University of Tabriz
Journal of Plant Physiology and Breeding
Print ISSN: 2008-5168 Online ISSN: 2821-0174

2024, 14(1): 33-50

Selecting superior groundnut (*Arachis hypogaea L.*) genotypes using multi-trait selection indices

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Article Info
Article type:
Research article

Article history:
Received: February 24, 2024
Revised: June 29, 2024
Accepted: June 29, 2024
Published online: June 30, 2024

Keywords:
Genotype-ideotype distance index (MGIDI), Ideal genotype selection index (IGSI), Multi-environment, Restricted maximum likelihood (REML)

Abstract

Objective: Groundnut (*Arachis hypogaea* L.) is an annual oilseed and proteinous crop whose production is mainly affected by genotype × environment interactions, making it hard to select superior genotypes. The multi-trait selection indices have been used to choose genotypes based on multiple traits.

Methods: In this study, 11 groundnut genotypes were evaluated based on a randomized complete block design with three replications in three locations, Talesh, Masal, and Rasht, Guilan province, Iran, during two growing seasons (2019-2020 and 2020-2021). Variance components were estimated using the restricted maximum likelihood method, and factor analysis was applied to grouping the traits. Multi-trait genotype-ideotype distance index (MGIDI) and ideal genotype selection index (IGSI) were calculated to select superior genotypes using 16 agronomical characteristics.

Results: Although by considering the 30% selection intensity, the genotypes selected by the MGIDI and IGSI indices in the three locations were somewhat different, the ICG192 groundnut genotype was selected as a superior genotype in all three areas based on both MGIDI and IGSI indices.

Conclusion: The results revealed relative compliance between the MGIDI and IGSI indices in the selection of superior genotypes, and they may be used for genotype selection based on multiple traits.

Cite this article: Rasekh SZ, Karimzadeh G, Ghassempour A. 2024. Selecting superior groundnut (*Arachis hypogaea* L.) genotypes using multi-trait selection indices. J Plant Physiol Breed. 14(1): 33-50. https://doi.org/10.22034/JPPB.2024.60718.1331

Introduction

Groundnut (*Arachis hypogaea* L.) is an important annual oilseed and protein crop cultivated on about 31.57 million hectares with a production of ~53.64 million tons worldwide (FAO 2022). The peanut cultivation area in Iran covers approximately 1300 hectares. An estimated 90% of Iran's peanut production occurs in the Guilan province, particularly in the Astana Ashrafieh area (Nobahar *et al.* 2019). The prevalent variety of peanuts in this area is Goli or NC2 which is known for its low harvest index and extended growth cycle. Introducing new germplasm is a crucial approach to fostering the early development of high-yielding cultivars in the region.

Critical genotype by environment (G×E) interaction intuitively decreases the association between genotype and phenotype, making it troublesome to distinguish top genotypes and achieve breeding advancement (Delacy *et al.* 1996). One of the important methods introduced in the analysis of multi-environment trial data is the restricted maximum likelihood (REML) method, which is based on Henderson's theoretical model (Henderson 1984), estimating variance components by providing genetic correlations, and flexibility in linear models for analysis. Balanced and unbalanced data, high usefulness in bulked and alpha lattice tests plus reduction of the negative estimates of genetic parameters are among the advantages of using this method (Searle *et al*. 1992; Liu *et al*. 1997; Holland 2006).

Grain yield is a complex trait influenced by polygenes and environmental factors. Successful selection of superior genotypes based on grain yield and other agronomic characteristics has stood as a challenge for plant breeders. Multivariate information is common in biological experiments and utilizing the data on different traits is crucial to form better choices for treatment suggestions or genotype determination. In any case, recognizing genotypes/treatments that combine high performance over several characteristics has been a challenging assignment. Several linear selection indexes (Céron-Rojas and Crossa 2018) can help breeders select better genotypes. A simple linear phenotypic selection index that is easy to use (Bhering *et al.* 2012; Bizari *et al.* 2017; Burdon and Li 2019; Jahufer and Casler 2015) is the Smith-Hazel (SH) index (Hazel 1943; Smith *et al.* 1936). To calculate the SH index, breeders use the matrix of phenotypic and genotypic (co)variances and the economic weight vector to determine how to select the vector of index coefficients to establish the relationship between genetic and phenotypic values. Since the SH index requires transformation of the phenotypic covariance matrix (Smith 1936), the presence of multicollinearity (which can occur when measuring more than one trait) can result in poorly conditioned matrices and biased index coefficients, thus, affecting the estimates of genetic gains. In addition to multicollinearity issues,

