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Analysis of Genotype-by-Environment Interaction, Farmers' Preferences, and Gender Response in Groundnut Breeding in Tanzania Using Triadic Comparison of Technologies

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ABSTRACT

High kernel yield and farmer- and market-preferred traits are overriding considerations for groundnut (*Arachis hypogaea* L.) breeding, production and adoption. However, yield expression and cultivar selection responses in groundnuts are influenced by genotype-by-environment interactions (GEI) and management conditions. Therefore, it is essential to evaluate GEI to identify high-yielding and stable groundnut genotypes preferred by farmers and markets for breeding or variety recommendations. The objectives of this study were to assess the GEI and farmers' preference traits in groundnut to facilitate the selection of superior genotypes for release and guide breeding with specific or broad adaptation while integrating farmers' and gender perceived traits. The study was conducted across 18 environments representing agroecological zones and potential groundnut production areas in Tanzania. Sixteen genotypes, including two commercial checks, were evaluated in selected locations using a randomized complete block design. Furthermore, on-farm decentralized trials were conducted across 42 locations following the tricot approach. Significant ($p < 0.05$) variations were detected among the tested genotypes (G), environments (E), and GEI effects on kernel yield. Genotype ICGV-SM 05534 had a relatively highest kernel yield of 927.232 kg ha^{-1}. The GGE biplot identified ICGV-SM 16645 and ICGV-SM 10014 as the most stable genotypes across locations, with mean kernel yields of 936.39 and 877.67 kg ha^{-1}, respectively. The triadic comparison of technologies (TRICOT) analysis identified gender differences in trait preferences among groundnut growers. Early maturity, ease of harvesting and shelling were the most preferred traits by female farmers, and haulm yield by males. Tan color and small-medium kernel seed size were identified as the top traits selected by farmers' overall varietal preferences. Additionally, early maturity is an important trait to consider in the market segment. Farmers' preference traits are crucial during the initial stage of designing the target product profile to increase the adoption of the deployed groundnut variety. The selected genotypes, test environments, and farmer-preferred traits are vital for breeding pipelines, targeted variety release, and production for different target population environments (TPEs) in Tanzania.

1 | Introduction

Groundnut (*Arachis hypogaea* L.) is a key food security and industrial seed oil crop globally. Groundnut kernel is rich in oil (48%–50%), protein (26%–28%), dietary fiber, minerals, and vitamins (Kumar et al. 2024); Pasupuleti et al. (2013). Globally, groundnut is grown in more than 100 countries situated in tropical, subtropical, and warm temperate regions (Upadhyaya et al. 2012). In sub-Saharan Africa (SSA), Tanzania is third in groundnut production. In 2021, Tanzania produced 720,000 tons of groundnut from an estimated cultivation area of 1,200,000 ha (FAOSTAT 2021). Tanzania is a major exporter of groundnut to the neighboring countries, including Rwanda, Burundi, Kenya, Uganda, Indonesia, and the Democratic Republic of Congo (OEC 2026).

Groundnut is a multipurpose crop cultivated mainly by women and resource-poor farmers in Tanzania for food and cash income. However, kernel yield in groundnut remains low in the country due to several production challenges such as biotic constraints (e.g., insect pests, and diseases), abiotic stresses (e.g., poor soil fertility, moisture and heat stress) (Daudi et al. 2018). The average yield of groundnut in sub-Saharan Africa (SSA) is below $1\,t\,ha^{-1}$, lower than the global average of $2.5\,t\,ha^{-1}$ (FAOSTAT 2021). There is a need to develop and deliver farmer- and market-preferred improved cultivars, modern production technologies and good agronomic practices for enhanced productivity and increased adoption in SSA. The development of improved cultivars relies on identifying sufficient genetic variation, selecting stable and superior genotypes for breeding, and incorporating both farmer and market preferences. Daudi et al. (2018); Yila et al. (2023) reported that both women and men emphasized the need for market-preferred traits in groundnut. However, eating quality or taste and easy shelling were highly preferred by women farmers. High kernel yield and farmer- and market-preferred traits are the overriding considerations for groundnut breeding, production, and adoption.

Yield expression and selection response in groundnuts are subject to genotype-by-environment interaction (GEI) and management conditions. In an attempt to select desirable genotypes for breeding, Daudi et al. (2020) selected new breeding populations and evaluated genetically diverse groundnut collections in Tanzania. The authors reported the presence of marked genetic variation for rust resistance, high yield, and farmer-preferred attributes in the assessed genotypes. Furthermore, the study found a significant influence of environmental variance on genotype selection. Several statistical methods are available to analyze GEI and guide cultivar selection. The genotype and genotype by environment (GGE) biplot depicts the response of a set of genotypes and their interaction with the environments to guide genotype and ideal production environment selection. Several past studies have reported significant GEI in groundnut varieties (Kona et al. 2024; Kumar et al. 2024; Lal et al. 2019; Lokeshwar Reddy et al. 2016). Nevertheless, most of these studies were conducted on-station, in controlled environments with access to agricultural inputs like fertilizer and irrigation (Ceccarelli 2017; Ceccarelli and Grando 2022). However, these on-station growing conditions are not consistent with farmer environments. Moreover, there is still limited research highlighting the evaluation of traits related to farmer preferences and gender on a large scale. A novel decentralized on-farm testing supported by citizen science, known as the triadic comparison of technologies (tricot), has emerged as a pioneering framework for on-farm evaluation. A tricot model is dependent on a larger sample number (N) and is a decentralized participatory approach demonstrating the ability to guide breeders to accelerate the selection of genotypes while mitigating the genotype × environment × management (G × E × M) interactions (de Sousa et al. 2021a; Occelli et al. 2024; Van Etten et al. 2019). The tricot approach is referred to as a citizen science approach because it involves many farmers with few breeding lines to test. The approach empowers farmers to actively participate in the evaluation of newly developed varieties and agricultural technologies, enabling the decentralized assessment of crop varieties or management practices under diverse local conditions (Van Etten et al. 2019).

Large-scale participatory trials, engaging many farmers groups, can generate robust data that enhances the external validity of experimental findings, providing insights into the performance of different crop varieties across varying environments (Van Etten et al. 2019). By leveraging farmer-generated data from tricot trials, agronomists and breeders can acquire up-to-date insights on farmers' and market preferences for new crop variety releases that align with both farmers' needs and market demands (Alamu et al. 2023; Nanyonjo et al. 2024). Tricot employs incomplete block designs and best-worst ranking assessments, allowing for scalable and cost-effective data collection (de Sousa et al. 2021a). The integration of farmer-generated rankings contributes to more inclusive and context-specific evaluations of agricultural technologies. Evaluating genotype-by-environment interactions (GEI) within this participatory framework is essential for identifying high-yielding and stable groundnut genotypes that align with farmers' preferences and market demands. In this context, this study aimed to assess GEI and farmers' preferred traits in groundnut to facilitate the selection of superior genotypes with specific or broad adaptation, incorporating farmer perspectives and gender-inclusive trait selection criteria using triadic comparison of technologies.

2 | Materials and Methods

2.1 | Study Design

A total of 16 groundnut genotypes were used for the on-station trial in this study (Table 1). The test accessions included elite breeding lines obtained from the International Crop Research Institute for the Semi-Arid Tropics (ICRISAT) and two released materials from the Tanzania Agricultural Research Institute (TARI), which were used as checks. The selected test materials were resistant to foliar disease and have good shelling percentage and yield.

Field trials were conducted using a randomized complete block design (RCBD) with four replications in the 2022 and 2023 growing seasons at nine locations, providing a total of 18 environments in Tanzania (Table 2). The study sites represented the major groundnut production areas and six out of the seven agroecological zones in Tanzania (Figure 1). Descriptions of the study sites are presented in Table 2. In general, the soil, climatic, and biological conditions of the study sites vary considerably.

