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Genetic Architecture and Yield Stability of Autumn-Sown Chickpea Landraces in Semi-Arid Environments

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Abstract

Shifting chickpea (*Cicer arietinum* L.) cultivation from spring to autumn is a promising strategy to escape terminal drought and maximize yield potential in semi-arid regions; however, success depends on identifying genotypes with suitable phenology and yield performance. This study evaluated 332 desi chickpea genotypes (330 landraces, two checks) over two seasons (2021–2022) under autumn-sown rainfed conditions in western Iran, using Linear Mixed Models (LMM), Genotype × Yield × Trait (GYT) biplots, Structural Equation Modeling (SEM), and the Multi-Trait Genotype-Ideotype Distance Index (MGIDI). Results revealed trait-dependent genetic variation, with heritability highest for hundred-seed weight (H^2 = 94.9%) and moderate for plant height (H^2= 40.6%) and days to flowering (H^2= 35.1%), while seed yield showed no detectable genotypic variance under the single-replicate design. No genotype excelled across all GYT combinations, though G313 ranked highest for yield × hundred-seed weight in both years, a promising parental candidate. SEM identified plant height as the dominant trait underlying agronomic performance in both seasons, with a direct positive association with seed yield emerging in 2022, while the top genotype for the yield–height combination shifted between years (G33 in 2021, G49 in 2022). Integrating both seasons, MGIDI ranked 114 landraces above the better commercial check, with G5 first overall, confirming its identification as a GYT winner. Plant height should be one component of a broader selection strategy rather than a standalone target, given genotype × year variability and lodging risk. The identified superior landraces (G5, G313) offer valuable genetic resources for breeding climate-resilient chickpea cultivars.

Keywords: Augmented design, *Cicer arietinum* L., GYT biplot, MGIDI, Structural Equation Modeling, Terminal drought tolerance.

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Introduction

Genetic diversity among landraces is fundamental for crop improvement, providing the raw material needed to combine desirable traits such as high yield potential, adaptability, and abiotic stress tolerance (Pandey et al., 2017). In chickpea (*Cicer arietinum* L.), exploiting this variability is particularly critical for improving yield stability under autumn-sown conditions in Southwest Asia, as climate change increasingly threatens stable yields across variable environments (Theodoridis et al., 2018). Iran is an important chickpea-producing country, with about 176 thousand tonnes produced in 2022, ranking among the top ten producers worldwide (FAOSTAT, 2022). however, the narrow genetic base of cultivated chickpea has limited breeding progress, emphasizing the need for comprehensive germplasm evaluation (Meuwissen et al., 2020; Thudi et al., 2016; Varshney et al., 2021).

The unbalanced nature of augmented experimental designs necessitates advanced statistical approaches beyond conventional ANOVA for reliable genotype evaluation (Aparicio et al., 2024; Piepho et al., 2022). Recent reviews emphasize that multivariate tools such as GYT (Genotype × Yield × Trait) biplots are crucial for visualizing trade-offs and selecting high-yielding cultivars across diverse traits (Kendal, 2019; Maleki et al., 2024; Yan & Frégeau-Reid, 2018), while Structural Equation Modeling (SEM) offers a powerful framework to dissect causal pathways and integrate latent variables, providing deeper insight into yield architecture than simple correlations (Devlieger & Rosseel, 2017; Istanbuli et al., 2024; Vadithya et al., 2025; Zhu et al., 2024). Despite these advances, their combined application to unravel the genetic stability of Iranian chickpea landraces remains underexplored. This study therefore aimed to: (i) assess genetic variability and heritability in a large desi chickpea panel using advanced mixed-model approaches; (ii) visualize genotype superiority and trade-offs by combining yield with agronomic traits via GYT biplots; (iii) dissect the direct and indirect pathways influencing seed yield through SEM; and (iv) identify genotypes with superior combined multi-trait performance using MGIDI. To the best of our knowledge, this is the first comprehensive evaluation of a large collection of Iranian desi chickpea landraces under autumn sowing conditions, integrating mixed-model-based genetic parameter estimation with structural equation modeling to identify yield-determining trait relationships. Ultimately, this integrated framework aims to enhance selection efficiency for autumn sowing in semi-arid environments.

Materials and Methods

Over two successive cropping seasons (2020–2021 and 2021–2022), an experiment was conducted at a research station in western Iran (47.30° E, 34.33° N) to assess phenotypic variation and key morpho-agronomic traits of Iranian desi chickpea. The study involved 332 genotypes, comprising 330 Iranian desi chickpea landraces and two commercial checks ('Kaka' and 'Pirouz'), evaluated under an augmented block design(Federer, 1956) with 15 incomplete blocks per year; checks were replicated once per block (15 replications/year), while landraces were unreplicated. Trials were sown in autumn to mitigate terminal drought. Mean seasonal temperatures were 15.25°C (2020–2021) and 13.9°C (2021–2022), with total precipitation of 317.5 mm and 227.5 mm, respectively (Figure 1).