breeders often face difficult choices about distributing economic value and translating it into true economic weights (Bizari *et al.* 2017). The MGIDI index was found to have many practical applications since it allows a unique and easy-to-interpret selection process. In addition to dealing with collinear traits, the MGIDI index doesn't require the use of economic weights such as in the SH index, in which one can predict genetic and economic gains for various possible combinations of genetic parameters and assumed economic weights (Bizari *et al.* 2017; Burdon and Li 2019). Olivoto and Nardino (2021) evaluated 44 wheat genotypes for 14 agronomic traits. In their study, the MGIDI index outperformed the FAI-BLUP and SH indexes in selecting traits with desired gains. Furthermore, the MGIDI index was computationally more efficient. Yue et al. (2022b) examined 12 agronomic traits of 28 maize genotypes in a 2-year field experiment across 24 environments. They compared MGIDI, FAI-BLUP, Smith-Hazel, and MTSI methods for genotype ranking. The study indicated MGIDI's superiority over the other methods, suggesting that it is an optimal tool for selecting genotypes based on multiple traits. Pour-Aboughadareh and Poczai (2021) studied 180 wild relatives of wheat and landraces from the *Triticum* and *Aegilops* genera under control and water-deficit stress. After 30 days of stress treatment, seedlings were sampled and 23 traits were assessed. MGIDI, Smith-Hazel (SH), and factor analysis and ideotype design (FAI) were employed to identify preferred accessions with favorable root and physiological traits. The findings underscored the effectiveness of selection indices, particularly MGIDI, for choosing superior plant genetic materials through multi-trait evaluation in the early growth phase. Also, the IGSI index has been used to select the best genotypes by integration of different drought tolerance indices (Zali *et al.* 2019), stability analysis parameters (Zali *et al.* 2015; Najafi Mirak *et al.* 2018), and different morphological and phenological traits (Abdollahi Hesar *et al.* 2020). These indices focus on the selection of superior genotypes using multiple traits. So, examining the overall response of genotypes and selecting superior genotypes becomes more efficient (Olivoto and Nardino 2020).

The lower the MGIDI value of a genotype, the smaller the distance from the ideal genotype, so it is considered a superior genotype. Concerning IGSI, the most superior genotypes have the lowest deviation from the positive perfect genotype and the highest distance from the negative one. The IGSI value is in the range of 0-1. If it is near 1, the genotype is near ideal; if it is near 0, the underlying genotype is near the non-ideal type. However, the application of these selection indices has not been detailed in groundnut breeding. This research aimed to select suitable peanut genotypes using the MGIDI and IGSI indices based on multi-trait considerations.

Materials and Methods

In this study, 11 groundnut (*A. hypogaea* L.) genotypes provided by the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) were evaluated during two cropping seasons (2019-2020 and 2020-2021) in three different locations, including Talesh, Masal, and Rasht, northern Iran. Descriptions of the experimental sites are given in Table 1. The experiment layout was a randomized complete block design with three replications. Each plot included three rows of five-meters long, a row space of 50 cm, and 20 cm between plants on the rows. The evaluated agronomic traits were plant height, number of secondary branches, pod number per plant, seed number per pod, 100-seed weight, pod length, pod width, seed length, seed width, dry forage yield, total pod yield, biomass, seed yield, harvest index, seed oil percentage, and oil yield.

The variance component estimates for each trait were obtained by REML, using the following model:

$$Y = Xr + Zg + Wi + e$$

Where Y is the data vector, Xr is the fixed effect, Zg is the random genotypic effect, Wi is the random effect of the G×E interaction, and e is the random residual.

The broad sense heritability for each trait was calculated based on variance component estimates as shown below:

$$h^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_p^2} = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \hat{\sigma}_r^2 + \hat{\sigma}_{gr}^2}$$

Where $\hat{\sigma}_g^2$ is the estimated genetic variance; $\hat{\sigma}_r^2$ is the estimated environmental variance, and h^2 is heritability on the plot mean basis. CV_g, the genetic coefficient of variation, and CV_r, the environmental coefficient of variation, were also calculated for the evaluated traits:

$$CV_g = \frac{\sqrt{\hat{\sigma}_g^2}}{\bar{X}} \times 100$$

$$CV_r = \frac{\sqrt{\hat{\sigma}_r^2}}{\bar{X}} \times 100$$

The significance of genotype, environment, and G×E interaction effects was verified using the likelihood ratio test. The analysis was performed in the R (V.4.2.3) software with the "metan" package.

We used MGIDI, proposed by Olivoto and Nardino (2020), to rank genotypes based on multiple traits. First, the data were rescaled between 0 and 100 to generate an idiotypic matrix followed by factor analysis, according to Olivoto and Nardino (2020). The MGIDI was then calculated as the Euclidean distance between a genotype and the ideal genotype based on each factor score:

Table 1. The experimental sites and geographical characteristics of test environments.

Location	Year	Latitude, longitude	Altitude (m)	Monthly precipitation (mm)						Monthly temperature (°C)					
				March	April	May	June	July	August	March	April	May	June	July	August
Talesh	2019	37.80° N	80	145.00	68.60	7.40	51.30	23.90	117.70	12.00	17.80	23.90	25.90	26.00	22.80
	2020	48.90° E		180.80	109.00	7.10	30.70	148.80	190.20	11.40	16.60	23.90	26.00	25.40	23.80
Masal	2019	37.36° N	84	107.60	60.00	6.30	91.70	24.50	67.30	13.20	18.50	25.70	27.00	26.80	23.80
	2020	49.13° E		100.00	47.90	2.90	10.40	138.00	27.80	13.10	18.80	25.40	27.50	26.30	25.10
Rasht	2019	37.27° N	4	122.70	74.50	6.20	171.10	25.30	138.00	13.20	19.30	24.70	26.20	25.80	22.90
	2020	49.59° E		135.50	67.50	0.30	19.80	103.20	97.70	12.20	17.90	24.80	26.70	25.20	24.00

$$\mathrm{MGIDI_i} = \left[\sum_{j=1}^{f}\left(\gamma_{ij} - \gamma_j\right)^2\right]^{0.5}$$

Where $MGIDI_i$ is the multivariate distance index from the ideal genotype for the i_{th} genotype, and γ_{ij} and γ_j are the scores of the ith genotype and the ideal type for the jth factor, respectively. The genotypes with the lowest MGIDI are close to the ideal genotype and thus provide desired values for the measured traits. A selection intensity of 30% was considered for calculating the selection differential for the studied traits. Also, the contribution of each factor in the MGIDI index of the i_{th} genotype (ω_{ij}), was used to determine the genotype advantages and disadvantages and was calculated as:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f}\sqrt{D_{ij}^2}}$$

where D_{ij} is the distance between the i_{th} genotype and the ideal genotype for the j_{th} factor (Olivoto and Nardino 2020).