TABLE 1 | Description of groundnut genotypes used in the study.

Sn	Designation	Pedigree	Source	Attributes	Release status: Not released (NR) or released (R)	Maturity (SD or MD)	Kernel color	Kernel size
1	ICGIL 17105	ICGV 87846 × ISATGR 265–5	ICRISAT-Malawi	Rust, LLS, and rosette resistance	NR	MD	Tan	Medium
2	ICGIL 17120	ICGV 87846 × ISATGR 265–5	ICRISAT-Malawi	Rust and LLS resistance	NR	MD	Tan	Medium
3	ICGIL 17123	ICGV 87846 × ISATGR 265–5	ICRISAT-Malawi	Rust and LLS resistance	NR	MD	Tan	Medium
4	ICGV-SM 02724	—	ICRISAT-Malawi	Rust and LLS resistance	NR	MD	Tan	Medium
5	ICGV-SM 03707	—	ICRISAT-Malawi	High shelling percent	NR	MD	Tan	Medium
6	ICGV-SM 05534	(VALENCIA R2 × ICGV-SM 93555) F2-P23-P59-P59-B1-B1-B1	ICRISAT-Malawi	Early maturity	NR	SD	Tan	Medium/Small
7	ICGV-SM 05702	(FLAMINGO × ICG 12991) F2-P11-P1-B1-B1-B1-B1	ICRISAT-Malawi	Early maturity and rust, LLS, and rosette resistance	NR	SD	Tan	Medium/Small
8	ICGV-SM 10014	(CHALIMBANA P23 × ICGV-SM 99568) F2-P5-P1-P1-P1-B1-B1	ICRISAT-Malawi	High shelling percent	NR	MD	Tan	Large
9	ICGV-SM 16514	(ICG 12991 × ICGV 86124) F2-P8-P1-B1-B1-B1-B1	ICRISAT-Malawi	High shelling percent and aphid resistance	NR	SD	Tan	Medium/Small
10	ICGV-SM 16519	(ICG 12991 × ICGV 86124) F2-P12-P1-B1-B1-B1-B1	ICRISAT-Malawi	High shelling percentage	NR	MD	Tan	Medium
11	ICGV-SM 16524	(ICG 12991 × ICGV 86124) F2-P15-P8-B1-B1-B1-B1	ICRISAT-Malawi	Early maturity and high shelling percent	NR	MD	Tan	Medium
12	ICGV-SM 16530	—	ICRISAT-Malawi	ELS	NR	MD	Tan	Medium
13	ICGV-SM 16645	(ICGV 91114 × OG 52–1) F2-SSD-SSD-SSD-P16-B1-B1	ICRISAT-Malawi	Shelling percent	NR	MD	Tan	Medium
14	ICGV-SM 17533	—	ICRISAT-Malawi	Short duration, LLS, and rust resistance	NR	SD	Tan	Medium/Small
15	MANGAKA 2009	ICGV 93437 × ICGV-SM 94586	TARI-Naliendele/ Commercial variety	High yielding	R	SD	Tan	Medium/Small
16	MNANJE 2009	(USA 20 × TMV 10) F2-P3-B1-B1-B1-B1-B1B1-B1-B1	TARI-Naliendele/ commercial variety	High yielding and good taste	R	MD	Red	Large

Abbreviations: ICRISAT = International Crop Research Institute for Semi-arid Tropics, LLS = Late leaf spot, MD = medium duration, SD = Short duration, Sn = serial number, TARI = Tanzania Agricultural Research Institute.

TABLE 2 | Description of the study locations in Tanzania and corresponding soil properties, and climatic conditions in 2022 and 2023 in Tanzania.

Agro-ecological zone	Location	Latitude (°S)	Longitude (°E)	Altitude (masl)	Soil		Max Temp (°C)		Min Temp (°C)		Total rainfall (mm)	
					Type	pH	2022	2023	2022	2023	2022	2023
Eastern	Chambezi	6.5167	38.9167	12	Sandy loam	5.00					499.5	327.3
Southern	Naliendele	10.3539	40.1682	135	Sandy loam	4.50	30.7	30.9	22.1	22.4	743.6	802.1
Western	Kihinga	4.8356	29.6777	825	Clay to clay loam	5.9–6.3					853.4	693.2
Central	Makutupora	5.5866	35.4609	1070								
Southern highland	Uyole	8.9094	34.4560	1798	Sandy loam	5.6–6.1	23.9	23.7	12.1	10.7	1197.2	497.9
Southern	Nachingwea	10.22	38.4545	474	Grey and red loam	4.5–6.5			19.5	19.7	901.6	585.4
Western	Tumbi	5.3456	32.4156	1190	Sandy loam	4.4–5.8	30.5	19.9	14.2	10.9	639.6	679.1
Lake	Ukiriguru	2.4300	33.1000	1236	Sandy loam	5.5–7.5	29.2	29.6	21.65	21.5	1237.7	887
Southern	Nakayaya	11.0400	37.2100	608	Sandy loam	4.5–6.5					1122	

Abbreviations: masl = meter above sea level, Max = maximum, Min = minimum, mm = millimeter.

2.2 | Field Establishment and Trials Management

Trials were conducted using experimental units (plots) that consisted of two rows that were 4 m long. One seed per station was planted with an inter-row spacing of 50 cm and an intra-row spacing of 10 cm. Two guard rows were planted at the beginning and end of each replication. The trials were done at Ukiriguru, Kihinga, and Tumbi sites and were established in October/November in both seasons, while trials at Naliendele, Nachingwea Makutupora, Nakayaya, and Uyole were established in December, and at Chambezi, the trials were established in February/March. Standard crop management practices were followed as recommended for the area (NARI 2010).

2.3 | Triadic Comparison of Technologies Trials

The above 16 groundnut genotypes were used for both on-farm and on-station trials in this study (Table 1). An additional local variety was added as a "local check" for the on-farm trials.

Decentralized on-farm trials were established as incomplete blocks of three following the tricot approach (de Sousa et al. 2024). Each plot consisted of two rows, 4 m long, with an inter-row spacing of 50 cm and an intra-row spacing of 10 cm, and one seed planted per hole. The study was conducted from 2021 to 2024 following the framework proposed by de Sousa et al. (2021a, 2021b). The approach consists of an adapted mother-baby trial (Witcombe et al. 2006) with centralized on-station locations being managed by researchers under an RCBD and decentralized on-farm trials managed by farmers under an incomplete block design of three following the tricot approach (de Sousa et al. 2024). The trials at all on-farm sites (Figure 1) were established under natural rainfall. Each farmer received a random and anonymous combination of three varieties to evaluate, denoted as A, B and C, which were assigned using ClimMob software (Quir'os et al. 2024). A total of 154, 178 and 871 farmers participated in 36 villages of 10 regions of Tanzania in 2021, 2022 and 2023, respectively.

2.4 | Data Collection

2.4.1 | Genotype-by-Environment Interaction Trails

At harvest maturity, pod yield (PDY) was measured by weighing the dried pods from each plot and recording the weight in grams per plot. The shelling percentage (SP) for each genotype was calculated from a random sample of pods weighing 200 g, as the proportion of shelled seed weight to the total weight of the unshelled pods (Pasupuelti et al. 2018). Kernel yield (KY, expressed in t ha-1) was estimated as the product of pod yield per plot and shelling percentage and was converted to kg ha-1 using the plot size (4 m^2) after adjusting for moisture content.

