of 0.25h and 0.02h area adjacent to the demonstrated plot was kept for farmers' practices as check. The package of practices used in the demonstrations were, seed rate @ 60kg/ha, seed treatment with Rhizobium and Phosphotika @ 20g/kg of seed, line sowing with proper spacing of 35cm between rows and 10cm between plants. Soybean variety JS-9560 was used in both years for demonstration. Details of the technologies used for the present study in the CFLD's and farmers traditional practices used for the comparison are presented in Table 1. The soil of the area under study was loamy, pH varied from 5.4 to 5.88 which is moderately acidic, organic carbon (OC) was found to be high at 1.6, available nitrogen (N) was found low at 275.9kg/ha, available phosphorus (P) was normal with 53.1kg/ha and available Potassium (K) was also found to be normal with 243.2kg/ha. Sowing was done from the 2nd fortnight of May to the 1st fortnight of June.

Thinning and weeding were done at 20 and 40 DAS to ensure recommended plant spacing within the rows and plants, and also to keep the field free from weeds. The economic parameters were calculated based on the prevailing price of the inputs and the minimum support price of the outputs. The output data were collected from both the CFLD and

farmers' practices, and finally, the technological gap, extension gap, technological index, along with the cost-benefit ratio, were calculated using the formula given by Samui *et al.* 2000. Benefit cost ration was calculated by the formula $B: C = \text{Net income (Rs. /ha)} / \text{cost of cultivation (Rs. /ha)}$.

Table 1: Practices followed on Demonstration and Farmers' practice.

S.No	Intervention	Demonstrated plot	Farmers plot	Critical inputs	
1	Land situation	Rainfed	rainfed	2023	2024
2	Variety	HYV	local	JS-9560	JS-9560
3	Seed treatment	Rhizobium and phosphotika	No seed treatment	Rhizobium and phosphotika @ 20g/kg	Rhizobium and phosphotika @ 20g/kg
4	Sowing time	2 nd fortnight of May-1 st fortnight of June	April to May	2 nd fortnight of May-1 st fortnight of June	2 nd fortnight of May-1 st fortnight of June
5	Seed rate	60kg/h	>80kg/h	60kg/h	60kg/h
6	Method of sowing	Line sowing	Random sowing	Line sowing	Line sowing
7	spacing	35cmX10cm	-	35cmX10cm	35cmX10cm
8	Weed management	Two-hand weeding.	One hand weeding	Two-hand weeding at 20 and 40 DAS	Two-hand weeding at 20 and 40 DAS
9	Plant protection	Neem-based pesticides and placing yellow sticky cards	No plant protection measure was adopted	Neem-based pesticides and placing yellow sticky cards	Neem-based pesticides and placing yellow sticky cards

RESULTS AND DISCUSSION

Seed yield

The average soybean grain yield under CFLD with improved production technologies varied from 1750kg to 1800kg/ha, with a mean yield of 1775kg/ha, and farmers' yield varied from 1100kg to 1140kg/ha, with a mean yield of 1120kg/ha. The year-wise average productivity under improved practices (CFLD) was 1800kg/ha, and 1750kg/ha, against the average farmer's yield of 1100kg/ha and 1140kg/ha in 2023 and 2024, respectively, in comparison to the farmer's practice. There was a 63.6% and 53.5% increase in the yield of soybeans under improved technologies in 2023 and 2024, respectively. The results of CFLD (Table 2) revealed that the yield of the improved soybean variety JS-9560 was higher than the farmer's practice. The average soybean yield for the two years was 1775kg/ha in the demonstrated plots as compared to 1120kg/ha in the farmer's field. The average percent increase in yield was 58.55, which is similar to the result reported by Tiwary *et al.* 2014. The low yield under farmers' practice may be attributed to various factors such as the use of local varieties, the use of uninoculated seed, uneven sowing dates, improper methods of sowing, which could be a reflection of a lack of technology adoption. A similar result was also reported by Diwedi *et al.* 2010. The higher grain yield of soybean in the demonstrated plot may be due to the use of the recommended improved variety,

which implies higher yield and productivity (Jain and Dubey 2009).

Gap analysis

The study (Table 2) revealed a mean technology gap of 225kg/ha in different years may be attributed to dissimilarity in the soil fertility status, water availability, plant protection measures and other environmental factors. These findings were similar to the findings of Katare *et al.* 2013 and Raj *et al.* 2013. Technology gap under these studies revealed that more demonstrations can be conducted with improved technology intervention to reduce the existing gap.

Studies under the extension gap revealed that, yield gap ranges from 700kg to 610kg/ha between demonstrated technologies and farmers' practice, with an average extension yield gap of 655kg/ha. The extension gap was highest (700kg/ha) in 2023 and lowest (610kg/ha) in 2024. Adoption of improved varieties, improved technologies, seed inoculation, weed management, maintaining proper plant population, and appropriate plant protection measures in the demonstrations might be the reason that has resulted in higher grain yield than the farmers' practices. The extension gap could be reduced by having proper planning with involvement from extension workers and the department as well. Similar findings were reported by Meena *et al.* 2016 and Bhargav *et al.* 2017.

Table 2: Yield, Technology gap, extension gap, and Technology index in soybean under CFLDs during kharif 2023 and kharif 2024.

Year	Primary branches/plant		Plant height (cm)		No. of seed yield /plant		Test weight		Potential yield (kg/h)	Average grain yield (Kg/h)	Percent increase (%)	Techno logy gap (kg/h)	Extensi on gap (kg/h)	Techno logy index (%)
2023/ JS- 9560	Demo	Farmer practice	Demo	Farmer practice	Demo	Farmer practice	Demo	Farmer practice	2000	1800	63.6	200	700	10
	6.80	6.20	46	56.80	336.00	228.20	180.70	162.8	2000	1100				
2024/ JS- 9560	Demo	Farmer practice	Demo	Farmer practice	Demo	Farmer practice	Demo	Farmer practice	2000	1750	53.5	250	610	12.5
	6.20	6.00	46.60	56.00	328.60	224.60	182.20	163.2	2000	1140				
Avera ge	Demo	Farmer practice	Demo	Farmer practice	Demo	Farmer practice	Demo	Farmer practice	-	1775	58.55	225	655	11.25
	6.50	6.10	46.3	56.40	332.300	226.400	181.45	163.00	-	1120				

The technology index shows the feasibility of the technology in the farmer's field. A higher technology index reflected the inadequate transfer of proven technology to the growers and insufficient extension services for the transfer of technology. The average of two years' technology index was recorded as 11.25%, which was 10% in 2023 and 12.5% in 2024. The findings of the present study were in line with the findings of Rai *et al.* 2016. This indicates that a gap existed between evolved technology and its adoption in the farmer's field. Therefore, awareness programs through trainings, method demonstrations, and adoption of improved varieties with the recommended scientific package of practices have increased during both years of study. These findings were in line with the studies carried out by Chandra 2010 and Khedkar *et al.* 2017.

Economics

The present study on economic analysis of soybean production (Table.3) revealed the two years average cost for soybean production i.e., labour cost for field preparation, seed cost, inoculants cost, sowing cost, cost for inter cultural

operations, harvesting, threshing etc, which were put into the whole operation was Rs. 54,400/ha in demonstrated plot as compared to Rs. 49,000/ha with farmer's practice. Similarly, cultivation of soybean under improved practices gave a higher net return of Rs. 74,400 and Rs. 74,050/ha compared to the farmers' practice net return of Rs. 30,600 and Rs. 33,900/ha during 2023 and 2024, respectively. The higher net returns in improved production practices were due to higher grain yield in the demonstrated plots as compared to farmers' traditional practice. Similar results have been reported by Suryavanshi *et al.* 2020.

The average benefit cost ratio under recommended practices was 1.36, and that of farmers' practice was 0.66, which could be due to the higher grain yield obtained under recommended practices compared to farmers' practice. A similar result was reported by Tomar 2010. From the results, it can be stated that all the economic indices show higher results under improved technology than the farmers' practices. Similar findings were reported by Hannah *et al.* 2023 and Singh *et al.* 2019.

Table.3: Economic Performance of soybean cultivated under CFLD and Farmers' practices during kharif 2022, kharif 2023, and kharif 2024.

year	Number of clusters	Area (h)	Cost of cultivation (Rs. /h)		Gross income (Rs./h)		Net income (Rs./h)		B.C Ratio	
			Demo	Farmer	Demo	Farmers Practice	Demo	Farmers Practice	Demo	Farmers Practice
2023	8	20	51,600	46,400	126,000	77,000	74,400	30,600	1.44	0.66
2024	6	10	57,200	51,600	131,250	85,500	74,050	33,900	1.29	0.66
Average	6.6	15	54,400	49,000	128,625	81,250	74,225	32,250	1.36	0.66

CONCLUSION

During 2023 and 2024, the Cluster Front Line Demonstration (CFLD) on soybeans in Nagaland's Zunheboto district successfully introduced improved production technologies to local farmers. The results clearly demonstrated significant increases in both yield and net returns compared to traditional farming methods.

Demonstration plots recorded a 58.55% higher grain yield, a notable improvement attributed to increased farmer awareness and targeted training on advanced techniques. Key components of this success included the adoption of improved varieties, effective method demonstrations, and enhanced crop protection measures.

The project's findings highlight an existing "extension gap" that necessitates further educating farmers on the latest technologies. To bridge this gap, robust and ongoing extension activities are essential to encourage the broader adoption of recommended agronomic practices.