Also, IGSI (Zali *et al.* 2015) was used to select desirable genotypes by considering multiple traits simultaneously. The normalized (r_{ij}) values of the j^{th} genotype (j = 1, 2, ..., n) for the i^{th} trait (i = 1, 2, ..., m) were calculated as:

$$r_{ij} = \frac{X_{ij}}{\sqrt{\sum_{ij}^{n} X_{ij}^2}}$$

Then, the r_i^+ and r_i^- values were determined, corresponding to the normalized values of the favorable and the unfavorable genotypes for each trait, respectively. The two distances denoted by d_i^+ and d_i^- were used to measure the distance of each genotype from either the favorable or unfavorable genotype:

$$d_i^+ = \sqrt{\sum_{i=1}^{n}\left(r_{ij} - r_j^+\right)^2}$$

$$d_i^- = \sqrt{\sum_{i=1}^{n}\left(r_{ij} - r_j^-\right)^2}$$

$$IGSI = \frac{d_i^-}{d_i^+ + d_i^-}$$

Additionally, a heatmap was generated to assess the interrelationships between various genotypes and corresponding traits. The heatmap was drawn in the R (V.4.2.3) software with the "gplots" package. Factor analysis based on principal component analysis was performed in the R (V.4.2.3) software with the "metan" package. In this method, factors with eigenvalues ≥ 1 were selected and factor loadings greater than 0.5, regardless of their sign, were considered significant coefficients for each independent factor. The largest factor coefficient among the coefficients of each factor represents the factor to which the said attribute is assigned.

Results and Discussion

A significant difference was observed through the likelihood-ratio test at a 1% probability among genotypes concerning various plant characteristics including plant height, number of secondary branches, 100-seed weight, pod length, pod diameter, dry forage yield, total pod yield, biomass, seed yield, harvest index, oil percent, and oil yield, as shown in Table 2. The environmental effect was notable across all characteristics examined, except for seed length. Furthermore, G×E interaction played a significant role in all traits as indicated in Table 2. The relative genotypic and environmental coefficients of variation were greater than 1.0 for certain traits such as plant height, pod diameter, dry forage yield, total pod yield, biomass, seed yield, seed oil percent, and oil yield, while they were below 1.0 for others like the number of secondary branches, pod number per plant, seed number per pod, 100-seed weight, pod length, seed length, seed diameter, and harvest index. The accuracy of genotype selection for 16 characteristics varied from 0 (seed length) to 0.975 (biomass), with biomass, total pod yield, and pod diameter exhibiting the highest selective accuracies. Notably, the most significant coefficients of genetic variance were observed as 15.51%, 15.1%, and 10.3%, for oil yield, seed yield, and fresh forage yield, respectively. Coefficients of determination for G×E interaction effects were high for seed length, seed diameter, and seed oil percent, underscoring the substantial contribution of the G×E interaction variance to the overall phenotypic variance, as shown in Table 2.

Heritability estimates based on entry mean suggested a predominant influence of genetic effects on most assessed traits.

The assessment of 12 morphological traits related to yield by Samadi Gorji *et al.* (2018) indicated significant differences between genotypes for all traits. The broad sense heritability in their study varied from 80.25% (seed width) to 99.54% (100-seed weight), with a value of 96.85% for seed yield. The highest phenotypic and genotypic variation coefficients were associated with pod weight. Fondra *et al.* (2000) identified pod number per plant, pod length, number of seeds per pod, seed weight, pod weight, and seed width as crucial traits in evaluating diversity among peanut genotypes. Additionally, Golaktya and Makneh (1991) pointed out that the main stem height and the ratio of seed to pod volume encompassed the most genetic diversity among 18 groundnut genotypes. Investigating 10

Table 2. Likelihood ratio test and estimates of genetic parameters for 16 agronomic traits of 11 groundnut genotypes.

Traits	Genetic parameters									
	LRT_g	**LRT_{ge}**	**E/F**	**δ^2_p**	**R^2_{ge}**	**h^2_g**	**As**	**CV_g**	**CV_r**	**CV_g/CV_r**
PH	10.953^{***}	100.429^{***}	80.70^{***}	82.7	0.517	0.757	0.87	8.01	6.24	1.28
NSB	17.1269^{***}	6.3179^{*}	25.20^{***}	2.42	0.152	0.823	0.907	9.75	14.4	0.679
NPP	16.313^{ns}	28.070^{***}	21.75^{***}	11.8	0.297	0.816	0.904	9.3	10.3	0.902
SNPP	0.66^{ns}	53.085^{***}	5.973^{***}	0.0075	0.547	0.317	0.563	1.21	3.33	0.363
SW	8.045^{**}	58.368^{***}	4.973^{***}	18.4	0.464	0.708	0.841	3.46	4.02	0.862
PL	8.006^{**}	44.683^{***}	18.93^{***}	6.49	0.42	0.707	0.841	3.6	4.65	0.774
PD	28.441^{***}	14.994^{***}	34.52^{***}	1.44	0.186	0.887	0.942	5.48	5.34	1.03
SL	0^{ns}	155.12^{***}	1.534^{ns}	3.06	0.834	0	0	0	4.77	0
SD	1.975^{ns}	132.597^{***}	9.419^{***}	0.375	0.714	0.474	0.689	3	3.63	0.825
DFY	25.911^{***}	78.992^{***}	5.764^{***}	306649	0.352	0.876	0.936	10.2	6.04	1.7
TPY	35.421^{***}	70.602^{***}	43.16^{***}	218689	0.282	0.911	0.954	9.95	5.16	1.93
BY	56.390^{***}	50.919^{***}	12.41^{***}	711163	0.172	0.951	0.975	9.66	4.19	2.31
SY	28.548^{***}	86.931^{***}	31.34^{***}	187925	0.342	0.888	0.942	15.1	8.03	1.88
HI	5.771^{*}	87.017^{***}	28.68^{***}	13.5	0.562	0.653	0.808	5.92	6.45	0.919
OP	9.057^{**}	276.966^{***}	25.73^{***}	2.74	0.662	0.727	0.853	1.76	0.626	2.81
OY	27.91^{***}	79.11^{***}	25.84^{***}	52612	0.3378	0.8851	0.9408	15.51	8.759	1.771