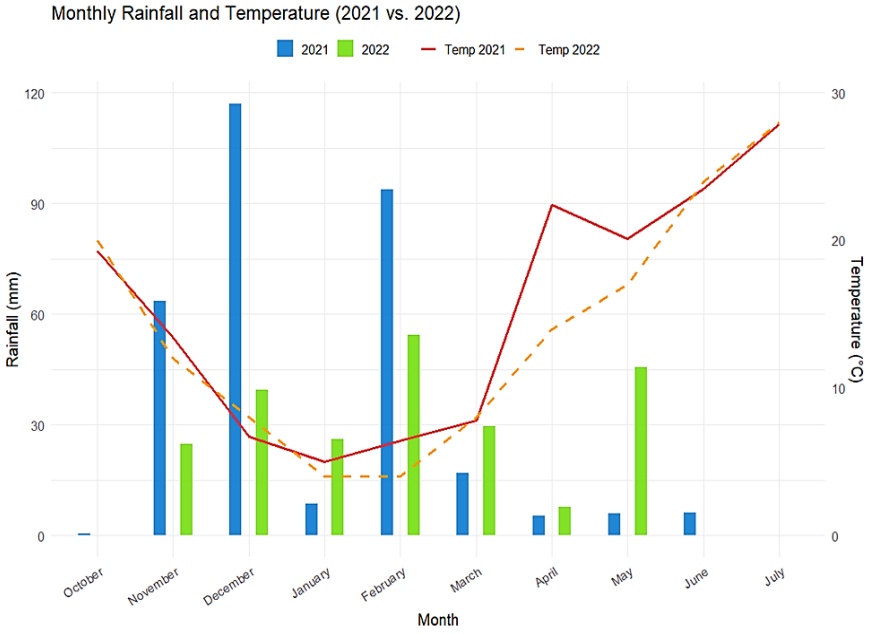

Figure 1. Monthly trends in temperature and precipitation for 2021 and 2022 at a research site located in western Iran.

Each incomplete block comprised 24 plots (22 landraces, 2 checks), with a 1.5 m gap between blocks. Plots consisted of two 4-m rows, 30 cm apart, with 8–10 cm intra-row spacing. Traits recorded followed chickpea descriptors (IBPGR, 1993): days to 50% flowering (DF), days to maturity (DM), plant height (PH, cm), primary (NPS) and secondary (NSS) stem number, pods per plant (PPP), 100-seed weight (HSW, g), and seed yield (SY, kg ha^{-1}).

Data were analyzed using R (R Core Team, 2025). based on mixed-effects models fitted via glmmTMB v1.1.7 (Brooks et al., 2017) with year and block as fixed effects and genotype and

genotype × year as random effects; year was fixed given only two available years, precluding reliable variance estimation (Piepho et al., 2008).

Broad-sense heritability (H^2) was estimated for all eight traits from Gaussian variance-component estimates obtained from the mixed-effects models, on the raw phenotypic scale. Following Holland et al. (2003) , heritability across the two years was calculated as:

$$H^2 = \frac{\sigma_G^2}{\sigma_G^2 + \frac{\sigma_{G\times Y}^2}{y} + \frac{\sigma_e^2}{y}} \quad [1]$$

where σ_G^2 is the genotypic variance, $\sigma^2_{G\times Y}$ is the genotype-by-year interaction variance, σ^2_e is the residual variance, and y is the number of years ($y = 2$). The same procedure was applied to all eight traits to ensure consistency and interpretability.

Genotype × Yield × Trait (GYT) biplot analysis followed Yan and Yan and Frégeau-Reid (2018). Yield-trait indices were calculated in Excel as the product of yield and each trait (Y×PH, Y×PPP, Y×NPS, Y×NSS, Y×HSW) or, for phenological traits, as the ratio of yield to DF/DM (Y/DF, Y/DM), favoring earlier genotypes. Indices were analyzed by PCA FactoMineR package v2.16 (Lê et al., 2008) visualized with ggplot2/ggrepel, and the top genotype per combination identified as the 'winning' genotype. Results were cross-validated against GGEBiplotGUI (Frutos et al., 2014) , yielding identical winners.

Structural Equation Modeling (SEM) was used to dissect causal relationships among traits and yield, partitioning correlations into direct/indirect effects while accounting for measurement error. The single-factor model initially included six traits (DF, DM, PH, HSW, PPP, SY) in 2021; HSW showed a non-significant loading in 2022 and was excluded, yielding a five-trait model that year. Multivariate outliers were removed via robust Mahalanobis distance (99% CI, $p < 0.01$; 14 of 332 genotypes excluded, final n = 318), followed by Yeo-Johnson transformation. Factor structure was defined by Exploratory Factor Analysis; fit was assessed via CFI, TLI, RMSEA, and SRMR using the 'lavaan' (Rosseel, 2012) and ‘semPlot’ (Epskamp et al., 2019) packages.

The Multi-Trait Genotype-Ideotype Distance Index (MGIDI) (Olivoto & Nardino, 2021) was calculated using the metan package (v1.19.0, R v4.5.2), based on adjusted trait means from both seasons (16 trait-year variables), given the lack of genotype replication across years. Lower values were favored for DF and DM; higher values for all other traits. Selection intensity was 15%, with six factors (eigenvalue > 1) retained. Final MGIDI figures were visualized in Python, with results numerically consistent with the R/metan output.

Results

Model Comparison and Genetic Parameters

The comparison of statistical models (Base, Interaction, and Augmented) demonstrated that accounting for spatial trends and interaction effects generally enhanced model fit (Table 1).

Table 1. Comparison of Base, Interaction, and Augmented mixed models (AIC) for eight agronomic traits in desi chickpea (2021–2022).