A low "technology index" was recorded, indicating that the new technologies are highly feasible and adaptable for local growers. Farmers expressed strong interest and satisfaction with the performance of the technologies and showed a clear willingness to adopt these advancements in future seasons.

Ultimately, the CFLD has proven to be an effective strategy for accelerating the adoption of improved agricultural practices and expanding the reach of advanced methods, which will boost soybean production and productivity in the region and var. JS-9560 is recommended as a suitable variety for

adoption by the farming communities for maximising profits.

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Impact of Front Line Demonstrations in Soybean [*Glycine max* (L.) Merrill] under North Western Himalayan Hills

VEDNA KUMARI^{1*}, AMAR SINGH¹ and S. D. BILLORE²

**¹Department of Genetics and Plant Breeding, College of Agriculture,
Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya,
Palampur 176062 and ²ICAR-National Soybean Research Institute,
Indore 452001, Madhya Pradesh**

Email: vednadr@gmail.com

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ABSTRACT

Front line demonstrations are conducted on farmer's fields for effective transmission of crop production and protection technologies generated under the close supervision of the researchers. For effective transfer of technology, it is pertinent to study the various constraints observed during demonstration of technology in the farmer's fields. The present study aims to assess the impact of improved technology, identify various constraints causing yield gaps and propose potential strategies to increase soybean production under North Western Himalayan hills. The study was carried out in 3.52 hectare area by involving 34 farmers of Kangra, Mandi and Chamba districts, 3.52 hectare by involving 32 farmers of Kangra and Mandi districts and 3.64 hectare with 33 farmers of Kangra, Mandi, Hamirpur and Bilaspur districts during kharif 2017, 2018 and 2019, respectively. Results revealed that by using improved variety of soybean and scientific recommendations, the net returns may be increased up to 67-68 % by increasing cost of cultivation about 21% only in the form of interventions. Among the varieties, Him Soya appeared to be more profitable compared to Hara Soya as the farmers prefer yellow seeded varieties for use as soya milk, tofu, dal, flour and other preparations. Green-seeded varieties need popularization among farmers by creating awareness and motivation to adopt appropriate recent production and protection technologies in the state. Results suggested that by adoption of improved package of practices, the farmers can realize higher yields and net profit in soybean cultivation under North Western Himalayas.

Keywords: Improved Technology, Farmer's Practice, Economics, Soybean

Soybean [*Glycine max* (L.) Merrill] is one of the oldest crops of the world, grown across diverse environments in tropical, subtropical and temperate climates. It has a prominent place among modern agricultural commodities as the world's most important seed legume and contributes about 25% to the global edible oil production, 65% of the world's protein concentrate for livestock feeding (Anonymous, 2020). It is a good source of vitamins and minerals like calcium, phosphorous, iron, molybdenum, vitamin K₁, copper,

manganese, etc. It contains antioxidants and phytonutrients that are linked to various health benefits. Food uses of soybean include beverages, fermented products like *soya* sauce and cheese, baked goods, biscuits and snacks. The amount of protein produced by soybean per unit land area is higher than any other crop and therefore, it is also called as 'golden bean', 'yellow jewel', 'nature's miracle protein' and 'meat of the field'. Soybean also contains numerous antioxidative compounds which are beneficial to human health as they reduce the risk of diabetes, cardiovascular diseases, breast cancer, osteoporosis, neurodegenerative disorders and menopausal symptoms. Soybean provides cholesterol free oil (20%) and high quality protein (40%). Its protein is rich in lysine (4-6%) and the oil is edible one (Katare *et al.*, 2013). Soybean is crop of food and nutritional security as it is consumed as a pulse as well as an oilseed. In India, large portion of the population being vegetarians, the crop like soybean has become an important crop due to its high protein content and yield potential.

India is fifth largest producer with area, production and productivity after Brazil, USA, Argentina and China. In India, soybean has emerged as a major oilseed crop starting with a meager area of 0.03 m ha in 1970, the crop has touched the figure of 11.13 m ha area with an estimated production of 13.26 m tons and productivity of 1191 kg/ha (<http://eands.dacnet.nic.in>). The crop is grown under rainfed conditions in diverse agro-ecological zones ranging from northern hill, northern plain, north eastern, central and southern zones and

among them, the agro-climatic conditions in hills are the most challenging and highly variable (Bhartiya and Aditya, 2016).

In Himachal Pradesh, soybean is grown as a major *kharif* oilseed crop in mid hills under rainfed conditions in an area of 600 ha with the production of 1006.2 tons and productivity of 1680 kg/ha (<http://www.fao.org/faostat/en/#data/QC>). The crop is primarily used as pulse, oil as well as a vegetable by the hill farmers. The main reasons for low productivity of soybean include the poor extension of improved technology, high cost of inputs, improper nutrient management, poor plant protection measures, erratic behavior of rainfall and cultivation on marginal and sub-marginal lands under rain fed conditions in the state. Hills represent most challenging agro-climatic conditions and differences in altitude and sunshine hours render significant impact on genotype $\times$ environment interaction in determining crop yields. Earlier, Bhartiya *et al.*, 2018 suggested that locations contributed maximum variation for days to maturity followed by grain yield and days to flowering.

At present, the existing gap in the production and requirement of soybean is a great threat to the nutritional and livelihood security of resource poor masses in hills. Although, soybean has emerged as a main oilseed crop and gained a vital status in the oil economy of the country still, a vast gap exists between potential yield and yield under real farming situations in all the soybean growing agro ecological zones (Bhatia *et al.*, 2006). To revamp this

gap with limited land holdings and resources in hilly region is a great challenge. The quantification of existing yield gaps could be a key strategy to understand their causes which can be helpful in focusing research and policy on areas where improvement can be made. The potential to increase production in a given area and an insight into yield limiting/reducing factors can be determined by estimating yield gaps, which in turn, will help in prioritization of research strategies (Stuart *et al.*, 2016).

Front line demonstration programme is a useful outcome of 'Technology Mission on Oilseeds'. The demonstrations are conducted on farmer's fields for effective transmission of technology generated under the close supervision of the scientists. It is pertinent to study the various factors contributing higher crop yield and constraints in field production observed while demonstrating the technologies in the farmer's fields.

Keeping this in view, the present study aims to assess the impact of improved technology, identify various constraints causing yield gaps and propose potential strategies to increase soybean production under North Western Himalayan hills.

MATERIAL AND METHODS

The present study was carried out during *kharif* seasons of 2017, 2018 and 2019 in different districts of Himachal Pradesh under All India Coordinated Research Project on soybean. Front line demonstrations were planned in the farmer's fields to demonstrate the

genetic worth of improved soybean varieties *viz.*, Hara Soya and Him Soya. Recommended package of practices were followed to raise the crop in comparison to farmer's practice as control to aware farmers in terms of overall higher yields, cost-benefit ratio and net returns in their own real farming situations. Before conducting the demonstrations, information about farmers and their farming systems, available resources, present cropping systems, use of inputs and productivity of major crops of the area was gathered through interaction (Table 1). Demonstration site was selected based on its easy accessibility, farm size and layout of the field in order to have better impact of the demonstrated technology. The demonstrated area was scattered due to small land holdings in the state.

The present study was carried out in 3.52 ha area by involving 34 farmers of Kangra, Mandi and Chamba districts, 3.52 ha by involving 32 farmers of Kangra and Mandi districts and 3.64 ha with 33 farmers of Kangra, Mandi, Hamirpur and Bilaspur districts during *kharif* 2017, 2018 and 2019, respectively. Crucial farm operations *viz.*, sowing, fertilizer application, weeding, draining of excess water due to high rainfall, plant protection measures, harvesting and post-harvest operations were ensured through time-to-time interactions with farmers. The crop was sown during last week of May to first fortnight of June or onset of monsoonal rains in all villages.

Estimation of technology gap, extension gap and technology index

In front line demonstrations, full package of practices were adopted whereas in the farmer's practice, existing practices being used by the farmers of the area were followed. The yield data were collected from the demonstrated plot and farmer's practice through personal interaction. The yield increase in demonstration plot over farmer's practice was calculated by using the following formula:

Yield increase over farmer's practice (%) = $\{(\text{Demonstration plot yield} - \text{Farmer's plot yield}) / \text{Farmer's plot yield}\} \times 100$

The data obtained were analyzed to estimate the technology gap, extension gap and technology index as per following formulae (Samui *et al.*, 2000):

Technology gap = (Potential yield – Demonstration plot yield)

Extension gap = (Demonstration plot yield – Farmer's plot field)

Technology index = $\{(\text{Potential yield} - \text{Demonstration plot yield}) / \text{Potential yield}\} \times 100$

Economic impact analysis

Cost of cultivation of soybean includes the cost of inputs like seed, fertilizers, plant protection measures, hired labour for various field and post-harvest operation charges while the farmer's family labour was not considered in the present study. The gross and net returns were calculated by considering cost of cultivation and price of seed and straw yield and cost-benefit ratio was worked out as a ratio of costs and corresponding returns.

RESULTS AND DISCUSSION

Results of front line demonstrations conducted during *kharif* 2017, 2018 and 2019 in farmer's fields indicated that the yields of demonstrated plots were invariably higher than the corresponding farmer's plot yield in all years which were due to the adoption of recommended practices in front line demonstrations (Table 2).

The improved production technologies resulted in yield increase varying between 24.5 to 27.3 percent in Hara Soya and 25.5 to 30.1 percent in Him Soya as compared to existing traditional practices which indicated the positive effects of improved varieties and cultivation practices over the farmer's practices towards enhancing the yield of soybean in hills. The results were in conformity with the earlier findings of Singh (2002); Dixit and Singh (2003); Patel *et al.* (2009) and Dubey *et al.* (2011).