2.4.2 | Triadic Comparison of Technologies Trials

At the tricot on-farm trials, farmers were guided to plant the three varieties side-by-side and on the same day, and next to

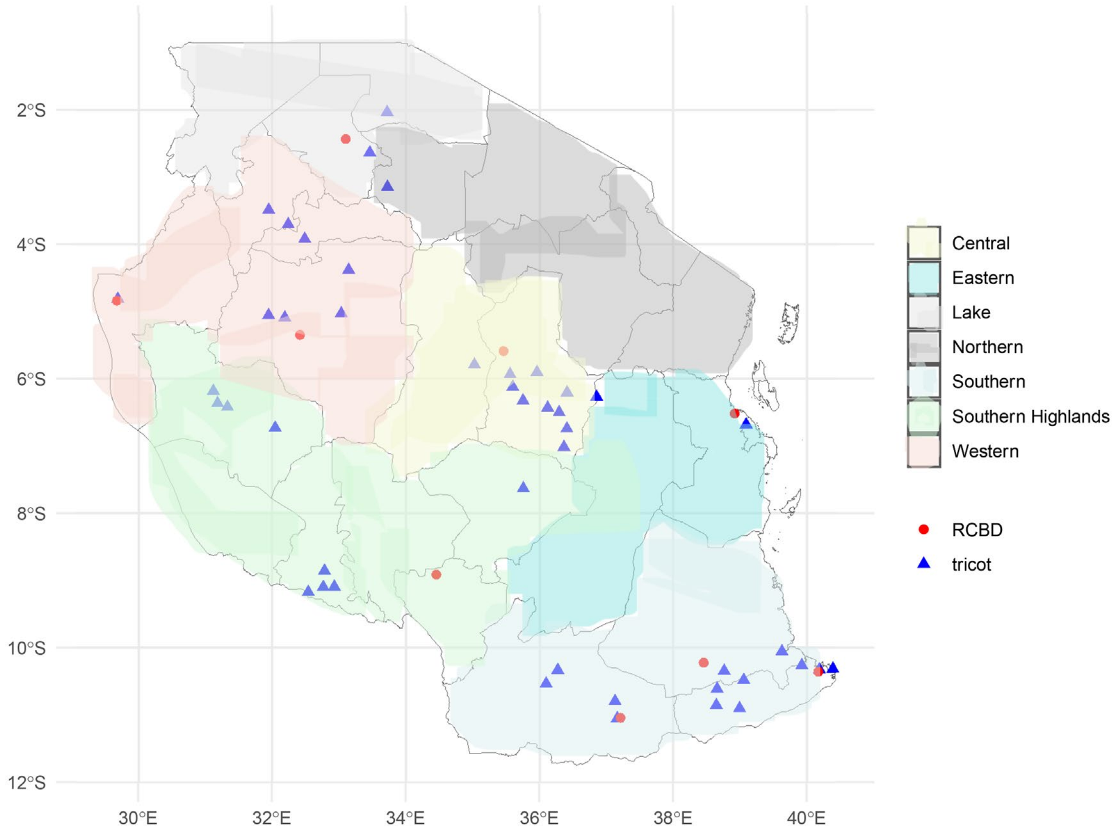

FIGURE 1 | Distribution of centralized randomized complete block design trial (RCBD, red dots) and on-farm decentralized incomplete blocks trial (tricot, blue triangles) across the agro-ecological zones of Tanzania. For data anonymization purposes tricot trials as displayed as centroids within 2–5 arc-min resolution.

their own crop under usual crop management. They were also instructed to evaluate their performance using the best-worst scaling for pre-determined traits based on the target product profile (TPP) designed for groundnut across different crop stages (e.g., shelled yield, pod yield, kernel color, vigor, maturity, harvest labor). Additional information such as Global Positioning System (GPS), location of the trial, farmer age and gender, and the previous use of the land where the trials were established were also collected at the seed delivery moment. For farmer-led variety performance evaluation, the data was digitally collected with the support of extension officers using Open Data Kit (ODK, https://getodk.org) on smartphones/tablets.

2.5 | Data Analysis

2.5.1 | On-Station Trials

A fixed-effect model was employed to analyze the yield trait from the RCBD trials using the R software (R Core Team 2021). In this analysis, each combination of year and location was treated as a distinct environment. Given that the trial spanned nine locations over 2 years, there were a total of 18 unique environments. For each of these individual environments, the following model was used.

$$Y_{ij} = \mu + G_i + R_j + \epsilon_{ij}$$

where:

Y_{ij} represents the observed response variable for the ith genotype and jth replication.

μ is the overall mean.

G_i represents the fixed effect of the ith genotype.

R_j represents the fixed effect of the jth replication.

Moreover, a mixed-effects model was employed by considering year, location, and genotype as the main effects, and replication as the nested effect within location and year. Additionally, all two-way interaction effects among year, location, and genotype, as well as the three-way interaction involving year, location, and genotype, were included in the model. To implement this, the following model was considered:

$$Y_{ijkl} = \mu + \gamma_i + E_j + R_{k(j,i)} + G_l + \gamma_i.E_j + \gamma_i.G_l + E_j.G_l + \gamma_i.E_j.G_l + \epsilon_{ijkl}$$

where:

Y_{ijk} represents the observed response variable for the lth Genotype in ith Year, jth Location, and kth Replication nested within Location.

μ is the overall mean.

γ_i represents the random effect of the ith Year.

E_j represents the random effect of the jth Location.

$R_{k(j,i)}$ represents the random effect of the kth Replication nested within the jth Location in ith Year.

G_l represents the random effect of the lth Genotype.

$\gamma_i . E_j$ represents the random interaction effect between Year and Location for the ith Year and jth Location.

$\gamma_i . G_l$ represents the random interaction effect between Year and Genotype for the ith Year and lth Genotype.

$E_j . G_l$ represents the random interaction effect between Location and Genotype for the jth Location and lth Genotype.

$\gamma_i . E_j . G_l$ represents the random 3-factor interaction effect between Year, Location, and Genotype for ith Year, jth Location, and lth Genotype.

2.5.2 | On-Farm Tricot Trials

On-farm data was analyzed using the Plackett-Luce (PL) model, independently proposed by Luce (1959) and Plackett (1975) to analyze ranking data. It is implemented in R by the package "PlackettLuce" (Turner et al. 2020). The Plackett-Luce model estimates the relative importance (probability of outperforming) of different technologies following Luce's Choice Axiom (Luce 1959), which states that the probability that one item (e.g., variety) outperforms another is independent of the presence or absence of any other items in the set, as the following equation explained;

$$P(i \succ j) = p_i / \left(p_i + p_j\right)$$

where p_i is a positive real-valued score assigned to individual i. The comparison $i \succ j$ can be read as "i is preferred over j".

The PL model determines the values of positive-valued parameters α_i (worth) associated with each item i. These parameters α are related to the probability (P) that item i outperforms all other n items in the set. We report log-worth values that are centered to 0 using the item(s) Local as the control treatment (check). The tricot trials used rankings of three varieties ($i \succ j \succ k$), which have the following probability of occurring according to the PL model:

$$P(i \succ j \succ k) = P(i \succ j, k) \cdot P(j \succ k)$$

We used Kendall Tau correlation to identify the traits most closely associated with farmers' overall preference for the tested varieties. For the modeling and data processing of on-farm data we used the R packages PlackettLuce, ClimMobTools, and gosset (Turner et al. 2020; Van Etten et al. 2019; van Ettena et al. 2023).

