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RESEARCH

Resilience of pea genotypes issued from different selection methods in Algerian subhumid condition

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Abstract Pea (*Pisum sativum* L.) is a key crop for animal feed, especially in rainfed agricultural systems. It stands out for its high protein content, storability, and flexibility in concentrate feed formulations, offering potential to enhance feed self-sufficiency in livestock production. To ensure its integration and sustainability under climate change, selecting resilient varieties is essential. Genotype-by-environment interaction (GEI) strongly influences yield in Mediterranean regions, requiring optimized selection methods to manage climatic variability. This study evaluated 37 field pea genotypes, including 30 pure lines derived from genomic and phenotypic selection, three evolutionary populations, 3 parental varieties, and one control. Trials were conducted over three cropping seasons (2021–2024) using a randomized complete block design with three replications. AMMI analyses revealed significant effects of genotype, environment, and their interaction on grain yield. Variance analysis showed that 50.26% of yield variation was due to environment, 7.22% to genotype, and 16.75% to GEI. These results were confirmed by the analysis of variance components. In contrast to other years, the 2022–2023 season revealed differences in yield between genomic and phenotypic selection lines across regions. Lines from the Algiers region were most productive, with a 2.54% yield increase over the mean of the parental lines. While not all genotypes from genomic selection showed stability, those that did were consistently superior to the reference mean yield. This study highlights the potential of genomic selection (GS) to improve pea breeding efficiency compared to phenotypic selection (PS), as the 2 top-performing genotypes were products of GS.

Keywords Pea feed · Phenotypic selection, genomic selection, genotype by environment interaction (GEI) · AMMI model · Rainfed agricultural systems

Introduction

The improvement of animal production relies not only on advances in livestock genetics and livestock

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health but also on the availability of appropriate animal feed (Almeida et al. 2024). In Maghrebian countries, natural pastures are no longer sufficient to meet the growing nutritional needs of livestock, due to the continuous increase in the demand for animal-derived products (Ghozlane 2018; FAO 2023). In response to this situation, the development of feed crops, both for biomass (e.g., hay, silage) and for grain (e.g., forage legumes or dual-purpose cereals), represents a key solution to improving farmers' self-sufficiency and reduce production costs (Eulmi 2024). This approach aligns with findings from global assessments of sustainable livestock systems, which emphasize the importance of integrating forage and grain production to enhance feed availability and system resilience (Rotz et al. 2017; Mekonnen et al. 2022).

Pea (*Pisum sativum* L.) is described as a widely cultivated legume, playing a major role in global food security and agricultural sustainability (Delvento et al. 2023). It is also noted as one of the most commonly grown legumes in semi-arid Mediterranean regions (Di Miceli et al. 2023). Pea is a cool-season annual crop (Li et al. 2023), characterized by its high protein content (20%–25%) in the grains, along with prebiotic carbohydrates, as well as a range of minerals and vitamins (Windsor et al. 2024). As a legume, pea can fix atmospheric nitrogen through symbiotic relationships with nitrogen-fixing bacteria in its root nodules (Neugschwandtner et al. 2021; Tripolskaja et al. 2023). On average, 35% of its total nitrogen comes from the atmosphere, which corresponds to 48.6 kg ha – 1 (Faligowska et al. 2022).

In 2023, field pea was among the most widely cultivated cool-season legumes in Europe, with a production of nearly 2 million tons (Terres Univia 2023). In this continent, pea (*Pisum sativum* L.) is primarily cultivated for grain production (protein pea), mainly intended for animal feed and, to a lesser extent, for human consumption. The cultivation of forage pea is significantly less common. In contrast, pea production in North African countries is very limited with more pea forages cultivated than field pea.

Algeria relies heavily on imported high-protein concentrates of almost soybean, with a dependency rate reaching 100% (Ghozlane et al. 2021). In the 2021–2022, the country imported approximately 900,000 metric tons of seed soybeans and 373,000 metric tons of soybean meal (USDA Foreign Agricultural Service 2023). In a context like Algeria, which is highly dependent on imported concentrate feeds, field pea represents a strategic priority over forage pea due to its high protein content, good storability, and strong potential to enhance feed self-sufficiency in livestock production. Pea adapts well to the various agroecosystems in Algeria. They can be grown under rainfed conditions, particularly in the semi-arid regions (Benider et al. 2022).