***Significant at $p \leq 0.001$; **Significant at $p \leq 0.01$; *Significant at $p \leq 0.05$; ^{ns}nonsignificant. LRT_g and LRT_{ge}: Likelihood ratio tests for genotype and genotype by environment interaction (GEI), respectively; E/F: The F value for environment effects; δ^2_p: Phenotypic variance; R^2_{ge}: The coefficient of determination for GEI effects; h^2_g: Heritability based on entry mean; As: The accuracy of genotype selection; CV_g and CV_r: The genotypic and environmental coefficients of variation, respectively; PH: Plant height; NSB: Number of secondary branches; NPP: Pod number per plant; SNPP: Seed number per pod; SW: 100-seed weight; PL: Pod length; PD: Pod diameter; SL: Seed length; SD: Seed diameter; DFY: Dry forage yield; TPY: Total pod yield; BY: Biomass; SY: Seed yield; HI: Harvest index; OP: Seed oil percent; OY: Oil yield.

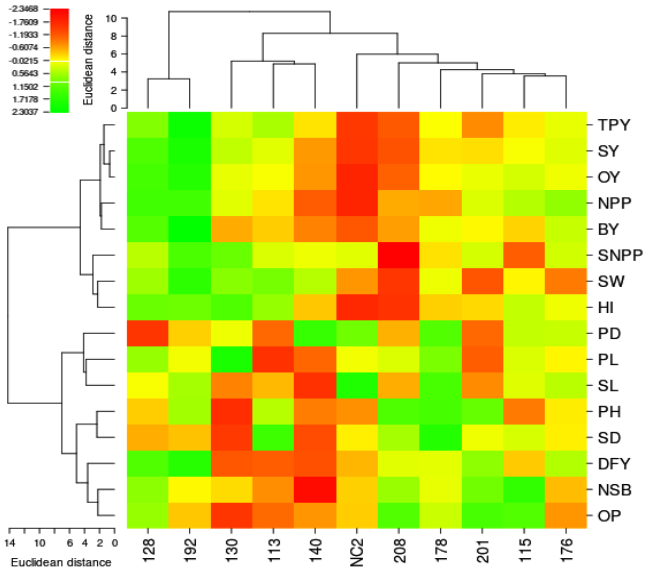
peanut genotypes, Vange and Maga (2014) discovered a substantial coefficient of genotypic variation and genetic advance for the number of pods per plant, the number of branches per plant, and seed yield.

Figure 1 shows the two-way heatmap clustering pattern to group the genotypes and analyze the measured traits based on the average of two years of data at each location. The genotypes were divided into two clusters in Talesh (Figure 1a). The first cluster included the genotypes 192 and 128. These genotypes had higher plant height, number of secondary branches, pod number per plant, seed number per pod, 100-seed weight, pod length, dry forage yield, total pod yield, biomass, seed yield, harvest index, seed oil percentage, and oil yield. The second cluster included other genotypes (115, 178, 176, 140, 201, 208, 130, NC2, and 113) that had lower values than the mean for all traits except pod diameter, seed length, and seed diameter (Figure 1a). The genotypes in Masal were divided into two clusters (Figure 1b). The first cluster included the genotype 192. This genotype had higher values than the mean for all traits except seed diameter and seed oil percentage. Other genotypes were included in the second cluster, which had lower values than the mean for all the traits except for seed diameter and seed oil percentage. In Rasht, genotypes were divided into two clusters (Figure 1c). The first cluster consisted of the genotypes 192 and 128. These genotypes had higher values than the mean for all traits. In contrast, genotypes in the second cluster (115, 178, 176, 140, 201, 208, 130, NC2, and 113) had lower values than the mean for all traits (Figure 1c). Therefore, the two-side dendrogram can show relationships between groundnut genotypes and measured traits. Likewise, Pour-Aboughadareh *et al.* (2021) used the two-way heatmap clustering pattern to find the relationships among the 20 investigated barley genotypes and 18 measured growth and physiological traits under salinity stress conditions. Considering the genetic diversity of 76 peanut genotypes from the National Plant Seed Bank of Iran, Aalami *et al.* (2007) observed relatively low diversity in morphological traits. Foundra *et al.* (2000) conducted cluster analysis and principal component analysis on 14 morphological traits in a population of 86 peanuts, highlighting pod length, number of seeds in the pod, pod weight, and seed weight as key characteristics for evaluating diversity. Cluster analysis using Ward's method classified these genotypes into nine groups.

