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PERFORMANCE OF NEW SOYBEAN GENOTYPES ON PHYSICO CHEMICAL AND QUALITY PARAMETERS UNDER DIFFERENT ROW SPACING IN VERTISOL SOIL

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ABSTRACT

A field investigation entitled "Performance of new soybean genotypes under different row spacing in Vertisol soil" was carried out at the Regional Research Centre, Amravati, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during the *kharif* season of 2021–22. The experiment was conducted in a split plot design with four replications and twelve treatment combinations. The treatments consisted of two row spacings, namely S_1 (30 × 7 cm) and S_2 (45 × 5 cm), along with six soybean genotypes *viz*., NRC-165, NRC-152, HIMSO-1689, JS-2172, AMS-1001 (PDKV Yellow Gold) and AMS-100-39 (PDKV Amba). The gross and net plot sizes were 3.6 m × 6.0 m and 2.7 m × 5.4 m, respectively. The crop was sown according to the assigned treatments. Periodic observations on growth parameters and yield attributing characters were recorded in addition to yield data. The results of the study indicated that row spacing S_1 (30 × 7 cm), S_2 (45 × 5 cm) and genotype was recorded non-significantly in terms of physico-chemical properties pH, EC, OC and Bulk density. Among the genotypes, AMS-100-39 (PDKV Amba) recorded the highest quality parameters such as oil content and protein content and also recorded highest nitrogen, phosphorus and potassium uptake. Available NPK was recorded non-significantly in terms of row spacing and genotype.

***Key words*:** Genotypes, Row spacing, Vertisols, Physico-chemical, Quality parameters.

Introduction

Soybean (*Glycine max* (L.) Merrill) is a globally significant leguminous oilseed crop owing to its vital role in food security, nutritional enhancement and soil sustainability. The crop contributes substantially to agricultural systems through biological nitrogen fixation and high biomass production, which together improve soil fertility and organic matter dynamics. Because of its diverse end uses as a source of edible oil, high-quality plant protein and industrial raw material, soybean has gained prominence as a strategic crop for sustainable intensification of agriculture across varied agro-ecological regions (Hartman *et al*., 2011, Salvagiotti *et al*., 2008).

Worldwide, soybean is cultivated extensively and ranks among the leading sources of vegetable oil and protein. In India, soybean cultivation has expanded rapidly, particularly in central India, contributing significantly to oilseed production and farmers income. However, despite large-scale adoption, productivity levels remain below global averages, largely due to suboptimal agronomic practices and limited genotype-specific recommendations. This highlights the need for refining crop management strategies to enhance yield potential and economic returns under region-specific soil and climatic conditions (Board and Kahlon, 2013, Gaspar *et al*., 2017.

Plant population management, achieved through

appropriate row spacing, is a critical non-monetary input influencing canopy structure, light interception and resource use efficiency in soybean. Row spacing determines the extent of inter-plant competition and regulates canopy microclimate, thereby affecting photosynthetic activity and biomass partitioning. Narrow row spacing may intensify competition for moisture and nutrients, particularly under rainfed environments, which can negate potential yield benefits (Heitholt and Egli, 2005, Liu *et al*., 2008). In contrast, optimum row spacing promotes uniform plant distribution, efficient radiation uses and enhanced dry matter accumulation, resulting in improved yield performance (Carpenter and Board, 1997, Andrade *et al.,* 2019).

The response of soybean to row spacing is strongly genotype-dependent, as genotypes vary in growth habit, branching pattern and physiological efficiency. A planting geometry suitable for one genotype may not be optimal for another, emphasizing the importance of genotype-specific agronomic evaluation. Alterations in row spacing influence nutrient uptake patterns, soil moisture utilization and canopy light distribution, which collectively determine yield and economic viability (De Bruin and Pedersen, 2008, Bastidas *et al.,* 2008).

Vertisol soils, characterized by high clay content and distinct moisture retention behaviour, present unique challenges for soybean cultivation. Under such conditions, optimization of row spacing becomes particularly important to ensure efficient utilization of soil moisture and nutrients. Therefore, systematic evaluation of newly released soybean genotypes under varying row spacing in Vertisol soils is essential to identify the most productive and economically sustainable planting geometry.