Pea is well adapted to Mediterranean climatic conditions, it requires about 300 mm of water, with a particularly high demand during key developmental stages such as the beginning of flowering and pod setting (Terres Unovia 2019). The increasing irregularity of rainfall in Mediterranean countries (Rodrigo-Comino et al. 2021) and the climate change (Del Pozo et al. 2019) are significantly affecting the productivity of pea and other rainfed crops.

In response to these challenges, the selection of new varieties emerges as a key strategy to strengthen the resilience of pea cultivation to often unpredictable environmental conditions. Among the main breeding approaches currently used to improve crop adaptation are phenotypic selection, genomic selection, and evolutionary selection (ES). GS is proving to be a powerful tool in pea improvement, offering the possibility to accelerate genetic progress while optimizing the use of germplasm collections (Annicchiarico et al. 2019; Bari et al. 2021). It allows for the more efficient identification of promising genotypes by relying on molecular markers, thereby reducing the time required to develop improved varieties. At the same time, PS remains an essential method as is confirmed by (Uhlarik et al. 2022). Finally, ES aims to gradually increase the frequency of favorable alleles within breeding populations. This method, which results in a genetically heterogeneous cultivar rather than an ordinary pure line cultivar, enhances target traits while improving the chances of identifying superior genotypes (Annicchiarico et al. 2023; Pereira De Castro et al. 2023). Moreover, it fits within a framework of continuous population improvement, now recognized as a key phase of breeding programs, alongside varietal development (Merrick et al. 2022; Pandey et al. 2021).

The evaluation of GEI relies on appropriate statistical methods. Before the introduction of the additive main effects and multiplicative interaction (AMMI) model, the most commonly used models were two-way ANOVA, linear regression, and the generalized linear model (GLM). However, these approaches present limitations when analyzing GEI effects (Guo et al. 2017). The AMMI model (Gauch 2006; Zobel et al. 1988) is now widely used to study these interactions by combining principal component analysis (PCA) and analysis of variance.

This research focuses on the evaluation of different selections of protein pea derived from three distinct methods, namely, phenotypic selection, genomic selection, and evolutionary selection, conducted at a sub-humid site of Algeria characterized by high annual variability. The main objective is to compare selection methods, to determine which approach may most effectively enhance the resilience of pea to annual climatic variations in low-input rainfed production systems. In addition, our study aimed to identify germplasm exhibiting the best performance in coastal Algeria in terms of resilience and yield stability.

Materials and methods

Genetic material

The pea genotypes derived from cross-breeding between 3 parent varieties: Attika (A), Isard (I), and Kaspa (K). The selection of these 3 varieties was based on their high yield performance and stability in Mediterranean and continental environments (Annicchiarico 2005; Annicchiarico and Iannucci 2008).

Isard is afila. tolerant to cold and low resistance to lodging. Attika and Kaspa have normal foliage, tolerance to water stress and lodging. Attika is notable for its cold tolerance, while Kaspa stands out for its high productivity and protein content (UNIP-ITCF 2001; Sadras et al. 2012; Terres Inovia 2015). From the crosses between AxK, AxI, and KxI, 60 recombinant inbred lines (RILs) were generated by selfing. The evolutionary populations (EPs) were obtained through natural and mass selection under different conditions (Italy, Algeria, and Morocco), before being grouped by region and subdivided for specific selection in Algeria, Morocco, and Italy.

Simultaneously, mass selection identified 30 F6 plants per cross after 4 cycles of natural selection in Italy, for PS and GS model construction, while 120 lower-ranking plants were selected for GS application. Details on the selection of inbred lines and evolutionary populations for three target regions (Italy, Algeria, and Morocco) are given in (Annicchiarico et al. 2020). This combined approach optimized the selection of lines based on. Selection at the country level allowed the identification of 10 genotypes for Algeria, 10 for Morocco, and 13 for Italy, as shown in Table 1. These selections (33) were the focus of this study. For comparison purposes, the three parent varieties were included in the study, as well as a control variety, Aviron, registered in 2012 by Florimond Desprez (Terres Inovia), which is a winter crop, late-maturing, and of the afila type. Thus, the total number of genotypes studied is 37.