Yield of the front line demonstrations (demonstration plot yield) and potential yield of the crop was compared to estimate the yield gaps (Table 2) between soybean varieties which were further categorized into technology and extension gaps (Hiremath and Nagaraju, 2009). Technology gap (Yield gap-I) indicates researchable issues for realization of potential yield, whereas the extension gap (Yield gap-II) indicates the role of extension functionaries towards the transfer of improved technologies (Joshi *et al.*, 2014).

The technology gap ranged from 497 kg/ha to 661 kg/ha in Hara

Soya and 316 kg/ha to 524 kg/ha in Him Soya. The technology gap observed may be attributed to growing of the crop under rainfed conditions, the variation in the soil fertility status, marginal and sub-marginal land holdings, undulating topography and prevailing weather conditions. Although, technology gap is considered difficult to abridge because of environmental differences between on-farm and research station situations but it gives an indication of the upper limits of productivity that can be achieved in a given environment. A very narrow yield gap suggests the need to generate further better performing technologies in a given environment (Bhatia *et al.*, 2006). Therefore, variety-wise location specific recommendation may be necessary to minimize the technology gap for yield under different situations.

The extension gap which ranged from 244 kg/ha to 291 kg/ha in Hara Soya and 259 kg/ha to 343 kg/ha in Him Soya emphasized the need to educate the farmers for adoption of improved agricultural production technologies to narrow-down the extension gap. Extension gap mainly arises as a result

of differences in the management practices followed by the traditional farmers such as use of sub-optimal or no doses of inputs and cultural practices as compared to the improved practices followed.

The technology index shows the feasibility of the evolved technology in the farmer's fields. The lower value of technology index, more is the feasibility of the demonstrated technology (Balai *et al.*, 2013). Reduction of technology index from 34.8 percent (2019) to 26.2 percent (2018) in Hara Soya and 29.1 percent (2019) to 17.6 percent (2018) in Him Soya exhibited the feasibility of technology demonstrated in farmer's fields for both soybean varieties. Therefore, as per technology index, Him Soya variety (17.6 percent) was found more feasible as compared to Hara Soya in hills. The location-wise variation in yield can be attributed to variation in climatic conditions, microclimate and agricultural production technology followed. More or less similar findings were reported by earlier workers (Sagar and Chandra, 2004 and Dubey *et al.*, 2011).

Table 1. Comparison of recommended production technology capsule and farmer's practice

Input/ Practice	Technology Demonstration capsule	Existing farmer's practice
Variety	Hara Soya and Him Soya	Soybean
Sowing time	June	May end to June/ on arrival of monsoon
Spacing	45 x 5-10 cm	Broadcast method
Seed rate (kg/ha)	75	100
Plant population	0.22 to 0.44 million/ha	Grown as mixed crop with maize
Depth of sowing	3-5 cm	3-5 cm
Manure and fertilizer	3 t FYM/ha + 20:60:40 N:P ₂ O ₅ :K ₂ O kg/ha	3 t FYM/ha
Seed treatment	Thiram 75 WP + Cabendazim 50 WP (2:1) @ 3.0 g/kg seed or Thiram + carboxin @ 2 g/kg seed	Nil
Weed control	Two hand weedings at 20 and 40 DAS or Pendimethalin @4.5lt/ha (pre emergence spray) and Turga-super + Quirine @ 750ml+37.5g/ha (post emergence spray)	Two hand weedings at seedling and before flowering stage

Table 2. Productivity, gap analysis and technology index of soybean grown under FLDs in North Western Himalayan hills

Year	Area (ha)	No. of farmers	Improved variety	Potential yield	Yield (kg/ha)		% increase over FP	Gap analysis (kg/ha)		Technology Index
2017	1.88	18	Hara Soya	1900	1354	1064	27.3	546	290	28.7
	1.64	16	Him Soya	1800	1461	1155	26.5	339	306	18.8
2018	2.38	23	Hara Soya	1900	1403	1112	26.2	497	291	26.2
	1.14	9	Him Soya	1800	1484	1141	30.1	316	343	17.6
2019	2.68	23	Hara Soya	1900	1239	995	24.5	661	244	34.8
	0.96	10	Him Soya	1800	1276	1017	25.5	524	259	29.1
Mean			Hara Soya	1900	1332	1057	26.0	568	275	29.9
			Him Soya	1800	1407	1104	27.4	393	303	21.8

Table 3. Comparative economic impact of soybean under front line demonstrations during kharif 2017, 2018 and 2019

Year	Improved variety	Cost of cultivation (Rs./ha)		Net returns (Rs./ha)		Additional cost of cultivation (Rs./ha)	Additional net returns (Rs./ha)	B:C Ratio	
		DP	FP	DP	FP			DP	FP
2017	Hara Soya	34350	29960	33331	23234	4390	10097	0.97	0.78
	Him Soya	34350	29960	38681	27774	4390	10907	1.13	0.93
2018	Hara Soya	38200	34540	34770	23293	3660	11477	0.91	0.67
	Him Soya	38200	34540	38962	24769	3660	14193	1.02	0.72
2019	Hara Soya	39403	34972	26248	17775	4431	8473	0.67	0.51
	Him Soya	39403	34972	28225	18903	4431	9322	0.72	0.54
Mean	Hara Soya	37318	33157	31450	21434	4160	10016	0.84	0.65
	Him Soya	37318	33157	35289	23815	4160	11474	0.95	0.72

Table 4. Constraints for yield gap and potential interventions perceived by farmers for improving the productivity of soybean in north western Himalayan hills

Constraints causing yield gap	Potential interventions to mitigate yield gaps
Wild life menace (bores, stray animals, rabbits, <i>Neel gai</i>)	Wild life management
Migration of working force and youth from villages to towns in search of white collar job	Employment generation in villages to stop migration
Scattered and small land holdings	-
Ignorance of farmers for improved cultivation practices	Strengthening of extension services and timely advisories
Non availability of improved seeds and other inputs	Timely and assured supply of various inputs
Non-existent marketing network and poor transportation facilities	Assured marketing network and transport facilities
Undulating topography and challenging conditions	Adoption of varieties for niche based areas
Unpredictable weather and changing climate	Adoption of climate resilient varieties

Varietal economic analysis of soybean

A comparative variety-wise economic impact of soybean revealed that per hectare average demonstration yield (1407 kg/ha) and farmer's plot yield (1104 kg/ha) of soybean variety Him Soya were higher than the variety Hara Soya giving 1332 kg/ha and 1057 kg/ha, respectively (Table 2).

The profitability analysis indicated that the variety Him Soya exhibited comparatively more returns both in demonstrations (Rs. 35289) and farmer's plot yield (Rs. 23815) compared to Hara Soya under front line demonstrations. The additional cost of Rs. 3660 to Rs. 4431 in both varieties gave additional net returns ranging from Rs. 8473 to Rs. 11477 in Hara Soya and Rs. 9322 to Rs. 14193 per hectare in Him Soya. The benefit: cost ratio revealed that cultivation of Him Soya is more profitable both under demonstrations (0.95) as well as farmer's plot (0.72) as compared to soybean variety Hara Soya which exhibited the benefit: cost ratio of 0.84 and 0.65, respectively (Table 3). This may be due to higher yields obtained under recommended practices compared to farmer's practices. Bhatnagar (2009) reported that the research emanated production technologies were capable of enhancement of productivity of soybean by 32.26 per cent through front line demonstrations while Meena *et al.* (2012) reported about 23.32 per cent increase in yield under improved technologies over farmer's practices. Similar enhancement in the productivity of soybean over farmers

practices by adoption of improved technology was observed by earlier workers (Raghuwanshi *et al.*, 2009; Raghuwanshi *et al.*, 2010; Badaya *et al.*, 2017; Singh, 2018; Singh *et al.*, 2018; Khedkar *et al.*, 2020).

Among the possible constraints observed for yield gap, the wild life menace followed by migration of youths from villages, scattered and small land holdings, poor extension services and ignorance of farmers for improved cultivation practices, non-availability of improved seeds and other inputs, undulating topography and unpredictable weather and changing climate appeared to be the prominent constraints causing yield gap in soybean (Table 4). Potential interventions perceived by farmers include wild life management, initiatives for youth employment generation, strengthening of extension services and timely availability of agricultural inputs like seed, fertilizer, pesticides, assured marketing network and awareness programmes for improving the production and productivity of soybean in North Western Himalayas.

The study suggested that by using improved variety of soybean and scientific recommendations, the net returns may be increased up to 67-68 % by increasing cost of cultivation about 21% only in the form of interventions. Among the varieties, Him Soya appeared to be more profitable compared to Hara Soya as the farmers prefer yellow seeded varieties for use as soya milk, *tofu*, *dal*, flour and other preparations while green-seeded varieties need popularization among farmers by creating awareness and

motivation to adopt appropriate recent production and protection technologies in the state. Hence, the result of front line demonstrations suggested that by adoption of improved package of practices, the farmers can realize higher yields and net profit in soybean cultivation under North Western Himalayas.