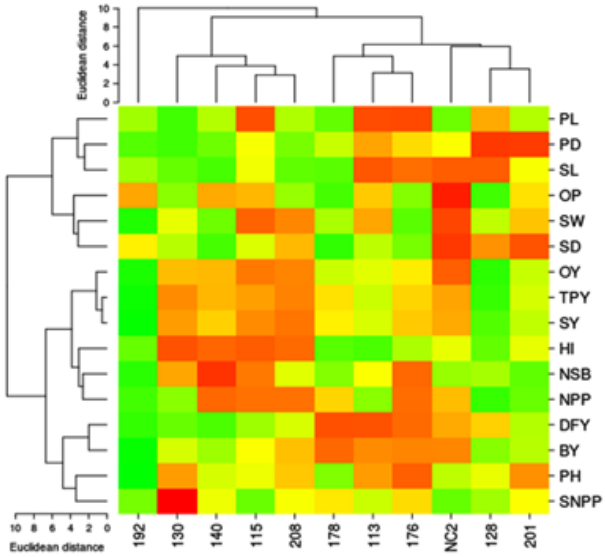
Based on the factor analysis in Talesh, four factors with eigenvalues greater than 1 were chosen, which determined 85.80% of the total variation (Table 3). Seed yield, oil yield, biomass, total pod yield, pod number per plant, harvest index, 100-seed weight, dry forage yield, and pod diameter were comprised in Factor 1. Factor 2 consisted of seed oil percentage, number of secondary branches, and seed number per pod. Factor 3 included pod length, seed width, and plant height, and Factor 4

included seed length and pod width. The average communality was 0.858 with a range of 0.506-0.997, which means that these factors explained a large part of the variables' variance (Table 3).

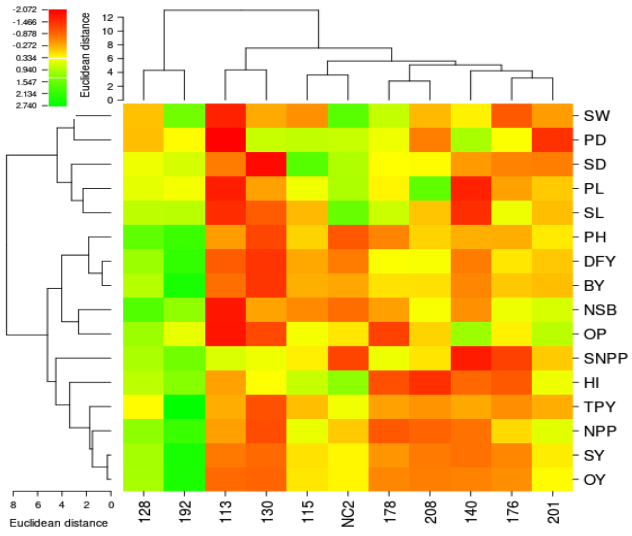
In Masal, five factors with eigenvalues greater than 1 were chosen, which explained 92.98% of the total variation (Table 3). Oil yield, seed yield, total pod yield, pod number per plant, biomass, number of secondary branches, 100-seed weight, and plant height were included in Factor 1. Factor 2 comprised of pod length, seed length, and pod diameter. Factor 3 included dry forage yield and harvest index, and Factor 4 included seed width. The remaining two traits, the number of seeds per



(a)



(b)



(c)

Figure 1. Heatmap and grouping of groundnut genotypes and traits in a) Talesh, b) Masal, and c) Rasht. Colors are representative of a relative scale (-2 to +2) derived after data standardization. The red indicates lower values, and the green indicates higher values.

SW: 100-seed weight; PD: Pod diameter; SD: Seed diameter; PL: Pod length; SL: Seed length; PH: Plant height; DFY: Dry forage yield; BY: Biomass; NSB: Number of secondary branches; OP: Seed oil percent; SNPP: Seed number per pod; HI: Harvest index; TPY: Total pod yield; NPP: Pod number per plant; SY: Seed yield; OY: Oil yield.

pod and seed oil percentage were included in Factor 5. The average communality was 0.93 with a range of 0.80-0.99, indicating that these factors explained a large part of the variables' variance (Table 3).

In Rasht, four factors with eigenvalues greater than 1 were chosen, which explained 84.95% of the total variation (Table 3). Factor 1 consisted of the number of secondary branches, plant height, dry forage yield, biomass, and seed oil percentage. Harvest index, seed yield, total pod yield, oil yield, and pod number per plant were included in Factor 2. Factor 3 comprised pod length, seed length, 100-seed weight, and seed diameter. Factor 4 included the seed number per pod and pod diameter. The average communality was 0.84 with a range of 0.52-0.99, which indicated that these selected factors explained a considerable portion of the variance of the variables (Table 3). Safari *et al.* (2012) found two significant canonical variables, with one concentrating on the weight of 100 seeds, oil yield, the weight of 100 pods, the ratio of seed volume to pod volume, and the number of pods per plant, playing a critical role in distinguishing cultivars.

Table 3. The eigenvalues and explained proportion of variance in the factor analysis, and the factor loadings after varimax rotation for groundnut traits in three regions.