Materials and Methods

A field experiment was conducted during the *kharif* season of 2021–22 at the Agronomy Farm of the Regional Research Centre, Amravati, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India. The experimental site was characterized by uniform and levelled topography with Vertisol soil. Initial soil analysis, carried out following standard procedures, revealed that the soil was low in available nitrogen (192 kg ha^{-1}), low in available phosphorus (16.50 kg ha^{-1}) and high in available potassium (325 kg ha^{-1}). The soil reaction was slightly alkaline with a pH of 7.75 and electrical conductivity of 0.35 dS m^{-1}, indicating non-saline conditions.

Geographically, the experimental location lies at 20°55’ 53.82” N latitude and 77°45’ 32.57” E longitude and falls under a semi-arid agro-climatic zone. Weekly meteorological data, including total rainfall, number of rainy days, maximum and minimum temperatures, relative humidity, evaporation and bright sunshine hours, were recorded throughout the crop growth period (June to December 2021) from the Agricultural Meteorological Observatory, P.D.K.V., Akola. During the entire cropping season, the experimental site received a total rainfall of 1139.8 mm, which supported normal crop establishment and growth.

The experiment comprised twelve treatment combinations involving two row spacings, namely S_1 (30 × 7 cm) and S_2(45 × 5 cm) and six soybean genotypes: NRC-165, NRC-152, HIMSO-1689, JS-2172, AMS-1001 (PDKV Yellow Gold) and AMS-100-39 (PDKV Amba). The treatments were evaluated using a split plot design with four replications, where row spacing was assigned to main plots and genotypes to sub-plots. The crop was sown as per the treatment specifications and all recommended agronomic practices, including fertilizer application, intercultural operations and plant protection measures, were uniformly followed to ensure optimal crop growth and to minimize experimental error. Soil pH and electrical conductivity were determined using standard pH meter and EC meter, respectively, following the methodology of Jackson (1973). Organic carbon was estimated using the Walkley-Black wet oxidation method. Available nitrogen was determined by the alkaline permanganate method (Subbiah and Asija, 1956). Available phosphorus was extracted using 0.5 M sodium bicarbonate (pH 8.5) and measured by the Olsen method (Olsen and Watanabe, 1965). Available potassium was determined by the neutral normal ammonium acetate extraction method using a flame photometer (Jackson, 1967). Total nitrogen in seed and straw was estimated by Kjeldahl’s method described by Jackson (1967), Phosphorus was estimated from di-acid extract by the Vanadomolybdate Phosphoric Acid yellow colourmethod using a UV based double beam spectrophotometer (Piper, 1966) and Total potassium estimated by di-acid extract using flame photometer method described by Piper (1966). The oil content of soybean was determined by ether extractions method (Soxhlet Extraction method) outlined by Sankaran (1966) and The protein content in seed was calculated by multiplying nitrogen content (%) of seed with the conversion factor of 6.25 as reported by Gupta *et al*., (1973).

Results and Discussion

Quatlity studies

From the data depicted in Table 1, found that effect of row spacing on oil and protein content (%) was found to be non-significant and the effect of oil and protein content on different genotypes was significantly

Table 1: Oil and Protein Content (%) of soybean as influenced by different treatment.

Treatment	Oil Content (%)	Protein Content (%)
Row spacing (cm)		
S_1 (30 × 7 cm)	20.31	40.83
S_2 (45 × 5 cm)	20.55	40.58
SE(m) ±	0.50	0.36
CD at 5 %	NS	NS
Genotypes		
G_1- NRC-165	19.55	38.80
G_2- NRC-152	20.00	40.58
G_3- HIMSO-1689	20.42	40.91
G_4- JS-2172	20.23	40.70
G_5- AMS-1001	20.65	41.32
G_6- AMS-100-39	21.68	41.90
SE(m) ±	0.50	0.52
CD at 5 %	1.47	1.54
Interaction (S × G)		
SE(m) ±	0.56	0.30
CD at 5 %	NS	NS
GM	20.43	40.70