The genomic selection (GS) strategy in this study followed the rigorous framework established by Annicchiarico et al. (2024), who demonstrated the feasibility and accuracy of GS for grain yield in diverse pea germplasm using genotyping-by-sequencing (GBS) and the BayesB prediction model. Our

Table 1 List of Pea Genotypes evaluated in this study with their country of selection and selection method

Country of selection	Selection method	Numbers	Genotype
Algeria	Genomic	6	AI_L15; AI_S118; KA_L250; KA_S106; KI_S125; KI_S78
	Phenotypic	3	AI_S6; KA_156; KI_S8
	Evolutionary	1	evpop_AL
Morocco	Genomic	6	AI_S144; KA_L10; KA_S127; KI_S184; AI_S260; KI_S94
	Phenotypic	3	KI_41; AI_41; KA_S7
	Evolutionary	1	evpop_MO
Italie	Genomic	9	KI_L166; AI_L155; KI_S92; KI_L61; AI_L231; KA_L247; KA_L175; AI_L104; KA_L72
	Phenotypic	3	AI_L23; KI_L16; KA_28
	Evolutionary	1	evpop_IT

pipeline targeted grain yield through factorial crosses between Mediterranean-adapted genotypes, high-density GBS genotyping (~ 10,000 high-quality SNPs after filtering), and multi-environment phenotyping. Genomic predictions were performed separately for each target environment (Algiers, Marchouch, Lodi, and controlled conditions) using a leave-one-environment-out cross-validation scheme to ensure robustness and avoid overfitting. Prediction accuracy, measured as the Pearson correlation between observed and predicted grain yield, ranged from 0.48 to 0.61 depending on the environment values confirming both the reliability of the GS approach and its potential as a cost-effective breeding tool for field pea in Mediterranean environments.

A key determinant of GS performance lies in the quality and relevance of the training population (TP)—the set of genotypes both phenotyped and genotyped to train predictive models. In our study, the TP comprised 12 representative genotypes of diverse origins (Algeria, Morocco, Italy, and lines from controlled crosses), tested over three years across multiple contrasting environments. Although the TP was not updated annually, it encompassed sufficient agro-climatic diversity and genetic variability to support robust predictions. This design reflects evidence from other legumes (Annicchiarico et al. 2022) and self-pollinated cereals, where a well-structured TP—even of moderate size—can yield satisfactory accuracy, provided the target population remains genetically related (Lorenz et al. 2011; Juliana et al. 2019).

While annual updating of the TP, as practiced in many wheat and barley programs, can improve prediction accuracy by progressively enlarging the dataset (Sallam et al. 2015; He et al. 2016), it also entails significant logistical and financial costs. Moreover, studies indicate that beyond ~ 300–400 genotypes in selfing species, gains in predictive accuracy are often marginal (Sallam et al. 2015; Rutkoski et al. 2015). When validated through rigorous schemes such as leave-one-environment-out cross-validation, prediction stability can be maintained without annual TP renewal (Crossa et al. 2014; Annicchiarico et al. 2022).

Given the high interannual climate variability typical of Mediterranean environments, our approach prioritizes inter-environmental stability of predictions over maximizing short-term genetic gain. Therefore, maintaining a fixed but geographically and genetically diverse TP represents a methodologically sound and pragmatically adapted strategy for breeding programs in these conditions.

Experimental sites

The experimental trials were conducted at the experimental station of the Higher National School of Algiers, located 12 km southeast of Algiers (36°43.143’ N, 3°9.045’ E, at an altitude of 10 m). The region has a Csa climate (Hot-summer Mediterranean climate) according to the Köppen–Geiger classification. The field experiment was conducted over the course of 3 growing seasons (2021–2022, 2022–2023, and 2023–2024). The average temperature and precipitation values for each month of the experiment are shown in Fig. 1 for the 3 growing seasons. The 3 growing seasons showed notable differences in rainfall patterns. The 2022–2023 season had the lowest total rainfall (277.3 mm) but a favorable distribution, with sufficient precipitation during key growth stages and dry conditions at maturity. The 2023–2024 season recorded the highest rainfall (337 mm) with consistent distribution, especially in February, supporting good flowering and grain filling. In contrast, the 2021–2022 season (307.7 mm) suffered from early drought and excessive rain late in the cycle, which hampered pod maturation and caused significant yield losses.

