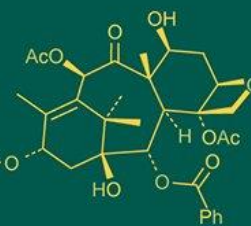
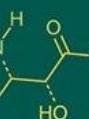
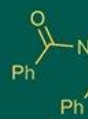


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Phenotypic characterization of soybean genotypes for rust (*Phakopsora pachyrhizi* Sydow) resistance

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Abstract

The present investigation was carried out to phenotypically characterize 30 soybean genotypes for resistance to rust caused by *Phakopsora pachyrhizi* Sydow. The genotypes were evaluated under field conditions at Agricultural Research Station, Kasbe-Digraj, Sangli, during Kharif 2018 in a randomized block design with three replications. Rust severity was assessed using the 0-9 disease-rating scale and percent disease intensity (PDI) was calculated following standard phytopathometric procedures. None of the genotypes showed an absolutely resistant reaction. KDS-753 recorded a highly resistant reaction, whereas CAUMS-1, KS-103, KDS-726, KDS-1009 and PS-1637 were moderately resistant. Six genotypes were susceptible and the remaining genotypes were highly susceptible. The identified highly resistant and moderately resistant genotypes may serve as useful donors for soybean rust resistance breeding, molecular characterization and gene-pyramiding programmes.

Keywords: *Glycine max*, *Phakopsora pachyrhizi*, soybean rust, PDI, phenotypic screening, resistance breeding

Introduction

Soybean (*Glycine max* (L.) Merr.) is an important oilseed and protein crop and is often described as a “miracle crop” or “golden bean” because its seed generally contains about 38-42% protein and 18-20% oil (Anonymous, 2022; Tiwari, 2022) [1, 34]. Soybean protein has a favorable amino-acid profile and contributes substantially to human food, livestock feed and vegetable-oil requirements (Anonymous, 2022; Tiwari, 2022) [1, 34]. Asian soybean rust, caused mainly by *Phakopsora pachyrhizi* Sydow, is one of the most destructive foliar diseases of soybean in tropical and subtropical soybean-growing regions (Bromfield, 1984; Goellner *et al.*, 2010; Reis, 2022) [4, 11, 29]. The pathogen is an obligate biotroph, produces abundant urediniospores and can infect leaves rapidly under humid conditions, resulting in premature defoliation, reduced pod filling and heavy yield losses under favourable epidemics (Miles *et al.*, 2003; Dalla Lana *et al.*, 2015; Godoy *et al.*, 2016) [24, 7, 12].

Rust symptoms commonly begin as small chlorotic to greyish lesions that later turn tan to reddish-brown, usually on the lower leaf surface, where uredinia develop and release spores (Miles *et al.*, 2005; Hartman *et al.*, 2015) [23, 13]. Disease development is favoured by moderate temperature, high humidity and prolonged leaf wetness, and the pathogen can spread over long distances through wind-borne urediniospores (Bonde *et al.*, 2006; Schmale and Ross, 2015; Belinelli *et al.*, 2025) [3, 32, 2]. In India, soybean rust has been reported as an economically important disease in several soybean-growing areas, including Maharashtra, Karnataka and Madhya Pradesh (Rao *et al.*, 1995; Mahajan *et al.*, 2019) [28, 20]. The epidemic occurrence of rust during favourable seasons has emphasized the need for systematic screening of germplasm and incorporation of resistance into adapted varieties (Khot *et al.*, 2010; Kurundkar *et al.*, 2011; Mahajan *et al.*, 2019) [15, 16, 20].

Host resistance is considered a sustainable component of rust management; however, resistance governed by single major genes can be overcome by virulent pathogen populations (Pham *et al.*, 2009; Twizeyimana and Hartman, 2012) [27, 35]. Therefore, resistant donor identification, differential reaction studies, new Rpp-source discovery and integration with molecular characterization are required for durable resistance breeding (Whitham *et al.*, 2016; Childs *et al.*, 2018; Dormatey *et al.*, 2020) [38, 6, 9]. Because soybean rust epidemics are influenced by airborne inoculum movement, host susceptibility and favourable weather, field

