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Screening of groundnut (*Arachis hypogea* L.) genotypes for yield performance in three agro-ecological zones of Tanzania

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Abstract

Groundnut is one of the most important oilseed crops and the most important food crop in the world. It is one of the four economically important oilseeds grown in Tanzania. Groundnut is normally produced by small-scale farmers, particularly women, as leverage crop for both food and cash crops in all Tanzanian agricultural and ecological zones. However, its production is constrained by several biotic and abiotic factors. The presence of environmental effects on the genotype performance (G*E) is one of the major constraints of production. This study sought to evaluate and identify widely adapted and high-yielding genotypes in three agro-ecological zones of Tanzania. A total of sixteen selected groundnut genotypes were evaluated under RCBD with three replications. Data on morphological traits, yield and yield components were collected and analysed. Results revealed the differential performance of the tested genotypes ($p < 0.001$). Three genotypes ICGIL 17113, NALX-22-18 and ICGV-SM 16528 have shown consistence performance across test environments that guaranteed the existence of potential to revert and combat both nutritional and better yield. The highest average yield was observed in genotype ICGV-SM 16528 having 1582 kg/ha while the lowest average yield was observed in genotype ICGV- SM 05534 having 733.05 kg/ha. Among the three genotypes, genotype ICGV-SM 16528 has shown consistent good performance across environments. As an oilseed crop, the nation may utilize those opportunities to solve the problem of the cooking oil insufficiency and nutritional issues of our communities since groundnut has important nutrients required for normal human health. Evaluated genotypes along with existing ones should be integrated in groundnut farming systems to enhance the production efficiency and the livelihoods of farming community. The breeders will use these findings to explore more genetic base of groundnuts for further improvement.

Key words: *Groundnut; genotypes; kernel yield; multi-environmental trial; experimental; genotype x environment interaction*

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Introduction

Groundnut or peanut (*Arachis hypogea* L.) is a self-pollinated species which belong to the Fabaceae family and subfamily Papilionaceae (Poojitha *et al.*, 2024). It is ranked the third most important source of vegetable protein, fourth source of edible oil and thirteenth most significant food crop globally (Dabalo *et al.*, 2024; N'Gbesso *et al.*, 2024). Groundnut provide excellent edible oil (48–50%) and easily digested protein (26–28%) (Bhattacharjee and Biswas, 2019; Das *et al.*, 2023). It provides approximately 5.6 calories per raw kernel and 5.8 calories per roasted kernel (Sendekie *et al.*, 2020). Groundnut provides almost half of the 13 essential vitamins (E, K, and B) and other essential minerals such as Potassium, Calcium, Magnesium and Zinc needed for normal human growth (Arya *et al.*, 2016; Nasehi, 2018). Groundnut significantly supports marginal farmers by providing them with income and nutritional food (Mwalongo *et al.*, 2020; Kotu *et al.*, 2022). The seeds can be eaten raw, roasted, boiled, or processed to make other food stuffs, confectionary products, and can also be grounded to produce peanut butter (Kongola, 2018). According to Katundu *et al.* (2013) and Karunia, (2016) 37% of groundnut produced is used to make confections, 12% to make seeds, and 50% of groundnut produce is used globally for oil extraction. After oil extraction, the residuals are utilized as a protein supplement in animal feed. As a legume, the crop is used in soil improvement as it fixes nitrogen in the soils (Witcombe and Tiemann, 2022).

In Sab-Saharan Africa (SSA), Nigeria is the largest producer followed by Sudan and the United Republic of Tanzania is the third in groundnut production (Shaibu *et al.*, 2021). In Tanzania, groundnut is cultivated mainly by smallholder farmer communities (Daudi *et al.*, 2018; Das *et al.*, 2023). Groundnut yields in Tanzania are at 0.72 t/ha lower than the average potential yield which range between 2 and 2.5 t/ha (Kongola, 2018; Daudi *et al.*, 2021).