3 | Results

3.1 | Climatic Conditions of Test Environments

Preliminary climatic data over the seasons showed a decrease in total rainfall in almost all the study sites and variable temperatures (Table 1). The highest rainfall in 2022 was 1237.7 mm at Ukiriguru, and 887 mm at Ukiriguru in 2023. Generally, 2022 received high rainfall compared to 2023. Chambezi received low rainfall in both years 2022 and 2023 (499.5 and 327.3 mm, respectively), and the highest rainfall site was Ukiriguru. The maximum temperature was 30.7 C in 2022 and 30.9°C in 2023 at Naliendele, and the minimum was 12.1°C in 2022 and 10.7°C in 2023 at Uyole.

3.2 | Response 16 Groundnut Genotypes for Kernel Yield When Evaluated in 18 Environments

The effect of groundnut genotypes on kernel yield when evaluated in 18 environments is presented in Table 3. The analysis revealed that the GEI was highly significant ($p < 0.001$). Also, highly significant ($p < 0.001$) effects were noted among the tested groundnut genotypes. Kernel yield exhibited highly significant ($p < 0.001$) environmental variability.

3.3 | Performance of Groundnut Genotypes

The top three genotypes with high kernel yield are ICGV-SM 16530 (936.393 kgha^{-1}), ICGV-SM 03707 (927.232 kgha^{-1}), and ICGV-SM 16524 (919.020 kgha^{-1}) (Table 4). The mean kernel yield across locations was 831.834 kgha^{-1}. The five bottom-performing genotypes in terms of kernel yield were ICGIL 17120 (676.543 kgha^{-1}), ICGV-SM 02724 (745.907 kgha^{-1}), ICGIL 17123 (756.369 kgha^{-1}), ICGV-SM 16514 (775.130 kgha^{-1}), and ICGIL 17105 (815.615 kgha^{-1}). These genotypes yielded below-average pod yield. The highest yield location was Nachingwea, and the lowest was Nakayaya (Table 4).

TABLE 3 | Analysis of variance and significant tests for kernel yield among 16 groundnut genotypes evaluated in 18 environments in Tanzania.

Source of variation	df	Component	St. error
Environment (E)	17	342,848.401	173,665.929***
Replication (year: location)	8	3668.692	1673.608
Block (replication)	36	342,848.401	173,665.929***
Genotype (G)	15	6876.455	3277.364**
G×E	255	16,862.378	2654.994***
Parameters			
Mean (kg ha^{-1})	831.834		
H^2	73.7%		
CV	31.413%		

Note: ** and *** represent significant differences at 0.01, 0.001 probability level, respectively.
Abbreviations: CV = coefficient of variation, DF = degrees of freedom, H^2 = Broad sense heritability.

TABLE 4 | Mean kernel yield (kg ha^{-1}) for the groundnut genotypes evaluated across 18 environments in Tanzania.

	Location and year											
Genotypes	**Year**	**Naliendele**	**Kihinga**	**Nakayaya**	**Nachingwea**	**Chambezi**	**Tumbi**	**Uyole**	**Ukiriguru**	**Makutupora**	**Overall**	**Overall**
ICGIL 17105	2022	839.115	225.204	136.320	2282.399	280.878	102.603	164.771	633.931	708.863	610.946	815.615
	2023	1224.716	790.667	560.695	1148.017	429.615	1772.699	630.782	919.166	1937.655	1044.394	
ICGIL 17120	2022	494.601	162.641	103.336	2098.491	118.008	33.771	243.746	516.813	347.474	519.663	676.543
	2023	916.302	553.361	403.570	850.669	371.794	1684.865	477.747	809.718	1771.745	883.179	
ICGIL 17123	2022	911.819	217.553	127.781	2427.254	376.982	26.987	311.387	801.695	458.890	631.765	756.369
	2023	915.656	530.045	304.406	865.748	281.168	1628.374	428.472	860.376	1712.295	851.102	
ICGV-SM 02724	2022	659.741	298.734	104.270	2251.492	141.467	49.415	402.503	755.493	412.765	589.260	745.907
	2023	1027.849	692.230	415.474	978.422	421.767	1618.961	452.038	811.689	1760.732	917.936	
ICGV-SM 03707	2022	1063.101	212.233	340.611	2347.403	230.627	43.767	254.321	693.769	773.296	653.493	882.423
	2023	1153.340	840.302	657.088	1183.717	680.147	1874.737	690.373	1054.578	2092.075	1127.585	
ICGV-SM 05534	2022	908.972	192.720	334.088	2440.281	354.043	72.711	509.357	841.127	862.250	693.958	927.232
	2023	1198.496	918.241	632.812	1271.126	491.343	1964.656	731.721	1088.100	2094.122	1144.406	
ICGV-SM 05702	2022	839.318	644.278	62.362	2358.515	221.997	48.164	410.467	702.095	666.593	653.105	833.982
	2023	1066.897	625.880	416.486	1178.102	446.391	1754.646	478.923	958.899	1948.835	989.201	
ICGV-SM 10014	2022	937.819	270.225	181.149	2364.730	291.224	552.709	272.541	770.003	692.573	680.680	877.669
	2023	1078.343	712.198	509.484	1113.543	459.483	1877.159	665.210	941.006	2019.162	1040.459	
ICGV-SM 16514	2022	838.312	256.704	211.779	2364.796	323.766	44.324	344.567	849.819	598.245	644.270	870.857
	2023	1194.783	945.559	564.589	1179.050	475.075	1939.109	676.457	1038.111	2037.001	1109.497	
ICGV-SM 16519	2022	790.095	276.453	45.701	2436.119	163.976	41.497	161.303	630.860	522.140	588.697	775.130
	2023	1134.792	675.297	444.060	1031.058	364.893	1770.054	658.956	838.819	1912.756	984.657	
ICGV-SM 16524	2022	929.842	200.230	519.238	2483.771	288.056	210.342	559.139	709.117	798.944	707.276	919.020
	2023	1114.647	835.852	556.285	1198.517	454.404	1908.297	687.162	1009.640	2084.034	1088.924	
ICGV-SM 16530	2022	887.262	356.828	113.775	2309.984	120.507	53.929	273.205	695.209	419.225	600.462	761.320
	2023	968.064	699.986	489.613	1039.624	395.821	1660.073	508.685	727.654	1798.371	929.071	
ICGV-SM 16645	2022	880.262	180.382	288.988	2448.748	489.178	45.342	215.267	709.581	973.895	673.311	936.393

(Continues)

TABLE 4 | (Continued)

	Location and year											
Genotypes	**Year**	**Naliendele**	**Kihinga**	**Nakayaya**	**Nachingwea**	**Chambezi**	**Tumbi**	**Uyole**	**Ukiriguru**	**Makutupora**	**Overall**	**Overall**
	2023	1243.118	914.508	782.282	1321.503	524.140	2057.043	825.222	1147.586	2151.651	1203.438	
ICGV-SM 17533	2022	996.111	195.383	203.559	2401.760	208.461	45.820	302.161	808.062	787.670	652.755	830.049
	2023	1038.806	738.188	456.260	1008.865	430.931	1775.088	555.252	867.814	1884.044	976.932	
MANGAKA 09	2022	1095.390	352.794	329.634	2443.767	181.054	42.844	189.021	704.835	645.887	655.391	864.645
	2023	1130.577	783.199	511.967	1113.678	512.212	1859.962	747.563	1029.409	2032.235	1075.812	
Mnanje 09	2022	1182.660	211.691	93.871	2482.077	324.731	110.079	163.564	740.685	453.122	639.192	836.188
	2023	1058.596	674.947	630.024	1126.806	515.065	1778.290	679.777	912.010	2006.669	1041.135	
Mean	2022	890.324	266.723	200.774	2367.402	258.049	96.502	299.353	722.499	632.625	730.358	831.834
	2023	1091.427	746.223	521.971	1100.375	454.556	1806.158	619.225	938.588	1950.823	933.310	
LSD (5%)	2022	233.383	110.72	96.685	590.59	118.18	23.439	156.297	ns	219.065	111.322	107.689
	2023	ns	263.202	265.868	299.805	ns	519.935	ns	ns	540.295	146.946	
CV%	2022	16.03	22.226	25.702	17.616	27.242	12.611	30.22	29.108	20.208	33.146	31.413
	2023	32.644	22.5	21.732	18.844	24.069	20.262	29.275	26.549	18.773	30.051	
H^2%	2022	86.61	92.209	95.21	72.79	88.139	99.717	84.731	26.553	92.698	50.963	73.7
	2023	49.324	70.499	97.654	68.533	60.554	70.809	53.185	51.401	78.094	73.342	

Abbreviations: CV = coefficient of variation, H^2 = heritability, LSD = least significant difference.