screening remains important for identifying resistant donors that can be confirmed later through molecular and multilocation studies (Hartman *et al.*, 2015; Martinelli *et al.*, 2015; Mueller *et al.*, 2016; Belinelli *et al.*, 2025) [13, 21, 25, 2]. Broadening the resistance base through wild and related legume sources, gene pyramiding and host-pathogen studies is important for improving the durability of soybean rust resistance (Kawashima *et al.*, 2016; Dormatey *et al.*, 2020) [14, 9]. Transfer of a pigeonpea-derived resistance gene into soybean demonstrated that related legumes can provide valuable resistance resources against Asian soybean rust (Kawashima *et al.*, 2016) [14]. Accurate phenotypic screening remains essential because molecular tools, image-based phenotyping and advanced disease-detection methods require reliable field-based disease classification for validation (Mayee and Datar, 1986; Martinelli *et al.*, 2015; Cavanagh *et al.*, 2021; Saleem *et al.*, 2024) [22, 21, 5, 31]. Hence, the present study was undertaken to characterize soybean genotypes for rust reaction and to identify resistant or moderately resistant genotypes useful for further crop improvement (Mayee and Datar, 1986; Martinelli *et al.*, 2015) [22, 21].

Material and Methods

Experimental material

The experimental material consisted of 30 soybean genotypes collected from different sources. The list of genotypes and their pedigree is presented in Table 1.

Table 1: List of soybean genotypes and pedigree included in the study

Sr. No.	Name of genotype	Pedigree
1	BAUS-100	JS 20-30/JS 335
2	CAUMS-1	Selection from NRC 2012-6-3-1-4-3
3	DS-3109	Pusa 12/F4C7-32
4	DS-3110	Pusa 12/F4C7-32
5	DSb-33	DSb 21/JS 95-60
6	GJS-3	Germ plasm line KB -85
7	Himso-1688	NRC 2007/B1-19
8	Himso-1689	NRC 2008/G-1-12
9	JS-21-71	JS 20-63/JS 95-60
10	JS-21-72	SL 738/JS 95-60
11	KDS-1009	AMS 99 33/EC 241780
12	KDS-1073	JS 20-05/EC 241780
13	KS-113	Selection from KS 103
14	MACS-1566	RKS 24/NRC 55
15	MACS-1620	RKS 25/NRC 55
16	NRC-138	JS 97-52/NRC 107
17	NRC-139	JS 97-52/NRC 101
18	NRC-146	Selection from 6A-34
19	NRC-147	Indigenous collection (IC 210)
20	NRC-148	NRC 7/AGS 191
21	NRCSL-2	JS 335/SL 525 EDV of JS 335
22	PS-1634	JS 9752/PS 1225
23	PS-1637	JS 9752/PK 472
24	RSC-11-15	JS 335/PS 1024
25	RSC-11-17	JS 97-52/JS 93-05
26	RVS-2007-4	RVS 2000-10/JS 95-60
27	RVS-2011-10	JS -335/PK 1042
28	KS-103	JS 335/EC 241780
29	KDS -726	JS 9305/EC 241780
30	KDS -753	JS 9305/EC 241780

Experimental method

The field experiment was conducted at Agricultural Research Station, Kasbe-Digraj, Sangli, during Kharif 2018.

The experiment was laid out in a randomized block design with three replications and all recommended agronomic practices were followed to raise a healthy crop according to university recommendations.

Screening for rust resistance

Rust severity was recorded on five randomly selected plants from each plot using the 0-9 scale proposed for plant-disease assessment (Mayee and Datar, 1986) [22]. The rating scale used for rust assessment is given in Table 2.

Table 2: Disease rating scale used for recording soybean rust reaction

Rating	Description
0	No lesions/pustules
1	1% leaf area covered with lesions/pustules.
3	1.1-10% leaf areas covered with lesions/pustules, no pustules on stem.
5	10.1-25% of the leaf area covered, no defoliation; little damage.
7	25.1-50% leaf area covered; some leaves drop; death of few plants; damage conspicuous.
9	More than 50% area covered, lesions/pustules very common on all parts, defoliation common; death of plants common; damage more than 50%.

Percent Disease Intensity (PDI) was calculated using the standard formula suggested by Wheeler (1969) [37]

$$PDI = \frac{\text{Sum of individual disease ratings}}{(\text{Number of plants examined} \times \text{Maximum disease grade})} \times 100$$

The categorization of soybean genotypes on the basis of PDI is presented in Table 3.

