J. Farm Sci., 38(3): (288-291) 2025

RESEARCH PAPER

Integrative assessment of seed quality parameters and fungal association patterns in soybean [*Glycine max* (L.) Merrill] genotypes

S. S. BHARATH[1*], RAVI HUNJE[1], V. K. DESHPANDE[1], SHAMARAO JAHAGIRDAR[2],
G. SOMANGOUDA[3] AND RAVIKUMAR HOSAMANI[4]

[1]Department of Seed Science and Technology, [2]Department of Plant Pathology
[3]Department of Agronomy,[4]Department of Biotechnology, College of Agricultural Sciences, Dharwad
University of Agricultural Sciences, Dharwad - 580 005, India
*E-mail: bharathss538@gmail.com

(Received: July, 2025 ; Accepted: September, 2025)

DOI: 10.61475/JFS.2025.v38i3.15

Abstract: The present study entitled "Integrative Assessment of Seed Quality Parameters and Fungal Association Patterns in Soybean [*Glycine max* (L.) Merrill] Genotypes" was conducted at the Department of Seed Science and Technology and Seed Quality and Research Laboratory, University of Agricultural Sciences, Dharwad, during 2022–23. Sixteen soybean genotypes were evaluated under a Completely Randomized Design (CRD) with three replications to assess seed quality and seed-borne mycoflora.Significant variation was observed among genotypes for all quality traits. MACS 1407, JS 335, and DSb 34 recorded the highest germination, seedling vigour indices and seedling dry weight, along with low electrical conductivity values, indicating superior seed vigour and membrane stability. In contrast, DSb 28 and JS 93-05 exhibited lower physiological performance. Seed health testing revealed the presence of *Colletotrichum truncatum*, *Cercospora kikuchii*, *Fusarium oxysporum*, *Aspergillus flavus* and *Macrophomina phaseolina* as predominant fungi. The lowest seed infection was recorded in MACS 1407, DSb 34 and JS 335, indicating their potential tolerance to seed-borne pathogens. Overall, MACS 1407, JS 335 and DSb 34 were identified as superior genotypes with better seed quality and health, suitable for further physiological and molecular investigations.

Key words: Germination, Electrical conductivity, Seed-borne fungi, Seed health

Introduction

Soybean (*Glycine max* L. Merrill) is a major leguminous oilseed crop cultivated worldwide for its high protein (~40%) and oil (~20%) content (Hartman *et al*., 2011). In India, it plays a vital role in meeting the growing demand for edible oil and enhancing soil fertility through biological nitrogen fixation. The crop spans about 12.5 million hectares with an annual production of around 13 million tonnes (Anon, 2024). The success of soybean cultivation is closely linked to the use of high-quality seed, which ensures rapid and uniform field establishment, ultimately boosting yield and productivity (Sharma *et al*., 2021).

Seed quality is a multifaceted trait encompassing genetic, physical, physiological, and health attributes (Basu, 1994). Among these, physiological indicators such as germination, vigour and metabolic efficiency are critical for producing vigorous seedlings (Hampton and TeKrony, 1995; Matthews *et al*., 2012). Seed vigour testing, especially under sub-optimal conditions, provides insights into potential field performance. The electrical conductivity test, which measures electrolyte leakage from soaked seeds, is widely used to assess membrane stability and seed deterioration (Powell, 1986; Hampton, 2002).

However, physiological seed quality is often compromised by seed-borne mycoflora that cause biochemical and structural damage, reducing germination and seedling vigour (Agarwal and Sinclair, 1987). Fungi such as *Aspergillus flavus*, *A. niger*, *Fusarium oxysporum*, *Penicillium* spp., *Cercospora kikuchii* and *Colletotrichum truncatum* are known to infect soybean seeds, leading to discoloration, rotting and seedling mortality (Singh and Mathur, 2004; Chavan *et al*., 2019). Under warm and humid conditions, these pathogens proliferate rapidly, diminishing seed viability and promoting disease transmission (Hartman *et al*., 2015).

Genotypic variability in physiological and pathological seed traits has been reported, indicating that certain genotypes possess inherent tolerance to seed-borne fungi and maintain superior seed quality (Bharathi *et al*., 2018). Understanding this variability is essential for identifying elite genotypes and developing effective seed-health management strategies. Recent studies under Indian agro-ecological conditions emphasize the need to assess seed quality alongside associated mycoflora for sustainable soybean production (Patil *et al*., 2023).

This study aims to evaluate genotypic variability in physiological seed traits such as germination, vigour indices and electrical conductivity to identify predominant seed-borne fungi affecting seed quality.