influenced. The significantly highest oil and protein content was recorded in genotype G_6- AMS-100-39 (PDKV Amba) which was at par with genotype G_5- AMS-1001 (PDKV Yellow Gold), G_4- JS-2172 and genotype G3- HIMSO-1689. Genotype G1- NRC-165 recorded lowest oil and protein content among all other genotypes. The variation in oil content of genotypes might be due to genetic makeup of individual genotype. Similar result was reported by Khandit *et al.*, (1991), Pandya *et al.*, (2006) and Zarger *et al.*, (2011). Interactions between row spacings and genotypes had no significant effect on oil and protein content (%).

Soil pH, EC (dS m^{-1}), OC (g Kg^{-1}) and Bulk density (Mg m^{-3})

Available NPK After Harvest:

From the data presented in Table 3, it was revealed that effect of different row spacings and genotypes on available nitrogen, phosphorus and potassium (kg ha^{-1}) was found to be non-significant.

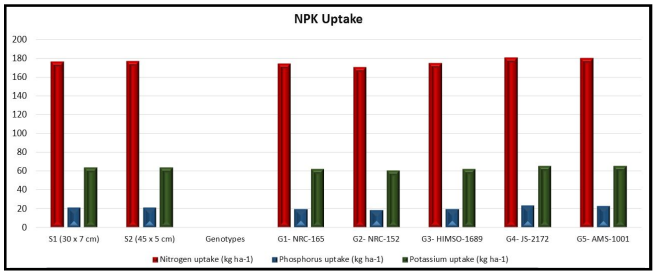


Fig. 1: Nitrogen, phosphorous and potassium uptake (kg ha^{-1}) by soybean as influenced by different treatment.

Table 2: pH, EC (dS m^{-1}), OC (g Kg^{-1}) and Bulk density (Mg m^{-3}) of soil after harvest as influenced by different treatments

Treatment	pH	EC	OC	BD
Row spacing (cm)				
S_1 (30 × 7 cm)	7.78	0.37	5.64	1.41
S_2 (45 × 5 cm)	7.81	0.36	5.68	1.44
SE(m) ±	**0.09**	**0.05**	**0.07**	**0.04**
CD at 5 %	**NS**	**NS**	**NS**	**NS**
Genotypes				
G_1- NRC-165	7.79	0.37	5.70	1.42
G_2- NRC-152	7.78	0.34	5.70	1.44
G_3- HIMSO-1689	7.63	0.35	5.68	1.46
G_4- JS-2172	7.88	0.36	5.45	1.40
G_5- AMS-1001	7.78	0.38	5.67	1.40
G_6- AMS-100-39	7.81	0.35	5.74	1.41
SE(m) ±	**0.07**	**0.07**	**0.15**	**0.03**
CD at 5 %	**NS**	**NS**	**NS**	**NS**
Interaction (S × G)				
SE(m) ±	**0.08**	**0.03**	**0.16**	**0.03**
CD at 5 %	**NS**	**NS**	**NS**	**NS**
GM	**7.79**	**0.36**	**5.66**	**1.42**
Initial status	**7.75**	**0.35**	**5.45**	**1.40**

EC: EC (dS m^{-1}); OC: OC (g Kg^{-1}); BD: Bulk Density (Mg m^{-3})

From the data presented in Table 2, it was revealed that effect of different row spacing and effect of different genotypes on pH, EC, OC and bulk density of experimental soil was found to be non-significant.

Available nitrogen, phosphorous and potassium (kg ha^{-1}):

Data regarding available nitrogen phosphorous and potassium kg ha^{-1} as influenced by different row spacing and genotypes are presented in Table 3 and Fig. 1. The mean available nitrogen 202.87, phosphorus 17.11 and potassium 331.48 kg ha^{-1}. Effect of different row spacing and effect of different genotypes on available nitrogen (kg ha^{-1}), phosphorus kg ha^{-1} and potassium kg ha^{-1} was found to be non-significant. The interaction effect between row spacing and genotypes on available nitrogen (kg ha^{-1}), phosphorus kg ha^{-1} and potassium kg ha^{-1} was found to be non-significant.