Like other food crops, groundnut is affected by abiotic and biotic factors that constrain the production and productivity (Daudi *et al.*, 2018). These include uneven rainfall distribution, incidences of diseases and pests, a lack of improved and high-yielding varieties, low soil fertility, aflatoxin contamination, and poor agronomic practices (Chintu, 2013; Martin *et al.*, 2023). Apart from aforementioned constrains, two-thirds of the production is under rain-fed systems in the semi-arid tropics. In this area rainfall is usually erratic and insufficient and annual production fluctuates as a result of the genotypes' sensitivity to various environmental factors (Dolinassou *et al.*, 2016). The heterogeneous nature of the environments causes the performance of various groundnut genotypes to differ both within and between environments. Ngirazi *et al.* (2017) reported that higher G*E interaction is usually expected to be a result of wide environmental variations. These kinds of interactions lead to one genotype yielding more in some environments than the others. There is limited knowledge on the level of interactions in the selection of genotypes across various environments (Gebeyehu, 2019). Although a number of major genes control yield traits, environmental factors frequently influence genotype performance (Dolinassou *et al.*, 2016; Gebeyehu, (2019). These call for testing genotypes in different locations to determine response of genotypes to environmental factors such as soil fertility, temperature, rainfall and humidity (NNgirazi *et al.*, 2017). According to Dolinassou *et al.* (2016) genotype is considered more adaptive or stable if it has a high mean yield but a low degree of fluctuation in yielding ability when grown in diverse environments. Quantifying and understanding the pattern and magnitude of GEI and stability is crucial.

Therefore, this study is designed to identify groundnut genotypes with high yield under different locations, identify groundnut genotypes with wide adaptations (stability) in three agro-ecological zones and ranking the suitability of environments based on the relative performance a given genotypes for guiding selection of genotypes in different agro ecologies for suitable high production.

Materials and methods

Description of test locations

Experiments were conducted at Naliendele, Makutupora, and Mwanhala agricultural research institutes of the Tanzania Agricultural Research Institute (TARI) during 2023/2024 cropping season. These agricultural research institutes are found in three different agro ecological zones of Tanzania, Southern zone (Mtwara), Central zone (Dodoma) and Western zone (Tabora) where farmers grow groundnut in large amount. Naliendele is located at 10° 22′ 20″S, 40° 10′ 34″E and 135 metres above sea level, it has a sandy loam soil with 4.5 pH, mean temperature ranging from 24.3^{0}C – 27^{0}C and mean rainfall of 820 – 1245 mm. Makutupora is located at 35^o, 46.093'E, 05^o, 58.669'S and 1 070 metres above sea level and has a pH of 5.69, mean temperature of 15^{0}C – 32^{0}C and rainfall of 400 – 660 mm and Mwanhala is located at 4^{0}35′94S, 33^{0}14′2^{0}E and 1300 metres above sea level and it has sandy loam soil, mean temperature of 28^{0}C -30^{0}C and rainfall of 650 – 1200 mm.

Groundnut genotypes

Sixteen (16) groundnut genotypes were evaluated for kernel yield and yield components. Thirteen genotypes were introduced from the International Crop Research Institute for the Semi-Arid Tropics (ICRISAT) (ICGV- SM 16514, ICGV- SM 16613, ICGV- SM 16579, ICGV- SM 16645, ICGIL 14466, ICGV- SM 16618, ICGV- SM 05534, ICGV- SM 16528, ICGV– SM 16630, ICGIL 17113, ICGV– SM 16524, ICGV – SM 16584 and ICGV- SM 16580 which is currently at advanced stage, one unreleased (advanced line NALX-22-18) and two (MANGAKA 2009 and MNANJE 2009) released varieties from the Tanzania Agricultural Research Institute (TARI), which were used as a standard check. The selected genotypes were improved for high yields, resistance to fungal diseases and aphids.

Field trial details

The field experiments at all three test locations (Naliendele, Makutopora and Mwanhala) were laid out using Randomized Complete Block Design (RCBD) with three replications, each replication consisted sixteen plots. Each groundnut genotype was planted on a plot of two rows with four meters long. The inter-row spacing was 50 cm, with an intra-row spacing of 10 cm one seed per hill. The total plot size for each genotype was 4.0 m^2. Hand- hoe weeding was done twice before and after flowering and fertilizer application was done before planting 5 g/hill. Fertilizer used was DAP 40 Pkg/ha at recommended rate. All agronomic practices for groundnut productions were followed as recommended by NARI, (2001). Trial at TARI-Naliendele was establishment in January 2024 and harvested in May 2024, at TARI-Makutupora it was established in December 2023 and harvested in April 2024, and at Mwanhala it was established in November 2023 and harvested in March 2024.