Based on the soil analysis performed in 2021, the site soil (0–30 cm) contained 19% clay, 22% fine silt, 42% coarse silt, 15% fine sand and 2% coarse sand (the soil texture is classified as silty, Soil Survey Staff) (Shahid et al. 2014). The pH of the soil was 8.8 (alkaline); total calcium carbonate content was 0.22% (non-calcareous); electrical conductivity (ECe) was 0.1 dS m -1 (no saline); organic matter content was 1.90% (poor); total nitrogen was 2.1% (rich); available nitrogen was 9.8% (poor); available phosphorus was 7.5 ppm (poor); and exchangeable potassium was 7.4 meq/100 g soil (moderately supplied).

Crop management and experimental design

The sowing dates were January 4, 2022, November 14, 2022, and November 8, 2023, for the three growing seasons of peas, while the harvests were carried out manually on May 19, 2022, April 28, 2023, and April 27, 2024. Each agricultural season, the

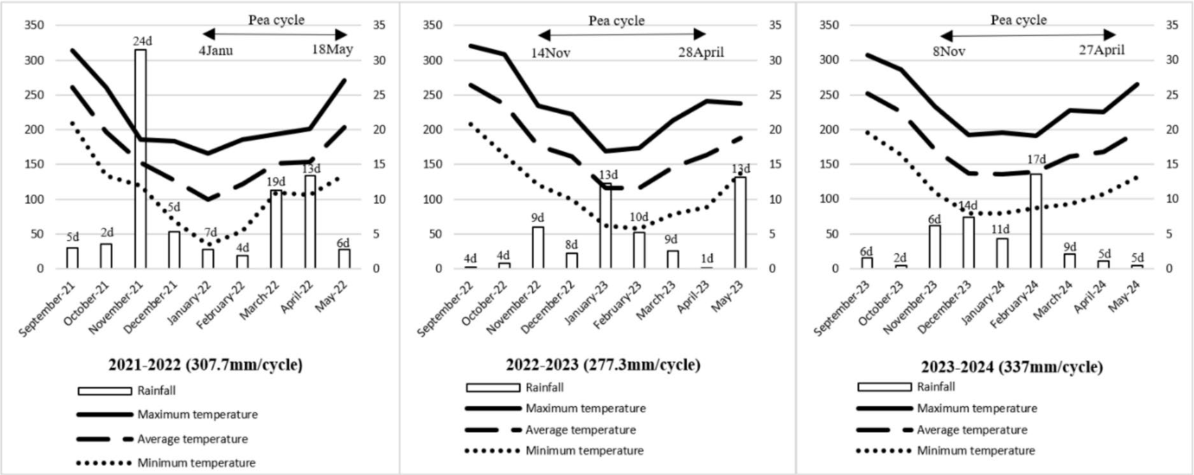

Fig. 1 Monthly rainfall and mean air temperatures (minimum, average, and maximum) at the experimental site during the 3 growing seasons

experiment was conducted using a completely randomized block design with 3 replications. Each genotype was sown on a 1.5 m^2 plot consisting of 4 rows, each 1.5 m long, spaced 25 cm apart. Each row contained 30 seeds, sown 5 cm apart, corresponding to a planting density of 80 plants/m^2 (144 kg/ha). Cultural practices were carried out according to minimum experimental requirements, and the experiment was conducted under exclusively rainfed conditions with low input.

Measurements

The study measured two key traits: Seed protein content and pea grain yield. Seed protein content was determined by near-infrared spectroscopy (NIRS) on 100 g of dry seed per plot, ground by a cutting mill with a 1 mm mesh sieve, by Nirflex 500 spectrometer (Büchi, Cornaredo, Italy) working in the 1000–2500 nm range. The reference data were obtained by the analysis of total nitrogen content by Dumas's method with a ThermoQuest NA1500 elemental analyzer (Carlo Erba, Milano, Italy) and atropine as a standard. The Partial Least Squares method within PLS Toolbox 8.9 (Eigenvector Research Inc., Washington, DC, USA) was employed to develop a prediction model, featuring an R2 of 0.78, while the calibration R2 amounted to 0.93. Seed protein content was obtained by multiplying the NIRS-estimated nitrogen content by 6.25. Grain yield was calculated based on the weight of the grains (adjusted to 12% moisture) measured per plot and converted to t/ha. Grain yield was assessed for all study years, except for protein content, which was measured only during the first year (2021–2022).