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Economic Positioning of Soybean: A Study of Growth Trends and Cost Comparisons with Kharif Crops in Major Soy-States of India

VISHAL S. THORAT^{1*}, B. U. DUPARE¹, Y. A. GARDE²,
R. NARGUND¹ AND R. K. VERMA¹

¹ICAR – National Soybean Research Institute, Indore (MP),

²ICAR – Indian Agricultural Statistics Research Institute, New Delhi

Email: vishal.thorat@icar.org.in

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ABSTRACT

This study analyses the dynamics of area, production and yield to assess the agricultural trajectory and economic viability of soybean cultivation in Madhya Pradesh and Maharashtra. A cross-state comparison reveals that while soybean production in Madhya Pradesh has stagnated with no yield gains over the years, growth in Maharashtra has been maintained, primarily led by yield improvements. From an economic standpoint, soybean cultivation is often at a comparative disadvantage relative to other Kharif crops, including paddy, maize, cotton, arhar and urad. This is further evidenced by the persistent profitability challenges confronting soybean farmers in both states under the current Minimum Support Price (MSP) framework. The findings suggest an urgent need to reorient agricultural policy to foster more equitable support for soybean producers and strengthen the overall sustainability of soybean cultivation in these critical regions.

Keywords: Kharif crops, profitability, yield improvements, comparative disadvantage

Soybean [*Glycine max* (L.) Merrill] introduced in early 1970s in India gained utmost importance among all the oilseeds through rapid area expansion in very short span of time. While the average global production of Soybean stands at 364.51 million tonnes from 2015 to 2024 with compound average growth of 3%, India have share of 10.57 million tonnes with compound average growth of 6% (USDA, 2025). In India Soybean generally grown in kharif season, which is heavily dependent on the monsoon. In this major season, states like Madhya Pradesh and Maharashtra play a pivotal role as crucial agricultural powerhouses, contributing substantially to the

national output of several key crops. Among the various Kharif crops, soybean has emerged as a dominant force, transforming the agro-economic landscape of central and western India. Often referred to as the "golden bean," soybean is not only a primary source of edible oil and protein but also a significant earner of foreign exchange. India is the fifth-largest producer of soybeans globally, and the domestic production is overwhelmingly concentrated in Madhya Pradesh and Maharashtra. These two states alone consistently account for over 80% of the country's total soybean output, with Madhya Pradesh, often called the

"Soybean State," and Maharashtra vying for the top position annually.

The performance of the agricultural sector is critically evaluated through the dynamics of area, production, and yield. Fluctuations in these three parameters are indicative of underlying shifts in cropping patterns, technological adoption, climatic variations, and policy impacts. An analysis of these trends for soybean and other major Kharif crops in Madhya Pradesh and Maharashtra is within these key states. Such an investigation provides valuable insights into the sustainability of current farming practices and the overall health of the agrarian economy in the region. therefore, essential to understand the trajectory of agricultural growth and identify constraints and opportunities

While tracking physical output is important, the economic viability of cultivation is what ultimately sustains the farmer. The profitability of farming is determined by the complex interplay between the costs incurred by the farmer and the revenue realized (Sharma *et al*, 2016; Shoko *et al*, 2016; Jaiswal and Hugar, 2011; Agarwal and Singh, 2014). In India, the Commission for Agricultural Costs and Prices (CACP) provide several measures of production costs, including Cost A2 (covering all paid-out expenses), Cost A2+FL (Cost A2 plus imputed value of unpaid family labor), and Cost C2 (a comprehensive cost including rentals and interest on owned land and fixed capital). The Minimum Support Price (MSP) is a crucial policy instrument designed to provide a safety net to farmers and incentivize production.

Therefore, a comparative analysis of these production costs with the declared MSP is critical to assess the remuneration and profitability of crop cultivation. This research paper focuses on the dynamics of area, production and yield of soybean and other principal Kharif crops in Madhya Pradesh and Maharashtra. Furthermore, it conducts a comparative analysis of the cost of cultivation (Cost A2, A2+FL, and C2) against the MSP to evaluate the economic sustainability of farming for the cultivators in these regions.

MATERIALS AND METHODS

Two prominent soybean producing states i.e. Madhya Pradesh (MP) and Maharashtra were considered for the study. The secondary data acquired from published sources of Directorate of Economics and Statistics, Ministry of Agriculture and Commission on Agricultural Costs and Prices (CACP). Data pertaining to area, production and yield of soyabean and other major kharif crops from year 2005-06 to 2024-25 (divided into two decades Period I (P1) – 2005-06 to 2014-15 and Period II (P2) – 2015-16 to 2024-25) was used. Further, data on cost of production (cost A2, A2+FL and C2) and Minimum Support Price (MSP) for last 10 years (2015-16 to 2024-25) was analysed.

For estimating the CAGR we have considered exponential functional form to be fitted to the collected data set for trend analysis of area, production and productivity of kharif crops in MP and Maharashtra. Exponential growth function of the form given below will be used for the purpose.

$$Y_t = ab^t e_t$$

where

Y_t = area/production/yield

a = intercept

b = Regression coefficient

t = time variable

e_t = disturbance term

The growth rate coefficient (b's) was computed by transforming $Y_t = ab^t e_t$ in log form as

$$\log Y_t = \log a + t \log b + \log e_t$$

Thus, compound annual growth rate (g) in % will be computed by

$$g = (Ant. (Log b) - 1) * 100$$

Significance of the reg. coefficient will be tested using the student's 't' test.

Instability Index also calculated for studying the fluctuation in area, production and productivity of soybean and other kharif crops with the help of Coefficient of Variation (CV).

$$CV = \frac{\text{Standard Deviation}}{\text{Mean}} \times 100$$

To evaluate the comparative profitability of kharif crops, data obtained from the cost of cultivation reports of the CACP were deflated using the wholesale price index (base 2011-12=100) and analyzed for the expenses associated with cultivating kharif crops and their corresponding returns.

RESULTS AND DISCUSSION

Dynamics of area, production and yield of kharif crops in Madhya Pradesh and Maharashtra

This section presents an analysis of the growth of area,

production and yield for soybean and its major competing Kharif crops in Madhya Pradesh and Maharashtra. The analysis is based on decadal data split into two periods: Period-I (2005-06 to 2014-15) and Period-II (2015-16 to 2024-25), as well as the overall period.

Madhya Pradesh

Madhya Pradesh, a major soybean-growing state, exhibits significant shifts in cropping patterns over the study period (table 1). The data reveals a concerning trend for soybean in Madhya Pradesh. While the overall period shows a positive Compound Annual Growth Rate (CAGR) in area (1.01%), this masks a recent reversal. In Period-I, the area grew at a healthy rate of 3.20% per annum. However, in Period-II, the area under soybean cultivation began to shrink, recording a negative CAGR of -0.60%.

This decline in area was compounded by a fall in productivity. The main factor affecting crop yields are agricultural inputs and weather parameters (Garde *et al.* 2020). Yield growth, which was 3.00% in Period-I, also turned negative (-0.30%) in Period-II. The combined effect of shrinking area and falling yield led to a significant decline in production growth, from a robust 7.60% in Period-I to -1.30% in Period-II. Furthermore, soybean production has become more volatile, with the Instability Index (II) increasing from 33.43% to 36.18%. This suggests that soybean cultivation in the state has faced challenges in the recent decade, possibly due to climatic factors, price volatility, or pest issues, leading to a loss of momentum.

Maize has emerged as a strong and dynamic competitor. Its area, production, and yield have shown remarkable growth in both periods, with acceleration in Period-II. The area under maize grew at an impressive 10.55% annually in Period-II, while production surged by 10.50%. This indicates a clear diversification trend among farmers, likely driven by better returns and resilience of maize. Whereas, Paddy has been a stable crop, with consistent positive growth in area, production and yield across both periods. Cotton, after experiencing a decline in area in Period-I (-0.20%), saw a significant revival in Period-II, with area growing at 5.71% and production at a very high rate of 10.70%.

The pulse crops present a mixed picture. While area growth for both Arhar and Urad decelerated sharply in Period-II, their yield growth was exceptionally strong (5.30% for Arhar and 8.10% for Urad). This suggests a shift towards productivity-led growth in pulses. However, their production remains highly unstable, with the Instability Index for Urad production reaching an extreme 73.70% in Period-II, highlighting the high risk associated with their cultivation.

Maharashtra

Unlike Madhya Pradesh, the area under soybean in Maharashtra has continued its strong expansionary trend, with a CAGR of 4.20% in Period-I and 4.10% in Period-II (table 2). This has resulted in a substantial increase in the mean area under cultivation from 3250.14 thousand hectares to 4342.57 thousand hectares.

However, this growth is almost entirely area-driven. Yield performance has been extremely poor, with a negative CAGR (-2.00%) in Period-I and a negligible recovery (1.00%) in Period-II, resulting in zero overall yield growth for the entire study period. Consequently, production growth (4.10% in Period-II) is merely a reflection of area expansion. The high and increasing Instability Index for production (from 34.92% to 41.71%) underscores the vulnerability of the crop, likely due to its rainfed nature and stagnant technology adoption. This indicates an extensification-led growth pattern without intensification, which is unsustainable in the long run.

Cotton is the most significant competitor in terms of acreage. It has maintained a steady, albeit slow, growth in area (1.60% overall) and yield (1.70% overall). Its production growth is stable, and importantly, its instability is considerably lower than that of soybean, making it a relatively less risky alternative for farmers. Similar to Madhya Pradesh, maize has shown positive growth across all three parameters in Maharashtra. While not as explosive as in MP, its consistent yield growth (1.20% overall) makes it an attractive option. Paddy appears to be losing ground, with a negative CAGR in area (-0.40%) during Period-II and sluggish overall growth in production and yield. Pulses in Maharashtra also struggle with area retention, with both crops recording an overall negative CAGR in area. Arhar showed a recovery in area growth in Period-II, which, coupled with strong yield growth (4.40%), boosted its production. Urad,

however, continued to lose area. As in MP, both pulse crops exhibit very high production instability. In brief, a cross-state comparison indicates that soybean in Madhya Pradesh has reached a plateau with stagnating yields and declining production, while in Maharashtra it has maintained momentum through yield-led growth.