3.4 | Genotype Main Effect and Genotype by Environment Interaction Analysis

Figure 2 presents a biplot of principal component analysis (PCA) illustrating the mean performance versus stability of different groundnut genotypes based on genotype-by-environment interaction (GEI) analysis. Principal component 1 (PC1) accounts for 55.4% of the total variation, while PC2 explains 9.47% of the variation (Figure 2). The graph is centred at the origin, with genotypes represented as green and blue labels, indicating different classification groups. The arrows denote stability and mean performance, with entries positioned further along the PC1 axis exhibiting higher mean performance. Genotypes clustered near the origin showed relative stability, while those farther away exhibited greater variability. Most assessed genotypes showed minimal deviation along the principal component axes, indicating consistent performance across different environments.

Genotype ICGV-SM 16645, had the closest proximity to the ideal genotype; it's the highest yielder, stable and, therefore, most desirable of all the tested genotypes, followed by genotype ICGV-SM 10014, which had higher yield advantage than the check (Figure 2).

3.5 | Which-Won-Where Analysis

"Which-won-where" analysis for genotype evaluation across multiple environments presented by a GGE biplot. The two principal components (PC1 and PC2) explained approximately 64.87% of the total genotype-environment interaction variation, with PC1 accounting for 55.4% and PC2 for 9.47% (Figure 3). The unexplained variation (35.13%) is a random or unaccounted variation attributable to interaction effects common in multi-environment field trials such as measurement inaccuracy, variable soil, climatic, and growing conditions. Prominent polygon vertices represent the genotypes with the best performance in respective agroecological zones. Best performing genotypes included Mnanje 2009, ICGV-SM 16445, ICGV-SM 05534, and ICGIL 17120 (Figure 3). These genotypes exhibited adaptation and superior yield potential within the different tested environments. Genotype Mnanje 2009 emerged as an outstanding with high stability and performance across multiple conditions. Specifically, ICGV-SM 16645, located at the corner of the polygon, was the best-performing genotype in most locations for the 2022 and 2023 seasons, except at Uyole in 2022; ICGV-SM 05534 was the best, and in 2022, Kihinga was the lowest yielding site with genotype ICGIL 17120 due to the severity of groundnut rosette. The Western part of Tanzania is often affected by groundnut rosette disease. Genotype Mnanje 2009 (check-2) performed better at Naliendele in 2022 and Chambezi in 2023.

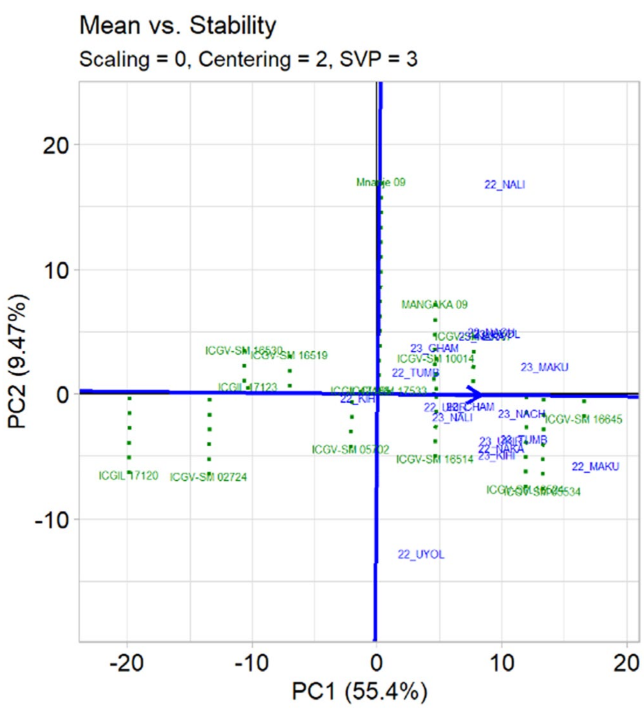

FIGURE 2 | The average environment coordination view comparison biplot comparing genotypes relative to an ideal genotype (the centre of the concentric circles). Names in blue denote the environment and in green the genotypes. Blue arrows represent ideal genotypes.

3.6 | Correlations Among the Assessed Groundnut Traits

Pearson correlation analysis between pairs of test environments by year and location for the 16 groundnut genotypes. The matrix revealed a clear clustering by year, with environments from 2023 (e.g., 23_MAKU, 23_NACH, 23_UKIR) exhibiting strong, significant positive correlations ($r = 0.66–0.91$) (Figure 4). This suggested consistent genotype performance patterns within this season. Similarly, moderate to high correlations were observed among 2022 environments, but with lower significance, which was indicative of variability in stability based on year. On the other hand, correlations between environments across years, for example, between 2022 and 2023, were relatively weaker and often non-significant, reflecting strong genotype×year interactions (Figure 4). These observations suggested that environmental conditions, particularly between growing seasons, had a substantial influence on genotype performance for kernel yield.

3.7 | The Triadic Comparison of Technologies Analysis

On-farm testing results extracted the farmer-stated preferences as explained by the Kendall correlation (Figure 5). Both men and women preferred varieties that are easy to sell (marketable) with all market-preferable traits presented in Figure 5. Results showed additional traits preferred by women, including early maturity, ease to harvest, and shelling (Figure 5). Pearson correlation coefficients between key varietal traits and the overall varietal preference scores were distinguished by gender. For both men and women, kernel size and color and marketability are common traits of importance. Tan-colored kernels with small to medium size are the most preferred, accounting for about 60% of the market share, followed by large red kernels. However, gender-specific differences became apparent in the mid-ranked traits. For men, yield was more strongly correlated with overall preference ($r \approx 0.5$) compared to oil content, whereas for women, oil content ($r \approx 0.5$) ranked slightly above yield (Figure 5). This suggested that women placed relatively greater value on