Model	DF	DM	PH	HSW	PPP	NPS	NSS	SY
Base Model AIC	3889.1	4038.1	4430.7	3660.3	5992.0	1909.1	2006.7	—
Interaction Model AIC	3835.7	3971.9	4426.7	3552.9	5983.6	1911.1	2004.3	11777.0
Augmented Model AIC	3832.8	3969.5	4424.4	3563.4	5987.0	1914.6	2005.3	11757.0

Abbreviations: DF, days to flowering; DM, days to maturity; PH, plant height; HSW, hundred-seed weight; PPP, pods per plant; NPS, number of primary stems per plant; NSS, number of secondary stems per plant; SY, seed yield.
—, model did not converge (non-positive-definite Hessian) under the applicable distribution at this model stage. HSW, PPP, NPS, and NSS are non-integer, right-skewed traits for which residual diagnostics indicated the Gaussian model was mis specified; AIC values for these four traits were obtained under a Tweedie distribution (log link), which outperformed the Gaussian model by 68–190 AIC points. DF, DM, PH, and SY were retained under the Gaussian model.

Table 2. Fixed- and random-effect estimates, variance components, and broad-sense heritability (H^2) from the final Augmented model for eight agronomic traits in desi chickpea (2021–2022).

Trait	Year effect	P	Var(G)	Var(G×Y)	Var(e)	Check−Test	P	H^2 (%)
DF	18.58	<0.0001	1.470	3.232	2.21	1.90	0.220	35.1
DM	29.19	<0.0001	0.789	5.453	2.16	1.03	0.562	17.2
PH	-1.52	<0.0001	3.252	2.415	7.12	1.26	0.464	40.6
HSW	-0.023 (log)	0.778	0.0804	0.00681	disp.=0.0232	0.942×	0.770	94.9
PPP	0.115 (log)	0.569	8.2×10^{-10}	0.0393	disp.=1.84	1.063×	0.560	~0
NPS	0.005 (log)	0.898	0.00537	2.0×10^{-10}	disp.=0.090	1.041×	0.511	14.5
NSS	0.193 (log)	<0.0001	0.00122	3.8×10^{-10}	disp.=0.175	1.041×	0.624	2.0
SY	-180.55	0.0056	0.003	0.009	82760	-14.38	0.674	~0

Var(G), genotype variance; Var(G×Y), year × genotype variance; Var(e), residual variance; Check−Test, estimated marginal mean difference or ratio between check and test genotypes (emmeans contrast); H^2, broad-sense heritability on a genotype-mean basis. All estimates are from the final Augmented model (value ~ year × type + block + (1|genotype)+(1|year :genotype)), weighted by replicate number (3 for checks, 1 for test genotypes).
For HSW, PPP, NPS, and NSS (fitted under Tweedie, log link), the year effect and variance components—including "Var(e)," the dispersion parameter—are on the internal log scale and not directly comparable to the untransformed values of the other four traits; Check−Test for these traits is reported as a back-transformed ratio rather than a difference, none differing significantly from 1.
$H^2 = Var(G) / [Var(G) + Var(G\times Y)/y + Var(e)/y]$ (Holland et al., 2003), y= 2 years, computed from Gaussian variance-component estimates on the raw phenotypic scale for all eight traits for consistency and interpretability. For HSW, PPP, NPS, and NSS, these Gaussian-scale H^2 values are not reproducible from the log-scale Tweedie components shown in this table, as they derive from a parallel Gaussian model; for DF, DM, PH, and SY, H^2 is directly reproducible from the values shown.

For seed yield, the genotype variance estimate (0.003) was unstable across REML/ML (0.003–0.09), and the boundary-corrected likelihood ratio test could not be completed due to non-

convergence of the reduced model; this is reported descriptively as evidence of a boundary estimate (Self & Liang, 1987) rather than a formal null result, reflecting a structural limitation of the single-replicate design.

Negative, significant year effects for PH and SY reflect less favorable conditions (lower/erratic rainfall, higher temperature stress during flowering/pod-filling) in 2022 versus 2021.

AIC favored the Augmented model for four of the eight traits (DF, DM, PH, SY); for HSW, PPP, and NSS the Interaction model was marginally preferred ($\Delta AIC < 11$), and for NPS the Base model was lowest. The Augmented model was nonetheless retained for all traits for consistency of reporting, as it uniquely incorporates the check-versus-test contrast central to the augmented design. Residual diagnostics showed a Gaussian distribution was inadequate for HSW, PPP, NPS, and NSS (non-integer, right-skewed traits); these were re-fitted under a Tweedie distribution, improving AIC by 68–190 points and yielding more stable variance-component estimates (Table 2). Broad-sense heritability (H^2) was high for HSW (94.9%), moderate for PH and DF (40.6% and 35.1%), and low for DM, NPS, and NSS (2–17%), while PPP and SY showed no detectable genotypic variance ($H^2 \approx 0\%$), confirmed by boundary-corrected likelihood ratio tests (Self & Liang, 1987). Year effects were significant for most traits, while the year × type interaction was non-significant for all eight ($P > 0.05$), indicating check cultivars and landraces responded similarly to environmental fluctuations. These results indicate substantial, trait-dependent genetic variation: HSW and PH are the most reliable targets for direct phenotypic selection, whereas PPP and SY selection will likely require multi-environment, replicated evaluation or indirect selection via correlated traits.