Competing cereals such as maize and paddy are gaining ground in Madhya Pradesh, whereas in Maharashtra soybean remains resilient despite competition. Pulses and cotton remain secondary but highly volatile crops in both states, influenced by climate and market fluctuations.

Table 1. Dynamics of area, production and yield of kharif crops in Madhya Pradesh

Crop	Variable	P1 (2005-06 to 2014-15)			P2 (2015-16 to 2024-25)			Overall	
		Mean	CAGR (%)	II (%)	Mean	CAGR (%)	II (%)	Mean	CAGR (%) II (%)
Soybean	Area ('000 ha)	5477.46	3.20*	11.01	5802.90	1.10*	8.21	5640.18	1.01* 9.84
	Production ('000 tone)	5950.70	3.00*	18.89	5463.79	-0.60*	13.78	5707.25	-0.30 ^{ns} 16.89
	Yield (Kg/ha)	1087.00	-0.20*	14.83	953.00	-1.70*	19.56	1020.00	-1.30*** 17.94
Maize	Area ('000 ha)	873.29	1.50*	10.55	1415.50	4.90*	18.44	1144.60	4.40* 29.44
	Production ('000 tone)	1439.40	9.40*	39.27	4040.91	6.90*	21.78	2740.16	10.50* 55.34
	Yield (Kg/ha)	1627.00	7.80*	32.45	2846.00	1.90*	11.02	2237.00	5.80* 33.75
Paddy	Area ('000 ha)	1730.55	1.80*	8.44	2553.80	6.90*	27.97	2142.17	3.80* 30.62
	Production ('000 tone)	2131.89	11.80*	40.68	5299.88	9.40*	32.63	3715.89	10.01* 56.54
	Yield (Kg/ha)	1208.00	9.80*	32.93	2063.00	2.30*	9.96	1635.00	6.01* 32.76
Cotton	Area ('000 ha)	608.70	-0.20*	3.34	593.90	-0.30 ^{ns}	5.71	601.30	-0.30 ^{ns} 4.70
	Production ('000 tone)	122.86	14.20 ^{ns}	60.83	288.55	-2.80 ^{ns}	18.16	205.70	10.40* 51.38
	Yield (Kg/ha)	204.00	14.40 ^{ns}	62.23	486.00	-2.50 ^{ns}	16.86	345.00	10.70* 51.63
Arhar	Area ('000 ha)	409.67	6.60*	29.40	332.20	-15.50*	64.71	370.93	-3.80*** 46.96
	Production ('000 tone)	277.86	7.60*	33.43	361.34	-18.10*	76.65	319.60	-1.10 ^{ns} 64.32
	Yield (Kg/ha)	698.00	0.90*	23.81	1022.00	-3.10 ^{ns}	18.72	860.00	2.80*** 28.04
Urad	Area ('000 ha)	584.59	4.50*	17.55	1336.90	-7.70 ^{ns}	42.92	960.75	5.30* 57.94
	Production ('000 tone)	222.02	6.80*	34.97	687.12	-8.00 ^{ns}	48.44	454.57	8.10* 73.70
	Yield (Kg/ha)	373.10	2.20*	16.13	530.00	-0.30 ^{ns}	28.11	451.00	2.70*** 30.27

Significant at *1%, **5% and ***10%. ns- non-significant, II – Instability index

Table 2. Dynamics of area, production and yield of kharif crops in Maharashtra

Crop	Variable	P1 (2005-06 to 2014-15)			P2 (2015-16 to 2024-25)			Overall	
		Mean	CAGR	II	Mean	CAGR	II	Mean	CAGR
Soybean	Area ('000 ha)	2957.72	4.20*	13.86	4342.57	4.10*	12.68	3650.14	4.00*
	Production ('000 tone)	3250.14	2.20 ^{ns}	34.15	5092.84	10.20*	29.73	4171.49	5.00*
	Yield (Kg/ha)	1119.00	-2.00 ^{ns}	34.92	1157.10	5.80**	22.59	1138.05	1.00 ^{ns}
Maize	Area ('000 ha)	777.36	8.20*	23.69	822.24	3.70 ^{ns}	14.96	799.80	2.00*
	Production ('000 tone)	1951.18	10.20*	33.77	2058.79	5.00*	35.86	2004.98	2.20*
	Yield (Kg/ha)	2473.78	1.90 ^{ns}	17.51	2492.70	1.20 ^{ns}	30.59	2483.24	0.20 ^{ns}
Paddy	Area ('000 ha)	1538.56	0.40 ^{ns}	2.44	1488.11	0.80*	3.24	1513.33	-0.10 ^{ns}
	Production ('000 tone)	2739.62	2.00 ^{ns}	11.71	3078.05	3.60*	11.95	2908.84	1.60*
	Yield (Kg/ha)	1777.57	1.60 ^{ns}	9.76	2065.60	2.80*	10.09	1921.58	1.70*
Cotton	Area ('000 ha)	3635.98	4.80*	14.82	4240.19	0.10 ^{ns}	5.40	3938.09	1.80*
	Production ('000 tone)	988.60	4.30 ^{ns}	31.60	1383.66	1.60 ^{ns}	18.54	1186.13	3.60*
	Yield (Kg/ha)	270.82	-0.50 ^{ns}	26.09	328.62	1.50 ^{ns}	22.09	299.72	1.70*
Arhar	Area ('000 ha)	1158.34	1.20 ^{ns}	7.26	1245.63	-1.30***	7.26	1201.99	0.50***
	Production ('000 tone)	844.66	-2.90 ^{ns}	26.21	1096.12	3.00 ^{ns}	26.93	970.39	2.00 ^{ns}
	Yield (Kg/ha)	729.72	-4.00 ^{ns}	25.11	875.80	4.40 ^{ns}	23.52	802.76	1.50 ^{ns}
Urad	Area ('000 ha)	401.64	-5.30*	22.98	348.22	1.00 ^{ns}	14.13	374.93	-1.50**
	Production ('000 tone)	202.67	-2.90 ^{ns}	40.96	176.29	9.80***	42.84	189.48	-0.30 ^{ns}
	Yield (Kg/ha)	495.30	2.50 ^{ns}	30.17	494.70	8.80*	35.38	495.00	1.20 ^{ns}

Significant at *1%, **5% and ***10%. ns- non-significant, II – Instability index

Cost of production vis-à-vis MSP

It was attempted to compare the price support received by farmers and actual cost incurred for different kharif crops.

Madhya Pradesh

The comparative analysis of cost of production (Real A2, A2+FL, and C2) against the Minimum Support Price (MSP) for soybean, paddy, maize, cotton, arhar and urad during the period 2015–16 to 2024–25 highlights marked inter-crop variations in economic viability (figure 1).

For soybean, the results reveal a persistent divergence between cost of production and MSP. During 2015–16, the real C2 was as high as ₹5328/ql, while the MSP was only ₹2370/ql, indicating a large negative margin. Although the gap narrowed in subsequent years, soybean consistently exhibited lower MSP relative to C2. In 2024–25, the real C2 stood at ₹2695/ql compared to an MSP of ₹3158/ql, suggesting partial improvement, yet the overall trend underscores soybean's disadvantage in price support.

In the case of paddy, the cost–MSP relationship appears more favourable. The MSP increased gradually over the years and often approached or exceeded the C2 cost. For example, in 2020–21, the real C2

was ₹1111/ql while MSP reached ₹1514/ql, ensuring remunerative returns. Similar trends persisted thereafter, positioning paddy as relatively better protected than soybean. For maize, MSP remained closer to the C2 cost throughout the period. Instances such as 2016–17, where MSP (₹1223/ql) exceeded C2 (₹1200/ql), and 2023–24, where MSP (₹1380/ql) was on higher side to that of C2 (₹1028/ql), illustrate maize's relatively balanced support structure.

Cotton displayed a distinctive trend of high production costs and proportionately higher MSP. Although in early years (2016–17) the MSP (₹3459/ql) lagged behind C2 (₹4734/ql), by 2024–25, MSP (₹4597/ql) nearly converged with C2 (₹4266/ql). This suggests greater policy emphasis on commercial crops like cotton compared to oilseeds such as soybean. For pulses, arhar and urad, the MSP trends reflect partial coverage of costs. For arhar, in 2019–20, MSP (₹4762/ql) was marginally higher than C2 (₹3592/ql), but in other years, the cost–MSP gap persisted. A similar situation is observed in urad, where MSP aligned closely with C2 in 2020–21 (MSP: ₹4862/ql; C2: ₹5694/ql), yet in later years, costs again outpaced support prices.