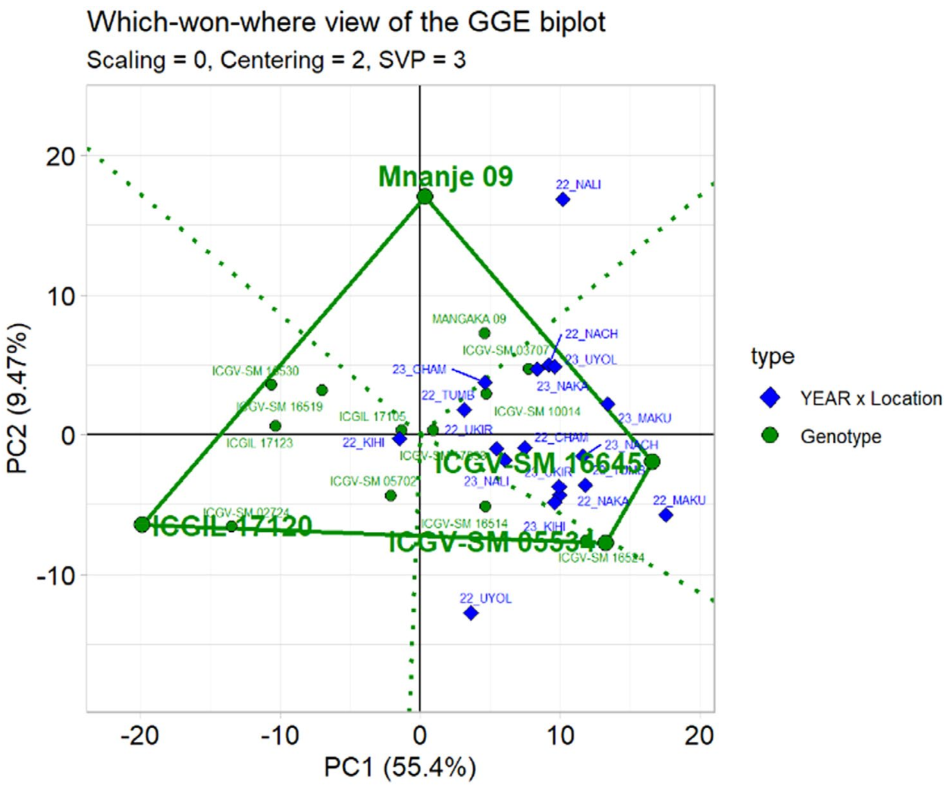

FIGURE 3 | "The which won where" polygon view of the GGE biplot showing which genotypes perform best in which environment. Blue circles represent the environment and green the genotype. Vertices of the polygon indicate superior genotypes in each sector.

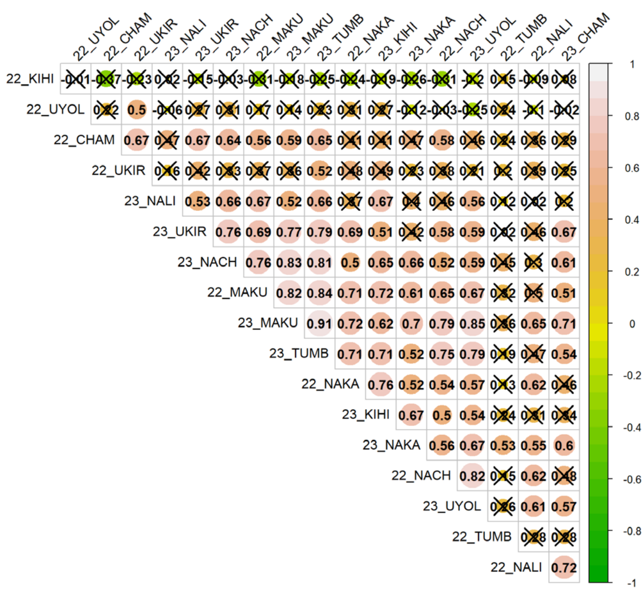

FIGURE 4 | Pairwise correlation matrix depicting the relationships among 18 test environments based on the performance of 16 evaluated genotypes. Correlation strength is represented by both color and circle size, green hues denote positive correlations, red hues indicate negative correlations, and color intensity corresponds to correlation magnitude. Non-significant correlation ($p > 0.05$) is marked with black crosses.

nutritional or processing-related traits, while men emphasized agronomic performance. Traits like pod yield, haulm yield, and shelling showed moderate correlations in both groups, indicating their intermediate importance. Additionally, harvest labor and maturity exhibited low correlations across both groups (<0.3), though women rated these marginally higher than men (Figure 5).

In aggregate (Figure 6), Central zone farmers' overall variety preferences skewed toward ICGV-SM 16514 linked to their kernel color. In the Eastern zone, Mangaka 2009 was overall preferred due to the kernel color (tan) and size (small-medium). ICGV-SM 16514 emerged as another popular variety, driven by maturity, harvesting labor, kernel and pod yield, but less by overall preference. The overall preferred varieties in the lake zone are ICGV-SM 17533, Mangaka 2009, ICGV-SM 10014, and ICGV-SM 02724 linked to maturity and kernel yield. In the Southern zone, there is a strong negative correlation between the preferred varieties and traits. Mangaka 2009 and ICGV-SM 16630 were overall preferred in the Southern highland zone due to seed size and kernel color. ICGIL 17105 emerged as another popular variety in the Southern highlands, driven by medium maturity (100–120 days) and harvesting labor but less by overall preference. Mangaka 2009 was overall preferred in the Western zone due to seed size. However, this breakdown ignores any possible segmentation of farmer preferences.

Figure 7 illustrates the on-farm performance of various varieties for kernel yield, using weighted coefficients as the basis. In the Central zone, the top three performing varieties are ICGIL 17120, ICGV-SM 16514, and ICGV-SM 17533. Varieties with high kernel yield in the Eastern zone include ICGIL 17105, Mangaka 2009, and ICGV-SM 16514. For Lake zones, the standout performers are ICGV-SM 17533, ICGV-SM 02724, and ICGV-SM 10014. In the Southern zone, the high-yielding varieties are ICGV-SM

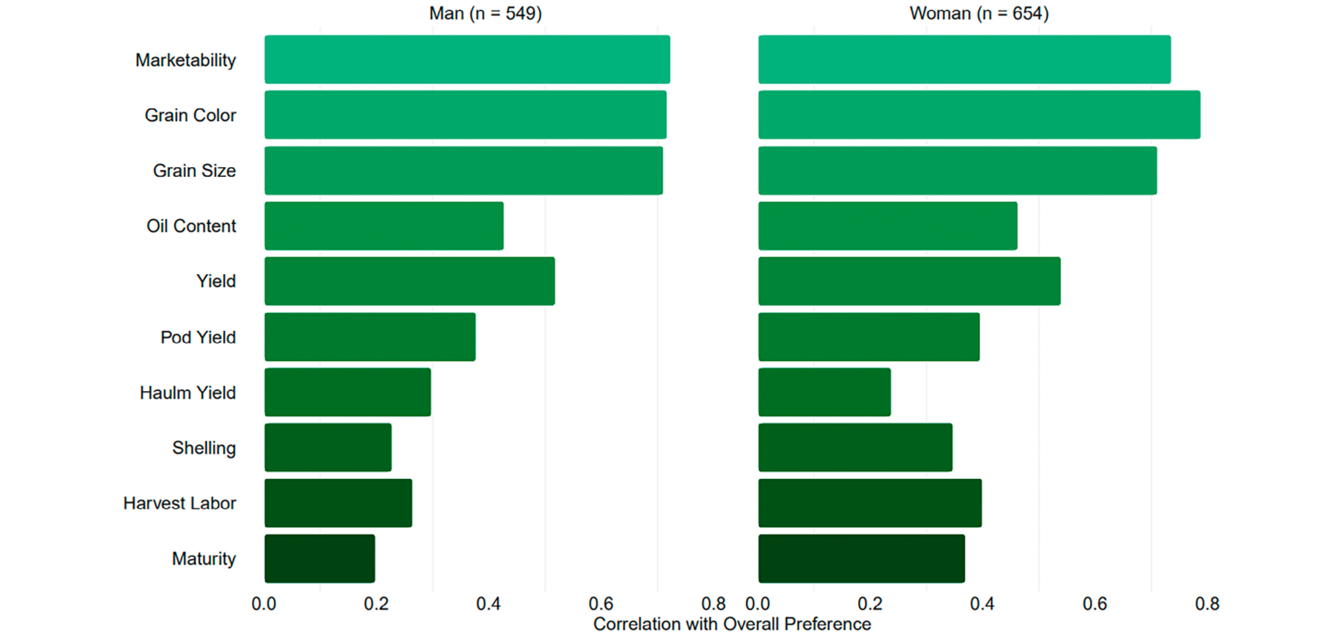

FIGURE 5 | Kendall correlation coefficients for trait preference with overall varietal preference among male ($n = 549$) and female ($n = 654$) respondents. The left panel represents responses from men, while the right panel reflects responses from women. The bars are ranked in descending order of correlation strength, illustrating which traits most strongly influence varietal choice for each gender group.