Genotype × Yield × Trait (GYT) Analysis

The GYT biplot analysis effectively visualized the dynamic interrelationships between yield and agronomic traits, revealing both environment-specific adaptation and genotype stability.

In the 2021 season (Figures 2 and 3), the biplots explained over 84% of the total variation. The analysis identified G33 as the superior genotype for the yield–plant height combination (Y×PH), while G5 and G15 led in yield combinations with pod number pee plant (Y×PPP) and primary stems (Y×NPS), respectively. Passport information and phenotypic summaries for these and other key genotypes referenced throughout the Results are provided in Table 4.

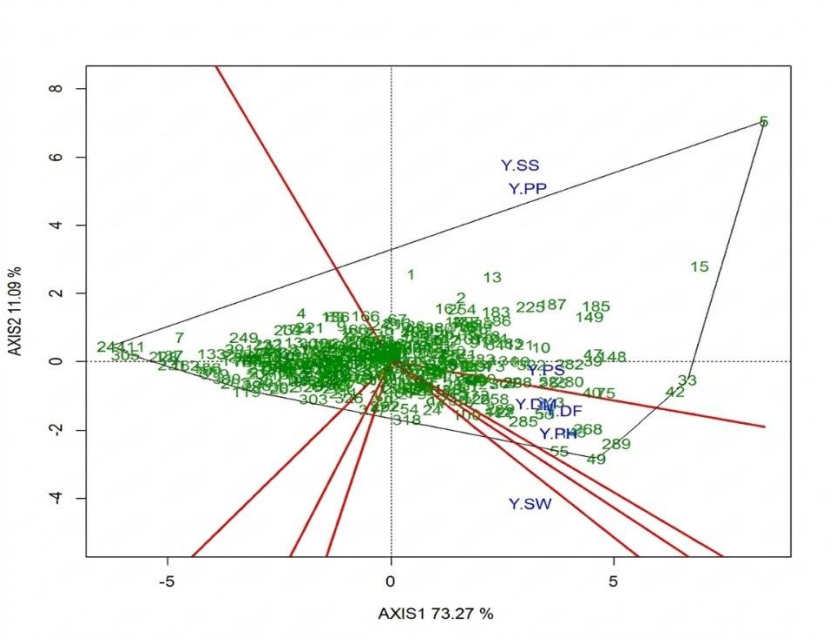

Figure 2. GYT (Genotype × Yield × Trait) biplot depicting the genotype × trait relationships based on yield performance, highlighting the winning genotypes for specific traits in 2021. The biplot was generated using the GGEBiplotGUI package in R version 4.5.0, following the GYT biplot methodology described by Yan and Frégeau-Reid (2018), with parameters set as: transform = 0, scaling = 1, centering = 2, and SVP = 2. For visual clarity, shortened labels were used in the biplot: PP for pods per plant (PPP), PS for number of primary stems per plant (NPS), and SS for number of secondary stems per plant (NSS). Other abbreviations: DF, days to flowering; DM, days to maturity; PH, plant height; SW for hundred seed weight (HSW); and Y for seed yield (SY).

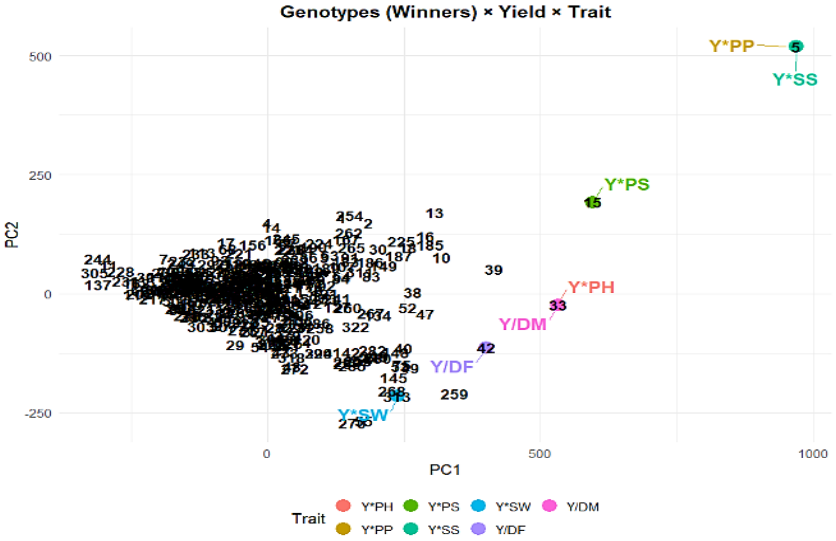

Figure 3. GYT biplot showing the winning genotypes for different agronomic traits based on yield performance in 2021, generated in R using the FactoMineR, ggplot2, and ggrepel packages.

In the 2022 season (Figures 4 and 5), the pattern of superiority shifted due to environmental changes. G49 replaced the previous winner for the yield–plant height index, and G52 emerged as the leader for yield–pod number per plant. Genotype G58 proved most effective for earliness indices (Y/DF and Y/DM) in this season.

Crucially, amidst this variability, genotype G313 exhibited remarkable stability, ranking first for the yield–seed weight (Y×SW) combination in both years. This consistent performance highlights G313 as a stable candidate for maximizing seed size, unlike other genotypes that showed transient superiority dependent on the season.