Statistical analysis

For each growing season, the analysis of grain yield and protein content was conducted using ANOVA in RStudio (version 4.3.3; R Core Team (2024). R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. < https://www.R-project.org/ > .

Grain yield data were analyzed using the AMMI model, which first accounts for the additive effects of genotypes (G) and environments (E), followed by the multiplicative effects of GEI through principal component analysis (PCA). The results of the AMMI analysis are presented as biplot graphs. The AMMI model, as described by (Gauch and Zobel 1990) and (Nowosad et al. 2016), is expressed using the following formula:

$$yge = \mu + \alpha_g + \beta_e + \sum_{k=1}^{N} \lambda n\gamma gn\delta en + Q_{ge}$$

where y_{ge} is the yield mean of genotype g in environment e, μ is the grand mean, α_g is the genotypic mean deviations, β_e is the environmental mean deviations, N is the number of PCA axis retained in the adjusted model, λ_n is the eigenvalue of the PCA axis n, γ_{gn} is the genotype score for PCA axis n, δ_{en} is the score eigenvector for PCA axis n, and Q_{ge} is the residual, including AMMI noise and pooled experimental error. The AMMI stability value (ASV) was used to compare the stability of genotypes as described by (Purchase et al. 2000):

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}\left(IPCA_1\right)\right]^2 + (IPCA_2)^2}$$

where SS is the sum of squares of $IPCA_1$ and $IPCA_2$, the first and the second interaction principal component axes, respectively; and the $IPCA_1$ and $IPCA_2$ scores were the genotypic scores in the AMMI model. The ASV (Additive Main Effects and Multiplicative Interaction Stability Value) is calculated as the distance from zero on a two-dimensional scatterplot of $IPCA_1$ (Interaction Principal Component Axis 1) scores against $IPCA_2$ (Interaction Principal Component Axis 2) scores. A higher IPCA score, whether positive or negative, suggests that a genotype is more specifically adapted to certain environments. In contrast, a lower ASV score indicates greater stability of the genotype across different environments. The Genotype Selection Index (GSI) was calculated for each genotype by combining the rankings of the ASV and Yield Stability Index (YSI), as outlined by (Farshadfar 2008). The GSI for the ith genotype is expressed as:

$$GSIi = RYi + RASVi$$

where $GSIi$ is the genotype selection index for the ith genotype, RYi is the rank of the mean yield for the ith genotype, and $RASVi$ is the rank based on the AMMI stability value for the ith genotype. AMMI analysis was performed in RStudio http://www.r-project.org/ using the "AMMI" function from the "agricolae" package (de Mendiburu 2023).

In order, to compare the precision of agricultural cultivar trials, and estimate the response to selection in plant breeding trials; broad-sense heritability (H^2) was calculated (Schmidt et al. 2019). H^2 is defined as the proportion of phenotypic variance that is attributable to an overall variance for the genotype, thus including additive, dominance, and epistatic variance (Holland et al. 2003; Falconer and Mackay 1996).

The broad-sense heritability (H^2) (Schmidt et al. 2019) is expressed by the following formula:

$$H^2 = \sigma_g^2 / \sigma_p^2 \text{ and } \sigma_p^2 = \sigma_g^2 + \frac{\sigma_{gy}^2}{n_y} + \frac{\sigma_e^2}{n_y * n_r}$$

where σ_g^2: genotypic variance,σ_p^2: phenotypic variance,σ_{gy}^2: genotype * year interaction variance,σ_e^2: residual plot error variance,n_y: number of years andn_r: replicates per year.