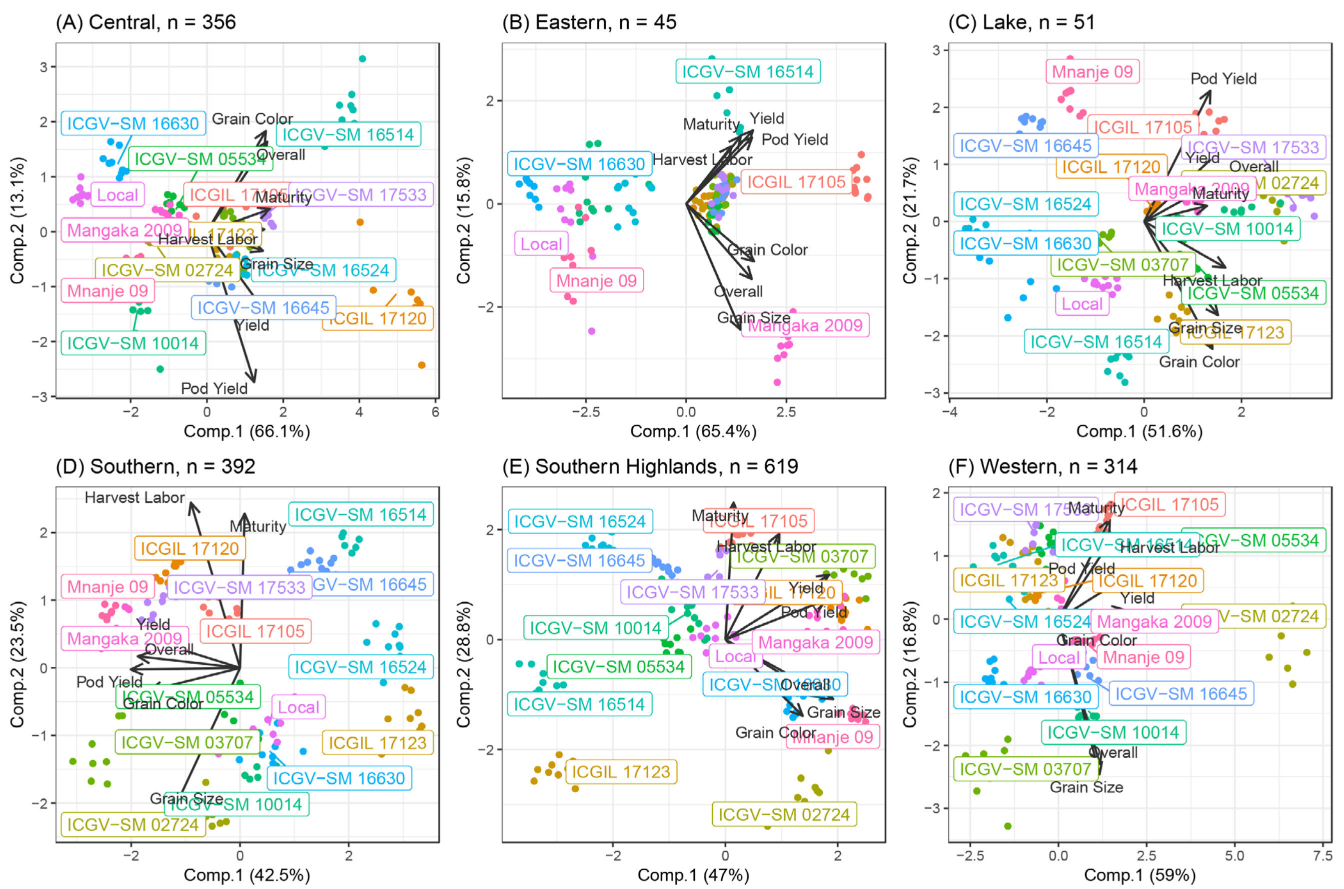

FIGURE 6 | Principal components of Plackett-Luce model estimates (log-worth) across agro-ecological zones in Tanzania. Each panel represents the performance of groundnut varieties by traits within the agro-ecological zone. The arrows indicate the direction and strength of the correlation between traits and variety performance within each agro-ecological zone, while the dots represent individual variety ranking based on the Plackett-Luce model.

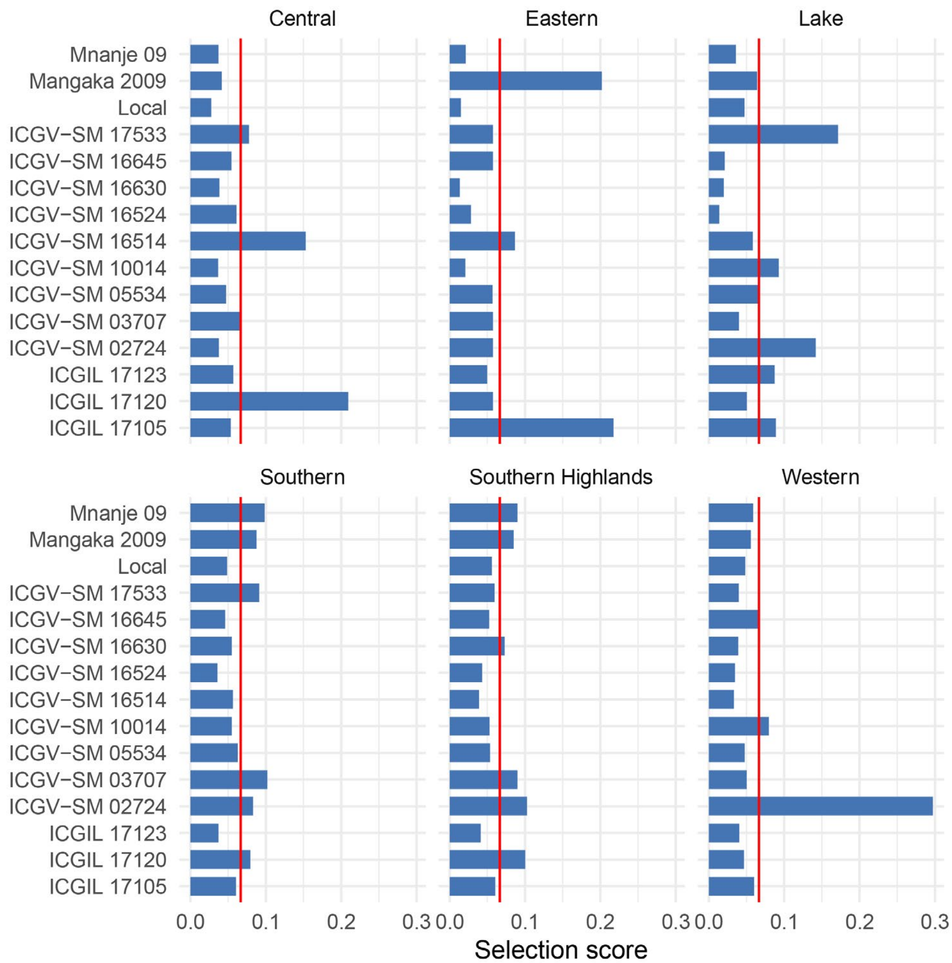

FIGURE 7 | Selection score based on weighted coefficients derived.