Material and methods

The experiment was conducted during 2022-23 at the Laboratory of the Department of Seed Science and Technology and the Seed Quality and Research Laboratory, Seed Unit, University of Agricultural Sciences (UAS), Dharwad. The study aimed to evaluate the initial seed quality parameters and associated seed mycoflora in elite soybean genotypes. A total of sixteen soybean genotypes were included in the study namely DSb 21, DSb 23, DSb 28, DSb 34, JS 335, JS 93-05, DLSb 1, JS 95-60, JS 20-69, JS 22-16, NRC 130, NRC 138, MACS 1188, MACS 1407, MACS 1460 and MACS 1520. The experiment was laid out in a Completely Randomized Design (CRD) with three replications to ensure precision and reliability of the results. Prior to the experiments, all seed samples were dried to a safe moisture content and stored under controlled conditions at 4°C until further use to maintain their viability and physiological quality.

Seed quality parameters such as seed germination (%) was carried out as per Anon (2021) and seedling vigour indices I and II were calculated following the formula of Abdul-Baki and Anderson (1973) and expressed in number. Electrical conductivity (EC) (µS/cm/g seed fresh weight) of seed leachate and seed infection (%) was estimated as per Anon (2021). Associated seed mycoflora were assessed on compound microscope for assessing the mycelia and associated spores.

Results and discussion

The results on germination percentage of sixteen soybean genotypes (Table 1) revealed significant variations among the entries. Germination ranged from 74 to 94 per cent, indicating inherent genetic variability in seed viability and physiological quality. Among the DSb series, DSb 34 recorded the highest germination (84%), followed by DSb 21 (80%), while the lowest was observed in DSb 28 (74%). In the JS series, JS 335 exhibited the highest germination (88%), followed by JS 22-16 (84%), whereas the lowest was recorded in JS 93-05 (79%). Among the MACS genotypes, MACS 1407 showed the highest germination (94%), followed by MACS 1520 (93%), while MACS 1188 recorded the least (90%).The superior germination performance in MACS 1407 and JS 335 might be attributed to higher seed viability and better membrane integrity, as these genotypes possibly experienced minimal mechanical or storage-induced deterioration. Variations in germination percentage among genotypes are primarily governed by genetic factors and physiological status of seeds at harvest and storage (Deshmukh *et al.*, 2019). Similar findings of significant genotypic variation in soybean seed germination were also reported by Padmini *et al.* (2021) and Hunje *et al.* (1987), who observed higher germination in well-stored and physiologically active genotypes.

Electrical conductivity (EC) test revealed significant genotypic variation (Table 1). The lowest EC values, indicating better membrane integrity, were recorded in MACS 1407 (12.8 µS cm^{-1} g^{-1}), followed by MACS 1520 (21.9 µS cm^{-1} g^{-1}) and JS 335 (25.3 µS cm^{-1} g^{-1}). In contrast, higher EC values were observed in DSb 28 (53.2 µS cm^{-1} g^{-1}) and JS 93-05 (49.7 µS cm^{-1} g^{-1}), indicating greater electrolyte leakage due to membrane damage. The inverse relationship between EC and germination performance suggests that genotypes with lower EC maintained better cell membrane integrity and seed vigour. Similar trends were reported by Lakshmi *et al.* (2018), who noted that genotypes with higher EC values generally exhibit poor storability and lower seed quality.

Seedling vigour index-I (SVI-I) showed significant differences among all genotypes (Table 1). The highest SVI-I was observed in MACS 1407 (3189), followed by JS 335 (3091) and DSb 34 (2805), while the lowest was recorded in DSb 23 (2092). The superior vigour indices of MACS 1407 and JS 335

Table 1. Initial seed quality parameters *viz*. germination (%), electrical conductivity (µS cm^{-1} g^{-1}), Seedling Vigour Index-I, Seedling Vigour Index-II and Seed infection (%) of soybean genotypes