	Talesh				**Masal**					**Rasht**			
Traits	**FA1**	**FA2**	**FA3**	**FA4**	**FA1**	**FA2**	**FA3**	**FA4**	**FA5**	**FA1**	**FA2**	**FA3**	**FA4**
BY	0.923	0.142	-0.185	0.165	0.729	0.110	0.661	-0.003	0.129	0.715	0.449	0.405	0.209
DFY	0.595	0.513	-0.313	0.279	0.203	0.292	0.927	0.007	0.074	0.795	0.264	0.424	0.236
HI	0.845	-0.152	0.326	-0.186	0.671	-0.183	-0.688	0.010	0.104	0.024	0.878	0.118	-0.056
NPP	0.893	0.365	0.099	-0.084	0.813	0.014	0.017	-0.424	-0.281	0.646	0.705	0.081	0.093
NSB	0.154	0.901	-0.001	0.199	0.671	0.378	-0.322	-0.454	0.183	0.889	0.054	0.238	-0.015
OP	-0.136	0.864	-0.298	-0.020	0.197	-0.052	-0.257	0.346	-0.758	0.710	0.185	0.048	-0.608
OY	0.978	0.133	0.025	-0.038	0.985	-0.084	-0.034	0.074	-0.098	0.575	0.754	0.301	0.062
PD	-0.492	-0.496	0.151	0.430	-0.189	0.642	0.386	0.479	0.101	-0.111	0.127	0.402	-0.676
PH	0.055	0.315	-0.874	0.036	0.622	0.456	0.114	0.200	0.552	0.847	0.431	0.057	0.239
PL	0.130	0.221	0.621	0.593	0.034	0.929	0.098	-0.171	-0.132	0.245	-0.071	0.863	0.077
SD	-0.130	0.158	-0.797	0.215	-0.103	0.063	-0.094	0.928	-0.220	0.182	0.311	0.621	-0.080
SL	-0.016	0.049	-0.257	0.909	-0.112	0.698	0.387	0.421	-0.174	0.263	0.225	0.827	-0.076
SNPP	0.608	-0.553	0.200	0.101	0.201	-0.345	-0.182	-0.100	0.837	0.208	0.333	0.111	0.820
SW	0.700	-0.544	0.157	0.022	0.645	0.071	0.173	0.634	-0.144	0.006	0.443	0.700	-0.311
SY	0.995	-0.009	0.084	0.002	0.981	-0.028	0.075	0.002	0.161	0.539	0.766	0.316	0.134
TPY	0.944	-0.250	-0.008	0.008	0.978	-0.131	0.038	-0.031	0.135	0.428	0.765	0.297	0.119
Eigenvalues	6.78	3.81	1.58	1.56	6.07	3.77	2.30	1.52	1.22	8.62	2.26	1.38	1.31
Variance (%)	42.37	23.78	9.88	9.77	37.95	23.55	14.40	9.48	7.60	53.87	14.14	8.64	8.20
Cumulative V. (%)	42.37	66.15	76.03	85.80	37.95	61.50	75.90	85.39	92.98	53.87	68.02	76.66	84.95

BY: Biomass; DFY: Dry forage yield; HI: Harvest index; NPP: Pod number per plant; NSB: Number of secondary branches; OP: Seed oil percent; OY: Oil yield; PD: Pod diameter; PH: Plant height; PL: Pod length; SD: Seed diameter; SL: Seed length; SNPP: Seed number per pod; SW: 100-seed weight; SY: Seed yield; TPY: Total pod yield.

Multi-trait genotype-ideotype distance index (MGIDI)

In Talesh, the selected genotypes using the MGIDI index were 192, 178, and 176 (Figure 2a), considering 30% selection intensity. The strengths and weaknesses of the genotypes showed that genotype 192 had the lowest values in Factor 1, Factor 3, and Factor 2. So, for traits that had the higher coefficients in these factors as seed yield, oil yield, biomass, total pod yield, pod number per plant, harvest index, 100 seed weight, dry forage yield, seed oil percentage, and number of secondary branches, this genotype was close to the ideal genotype (Figure 2b). Also, two selected genotypes 178 and 176 showed the lowest values for Factors 2 and 3 and were close to the ideal genotype regarding traits such as seed oil percentage, number of secondary branches, plant height, and pod length which had higher coefficients in these factors.

In Masal, the genotypes 192, 178, and 140 were selected based on the MGIDI index (Figure 2c). These genotypes were close to the ideal genotype for traits that had higher coefficients in Factor 1 (for genotype 192), Factor 2, Factor 3, and Factor 4 (for genotype 178), and Factor 3 and Factor 4 (for genotype 140). This shows that for oil yield, seed yield, total pod yield, pod number per plant, biomass, number of secondary branches, 100-seed weight, and plant height, the best-selected genotype (192) had the lowest difference from the ideal genotype. These traits were the most effective characteristics in selecting the superior genotypes (Figure 2d).

In Rasht, the genotypes 192, 128, and 115 were selected using the MGIDI index (Figure 2e). Also, based on the strengths and weaknesses of the genotypes, the best-selected genotype (192) had lower values concerning Factor 1, Factor 2, and Factor 3 and had a higher number of secondary branches, plant height, dry forage yield, biomass, seed oil percentage, harvest index, seed yield, total pod yield, oil yield, pod number per plant, pod length, seed length, 100-seed weight, and seed diameter (Figure 2f). MGIDI index has been used to select suitable genotypes in some crops. Maranna *et al.* (2021) evaluated sixty-eight advanced breeding lines of soybean (*Glycine max* L.) for yield and attributing traits. They showed that the presence of multicollinearity and difficulty in assigning economic weightage to the traits under consideration in the case of the SH index can affect genetic gain. Therefore, to overcome these weaknesses, the genotype-ideotype distance index (MGIDI) was developed which accounted for the multicollinearity issue and selected all the traits under consideration favorably. Pour-Aboughadareh *et al.* (2021) used the MGIDI index to choose the salt-tolerant barely genotypes considering all measured traits. Their results suggested that using the MGIDI index in the early growth stage can accelerate screening nurseries in barley breeding

programs. Also, Yue *et al.* (2022a) and Vahedi *et al.* (2023) used MGIDI based on multiple traits for selecting superior maize and cow cockle genotypes, respectively.