Nutrient Studies

Nitrogen, phosphorous and potassium Uptake (kg ha^{-1}):

Data regarding seed, straw and total nitrogen, phosphorous and potassium uptake kg ha^{-1} as influenced by different row spacing and genotypes are presented in Table 4. The mean seed, straw and total uptake were recorded as 143.01, 34.22 and 177.26 kg ha^{-1} for nitrogen; 11.79, 9.02 and 20.81 kg ha^{-1} for phosphorus; and 29.84, 34.11 and 63.96 kg ha^{-1} for potassium, respectively.

Table 3: Available nitrogen, phosphorus and potassium (kg ha^{-1}) in soil after harvest as influenced by different treatments.

Treatment	Available N(kg ha^{-1})	Available P(kg ha^{-1})	Available K(kg ha^{-1})
Row spacing (cm)			
S_1 (30 x 7 cm)	201.91	16.88	330.54
S_2 (45 x 5 cm)	203.84	17.34	332.42
SE(m) ±	**2.40**	**0.45**	**1.92**
CD at 5 %	**NS**	**NS**	**NS**
Genotypes			
G_1- NRC-165	202.65	17.14	331.76
G_2- NRC-152	202.49	16.98	331.91
G_3- HIMSO-1689	201.91	16.93	330.14
G_4- JS-2172	203.48	17.05	330.78
G_5- AMS-1001	202.79	16.99	331.32
G_6- AMS-100-39	204.37	17.53	332.96
SE(m) ±	**4.30**	**0.32**	**2.46**
CD at 5 %	**NS**	**NS**	**NS**
Interaction (S × G)			
SE(m) ±	**1.89**	**0.30**	**1.58**
CD at 5 %	**NS**	**NS**	**NS**
GM	**202.87**	**17.11**	**331.48**
Initial status	**192**	**16.50**	**325**

Nitrogen uptake (kg ha^{-1}):

It is revealed that seed and straw nitrogen uptake kg ha^{-1} were significantly influenced due to different row spacing. Row spacing S_2 (45 × 5 cm) recorded significantly higher seed nitrogen uptake than S_1 (30 × 7 cm) due to higher seed yield, whereas produced higher straw yield and resulting straw N uptake. However, row spacing had a non-significant effect on total N uptake, consistent with Sikka *et al*., (2018). Genotypes significantly influenced all N uptake parameters: G_6 (AMS-100-39 / PDKV Amba) registered the highest seed and total N uptake (statistically at par with G_4-JS-2172 and G_5-AMS-1001 for total uptake), driven by its superior seed yield. G_4 (JS-2172) achieved the highest straw N uptake, while G_2 (NRC-152) recorded the lowest seed and straw uptake. The interaction effect between row spacing and genotypes was non-significant for seed, straw and total N uptake.

Phosphorus uptake (kg ha^{-1}):

Row spacing and genotype significantly influenced individual phosphorus (P) uptake components, whereas total P uptake was influenced only by genotype, with no significant spacing genotype interaction observed across any parameter. Seed P uptake reached its maximum in the S_2 (45 × 5 cm) row spacing owing to superior seed yield, aligning with the findings of Sikka *et al*., (2018), while the lowest uptake was recorded in S_1 (30 × 7 cm). Conversely, straw P uptake was highest in S_1 due to greater straw biomass production. Among the evaluated genotypes, G_6 (AMS-100-39 / PDKV Amba) exhibited the highest seed and total P uptake- driven by its significantly superior seed yield and remained statistically at par with G_5 (AMS-1001 / PDKV Yellow Gold) for seed P uptake and with both G_4 (JS-2172) and G_5 for total P uptake. Straw P uptake was highest in G_4 (at par with G_5) and lowest in G_2 (NRC-152).

Table 4: Nitrogen, phosphorous and potassium uptake (kg ha^{-1}) by soybean as influenced by different treatment.