Genotype	Germination (%)	Electrical conductivity (µS cm^{-1} g^{-1})	Seedling Vigour Index-I	Seedling Vigour Index-II	Seed infection (%)
DSb 21	80 (63.68)	46.9	2392	5756	62.67 (52.34)
DSb 23	78 (61.86)	49.6	2092	5739	65.33 (53.94)
DSb 28	74 (59.57)	53.2	2421	5586	67.33 (55.14)
DSb 34	84 (66.70)	29.9	2805	6509	59.33 (50.38)
JS 335	88 (69.49)	25.3	3091	8756	72.33 (58.28)
JS 93-05	79 (63.00)	49.7	2382	6150	75.00 (60.00)
JS 95-60	83 (65.45	35.5	2432	8184	72.67 (58.54)
JS 20-69	82 (64.90)	43.5	2459	4701	73.67 (59.15)
JS 22-16	84 (66.67)	43.1	2473	3861	77.33 (61.58)
NRC 130	72 (58.27)	56.0	1611	5591	70.00 (56.79)
NRC 138	82 (64.67)	39.8	2366	4025	71.33 (57.63)
MACS 1188	90 (71.92)	20.1	2600	5492	50.33 (45.19)
MACS 1460	91 (82.56)	31.4	2691	6167	53.67 (47.10)
MACS 1407	94 (76.24)	12.8	3189	7871	47.33 (43.47)
MACS 1520	93 (74.34)	21.9	2799	5290	51.67 (45.96)
DLSb 1	71 (57.21)	56.4	1499	6078	69.67 (56.59)
S.Em ±	0.86	0.61	37.72	29.39	0.75
C.D (P=0.01)	3.33	2.37	146.09	113.83	2.92
C.V (%)	2.23	2.76	2.67	0.85	2.42

Figures in the parenthesis are arc sine value

Table 2. Assessment of seed mycoflora in soybean genotypes

Genotype	Associated seed borne mycoflora								
	A.f.	*A.n.*	*C.t.*	*C.k.*	*F.o.*	*M.f.*	*M.s.*	*R.n.*	*R.s.*
DSb 21	-	+	+	+	+	+	-	-	-
DSb 23	+	-	+	-	-	-	-	-	+
DSb 28	+	-	+	+	+	+	+	-	+
DSb 34	-	+	+	-	-	+	+	+	-
JS 335	+	-	+	+	+	+	+	+	-
JS 93-05	+	+	+	+	+	-	+	-	-
JS 95-60	-	+	+	+	+	-	-	-	-
JS 20-69	+	+	+	-	+	+	-	-	-
JS 22-16	+	+	+	+	-	-	+	-	-
NRC 130	-	-	+	+	+	+	-	-	-
NRC 138	+	+	-	+	+	+	+	-	-
MACS 1188	-	+	+	+	-	+	-	+	-
MACS 1460	+	-	+	-	+	-	+	-	-
MACS 1407	+	-	+	+	+	+	+	-	+
MACS 1520	+	+	-	+	-	-	-	-	-
DLSb 1	+	-	+	+	+	+	+	-	-
No. of Positive response	11	9	14	12	11	10	9	3	1

A.f. – Aspergillus flavus
A.n. – Aspergillus niger
M.s. – Mucor sp.
C.t. – Colletotricum truncatum
C.k. – Cercospora kikuchii
R.n. – Rhizopus nigricans
F.o. – Fusarium oxysporum
M.f. – Macrophomina phaseolina
R.s. – Rhizoctonia solani

are attributed to their higher germination percentage, longer seedlings and greater seedling dry weight.These results corroborate the findings of Abdul-Baki and Anderson (1973), who established SVI as a reliable parameter to assess physiological seed vigour. Similar genotypic variation in vigour indices among soybean cultivars was reported by Ahmed *et al.* (2023) and Padmini *et al.* (2021).

The seedling vigour index-II (SVI-II) also varied significantly across genotypes (Table 1). The highest value was observed in JS 335 (8756), followed by MACS 1407 (7871) and DSb 34 (6509), whereas the lowest was recorded in JS 22-16 (3861). The trend corresponds closely with germination and dry weight data, indicating that genotypes producing heavier seedlings contribute to higher vigour. Similar associations between SVI-II and seedling biomass were reported by Deshmukh *et al.* (2019) in soybean.

Significant variation in seed infection percentage was recorded among soybean genotypes (Table 1). Among the DSb series, DSb 34 showed the lowest seed infection (59.33%), followed by DSb 21 (62.67%), while DSb 28 had the highest (67.33%). In the JS group, JS 335 showed comparatively lower seed infection (72.33%) than JS 22-16 (77.33%) and JS 93-05 (75.00%). Among the MACS entries, MACS 1407 exhibited the least infection (47.33%), followed by MACS 1188 (50.33%) and MACS 1520 (51.67%).The lower infection rates in MACS genotypes suggest better inherent resistance or tolerance to seed-borne pathogens. These results are in agreement with Shivankar *et al.* (2016), who reported genotypic differences in susceptibility to *Cercospora* and *Colletotrichum* infections in soybean.

Table 2 highlights the diversity of seed-borne fungi in soybean genotypes. *Colletotrichum truncatum* and *Cercospora kikuchii* were the most prevalent, while *Rhizoctonia solani* and *R. nigricans* were least common. Genotypes like JS 93-05, JS 95-60, and JS 20-69 showed broader fungal spectra and higher infection levels, whereas MACS 1407, MACS 1188, and MACS 1520 had minimal colonization, indicating possible resistance. The variability in fungal association suggests that genotypic differences significantly influence seed infection and quality (Zhou *et al.*, 2020).