Data collection

The data were collected from randomly taken sample plants following the procedures described by IBPGR and ICRISAT (1992).

Phenological data

Days to 50% emergence was recorded as the number of days from sowing to the date when 50% of the plants in a plot emerged from the soil. Days to 50% flowering was recorded as the number of days from the date of 50% emergence to the date when 50% of the plants in a plot produced at least one flower. Days to maturity was recorded from the number of days from the date of emergence to the stage when 90% of the plants in a plot have reached physiological maturity.

Yield and yield component

Total number of pods per plant was recorded as the total number of pods per plant from five randomly selected plants per plot then averaged. Number of mature pods per plant was recorded when all fully filled and sound pods were recognized and five randomly selected plants per plot were averaged. Number of seeds per pod was obtained by calculating the mean numbers of seeds obtained from five plants selected to determine the number of pods per plant from each plot.

Hundred seed weight (g) was recorded by counting a hundred seeds randomly from a bulk of shelled seeds and then weighing using a sensitive balance. Pod yield (kg/ha) was obtained by weighing the yield from the plot after being sundried and then converted into kilograms per hectare (kg ha-1). This was arrived by using the formula that Pod yield (kg ha-1) = (pod weight (kg plot-1))/ (plot size (m^2)) × 10,000 m^2. Shelling percentage (%) was calculated by taking a sample of about 200 g of mature pods per plot randomly. This was then calculated as follows:

SP = SYx 100, where SP = shelling percentage, SY = seed yield, and PY = pod yield weight (200 g). Kernel yield (kg/ha) was obtained by taking pod yield (kg/ha) x shelling/100, and kernel yield was taken into consideration for statistical analysis in this study.

Statistical analysis

The data for Analysis of variance (ANOVA) on yield and yield components from each test location and combined across the locations was performed using the GenStat 15th edition statistical package to determine significant variability among genotypes for yield and yield components. We carried out the mean separation using the least significant difference (LSD at 0.05). Olanrewaju *et al.* (2021) and Kona *et al.*, (2024) indicated that in order to determine the effects of genotypes, environments, and their interactions and to identify stable high yielder genotypes, GGE biplot is employed; therefore, the GGE biplot methodology was used to analyze the multi-location genotype yield trial data to evaluate the grain yield stability and identify superior genotypes

Results

Mean Performance of Groundnut Genotypes Kernel Yield Across Locations

Kernel yield analysis of the tested groundnut genotypes revealed significant differences among various locations. A highly significant difference ($P < 0.001$) was observed among genotypes in the Makutupora testing site, but there were no significant differences found in any other locations (Table 1). Tests on genotypes show that the Makutupora site had the best kernel yields. Genotype ICGV-SM 16528 produced 3070.61 kg/ha in the most intense genetic gain sense, obtaining an excellent result. On the opposite end, ICGV-SM 05534 yielded only 1394.75 kg per hectare. The average yield for all genotypes tested at Makutupora was 2232.68 kg/ha, indicating a generally favorable environment for growing groundnuts. For the performance of genotypes varied significantly at Mwanhala, ICGV-SM 16528 showed a high yield of 1404.54 kg/ha, while the lowest yield was recorded for ICGV-SM 16618, which only gave 486.08 kg/ha. The mean yield for all genotypes at Mwanhala was significantly less than at Makutupora, averaging only 945.31 kg/ha. Naliendele had the lowest average yield performance of the three sites. The highest yield recorded was for ICGV-SM 16584, producing 477.65 kg/ha, while ICGV-SM 16630 yielded the least at 54.99 kg/ha, reflecting the challenging growing conditions at this site. The average yield for all tested genotypes at Naliendele was only 266.32 kg/ha. The average yield across all tested genotypes at Naliendele was 266.32 kg/ha, which, despite being lower than Makutupora and Mwanhala.

Table 1.