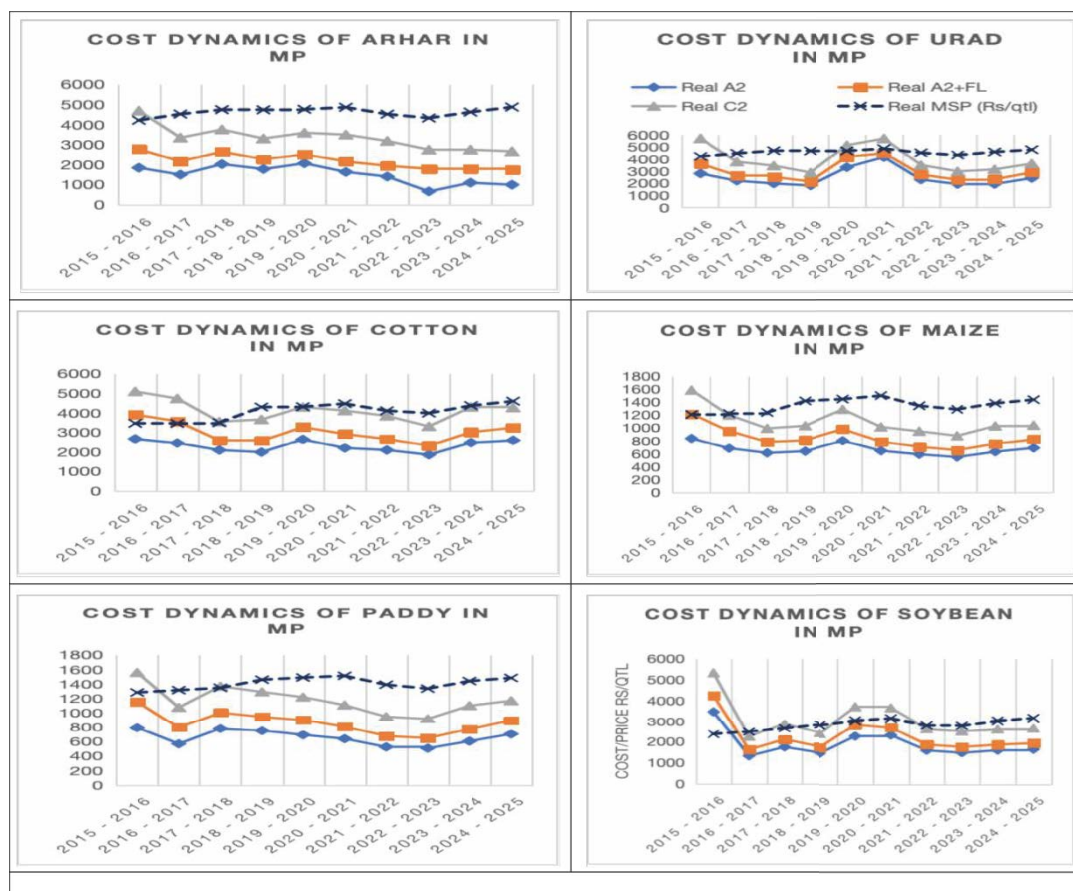


Figure 1: Real Cost of Production (Rs/ql) and MSP in Madhya Pradesh

The comparative perspective reveals that soybean is at a relative disadvantage when benchmarked against cereals (paddy and maize), cotton and even pulses like arhar and urad in certain years. While cereals benefit from closer MSP–C2 alignment and cotton shows policy-driven MSP enhancement, soybean continues to suffer from inadequate MSP coverage. Pulses, despite variability, also fare relatively better in select years. Graphical analysis corroborates these findings, where soybean consistently shows the widest gap between cost and MSP, highlighting the crop’s weak

economic viability under the current support framework.

Maharashtra

In figure 2 it can be seen that, for soybean, the results consistently highlight a mismatch between the cost of cultivation and MSP. In the initial year (2015–16), the real C2 was ₹4294/ql against an MSP of only ₹2370/ql, indicating a substantial negative margin. Although the gap narrowed in later years, soybean never achieved full cost coverage through MSP. By 2024–25, the C2 was ₹3200/ql while MSP stood at ₹3158/ql, reflecting near convergence

but still underscoring the crop's vulnerability compared to others.

In contrast, paddy demonstrates relatively better price support. During 2015–16, the C2 was ₹2251/ql and MSP ₹1285/ql, showing an initial shortfall. However, over time, MSP moved closer to costs, and in 2020–21 the MSP (₹1514/ql) exceeded C2 (₹1096/ql), ensuring positive returns. This suggests that paddy producers in Maharashtra benefited from stronger price protection compared to soybean growers. For maize, MSP remained close to or above the C2 cost in several years, particularly in 2017–18 (MSP was ₹1349/ql and C2 was ₹836/ql) and 2023–24 (MSP was ₹1442/ql and C2 was ₹1151/ql). This alignment demonstrates a relatively balanced support structure that provided maize cultivators with greater income security than soybean farmers.

Cotton displayed consistently higher production costs but also higher MSP, reflecting the importance of this commercial crop in Maharashtra's agrarian economy. In 2015–16, the C2 was ₹4196/ql and MSP ₹3464/ql, while by 2024–25 the MSP (₹4597/ql) nearly matched C2 (₹4609/ql). This

convergence indicates that policy mechanisms are more favourable for cotton compared to oilseeds like soybean.

In pulses like arhar and urad, the trends are mixed but generally more favourable than soybean in certain years. In 2019–20, arhar recorded a C2 of ₹3149/ql against an MSP of ₹4762/ql, offering substantial positive margins. Similarly, urad achieved near cost coverage in 2020–21 (C2 was ₹5314/ql and MSP was ₹4862/ql) and again in 2024–25 (C2 was ₹5442/ql and MSP was ₹4777/ql). Despite some fluctuations, pulse crops frequently received stronger MSP backing than soybean.

Relatively, soybean remains at a relative disadvantage vis-à-vis other crops in Maharashtra. While paddy and maize often benefitted from MSP levels approaching or exceeding cultivation costs, and cotton received consistent commercial crop support, soybean's MSP lagged behind cost C2 for most years. Arhar and urad also showed more favourable MSP–cost relation, particularly in arhar, underscoring policy emphasis on pulse promotion in recent years.

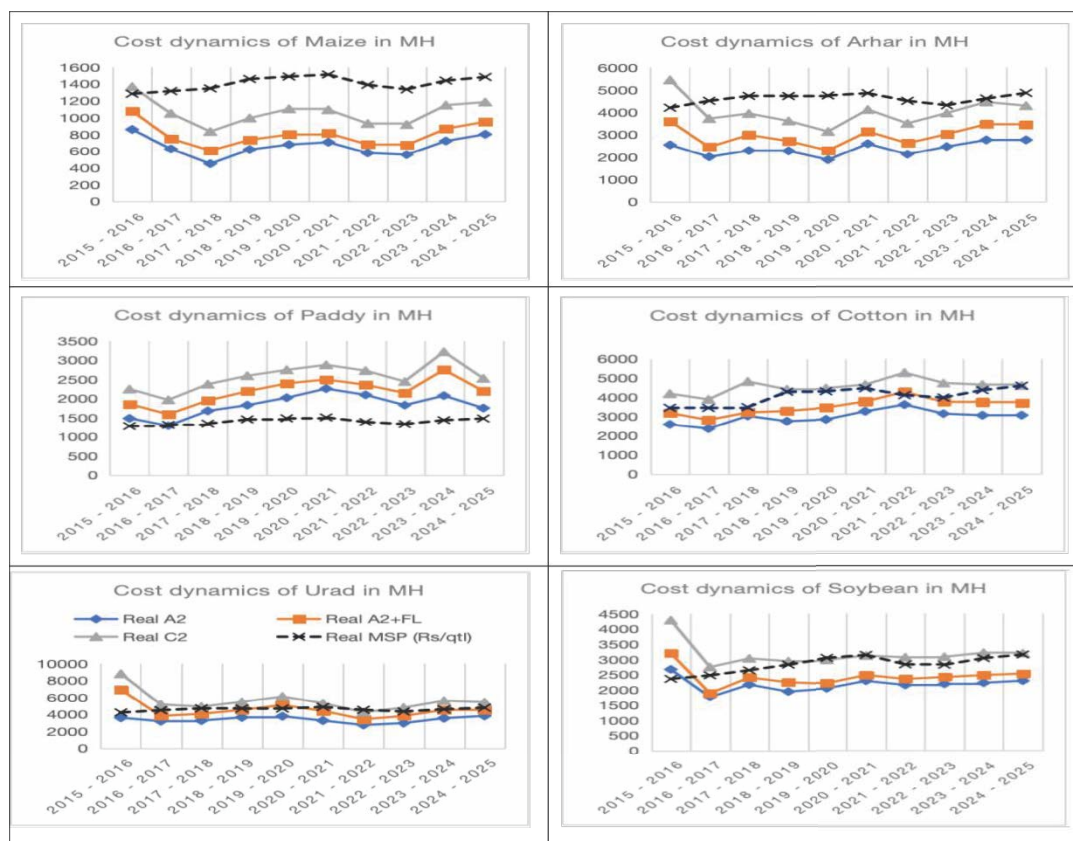


Figure 2: Real Cost of Production (Rs/qtt) and MSP in Maharashtra

Overall, the findings highlight that soybean farmers in Maharashtra, similar to those in Madhya Pradesh, face persistent profitability challenges under the current MSP regime. The comparative disadvantage of soybean vis-à-vis cereals, cotton, and pulses suggests the need for policy reorientation to ensure equitable support for soybean growers and to enhance the sustainability of soybean cultivation in the state.

CONCLUSION

Across both Madhya Pradesh and Maharashtra, soybean occupies a distinctive place in the cropping system. In Madhya Pradesh, its cost of cultivation is generally higher than

paddy and maize but broadly comparable with, or slightly below, cotton and pulses such as arhar. A similar pattern is evident in Maharashtra, where soybean falls in the mid-range of production costs above cereals but below high-cost crops like cotton, arhar and urad. This positioning makes soybean neither the cheapest nor the costliest option, but rather a commercially viable crop supported by strong domestic demand for edible oil and established processing networks, along with opportunities in export markets. The sustained importance of soybean in both states, however, will depend on continued improvements in production efficiency, access to improved technologies, and better

market integration to safeguard farmer profitability in the face of fluctuating margins.