Table 3: Categorization of soybean genotypes based on PDI

PDI	Category
0.00	Absolutely Resistant (AR)
0.01 - 11.11	Highly Resistant (HR)
11.12 - 33.33	Moderately Resistant (MR)
33.34 - 55.55	Moderately Susceptible (MS)
55.56 - 77.77	Susceptible (S)
77.78 - 100	Highly Susceptible (HS)

Results and Discussion

Considerable variation was observed among the soybean genotypes for flowering, maturity, plant height, branches, pods per plant, seeds per pod, seed yield per plant, seed weight, SPAD value, protein content, oil content and rust reaction. Such variation indicates the presence of useful phenotypic diversity that can be exploited in soybean improvement programmes (Singh and Vatsa, 2009; Li *et al.*, 2019; Kuswanto, 2019) [33, 19, 17].

Days to 50% flowering ranged from 35.33 days in NRC-138 to 46.33 days in KS-113, whereas days to maturity ranged from 88.00 days in NRC-146 to 105.33 days in KDS-1009. Plant height varied from 32.06 cm in CAUMS-1 to 68.31 cm in KS-113, and primary branches per plant ranged from 3.00 to 4.11. Such variation is important in resistance breeding because donor genotypes must be evaluated not only for disease reaction but also for agronomic suitability (Singh and Vatsa, 2009; Li *et al.*, 2019; Kuswanto, 2019) [33, 19, 17].

Seed yield per plant ranged from 3.71 g in KDS-1073 to 14.80 g in DSb-33. DSb-33 was the highest-yielding genotype and was followed by KDS-726, KDS-753, NRC-138 and KDS-1009. The genotype KDS-753 combined a highly resistant rust reaction with comparatively good seed yield, indicating that it may be a useful donor for resistance

breeding after further multilocation confirmation (Rodrigues *et al.*, 2015; Mahajan *et al.*, 2019; Dalla Lana *et al.*, 2015) [30, 20, 7]. The comparative performance of the top-yielding genotypes and the relationship between rust severity and seed yield are illustrated in Fig. 1 and Fig. 2.