Mean kernel yield (kg/ha) of sixteen genotypes evaluated over three locations

Genotype	Genotype code	Naliendele	Makutopora	Mwanhala	Overall mean
ICGV-SM16514	G1	329.51 a	1838.24 abc	687.04 a	951.60 abc
ICGV-SM 16613	G2	378.71 a	2065.33 abcd	1105.98 a	1183.34 abcde
ICGV-SM 16579	G3	59.14 a	1688.11 ab	687.25 a	811.50 a
NALX-22-18	G4	**332.96 a**	**3014.67 f**	**1053.64 a**	**1467.09de**
ICGV-SM 16645	G5	304.79 a	2432.10b cdef	898.23 a	1211.71 abcde
MANGAKA 2009	G6	319.72 a	2290.19 bcdf	993.01 a	1200.97 abcde
ICGIL 14466	G7	171.59 a	2683.66 def	603.79 a	1153.02 abcde
ICGV-SM 16618	G8	57.49 a	2009.22 abcd	486.08 a	850.93 ab
ICGV-SM 05534	G9	159.48 a	1394.75 a	644.91 a	**733.05 a**
ICGV-SM 16528	G10	272.98 a	**3070.61 f**	**1404.54 a**	**1582.71 e**
ICGV-SM 16630	G11	54.99 a	2283.23 bcdf	757.88 a	1032.04 abcd
MNANJE 2009	G12	195.97 a	2628.09 cdef	807.68 a	1210.58 abcde
ICGIL 17113	G13	196.35 a	**2948.62 ef**	926.34 a	**1357.11 cde**
ICGV-SM 16524	G14	62.05 a	2304.47 bcdf	998.92 a	1121.81 abcde
ICGV-SM 16584	G15	**477.65 a**	2297.41 bcdf	**1187.21 a**	**1320.76 bcde**
ICGV-SM 16580	G16	114.99 a	2157.37 abcde	878.55 a	1050.30 abcd
Means		218.02	2319.13	882.57	1139.91
LSD at 5%		388.796	455.568	605.496	276.16
CV%		24.9	13.7	1.8	25.9
P-value		P < 0.523	***	P < 0.25	***

Where ***= highly significant difference at $p<0.001$, CV (%) = coefficient of variation, LSD = Least significance difference and means within column followed by same letter(s) are not significantly different at 5 % according to LSD.

Mean Grain Yield Across Locations

The overall mean grain yield over the three testing sites varied significantly among genotypes. The mean yields ranged from a low of 733.05 kg/ha for ICGV-SM 05534 to a high of 1582.71 kg/ha for ICGV-SM 16528, with a grand mean yield of 1157.88 kg/ha across all genotypes. Out of the sixteen genotypes evaluated, eight genotypes, including ICGV-SM 16613, MANGAKA 2009, ICGV-SM 16645, ICGV-SM 16584, ICGIL 17113, NALX-22-18, and ICGV-SM 16528, achieved yields above the grand mean, indicating their potential as superior cultivars. The remaining eight genotypes fell below this average yield. Among the top performers, four genotypes ICGV-SM 16584, ICGIL 17113, NALX-22-18, and ICGV-SM 16528 produced the highest average kernel yields, ranging from 1320.76 kg/ha to 1582.71 kg/ha across the three locations. These four genotypes had significant yield advantages over the best standard checks, Mangaka 2009 and Mnanje 2009.

Genotype by Environment Interaction (GEI)

The combined analysis of variance results show that G, E, and GEI are significant ($p < 0.001$) for kernel yield among 16 groundnut genotypes (Table 2). The highest average kernel yield was found at Makutupora (3070.61 kg/ha), while the lowest average kernel yield was recorded at Naliendele (54.99 kg/ha). These results indicate that there was substantial variation in kernel yield performance from site to site of study, demonstrating a lack of meaningful consistency in genotype performance. The highest means for kernel yields were obtained across locations by genotypes such as ICGV-SM 16528, NALX-22-18, ICGIL 17113, and ICGV-SM 16584, while ICGV-SM 05534, ICGV-SM 16579, and ICGV-SM 16618 consistently gave the lowest yields. This variability indicates a wide genetic variance among the tested genotypes, influenced by diverse environmental conditions that complicate genotype selection across the testing sites.

Table 2.

Summary of analysis of variance of the G × E interaction for kernel yield among sixteen (16) groundnut genotypes evaluated across three locations.