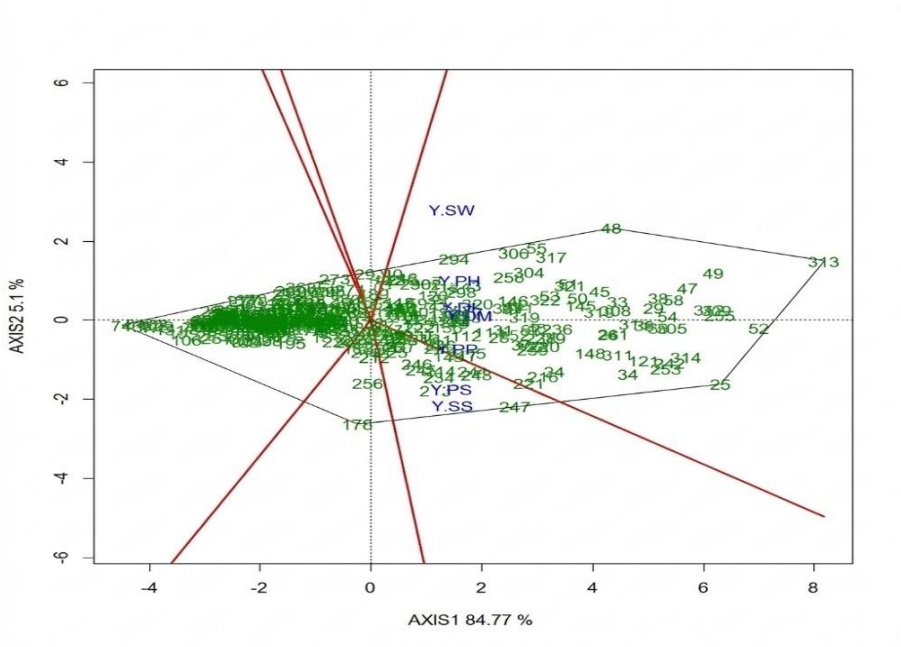

Figure 4. GYT (Genotype × Yield × Trait) biplot depicting the genotype × trait relationships based on yield performance, highlighting the winning genotypes for specific traits in 2022. The biplot was generated using the GGEBiplotGUI package in R version 4.5.0, following the GYT biplot methodology described by Olivoto and Nardino (2021), with parameters set as: transform = 0, scaling = 1, centering = 2, and SVP = 2. For visual clarity, shortened labels were used in the biplot: PP for pods per plant (PPP), PS for number of primary stems per plant (NPS), and SS for number of secondary stems per plant (NSS). Other abbreviations: DF, days to flowering; DM, days to maturity; PH, plant height; SW for hundred seed weight (HSW); and Y for seed yield (SY).

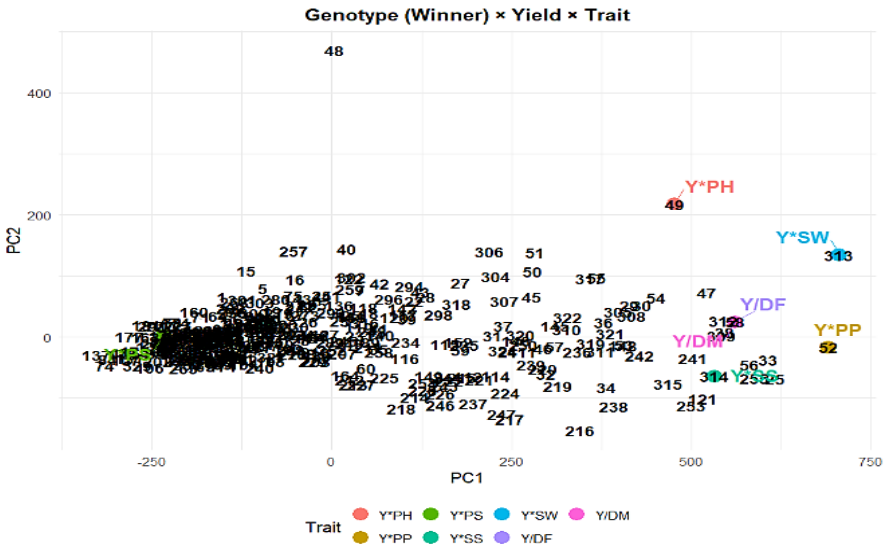

Figure 5. GYT biplot showing the winning genotypes for different agronomic traits based on yield performance in 2022. The plot was generated using the FactoMineR, ggplot2, and ggrepel packages in R.

Structural Equation Modeling (SEM) Analysis

SEM analysis provided a quantitative dissection of the causal pathways driving agronomic performance across the two distinct environments (Table 3; Figures 6 and 7). The single-factor model initially included six agronomic traits (DF, DM, PH, HSW, PPP, and SY) in 2021; however, hundred-seed weight (HSW) exhibited a non-significant factor loading in the 2022 dataset and was therefore excluded to improve model parsimony and fit, resulting in a five-trait structure (DF, DM, PH, PPP, and SY) for that year.

In 2021, the model demonstrated an excellent fit (CFI > 0.99), with PH and HSW showing the strongest standardized loadings on the latent agronomic performance variable. A key finding was the significant negative residual covariance between PPP and HSW, quantitatively confirming the physiological trade-off between seed number and size under the conditions of the first year.