03707, Mnanje, and ICGV-SM 17533. ICGIL 17120, ICGV-SM 02724, and ICGV-SM 03707 are the best varieties in the Southern highland, and for the Western zone, varieties ICGV-SM 02724, ICGV-SM 10014, and ICGV-SM 16645 yield better.

4 | Discussion

The large sum of squares for environments in the combined analysis of variance indicated that the environments were diverse (Table 3). This presents a differential response of tested genotypes to environmental conditions, confounding genotype selection across the test environments. Selecting superior genotypes is complicated when genotype performance is not consistent over several test environments, which prolongs the breeding process (Funnah and Mak 1980). The differential performance of genotypes across environments was indicative of variation in climatic and soil conditions in the different growing environments. Variability in climatic factors such as temperature, rainfall, and humidity is an important factor affecting plant growth and development that ultimately leads to differences in yield productivity. A large contribution of the environment affecting yield stability was reported in several studies (Nzuve et al. 2013; Sibiya et al. 2012; Yan and Kang 2003). The genotypic variation observed in kernel yield within a site is a result of differences in the genetic composition of test genotypes.

Yield is a quantitative trait conditioned by polygenes, and its expression varies across test genotypes and environments. Genetic variation is fundamental in plant breeding programs, which allows identification of superior genotypes for enhanced genetic gain. Previous studies reported significant genetic variation after evaluating a large panel of groundnut germplasm (Daudi et al. 2020; Lal et al. 2019; Narasimhulu et al. 2012). The presence of GEI reduces correlations between genotype and phenotype expression and leads to longer breeding cycles or failure to identify superior genotypes (Bustos-Korts et al. 2018). Crop improvement depends on the availability of genetic variation with stable performance for economic traits (Khan et al. 2015). Genotype × environment interaction effects were significant for kernel yield (Table 3), suggesting that environmental variability and change in climatic conditions affect the phenotypic expression of the tested groundnut genotypes. Environmental variability presents challenges for selection as it reduces the correlation between genotype and phenotypic expression. Mekontchou et al. (2006) and Bucheyeki et al. (2008) reported significant genotype, environmental, and genotype × environment interaction variations for agronomic traits in groundnuts.

To find which genotype won in which environments and to display mega-environments, GGE analysis was the model of choice. In the GGE biplot analyses, useful information was extracted from the different biplot graphs. From the GGE biplot (Figure 3), it was possible to visualize the interrelationships among the environments. It is possible that fewer but better test locations can provide equally or more informative data for cultivar evaluation (Yan and Kang 2003). Figure 3 shows that the rays of the biplot divide the plot into four sections, with fourteen environments all appearing in one sector and the remaining five appearing in three different sectors. These environments also show high correlation as indicated in Figure 4. These sectors had a different high-yielding vertex genotype each. It thus suggests that there are at least four groundnut mega-environments (shown in blue circles, Figure 3) in Tanzania. In mega environment 1, which consists of 14 locations, ICGV-SM 16445 was the high-yielding genotype, and mega environment 2 of Uyole 2022 location ICGV-SM 05534 was the leading. Check variety (Mnanje 2009) has high yielding at Naliendele in the year 2022. The low-yielding site was Kihinga 2022 with genotype ICGIL 17120. These genotypes showing high positive interaction with the environments could exploit specific agroecological conditions of the environments and therefore are best suited to those environments (Kandus et al. 2010). According to Yan et al. (2007), when different environments fall into different sectors, it implies that they have different high-yielding cultivars for those sectors and it shows crossover G×E, suggesting that the test environments could be divided into mega environments. The information on GEI will be useful in dividing the target environment into different mega-environments (Gauch and Zobel 1997) and deploying different genotypes in different mega-environments. Cultivar evaluation within a mega-environment should therefore be based on both mean performance and stability to avoid the random GEI (Yan and Kang 2003). This could be done by identifying the ideal genotype. Yan and Kang (2003) defined an ideal cultivar by two criteria: (1) it has the highest yield of the entire set of genotypes; and (2) it is stable, as indicated by the small circle being located on the AEC abscissa and with an arrow pointing to it (Figure 2). Although such an ideal genotype exists rarely in reality, it can serve as a reference for cultivar evaluation. Therefore, as indicated in Figure 2, genotypes ICGV-SM 16645 and ICGV-SM 10014 that consistently perform across seasons and locations will be ideal for selection. Farmers' preferences are a very important component to consider in any breeding program to accelerate adoption and variety turnover of the varieties (Eldon et al. 2020; Snapp et al. 2003). Having farmers test potential innovations in their own environment and use socio-economic context means that farmers have an opportunity to express their views on many aspects of suitability such as overall appreciation, marketability, maturity, and labor requirements. Inclusive farmers' preferences need to consider the gender dimension. The gender-sensitive approach helped to unpack the variation across genders and is especially critical where female members of the farming community take significant responsibilities in farming activities (Nidumolu et al. 2022). Historically, gender inequality remains a deeply entrenched institutional barrier to economic empowerment in development settings (Hansda 2018). Gender-specific preferences helped with highlighting differences in perspectives between male and female farmers. Both men and women preferred marketability, kernel color, and kernel size as their most important traits (Figure 5). This suggested that there was a shared emphasis on traits linked to visual appeal and market-related value, probably due to their direct influence on income potential. Our findings also showed that women placed relatively greater value on the traits, which reduce cost of labor such as shelling and harvest labor, while men emphasized yield performance. Farmers' overall preferences for groundnut in Tanzania in different agroecological zones related primarily to kernel color and seed size. Maturity appears also as an important factor leading farmers in the selection of the variety to grow though it is not in the overall preferences (Figure 6). These bear resemblance to priority traits documented in other studies (Daudi et al. 2018; Yila et al. 2023). Notably, although kernel color (Tan/red) and seed size (Small/large) emerged as a key factor driving farmers' preferences and market segment of the groundnut, it is not consistently included in breeding programs as a priority trait. Breeding programs of groundnut should account for color and seed size from the early stages during development of target product profile as CIMMYT Eastern and Southern groundnut breeding program has started doing. The convergence on easy to sell in the market (marketability), small-medium kernel size, and tan color as top-ranked traits underscores the need for breeders to prioritize market-preferred phenotypes. Simultaneously, the nuanced divergence on traits like oil content and labor-related features highlights the value of tailoring breeding pipelines to address gender-differentiated trait priorities, which will consequentially increase adoption rates and varietal turnover. On-farm ranking observations aggregated from many farmers have been shown to be useful for distinguishing different performances of agricultural technologies (Steinke et al. 2017; Van Etten et al. 2019).

5 | Conclusions

Kernel yield is a winning trait in groundnut breeding and production. Using GGE, genotypes ICGV-SM 16645 and ICGV-SM 10014 were identified as best performers for being close to the ideal cultivar in the GGE biplot analysis. The GGE analysis delineated the test environments into four mega-environments and is useful for the targeted evaluation of genotypes and for effective breeding and seed production. Over the years data are required to have a clear understanding of testing locations for groundnut in Tanzania and reduce the cost of using the location of the same results. Crop improvement programs need to consider the gender dimension and its critical role in groundnut variety to cultivate decision-making. Further study is required to segment more farmers' preference to include young men and women. In this study, we identified the top traits of interest for farmers: Kernel color and seed size drove farmers' overall varietal preferences. Farmers' selection criteria differ from one location to another. Therefore, it is very important to involve farmers from different locations in testing our breeding material before proposing for release. The findings can help guide breeding programs and seed companies in expanding access to suitable diversity of improved groundnut varieties, and specifically to fit different market segments. While the on-farm data may support informed breeding programs in product profile designing, the outcomes of the accelerated adoption rate of improved varieties and food security will be a diffused pathway.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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