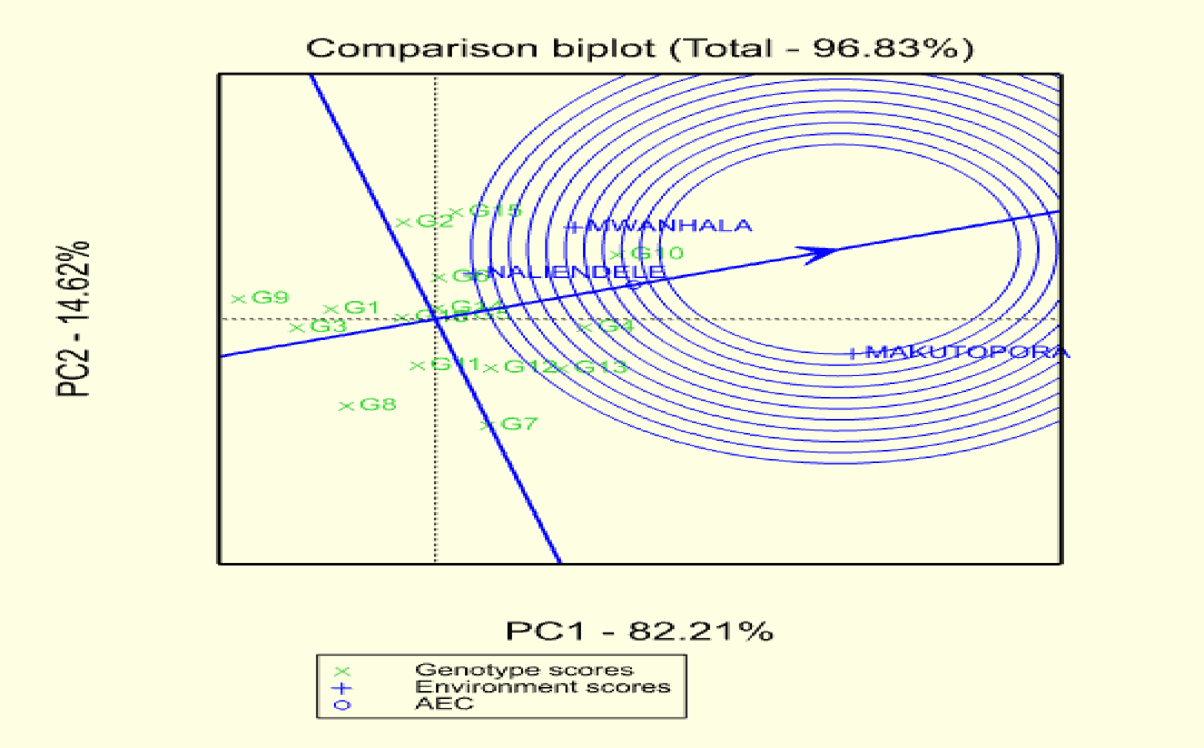
Location (L)	2	110719694***	55359847***
Replication	2	827613	413806
Genotypes (G)	15	7301558***	486771***
Interaction (L×G)	30	6136419***	204547***
Residual	90	7825660	86952

Note: *, ** and *** represent significant differences at 0.05, 0.01 and 0.001 probability levels, respectively.

Genotype and genotype by environment (GGE)—Biplot analysis

The GGE biplot analysis was studied in order to distinguish genotype and genotype by environment interaction. The first two principal components (PC1 and PC2) accounted for 82.21% and 14.62% of the variation in kernel yield, respectively, leading to a cumulative explanation of 96.83% (Fig. 1). This significant percentage indicates a strong and complex GEI in the multi-environment trial performance. The GGE biplot is an effective tool for identifying ideal genotypes, ideal environments, and genotypes that are best adapted to specific environments. It gives a clear picture of how one genotype compares to the ideal, which is characterized by high mean yield and stability across locations. Generally, the detailed results highlight the variability in performance among groundnut genotypes across different locations, emphasizing the importance of multi-location trials and the influence of environmental factors on yield outcomes. The identification of high-performing genotypes provides valuable information for breeding programs aimed at developing resilient and adaptable groundnut varieties.

Figure 1.
The average-environment coordination (AEC) view to show the mean performance and stability of the genotypes.