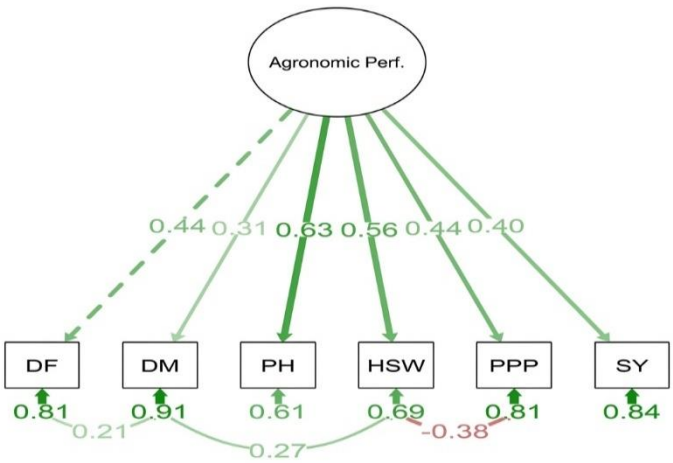

Figure 6. Structural equation modeling (SEM) of agronomic traits assessed in 2021 across a panel of 332 desi chickpea genotypes (330 landraces and 2 checks), with standardized path coefficients displayed. Plant height (PH) exhibited the highest standardized loading (β = 0.63) among all traits, indicating it was the strongest contributor to overall agronomic performance. Abbreviations: DF, days to flowering; DM, days to maturity; PH, plant height; HSW, hundred seed weight; PPP, pods per plant; SY, seed yield.

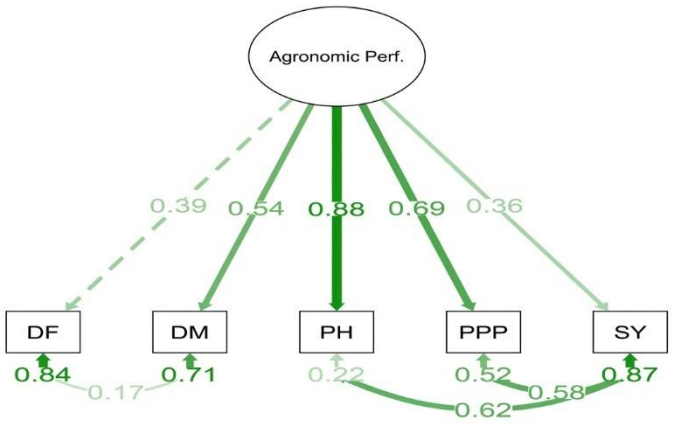

Figure 7. Path diagram of the single-factor SEM for five agronomic traits based on the 2022 dataset from the evaluation of 332 desi chickpea genotypes (330 landraces and 2 checks), with standardized coefficients indicated. Plant height (PH) exhibited the highest standardized loading (β = 0.88) among all traits, confirming its intensified role as the dominant driver of agronomic performance in this season. Abbreviations: DF, days to flowering; DM, days to maturity; PH, plant height; PPP, pods per plant; SY, seed yield.

In 2022, the architectural influence intensified. PH emerged as the dominant driver, exhibiting the highest standardized loading among all traits. Unlike the trade-offs observed in the previous year, the 2022 model revealed strong positive residual covariances (synergies) between PPP and SY, as

well as between PH and SY. These year-specific strong associations suggest that under the conditions of the second year, increased vegetative biomass and reproductive potential directly translated into yield seed without compromising other trait functions.

Table 3. Fit indices for original and modified SEM models in two independent datasets (2021 and 2022).

Index	Original (2021)	Modified (2021)	Original (2022)	Modified (2022)
Chi-square	20.579	6.409	60.112	2.721
df	7	6	5	2
p-value	0.004	0.379	0.000	0.256
CFI	0.940	0.998	0.876	0.998
TLI	0.871	0.995	0.751	0.992
RMSEA	0.078	0.015	0.198	0.036
RMSEA CI Lower	0.040	0.000	0.155	0.000
RMSEA CI Upper	0.118	0.076	0.244	0.129
SRMR	0.047	0.027	0.076	0.013
AIC	5343.064	5280.609	3486.732	3435.342
BIC	5395.777	5336.992	3523.151	3482.687

Abbreviations: Chi-square = Chi-square statistic; df = degrees of freedom; p-value = significance level; CFI = Comparative Fit Index; TLI = Tucker–Lewis Index; RMSEA = Root Mean Square Error of Approximation; SRMR = Standardized Root Mean Square Residual; AIC = Akaike Information Criterion; BIC = Bayesian Information Criterion.

Multi-Trait Genotype-Ideotype Distance Index (MGIDI)

Based on the MGIDI ranking, 114 and 59 landraces outperformed the commercial checks 'Kaka' (Check1, ranked 116th) and 'Pirouz' (Check2, ranked 60th) out of 332 genotypes, respectively, indicating that a substantial proportion of the desi chickpea landraces possess multi-trait performance superior to the currently available commercial cultivars. The top 20 highest-ranked landraces (Figure 8), led by G5, G255, G254, G145, and G245, represent the most promising genotypes for simultaneous improvement of the evaluated agronomic traits and are recommended as priority candidates for future breeding programs. Notably, genotype G5, independently identified as the winning genotype for pods per plant (YPP) and secondary stems (YSS) in the 2021 Genotype × Yield × Trait (GYT) analysis, was also ranked first overall by MGIDI (MGIDI

= 5.95), reflecting strong concordance between two independent multi-trait analytical approaches.