Treatment	Nitrogen uptake (kg ha^{-1})			Phosphorus uptake (kg ha^{-1})			Potassium uptake (kg ha^{-1})		
	Seed	Straw	Total	Seed	Straw	Total	Seed	Straw	Total
Row spacing (cm)									
S1 (30 × 7 cm)	141.88	35.15	177.03	11.28	9.43	20.71	29.33	34.62	63.95
S2 (45 × 5 cm)	144.15	33.30	177.50	12.30	8.62	20.92	30.36	33.61	63.97
SE(m) ±	**0.64**	**0.58**	**1.35**	**0.28**	**0.26**	**1.07**	**0.29**	**0.05**	**0.36**
CD at 5 %	**1.89**	**1.72**	**NS**	**0.82**	**0.78**	**NS**	**0.86**	**0.15**	**NS**
Genotypes									
G1- NRC-165	142.15	32.55	174.73	11.18	8.18	19.37	29.35	8.18	62.58
G2- NRC-152	138.81	32.11	170.93	10.21	7.62	17.85	27.87	7.62	60.53
G3- HIMSO-1689	141.41	33.70	175.18	10.56	8.65	19.21	28.49	8.65	62.27
G4- JS-2172	143.96	37.07	181.09	11.96	10.90	22.86	30.02	10.90	65.69
G5- AMS-1001	144.98	35.34	180.42	12.82	9.61	22.42	30.77	9.61	65.59
G6- AMS-100-39	146.75	34.53	181.24	13.99	9.18	23.18	32.54	9.18	67.13
SE(m) ±	**1.31**	**0.59**	**1.21**	**0.64**	**0.30**	**0.77**	**0.51**	**0.30**	**0.88**
CD at 5 %	**3.87**	**1.73**	**3.58**	**1.89**	**1.41**	**2.26**	**1.50**	**1.41**	**2.58**
Interaction (S × G)									
SE(m) ±	**1.14**	**0.50**	**0.78**	**0.33**	**0.27**	**0.64**	0.33	0.27	0.83
CD at 5 %	**NS**	**NS**	**NS**	**NS**	**NS**	**NS**	NS	NS	NS
GM	**143.01**	**34.22**	**177.26**	**11.79**	**9.02**	**20.81**	29.84	9.02	63.96

Potassium uptake (kg ha^{-1}):

Row spacing and genotype significantly influenced seed and straw potassium (K) uptake, whereas total K uptake was affected only by genotype, with no significant spacing genotype interaction. Seed K uptake was significantly higher under row spacing S_2 (45 × 5 cm) compared to S_1 (30 × 7 cm), driven primarily by superior seed yield. Conversely, straw K uptake was greater in S_1 due to higher straw biomass accumulation. Among the evaluated genotypes, G_6 (AMS-100-39 / PDKV Amba) recorded the highest seed and total K uptake owing to its significantly higher seed yield with total K uptake remaining statistically at par with G_4 (JS-2172) and G_5 (AMS-1001 / PDKV Yellow Gold), while G_5 followed G_6 for seed K uptake. Straw K uptake was highest in , which was statistically at par with both G_5 and G_6. Interaction effect between row spacing and genotypes on seed, straw and total potassium uptake kg ha^{-1} were found to be non-significant.

Conclusions

The soil physico-chemical properties were non-significantly influenced by varying row spacings and genotype selections. However, significant variations were observed regarding nutritional uptake and quality attributes. Among the evaluated treatments, the soybean genotype AMS-100-39 (PDKV Amba) exhibited superior performance, demonstrating enhanced quality parameters alongside significantly higher nitrogen (N), phosphorus (P) and potassium (K) uptake. Furthermore, a closer row spacing of 45 × 5 cm (S_2) optimized nutrient removal efficiency, yielding the highest uptake values for N, P and K. Consequently, combining the high-yielding genotype AMS-100-39 with an optimal planting geometry of 45 × 5 cm (S_2) can be recommended to maximize nutrient uptake and crop quality without compromising the fundamental soil physico-chemical characteristics.

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