Discussion

The findings from this study greatly underscore how a vital role is played by genotype and environment interaction (GEI) in the performance of groundnut genotypes in different agro-geological environments. The GEI result is highly significant ($p < 0.001$), indicating that the yield of groundnut genotypes is influenced not only by their genetic makeup but also by the fact that the yield for any groundnut genotype is the product of particular environmental conditions that array it. This is consistent with previous studies by Ngirazi *et al.* (2017) and Open *et al.* (2024) which have highlighted the complexities and consequences of environmental effect on performance of groundnut genotypes. Differences from one place to another in kernel yields point to the great influence of environmental factors such as soil type, rain, temperature, humidity, and management practices upon plant growth and harvest. For example, the highest yield recorded at Makutupora (3070.61 kg/ha) compared with the lowest ever at Naliendele (54.99 kg/ha) demonstrates how the actual growing conditions in each case can affect genotype performance. This variability stresses the need for multi-location trials to discover which genotypes can accept diverse environmental conditions.

The results also revealed that some genotypes, such as ICGV-SM 16528, NALX-22-18, and ICGIL 17113, were consistently superior with high mean performance and stability over different environmental locations. These genotypes both exceeded the grand mean of 1157.88 kg/ha and showed superiority over standard checks (Mangaka 2009 and Mnanje 2009). Such findings align with the study of Okori *et al.* (2019), who observed higher mean performance of test genotypes than standard checks. The capacity of these genotypes to show high yield stability over various environments is important for breeding programs that are focused on developing varieties that can adapt to various growing conditions. In contrast, other genotypes, such as ICGV-SM 05534 and ICGV-SM 16618 recorded well below average results in all environments. This suggests that these genotypes may not be suitable for cultivation in the environments under test and other related environments. Ngirazi *et al.* (2017) and Tesfaye *et al.* (2022) highlight the importance of testing genotypes, and it shows why genotypes must be tested for both their mean performance and their stability across environments.

The information learned from GEI can help in guiding breeding strategies that concentrate on selecting genotypes featuring desirable traits that can stand up to environmental fluctuations. The importance of field trials is further illustrated by the existence of cross-over genotype-environment interaction, genotypes had different rankings at each location. For example, ICGV-SM 16524 showed high yield at Makutupora but ranked low at Naliendele and Mwanhala. Such frequent irregularities highlight the need for comprehensive testing over a range of environments so as to ensure that selected genotypes are robust and adaptable. Research by Endale *et al.* (2022) indicates that without multi-location trials it is difficult to identify superior genotypes that perform consistently well.

The GGE biplot technique used in this study can give a good measure of how well different groundnut genotypes perform when grown under ideal conditions. A strong GEI would explain that two principal components accounted for a high percentage of the variability (96.83%), which indicates a strong and complex genotype by environment interaction (GEI) in the multi-environment yield trial data, suggesting therefore it captures much of the underlying variability in genotype performance. Mullualem *et al*. (2024) reported similar results. In the GGE biplot, identifying ICGV-SM 16528 as the most suitable genotype, this example illustrates just how useful this tool can be used for breeding programs. Through using GGE biplots, breeders are able not only to see how different genotypes perform in many environments but also to simultaneously capture high yield potential with reasonable stability. Furthermore, understanding the specific characteristics of each location, including soil fertility, climate, and management practices, can significantly enhance the selection process for stable genotypes. As noted by Egea-Gilabert *et al.* (2021) and Mullualem *et al*. (2024), the choice of testing environments plays a crucial role in the success of breeding programs and can influence the identification of genotypes that are well-adapted to specific conditions.

Conclusions and recommendations

The results of this study show that both environmental factors and genotype are critical for breeding programs. The present significant GEI indicates that good genotype selection needs to have a clear understanding of how genotypes perform across different environments. With multi-location testing combined with analytical tools such as GGE biplots, superior high-yielding genotypes may be identified that are at the same time very stable and well adapted to differing environments. The analysis identified three genotypes, ICGIL 17113, NALX-22-18, and ICGV-SM 16528, as stable and high yielders for kernel yield with 1357.11 kg/ha, 1467.09 kg/ha, and 1582.71 kg/ha values, from which ICGV-SM 16528 was the most desirable genotype. Therefore, these three advanced genotypes are recommended to be included in the breeding program. Further, repeating the study for subsequent years and conducting molecular characterization is recommended. Also assessing additional quality parameters such as oil content, protein content, and other important nutritional contents for release as new varieties, hence increasing the variety portfolio of this oilseed crop.

Conflict of interests

The authors have not declared any conflict of interests.

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