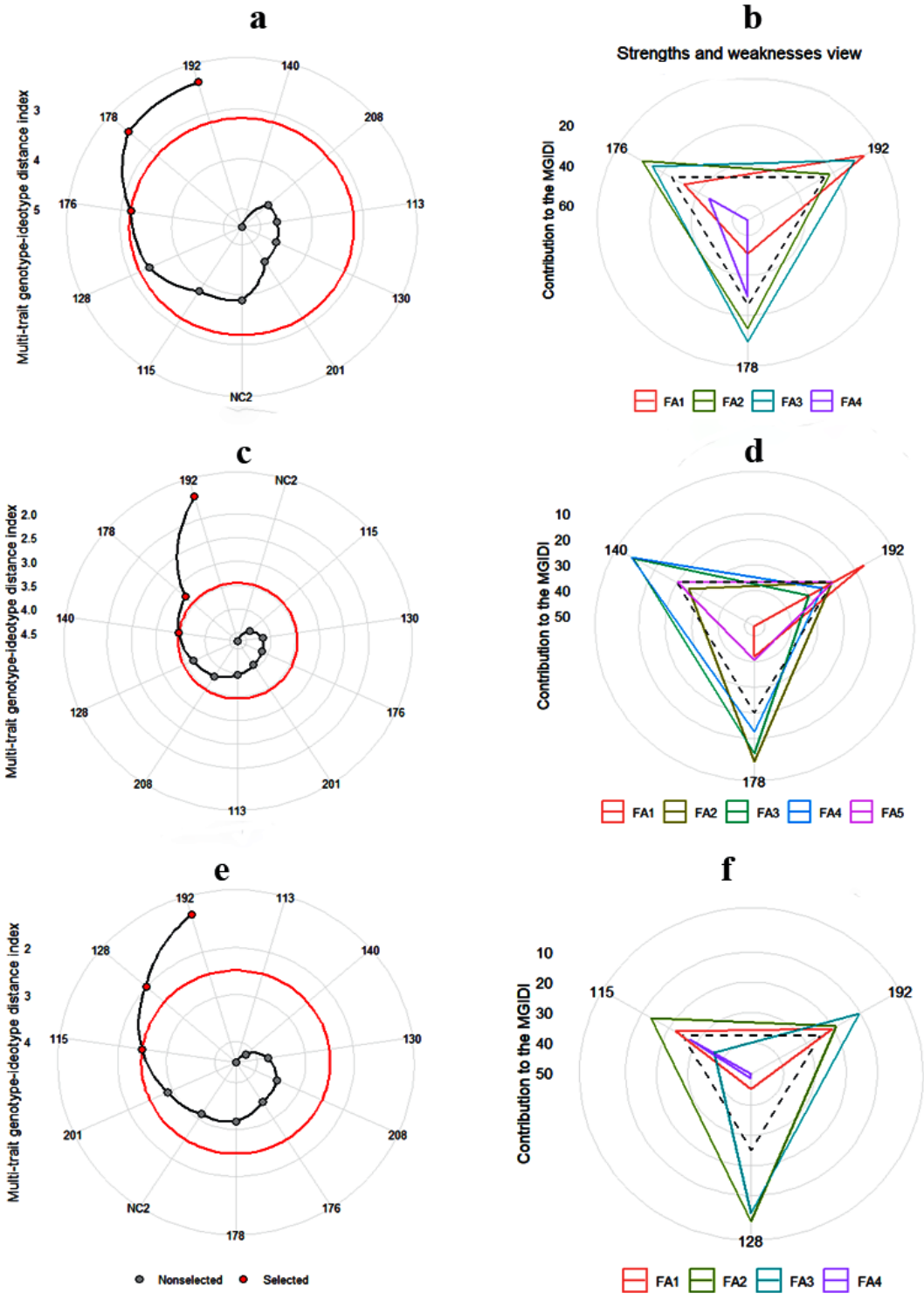


Figure 2. Genotype ranks obtained by the MGIDI index and the strengths and weaknesses of the selected genotypes based on the MGIDI index in Talesh (a, b), Masal (c, d), and Rasht (e, f). The selected genotypes are represented in red circles considering 30% selection intensity.

In Talesh, the selection differential was positive for all traits except for seed oil percentage and the number of secondary branches. Among the characteristics, oil yield (14.40%), seed yield (14.38%), and dry forage yield length (12.18%) showed the highest selection differential percentage (SD%) (Table 4). In Masal, the selection differential was positive for all traits except for pod number per plant. Seed yield (7.26%), seed length (7.49%), and seed diameter (6.55%) showed the highest SD% in this location (Table 4). In Rasht, selection differentials were positive for all traits. Oil yield (21.52%), seed yield (20.43%), and plant height (16.81%) showed the highest SD% (Table 4).

IGSI index

According to IGSI in Talesh, the genotypes 192 and 128 as evidenced by their highest IGSI values (0.80 and 0.72, respectively) showed the most favorable performance. Conversely, genotypes NC2, 140, and 208 displayed poorer performance, indicated by their low IGSI values of 0.22, 0.27, and 0.35, respectively (Table 5). In Masal, genotype 192 had the highest IGSI value (0.86), and genotypes

Table 4. Estimates of the grand mean (X_o), mean of the selected genotypes (X_s), and selection differential percentage (SD%) in three locations for groundnut.