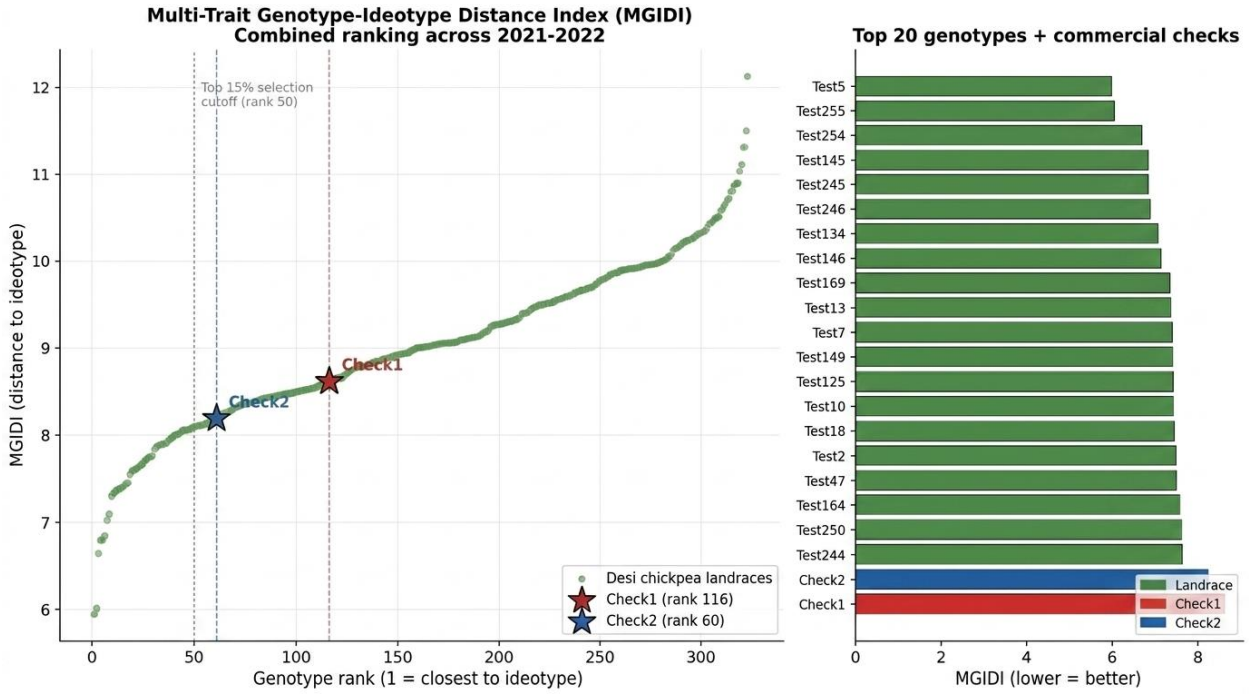

Figure 8. Multi-Trait Genotype-Ideotype Distance Index (MGIDI) ranking of 332 desi chickpea genotypes based on combined adjusted trait means from the 2021 and 2022 growing seasons. (Left) Scatter plot showing genotype rank (x-axis, 1 = closest to the ideotype) versus MGIDI value (y-axis, lower values indicate closer proximity to the ideal genotype). The dashed vertical line indicates the top 15% selection cutoff (rank 50). The commercial checks 'Kaka' (Check1, ranked 116th, MGIDI = 8.62) and 'Pirouz' (Check2, ranked 60th, MGIDI = 8.20) are highlighted with red and blue stars, respectively. (Right) Bar chart of the top 20 ranked landraces alongside the two commercial checks for comparison. MGIDI values were calculated using the metan package (v. 1.19.0) in R version 4.5.2 (2025-10-31 ucrt); the figure was generated in Python (Matplotlib) for visualization purposes.

Table 4. Passport and 2021 phenotypic summary of key landraces repeatedly referenced in the results (top performers in GYT and SEM analyses).

Origin	SY	PH	DF	Landrace
East Azerbaijan	1529	24	129	G5
Kurdistan	1492	30	136	G15
Kurdistan	1750	33	139	G33
West Azerbaijan	1658	31	136	G49
West Azerbaijan	1433	27	136	G52
West Azerbaijan	1171	26	134	G58
Kurdistan	1358	26	137	G313

DF, days to flowering; PH, plant height (cm); SY, seed yield (kg ha^{-1}).

Discussion

By combining mixed-model-based genetic parameter estimation with structural equation modeling in a large panel of Iranian desi chickpea landraces evaluated under autumn sowing, this study provides, to our knowledge, the first integrated statistical and physiological dissection of yield-determining trait relationships in this cropping system in Iran. The following sections interpret these findings in relation to genotype stability, trait architecture, and their implications for breeding strategy.

Model Comparison and Genetic Parameters

The transition from spring to autumn sowing in semi-arid regions is a critical strategy for escaping terminal drought and maximizing water use efficiency in chickpea production (Pandey et al., 2017), though success relies on identifying genotypes combining high yield potential with genetic stability across variable climatic conditions (Theodoridis et al., 2018; Varshney et al., 2021). Significant genotype × year interactions confirmed that environmental fluctuations in western Iran strongly influence yield performance (Yan HongPing et al., 2004), and the identification of stable genotypes highlighted the potential of specific landraces to outperform standard checks. Unlike approaches relying solely on yield per se, our integrated analysis revealed that stability is driven by specific architectural traits, particularly PH, which likely buffers environmental variability and facilitates mechanized harvesting (Thudi et al., 2016; Yadav et al., 2007).