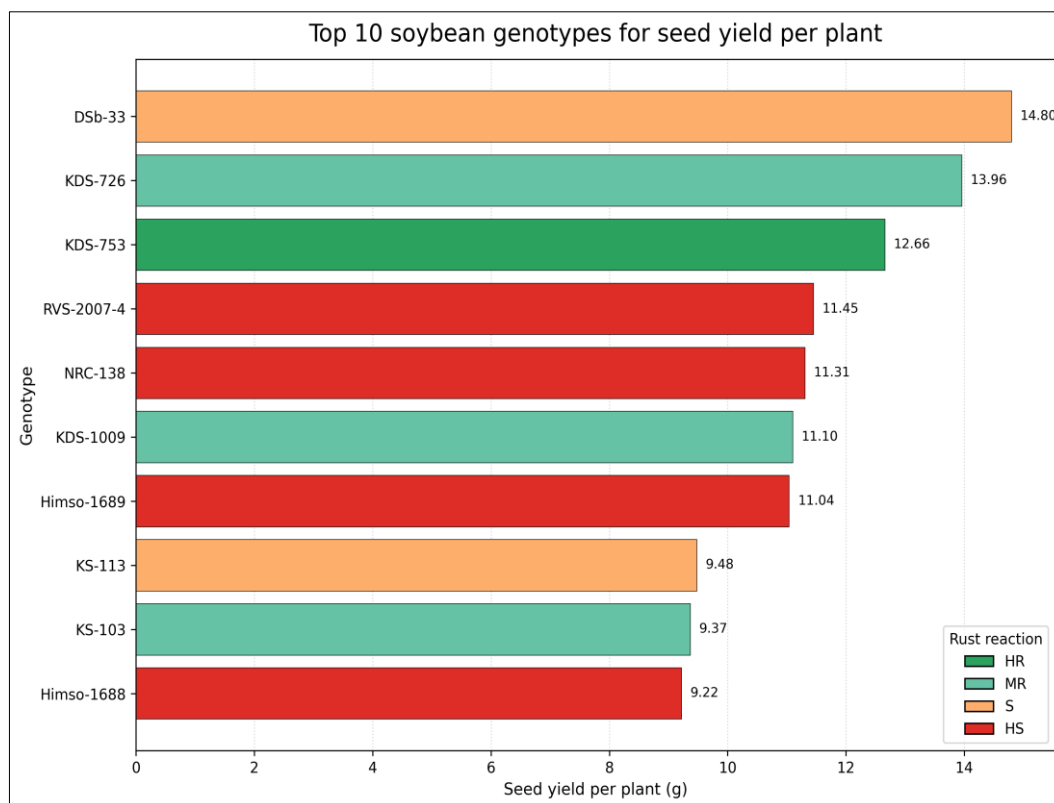


Fig 1: Top 10 soybean genotypes for seed yield per plant

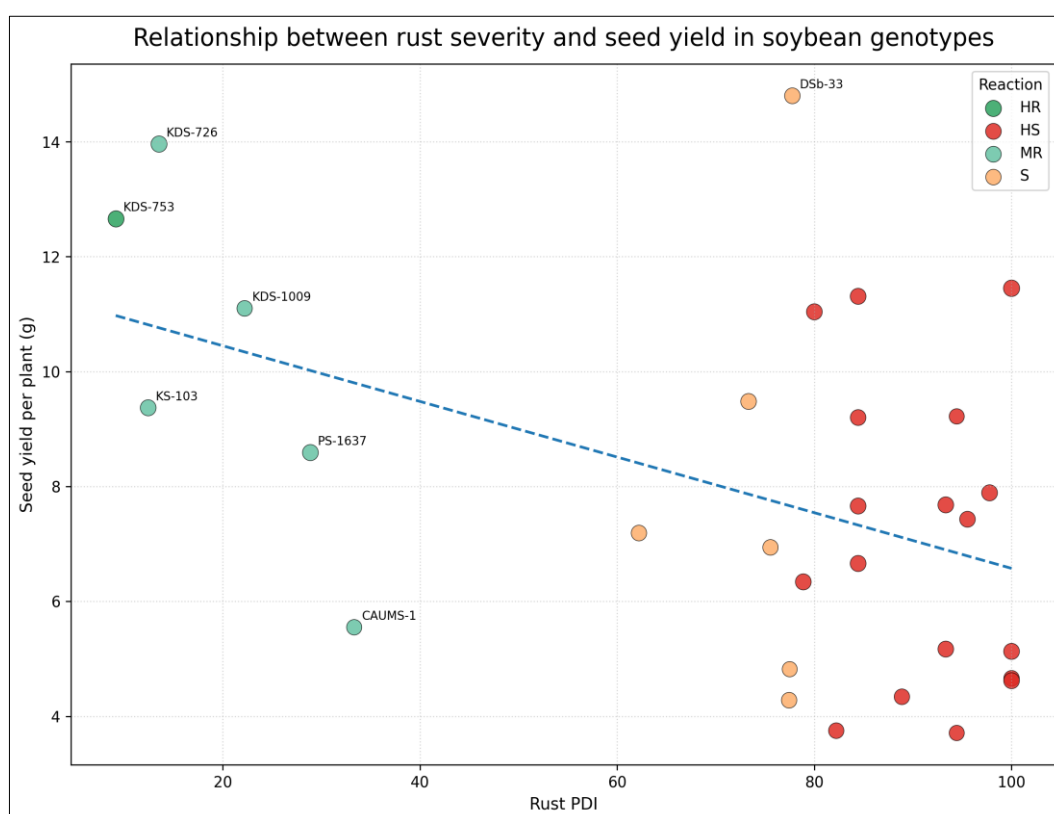


Fig 2: Relationship between rust severity (PDI) and seed yield per plant. Bubble size is proportional to SPAD value

Reaction of soybean genotypes to rust

The rust reaction of the 30 soybean genotypes revealed that none of the genotypes was absolutely resistant. KDS-753 recorded a highly resistant reaction with a PDI of 9.145. Five genotypes, namely CAUMS-1, KDS-1009, PS-1637,

KS-103 and KDS-726 showed moderately resistant reaction, whereas six genotypes were susceptible and the remaining genotypes were highly susceptible. The overall rust-response pattern is illustrated in Fig. 3 and Fig. 4.