Traits	Masal				Rasht				Talesh			
	Factor	X_o	X_s	%SD	Factor	X_o	X_s	SD%	Factor	X_o	X_s	SD%
BY	FA1	7425.30	7797.78	5.02	FA3	6816.67	7663.89	12.43	FA1	7615.30	8458.33	11.07
DFY	FA5	3788.64	3986.11	5.21	FA3	4037.88	4611.11	14.20	FA1	3419.70	3836.11	12.18
HI	FA5	28.94	29.52	2.00	FA1	21.31	22.95	7.71	FA1	33.13	34.20	3.23
NPP	FA1	21.64	21.59	-0.25	FA1	16.28	18.81	15.56	FA1	24.33	26.24	7.82
NSB	FA1	8.06	8.39	4.03	FA3	6.13	6.47	5.53	FA2	10.53	10.35	-1.74
OP	FA4	53.18	53.19	0.03	FA3	52.01	52.80	1.52	FA2	49.22	48.72	-1.01
OY	FA1	1139.32	1208.94	6.11	FA1	762.03	926.00	21.52	FA1	1242.56	1421.44	14.40
PD	FA2	13.88	14.75	6.21	FA2	15.19	15.46	1.84	FA2	13.33	13.67	2.50
PH	FA1	57.34	60.87	6.16	FA3	42.40	49.53	16.81	FA3	87.06	94.94	9.06
PL	FA2	31.07	32.48	4.54	FA4	34.77	35.49	2.09	FA3	33.27	33.68	1.24
SD	FA3	6.82	7.27	6.55	FA4	6.92	7.32	5.80	FA3	7.13	7.34	3.00
SL	FA2	14.56	15.65	7.49	FA4	15.16	15.83	4.38	FA4	14.74	15.36	4.25
SNPP	FA4	1.66	1.67	0.72	FA2	1.56	1.60	2.89	FA1	1.72	1.75	2.05
SW	FA1	59.13	61.79	4.50	FA4	57.48	58.42	1.63	FA1	60.85	62.04	1.96
SY	FA1	2144.62	2300.28	7.26	FA1	1466.74	1766.39	20.43	FA1	2549.55	2916.11	14.38
TPY	FA1	3631.06	3811.11	4.96	FA1	2778.79	3052.78	9.86	FA1	4195.61	4622.22	10.17

BY: Biomass; DFY: Dry forage yield; HI: Harvest index; NPP: Pod number per plant; NSB: Number of secondary branches; OP: Seed oil percent; OY: Oil yield; PD: Pod diameter; PH: Plant height; PL: Pod length; SD: Seed diameter; SL: Seed length; SNPP: Seed number per pod; SW: 100-seed weight; SY: Seed yield; TPY: Total pod yield.

176, 115, and NC2 exhibited inferior performance, indicated by their low IGSI values of 0.28, 0.30, and 0.38, respectively (Table 5). In Rasht, genotypes 192 and 128 with scores of 0.92 and 0.63 were superior. In contrast, the genotypes 113, 130, and 140 had the lowest IGSI values (0.16, 0.17, and 0.22, respectively), categorizing them as the weakest genotypes (Table 5).

The present study indicated that utilizing IGSI as a selection index can help identify suitable genotypes under varying environmental conditions. The IGSI index has been used to convert drought tolerance indices and various traits into a singular index or employ stability parameters to select superior genotypes. Zali *et al.* (2015) using the IGSI index based on various drought tolerance indices, assessed canola genotypes to identify tolerant genotypes. They indicated the efficacy of the IGSI index for the identification of drought-tolerant canola genotypes. They showed that the best genotype would be the one that has the least deviation from the positive ideal parameter and the highest deviation from the negative ideal parameter. Also, Hemadesh *et al.* (2021) employed this approach to identify the most superior barley cultivars. Our study based on the IGSI index identified genotypes 192 and 128 as superior groundnut genotypes across all three locations in northern Iran.

Conclusion

This study evaluated 16 traits of 11 groundnut genotypes across three locations in a two-year field experiment. The groundnut genotype 192 was selected as superior in all three locations based on MGIDI and genotypes 192 and 128 were superior groundnut genotypes based on the IGSI index.

Table 5. Ideal genotype selection index (IGSI) values, and the ranking of groundnut genotypes in the three studied locations.

Genotype	Code	Talesh		Masal		Rasht	
		IGSI	Rank	IGSI	Rank	IGSI	Rank
ICG130	130	0.47	8	0.42	5	0.17	10
ICG140	140	0.27	10	0.39	6	0.22	9
ICG113	113	0.50	7	0.38	8	0.16	11
ICG115	115	0.52	4	0.30	10	0.39	4
ICG128	128	0.72	2	0.55	2	0.63	2
ICG176	176	0.52	3	0.28	11	0.31	8
ICG178	178	0.51	5	0.50	4	0.32	6
ICG192	192	0.80	1	0.86	1	0.92	1
ICG201	201	0.50	6	0.51	3	0.39	5
ICG208	208	0.35	9	0.38	7	0.31	7
NC2	NC2	0.22	11	0.38	9	0.40	3

Acknowledgments

We thank the Vice-chancellor for Research and Technology at the University of Mohaghegh Ardabili, Ardabil, Iran, and the Rasht Agricultural Research, Education, and Extension Organization (AREEO) in Rasht, Iran, for their funding and support.

Ethical considerations

The authors avoided data fabrication and falsification.

Conflict of interest

The authors declare that they have no conflict of interest with any organization concerning the manuscript's subject.

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