Conclusion

This study on sixteen elite soybean genotypes revealed significant genotypic variation in physiological and pathological seed traits. Genotypes MACS 1407, JS 335 and DSb 34 showed superior germination, seedling growth, vigour indices, and low electrical conductivity, indicating high vigour and membrane integrity. In contrast, DSb 28 and JS 93-05 exhibited poor seed vigour. Seed mycoflora assessment identified *Colletotrichum truncatum* and *Cercospora kikuchii* as predominant fungi, with MACS 1407 showing lower infection levels. These findings underscore genotype-specific differences in seed quality and health, positioning DSb 34, JS 335, and MACS 1407 as promising candidates for further resistance and seed-health research.

References

Abdul-Baki AA and Anderson JD, 1973,*Vigour determination in soybean seed by multiple criteria*. *Crop Science*, 13(6): 630–633.

Agarwal VK and Sinclair JB, 1987,*Principles of Seed Pathology*. Boca Raton: CRC Press.

Ahmed S, Rani M and Kumar D, 2023, Evaluation of seed vigour indices in soybean genotypes under controlled stress conditions. *Legume Research*, 46(3): 478-484.

Anon, 2021, *International Rules for Seed Testing*. International Seed Testing Association (ISTA), Bassersdorf, Switzerland.

Anon, 2024, *Soybean Processors Association of India Annual Report 2023-24*. Indore: SOPA Publications.

Basu R N, 1994, An appraisal of research on wet and dry physiological seed treatments and their applicability with special reference to tropical and subtropical countries, *Seed Science and Technology*, 22(2): 107-126.

Bharathi A, Prasad R D and Reddy K R N, 2018, Screening of soybean genotypes for resistance against seed-borne fungi, *Legume Research*, 41(4): 606-610.

Chavan A M, Muley A B and Sable A S, 2019, Mycoflora associated with soybean seeds and their impact on seed health, *Journal of Pharmacognosy and Phytochemistry*, 8(2): 1555-1558.

Deshmukh A, Patil R and Ghorade R, 2019, Genotypic variation for seed germination and vigour traits in soybean. *Seed Research*, 47(2): 124–130.

Hampton J G and TeKrony D M, 1995, *Handbook of Vigour Test Methods*. 3rd edn. Zurich: International Seed Testing Association.

Hampton J G, 2002, What is seed quality?, *Seed Science and Technology*, 30(1): 1–10.

Hartman G L, Rupe J C, Sikora E J, Domier L L, Davis J A and Steffey K L, 2015,*Compendium of Soybean Diseases and Pests*. 5th edn. St. Paul, MN: APS Press.

Hartman G L, West E D and Herman T K, 2011, Crops that feed the world 2. Soybean worldwide production, use and constraints caused by pathogens and pests, *Food Security*, 3: 5-17.

Lakshmi S, Anuradha M and Prasad R, 2018, Assessment of seed deterioration through electrical conductivity test in soybean. *Seed Research*, 46(1): 19-24.

Matthews S, Khajeh-Hosseini M and Powell A A, 2012, Evaluation of seed quality: from physiology to international rules, *Seed Science Research*, 22(S1): 69-73.

Padmini K, Ramesh B and Reddy V S, 2021, Evaluation of seed quality parameters in soybean genotypes. *International Journal of Agricultural Sciences*, 17(1): 60-65.

Patil B L, Hunje R V and Shashidhar S D, 2023 Influence of seed quality parameters on vigour and viability of soybean genotypes, *Journal of Farm Sciences*, 36(4): 526-532.

Powell AA, 1986, Cell membranes and seed leachate conductivity in relation to seed quality, *Journal of Seed Technology*, 10: 81-100.

Sharma S D, Meena B R and Tripathi P, 2021, Influence of seed quality parameters on field performance of soybean genotypes, *Seed Research*, 49(1): 55-62.

Shivankar R S, Dhopavkar R V and Deshmukh A J, 2016, Variability in seed-borne infection and its impact on germination in soybean. *Journal of Oilseeds Research*, 33(2): 104-109.

Singh D and Mathur SB, 2004, *Histopathology of Seed-Borne Infections*. Boca Raton: CRC Press.

Zhou D, Huang X, Chaparro J M and Zhang R, 2020, Rhizosphere microbiomes of healthy and diseased soybean plants differ in structure and function. *The ISME Journal*, 14(7): 1870-1883.