These biological insights were underpinned by a robust statistical framework: comparing base, interaction, and augmented mixed-effect models confirmed their value for multi-year, unbalanced breeding data (Piepho et al., 2008; Smith et al., 2005). The augmented model gave the lowest AIC for four traits (DF, DM, PH, SY), the interaction model was marginally preferred for three (HSW, PPP, NSS), and the base model was lowest for NPS (Table 1), reflecting broadly comparable fit once the appropriate error distribution was used. Residual diagnostics showed a Gaussian distribution was inadequate for four traits (HSW, PPP, NPS, NSS), re-fitted under a Tweedie distribution—underscoring the value of distribution checking over assuming normality by default (Akaike, 2003; Burnham & Anderson, 2004). Significant year effects reflected strong annual environmental influence, while genotype × year terms effectively reduced unexplained variance, particularly for environmentally sensitive traits like flowering and plant height. For PH, the comparable magnitude of genotype and genotype × year variance components indicate that year-

to-year fluctuations should be considered in selection, given potential trade-offs with lodging resistance and harvest index in taller genotypes.

Genotype × Yield × Trait (GYT) Analysis

Regarding genotype performance, the panel showed extensive genotypic diversity, confirming the rich germplasm base documented in Iranian and global collections (Fayaz et al., 2022; Varshney et al., 2021). GYT biplots allowed us to move beyond simple yield ranking by combining yield with key agronomic traits into integrated indices (Kendal, 2019; Yan & Frégeau-Reid, 2018). Genotype superiority proved dynamic across years, reflecting substantial G × E effects: G313 consistently ranked first for Y × HSW in both years, suggesting a stable candidate for concurrent improvement of yield and market quality, whereas other rankings shifted between seasons (2021: G33 for YPH, G5 for YPPP; 2022: G49 for YPH, G52 for YPPP). This dynamic ranking implies that chickpea yield is fundamentally driven by environment-dependent variation in yield components (Roorkiwal et al., 2020), reinforcing the need for environment-specific, trait-targeted selection (Annicchiarico et al., 2025).

While PH was consistently associated with yield, its relevance extends beyond this link: harvest is the largest cost component in chickpea production, and combine-based mechanized harvesting—already used in western Iran—is increasingly favored given the substantial losses of manual harvesting (Golpira, 2013). The identification of distinct winning genotypes for earliness indices each year, including one dominating both flowering and maturity efficiency in 2022, underscores the importance of the "drought escape" strategy: genotypes initiating reproductive growth early and completing grain filling before severe heat maximize "yield per day" efficiency under Mediterranean-type climates (Turner et al., 2001). That a tall, high-yielding genotype also excelled in maturity efficiency in 2021 suggests height and earliness are not mutually exclusive, whereas the 2022 drought-escaping genotype represents a classic escape ideotype. Selection strategies must therefore balance the architectural stability of lines like G313 with the phenological agility of earliness-focused genotypes.

Structural Equation Modeling (SEM) Analysis

Structural Equation Modeling (SEM) further illuminated patterns of association among agronomic traits. PH consistently showed the strongest standardized loadings across both seasons, indicating it was the most stable indicator of the latent agronomic performance construct under autumn-sown

conditions, while traits such as PPP and SY varied by year. Residual covariances revealed a negative PPP–HSW association in the first year, consistent with known physiological trade-offs in legumes (Barmukh et al., 2022; Zhu et al., 2024).

Multi-Trait Genotype-Ideotype Distance Index (MGIDI)

The MGIDI results provide a practical, single-value ranking system, offering an actionable selection tool that corroborates the multi-trait relationships identified through the correlation and SEM analyses. Similar approaches have proven effective in chickpea for identifying heat-tolerant and multi-trait superior landraces (Jorben et al., 2022), reinforcing MGIDI's applicability to this species. The substantial number of landraces outperforming the top commercial check underscores the largely untapped genetic potential within this germplasm for combined improvement of phenology, yield components, and seed characteristics. Notably, G5's top MGIDI rank converged with its independent selection as a GYT-winning genotype, demonstrating that MGIDI, despite condensing sixteen trait-year variables into a single distance metric, captures genotype-specific strengths rather than merely an averaged compromise across traits (Olivoto & Nardino, 2021). Prioritizing these top-ranked landraces thus offers a more balanced breeding alternative to single-trait selection, which risks overlooking unfavorable trade-offs such as the negative association between pod number and seed weight.

Conclusion

This study demonstrates the substantial breeding value of Iranian desi chickpea landraces for autumn sowing under terminal drought conditions. Integrated analysis (LMM, GYT, SEM, and MGIDI) showed that yield stability is driven by architectural traits rather than yield alone, with plant height consistently linked to seed yield across seasons, though the top-performing genotype shifted between years (G33 in 2021, G49 in 2022). The MGIDI ranking identified G5 as the top multi-trait candidate, outperforming both commercial checks, while GYT analysis highlighted G313 for its stable yield × seed-weight performance across both years. These findings identify promising parental candidates and confirm that combining LMM, GYT, SEM, and MGIDI offers an effective framework for multi-trait selection, which future work should extend to multi-location trials with marker-assisted selection.

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