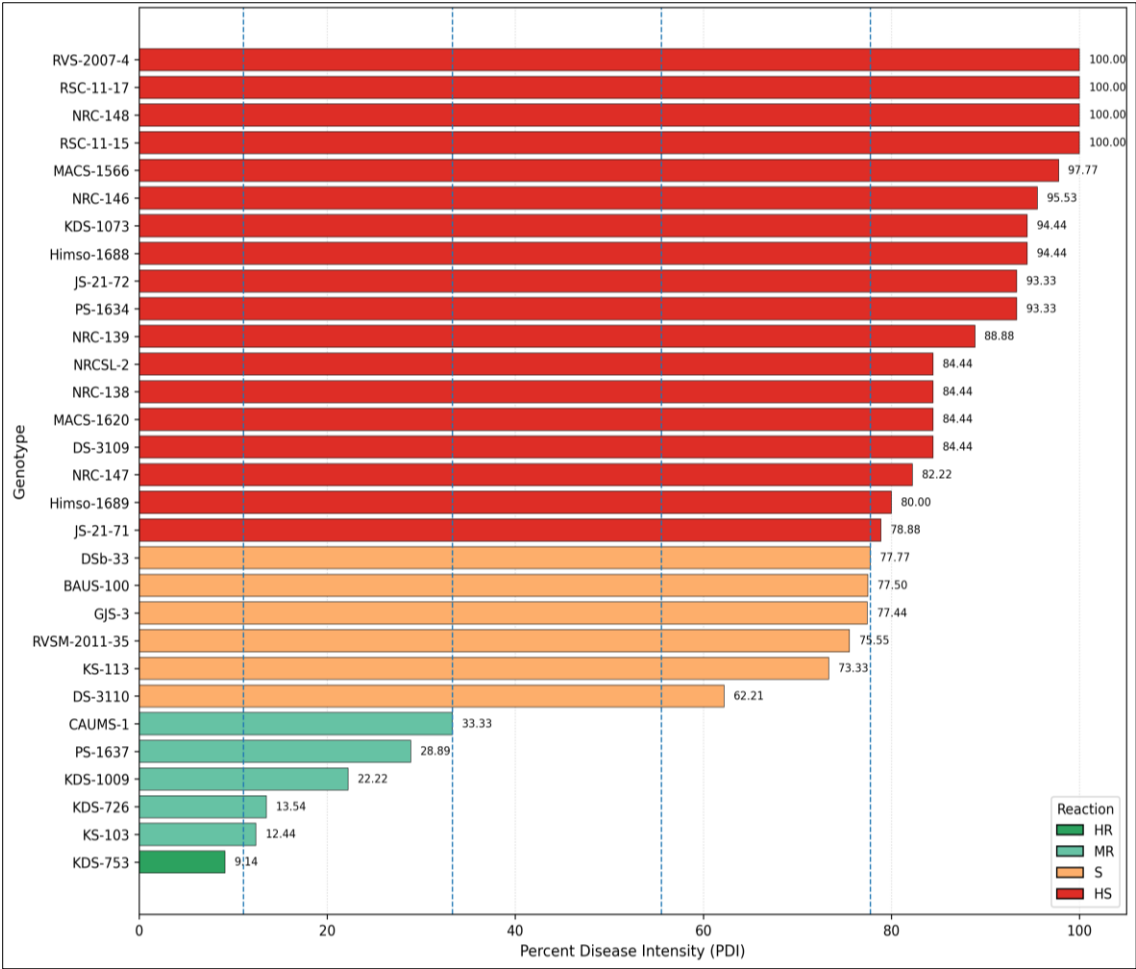


Fig 3: Soybean genotypes ranked by rust severity (PDI)