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Life Cycle and Morphometric Studies of Tobacco Caterpillar (*Spodoptera litura* Fab.): A Stealthy Threat to Soybean Crop under Manipur Valley Conditions

KUMAR AKASH DEEP AND NILIMA KARAM

Department of Entomology, College of Agriculture, Central Agricultural University, Imphal-795004, Manipur

Email: nilikaram@gmail.com

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ABSTRACT

The experiment was carried out at the Department of Entomology, COA, CAU, Imphal to study the life cycle and morphometric characteristics of S. litura. The study revealed that eggs were round in shape with a mean diameter of 0.5 mm and the incubation period was 2-3 days. The total larval period was 12-17 days. The 1st, 2nd, 3rd, 4th, 5th and 6th larval instar period were 2-3, 2-3, 3-4, 2-3, 2-4, 1-2 days, respectively. The pupal period was 6-8 days while the adult longevity of male and female moth was 6-7 and 7-9 days, respectively. The total life period of male and female moth was 29-33 and 30-34 days, respectively. The preoviposition and oviposition period of female moth was 2-3 and 3-4 days, respectively. Fecundity was found to be 186-243 eggs/female. The sex ratio was observed to be 1:1.

Keywords: Soybean, Tobacco caterpillar, life cycle, morphometric characteristics, Fecundity, Sex ratio

Soybean [*Glycine max* (L.) Mirrill] is a very popular oilseed crop grown all over the world. Soybean is packed with nutrients: about 40-42% protein, 20-22% oil, 35% carbohydrates, 6-7% minerals, 5-6% fibre and 5% ash. It's also rich in polyunsaturated fats, especially Omega-6 and Omega-5 fatty acids (Chauhan and Joshi, 2005). These characteristics have made soybean fit well in sustainable agriculture. Soybean not only improves the socio-economic situations of small and marginal farmers, but also contributes to the country's total edible oil requirement (Bhatia *et al.*, 2008). Soybean is native to East Asia (China) and Manipur being located in the easternmost of India, the crop is also

cultivated widely in the foothills and mid-hills of the state. Soybean is grown in the state since time immemorial for making various non-fermented and fermented food products. About 70 per cent of soybean production in Manipur is used for the production of a traditional fermented food item known as *Hawaijar*. (Devi *et al.*, 2023)

The tobacco caterpillar, *Spodoptera litura* (Fab.), is an economically important polyphagous insect being the most destructive soybean insect pest in India causing high yield loss (Natiker and Balikai, 2015; Babu *et al.*, 2015). Manipur is a great biodiversity hotspot and the

agroclimatic conditions are very conducive for the growth and multiplication of many species of insect pests. *S. litura* is also one important pest of soybean in North Eastern Hill (NEH) region (Azadthakur *et al.*, 2012). Larvae of *S. litura* are voracious feeders and feed gregariously commencing from leaves and eventually feeding whole plant parts (Ahmad *et al.*, 2013). *S. litura* causes economic losses of crops from 25.8 -100 % based on crop stage and its infestation level in the field. (Dhir *et al.*, 1992).

The study on the life cycle of *S. litura* can help in understanding the life cycle, nature of damage, feeding habits and morphological characteristics of the pest. This will help in the taxonomic studies and proper management of the pest in the field. Available literature revealed that studies on the biology of the pest infesting soybean crop under Manipur valley conditions are limited.

MATERIALS AND METHODS

The research experiment was undertaken in the laboratory of Department of Entomology, COA, CAU, Imphal maintained at a temperature of 25-30°C and RH of 60% to 70%. To raise the initial culture of *S. litura* in the laboratory, a large number of larvae were collected from untreated soybean field where no plant protection measures were taken. The collected larvae were reared on fresh and clean tender soybean leaves of insect susceptible variety JS 335. The leaves were kept on pre-sterilized petriplates (21cm diameter) and the larvae were reared on them. The mouth of the petriplates was covered with fine muslin cloth held in position by rubber band. Every day sufficient

amount of fresh leaves of soybean was provided to the larvae after removing partially eaten leaves and excreta from the petriplates till the larvae changed to pre-pupal form. Before the formation of the pre-pupal stage, a set of glass jars of 0.5 litre capacity were filled with moist loose soil for pupation. Pupae thus obtained were separated for adult emergence. A pair of newly emerged male and female moths were confined in a 2 litre capacity glass jar containing 4-5 leaf stage of variety JS 335 grown in disposable plastic cups for resting and oviposition so as to begin a new cycle. The soybean plants in disposable cups inside the glass jar were replaced with fresh ones daily. A small container containing cotton swabs dipped in a 10% honey solution was also placed in the rearing jar as diet for the moths and were changed every two days. The open end of the glass jar was covered with fine muslin cloth and secured in position with the help of a rubber band. The adults were monitored daily for mortality and oviposition. Egg masses oviposited on the plants and muslin cover by each female were collected and counted daily until the female dies. Newly emerged larvae which are the first offspring (F1 generation) were observed for the study on life cycle of the pest. Freshly hatched larvae were isolated and transferred carefully with the help of a fine camel hair brush on the fresh foliage of leaves kept separately in the petriplates having moist tissue paper at the bottom. First, second and third instar larvae were mass reared in petriplates and from fourth instar onwards was reared singly to avoid cannibalism.

RESULTS AND DISCUSSION

Biological and morphometric description of *S. litura*

Egg stage

Female moth deposited eggs on the upper surface of soybean leaves and on the muslin cloth in clusters of 183 to 246 eggs in a group of 2 to 3 layers. Eggs were round in shape with a mean diameter of 0.5 mm. Similar findings by Solanki *et al.* (2022) stated that eggs of *S. litura* are laid in mass in three layers in rows. Eggs were creamish white and were covered with pale brown scales from the abdominal tip of the female moth. This result is in accordance with the results of Ramaiah and Maheswari (2018) who reported that tobacco caterpillar eggs were brown and spherical covered with brown hairs. Before hatching, the eggs turned into light brown to black. Female moth usually laid eggs during night time. Incubation period was 2 to 3 days with an average of 2.50 ± 0.5 days. However, incubation period of *S. litura* on a different crop, castor was 4 to 5 days as reported by Cardona *et al.* (2007). This indicated that incubation period was less in soybean crop.

Larval stage

Larva of *S. litura* was observed to moult five times and had six instars. This contradicts the report made by Latha *et al.* (2014) that *S. litura* has five larval instars. The young larvae were pale green with black heads whereas fully grown larvae were earthy brown to blackish with a typical inverted Y-shaped marking on their head capsule.

(i) First instar

The first instar larva was very small and without egg shells. Larva was yellowish to pale green with a head being comparatively large, black in colouration with black spots on the body. Similarly, Cardona *et al.* (2007) reported that first instar larvae had wider head and tapering abdomen. Thin minute hair covered the body on the lateral side. The duration of the first instar larvae ranged from 2 to 3 days with an average of 2.4 ± 0.49 days. Length of the larvae varied from 1.42 – 1.54 mm with an average of 1.48 ± 0.04 mm and the weight ranged from 0.0032 – 0.0054 g with an average of 0.0043 ± 0.0007 g. Newly emerged larvae were sluggish and fed gregariously on soybean leaves at night time causing whitish scratch markings on the leaves. This is in close conformity with that reported by Latha *et al.*, (2014) that indicated young larvae are slow moving with average length of 1.4 mm.

(ii) Second instar

The second instar larvae were pale green to light yellow and hairs on the body were absent. They had stripes on the lateral side of the body with black markings on either side of the mid-dorsal line of the first abdominal segment. Larvae possessed three pairs of true legs and five pairs of pro legs. Larval duration of the second instar larva ranged from 2 – 3 days with an average of 2.5 ± 0.5 days. Larval duration as observed by Latha *et al.* (2014) was also 2-3 days. Length of the 2nd instar larvae ranged from 3 – 7 mm with an average of 5.3 ± 1.3 mm and

the weight ranged from 0.0095 – 0.0124 g with an average of 0.011 ± 0.001 g. Larvae fed by scraping the green parts of the leaves.

(iii) Third instar

The third instar larva were dark green with two black spots on the dorsal surface of first abdominal segment. Two sub-dorsal lines run along the whole body of larvae. Larvae possessed dark spots on the abdominal segments in which the first and eighth abdominal segments had the largest spots. An inverted Y-shaped spot is present on the dorsal side of head region. A recent report by Solanki *et al.* (2022) also indicated the same result as the present study. The larval duration of third instar varied from 3 – 4 days with an average of 3.4 ± 0.49 days. The length of the larvae ranged from 8 – 13 mm with an average of 10.6 ± 1.7 mm and the weight ranged from 0.0268 – 0.0421 g with an average of 0.0345 ± 0.006 g.

(iv) Fourth instar

Colour of fourth instar larvae changed to brown with light green on the ventral surface of the body. Three longitudinal yellow stripes were present all along the body with one dark and mid-dorsal and two lateral lines. Black spots with tiny white markings appeared on the lateral lines dorsally. The larval duration of fourth instar ranged from 2 – 3 days with an average of 2.4 ± 0.49 days. Length of larva ranged from 20 – 25 mm with an average of 22.7 ± 1.6 mm and weight ranged from 0.1350 – 0.2565 g with an average of 0.1996 ± 0.036 g. Third and fourth instar larvae voraciously fed on leaves leaving only midribs and veins intact. Supportive literature by Ramaiah

and Maheswari (2018) also stated that larval period of fourth instar larvae lasted for 2-3 days with an average of 2.5 ± 0.71 days and that third, fourth and fifth instars eat the whole leaf blade leaving only the midrib.