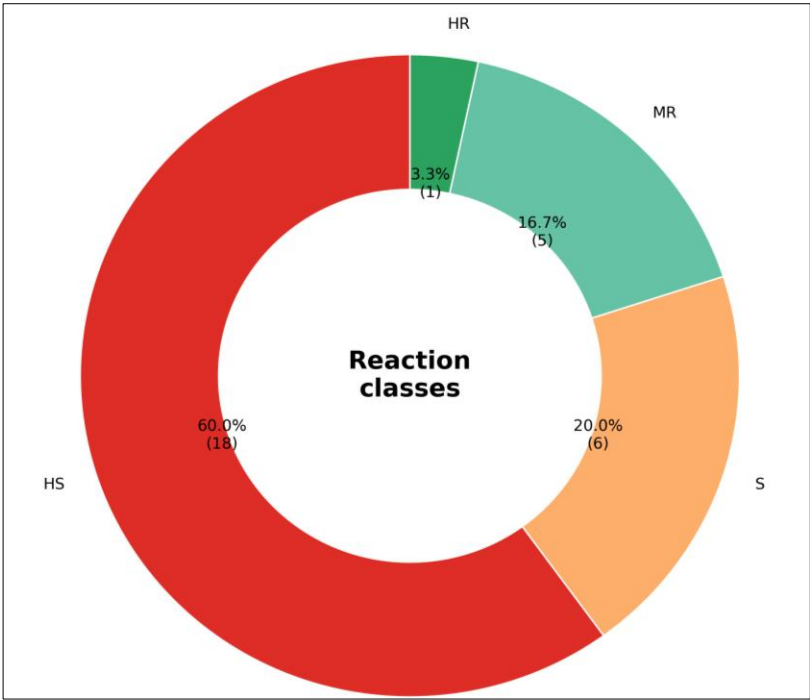


Fig 4: Distribution of soybean genotypes across rust-reaction classes

The observed separation of genotypes into highly resistant, moderately resistant, susceptible and highly susceptible groups is useful for breeding because phenotypic field screening can identify resistance sources for subsequent molecular confirmation, gene pyramiding and multi-location validation (Twizeyimana and Hartman, 2012; Childs *et al.*, 2018; Dormatey *et al.*, 2020; Saleem *et al.*, 2024) [35, 6, 9, 31].

The identification of KDS-753 as a highly resistant genotype and CAUMS-1, KDS-1009, PS-1637, KS-103 and KDS-726 as moderately resistant genotypes is in agreement with earlier reports that resistant and moderately resistant sources exist within soybean germplasm (Patil *et al.*, 2004; Pham *et al.*, 2009; Khot *et al.*, 2010; Kurundkar *et al.*, 2011) [26, 27, 15, 16]. However, most cultivated materials remain vulnerable to Asian soybean rust, which supports continued screening of germplasm for resistance breeding (Mahajan *et al.*, 2019; Godoy *et al.*, 2016) [20, 12].

The predominance of susceptible and highly susceptible reactions in the present study also supports the need for continuous resistance screening because *P. pachyrhizi* populations show pathogenic variation and can overcome single-source resistance (Bonde *et al.*, 2006; Twizeyimana and Hartman, 2012) [3, 35]. Therefore, identified resistant genotypes should be further evaluated across locations and seasons and integrated with molecular-marker analysis for durable resistance breeding (Whitham *et al.*, 2016; Godoy *et al.*, 2016; Childs *et al.*, 2018) [38, 12, 6].

The moderately resistant genotypes identified in this experiment may also be useful in breeding programmes where resistance is combined with yield and maturity traits (Singh and Vatsa, 2009; Rodrigues *et al.*, 2015) [33, 30]. Gene pyramiding and marker-assisted selection can help combine complementary resistance sources and improve the durability of rust resistance compared with reliance on a single donor genotype (Kawashima *et al.*, 2016; Dormatey *et al.*, 2020) [14, 9].

Biological and metabolite-based approaches have been explored for Asian soybean rust management, but host resistance remains a central strategy for reducing disease pressure and fungicide dependence (Hartman *et al.*, 2015; El-Hasan *et al.*, 2022; Reis, 2022) [13, 10, 29]. Therefore, field-based phenotypic screening such as the present investigation provides a practical foundation for subsequent molecular characterization and breeding use (Martinelli *et al.*, 2015; El-Hasan *et al.*, 2022) [21, 10].

Conclusion

The study demonstrated clear variation among 30 soybean genotypes for rust reaction and associated agronomic traits. Among the evaluated genotypes, KDS-753 showed a highly resistant reaction, while CAUMS-1, KS-103, KDS-726, KDS-1009 and PS-1637 showed moderately resistant reaction. These genotypes may be used as potential donor sources in soybean rust resistance breeding after confirmation under multilocation and multi-season testing. The identified resistant sources should also be subjected to molecular characterization and gene-pyramiding approaches for developing durable rust-resistant soybean cultivars.

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