(v) Fifth instar

Body colour of fifth instar larvae were earthy brown with longitudinal stripes more pronounced and distinct. Larvae appeared to be light brown in the dorsal region between the two dorsal stripes and remaining body was dark in colour because of the larger spots on the first and eighth abdominal segments. Along each yellow stripe, black spots were visible. Two parallel rows of black triangular spots were present on top of the whole larval body. Larval duration of fifth instar ranged from 2 – 4 days with an average of 3.05 ± 0.67 days. These observations are closely related to the observations made by Solanki *et al.* (2022). Length of larva ranged from 32 – 38 mm with an average of 35.8 ± 1.7 mm and weight ranged from 0.4145 – 0.6515 g with an average of 0.5778 ± 0.065 g. Larvae voraciously fed on leaves making big holes.

(vi) Sixth instar

The sixth instar larvae appeared to be black. Lateral sides of larval body were dark and ventral side were light coloured. Dark black spots present on the first and eighth abdominal segments were clearly visible. A bright yellow stripe was present along the length of the dorsal surface. Abdominal end was slightly tapered. Larval duration of sixth larvae ranged from 1 – 2 days with an average of 1.45 ± 0.5 days. Length of larvae ranged from 34

– 39 mm with an average of 36.5 ± 1.5 mm and weight ranged from 0.4225 – 0.6232 g with an average of 0.5348 ± 0.073 g. Sixth instar fed voraciously in the starting but later on, started to decline in feeding and transformed into an inactive pre-pupal stage.

Total larval period

Total developmental period of larva of *S. litura* ranged from 12 – 17 days with an average of 16.62 ± 1.89 days. Farahani *et al.* (2011) also reported duration of larval period of *S. litura* on soybean as 13.10 days.

Pupal stage

As soon as the sixth instar larva fully developed, larva avoided feeding and become sluggish and get curled into C-shape before pupation. This stage is called the pre-pupal stage. It then moved inside the soil and constructed an earthen cocoon in which pupation took place. Gupta *et al.* (2015) in his publication also reported that pupation of *S. litura* occurs in soil. Initially, pupa appeared to be light yellowish green and later on, turned into reddish brown. Pupa was obiect type with tapering ends. Seven pairs of spiracles were visible. A dark brown stripe was present on the mid-dorsal line and the two-pointed structures were present at the last abdominal segments. Pupal duration ranged from 6 – 8 days with an average of 7.00 ± 0.71 days. Some differences in previous findings were observed with longer pupal period on castor, green gram and arvi which ranged from 8.04–9.74 days. The pupal period of *S. litura* differs when reared on different crops such as a longer pupal period of 8.38 days on green gram, 9.05 days on cotton,

9.74 days on arvi and 12.26 days on cauliflower. The results revealed that pupal weight and duration were affected by the differences in the nutritional quality and quantity of host plants (Bhalani, 1989). Length of the pupa ranged from 15 – 18 mm with an average of 16.6 ± 1.2 mm and the weight ranged from 0.1077 – 0.3084 g with an average of 0.1773 ± 0.06 g. Similarly, Bayu and Krisnawati (2016) reported the pupal weight of *S. litura* on soybean as 0.32 g.

Adult stage

Adult was a medium-sized moth having dark- coloured forewings and light-coloured hindwings. Forewings appeared to be greyish brown with a crisscross variegated pattern with pale white lines while hindwings were off-white in colouration with brown venation and dark margin. Sexual dimorphism was clearly visible. Female moths were larger with stout bodies than male moths with a brown tuft of hairs on the abdominal tip which was absent on male. Male moth had an ashy grey patch on the apical margin of its forewings which was absent in female moths. Adult longevity of male moth ranged from 6 – 7 days with an average of 6.5 ± 0.5 days while that of female ranged from 7 – 9 days with an average of 8.125 ± 0.6 days. Contrasting results could be observed with the reports made by Kumar and Bhattacharya (2019) who stated that *S. litura* adult has shorter life span of 3.67 days only when fed on cabbage and cauliflower. However, similar results were given by Pramod *et al.* (2015) who reported longevity of adult female and male to be 9 and 6 days with an

average of 9.0 ± 0.0 and 5.5 ± 0.21 respectively. Body lengths of male and female were found to be 1.4 – 1.7 mm and 1.6 – 1.9 mm with an average of 1.54 ± 0.10 mm and 1.75 ± 0.09 mm, respectively. Length observed on wing span of male and female moths was found to be 3.5 – 3.9 mm for both with an average of 3.68 ± 0.12 cm and 3.74 ± 0.13 cm, respectively.

Pre-oviposition and oviposition period

Pre-oviposition period varied from 2 – 3 days with an average of 2.625 ± 0.48 days. Oviposition occurred during night time. Female moths laid eggs in masses three to four days after emergence. Oviposition period ranged from 3 – 4 days with an average of 3.5 ± 0.5 days.

Total life span

Total life cycle of *S. litura* took around 29 – 34 days to complete. Total life period of male moth ranged from 29 – 33 days with an average of 31.75 ± 1.30 days while that of female ranged from 30 – 34 days with an average of 32.25 ± 1.30 days. The result corroborates with

the results of Sharma (1994) who reported that total developmental period of *S. litura* was 32.67 days in soybean.

Fecundity

Female moths initiated laying of eggs after three to four days of emergence. There was considerable variation in the egg-laying of each female which ranged from 186 – 243 with an average of 212.375 ± 18.28 eggs per female. However, fecundity was observed higher in cabbage (283.5) and sweet potato (282.1) as per the earlier work of Xue *et al.* (2010).

Sex ratio

Sex ratio denotes the number of females per male. Out of 20 pupae, only 16 emerged as adults of which 8 were male and 8 were female. So, male: female ratio was 1:1. This contradicts the findings of Narvekar *et al.* (2018) that revealed that sex ratio of *S. litura* was female biased and that more female adults emerged than male adults.

Table 1. Life cycle of tobacco caterpillar (*Spodoptera litura* Fab.) infesting soybean

Stages of insect	No. of observation	Minimum	Maximum	Mean	±SD
Incubation period (days)	20	2	3	2.50	0.5
Larval period (days)	20				
I Instar	20	2	3	2.40	0.49
II Instar	20	2	3	2.50	0.5
III Instar	20	3	4	3.40	0.49
IV Instar	20	2	3	2.40	0.49
V Instar	20	2	4	3.05	0.67
VI Instar	20	1	2	1.45	0.5
Total larval period (days)	20	12	17	16.62	1.89
Pupal period (days)	20	6	8	7.00	0.71
Adult longevity (days)	16				
Male	8	6	7	6.50	0.5
Female	8	7	9	8.125	0.6
Sex ratio (Male: Female)	16			1:1	
Total life period (days)	16				
Male	8	29	33	31.75	1.30
Female	8	30	34	32.25	1.30
Pre oviposition period (days)	8	2	3	2.62	0.48
Oviposition period (days)	8	3	4	3.50	0.5
Fecundity (no. of eggs/ female)	8	186	243	212.38	18.28

Table 2. Morphometric characteristics of different life stages of *S. litura*

Life stages	Minimum	Maximum	Mean	±SD
I Instar larva				
a. Length (mm)	14.2	15.4	14.83	0.36
b. Weight (gm)	0.0032	0.0054	0.0043	0.0007
II Instar larva				
a. Length (mm)	3.0	7.0	5.3	1.3
b. Weight (gm)	0.0095	0.0124	0.011	0.001
III Instar larva				
a. Length (mm)	8.0	13.0	10.6	1.7
b. Weight (gm)	0.0268	0.0421	0.0345	0.006
IV Instar larva				
a. Length (mm)	20.0	25.0	22.7	1.6
b. Weight (gm)	0.1350	0.2565	0.1996	0.036
V Instar larva				
a. Length (mm)	32.0	38.0	35.8	1.7
b. Weight (gm)	0.4145	0.6515	0.5778	0.065
VI Instar larva				
a. Length (mm)	34.0	39.0	36.5	1.5
b. Weight (gm)	0.4225	0.6232	0.5348	0.073
Pupa				
a. Length(mm)	15.0	18.0	16.6	1.2
b. Weight(gm)	0.1077	0.3084	0.1773	0.06
Adult (male)				
a. Body length (cm)	1.4	1.7	1.54	0.10
b. Wing span (cm)	3.5	3.9	3.68	0.12
Adult (female)				
a. Body length (cm)	1.6	1.9	1.75	0.09
b. Wing span (cm)	3.5	3.9	3.74	0.13

CONCLUSION

The study on the life cycle of *Spodoptera litura* will help to identify the different stages of the insect in field condition. It will further help in planning management tactics during early stages which will help prevent the insect reaching ETL. The data on morphometric features of the pest at different stages also provides a clear

picture of the complete identification of the insect.

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Dr. Sanjay Gupta, Principal Scientist (Plant Breeding), ICAR-National Soybean Research Institute, Indore, Madhya Pradesh

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Dr. Mahaveer Sharma, Principal Scientist (Microbiology), ICAR-National Soybean Research Institute, Indore, Madhya Pradesh

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Pansae V G and Sukhatme P V. 1978. *Statistical Methods for Agricultural Workers*. Indian Council of Agricultural Research, New Delhi. pp.186. **(Book)**

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