In order to compare the broad-sense heritability for each study year, (Holland et al. 2003) proposed this formula: $H^2 = \frac{\sigma_g^2}{\sigma^2_{g+\frac{\sigma^2_{error}}{r}}}$, Where σ_g^2 : genotypic variance, σ^2_{error} : residual variance, and r: number of replicates.

Results

Although all 3 growing seasons showed high coefficients of variation (CV), indicating considerable phenotypic variability, only the first 2 seasons (2021–2022 and 2022–2023) revealed statistically significant differences among genotypes. Interestingly, despite the lack of statistical significance in 2023–2024 (Table 2).

The 2022–2023 growing season recorded the highest average grain yield (4.51 t/ha), followed by the 2023–2024 season (3.48 t/ha) and the 2021–2022 season (1.97 t/ha).

The broad-sense heritability (H^2), consistently greater than 0.7 across all years studied, indicates that yield variation was mainly attributable to genetic effects. This trend highlights a strong genetic control of yield under the evaluated experimental conditions.

Table 2 Analysis of variance *F* test results, total mean yield, coefficient of variation (CV), broad-sense heritability (H^2) for grain yield of 37 pea genotypes grown in subhumid for 3 years

Analysis	2021–2022	2022–2023	2023–2024
Total mean yield (t/ha)	1.97	**4.51**	3.48
CV (%)	32.8	36.6	43.6
H^2	0.83	0.93	0.7
LSD ($P < 0.05$)	0.03*	1,91e-08 ***	0.74

Bold values highlight that the year 2022–2023 represents the highest total mean yield

During the first growing season, the selected genotypes clustered with the parental varieties that exhibited the highest yield. In contrast, the genotypes AI_L104 (GS), KA_L247 (GS), KA_S106 (GS), and KI_L16 (PS) displayed the lowest yields and thus formed a separate group. In the second growing season, five pure lines stood out, with yields ranging from 5.63 to 7.28 t/ha, surpassing the parental yields (4.46 t/ha), representing a notable improvement of 42.79% through differential selection. Among these lines, 3 (AI_S6, KA_156, and KI_S8) were selected based on phenotypic criteria, while the other 2 (KA_S106 and KI_S125) were selected based on genomic criteria. However, the evolutionary populations did not show superiority over the parental genotypes. The third growing season revealed no significant differences among the genotypes.

For the 2022–2023 season, the analysis of the mean grain yield across the different selection types (PS, GS, and EP) revealed a significant difference. The Algerian PS and GS lines recorded the highest yields, grouping into the same statistical category (Table 3). Moreover, these lines exhibited higher yields with an increase of approximately 24.88% for Algerian GS lines and 33.40% for Algerian PS lines compared to the mean of the parental lines, thus confirming their superior agronomic potential. These results highlight the superiority of the Algerian genotypes (+29%) compared to the Moroccan (−9%) and Italian genotypes (−11%) compared to the mean of the parental lines under the conditions of this agricultural season.

When analyzing grain yield per agricultural season across the three selection types (PS, GS, EP) from all regions combined (Algeria, Morocco, and Italy), as well as that of the parental varieties and the control, no significant differences were recorded.

The analysis of variance for grain yield over the 3 years revealed a significant difference between genotypes, Environment and a highly significant GEI. On the overall average of the lines, the Algerian selections exhibited the highest grain yield (3.64 t/ha). The best-performing lines were 2 Algerian lines selected phenotypically, AI_S6 (3.92 t/ha) and KI_S8 (3.98 t/ha), along with one Italian line selected genotypically, KI_S92, with a yield of 4.04 t/ha (Table 4). The evolutionary populations (EP), regardless of their region of origin, displayed similar yields, which were close to the general average yield of all lines.

The analysis of variance of 37 field pea genotypes across three cropping seasons revealed a significant influence of the studied factors on grain yield (Table 5). The interannual variability was significant and accounted for 1.22 of variance. Although the genotypic effect was also significant but its genotypic variance is null. The genotype* year interaction was

Table 3 Analysis of variance *F* test results for grain yield of phenotypic (PS), genotypic (GS), evolutionary population (EP), parents, and control pea genotypes grown in subhumid for 3 years

Type of Selection	Region of selection	Number of genotypes	Years			
			2021–2022	2022–2023	2023–2024	2021–2024
Lines from GS	Algeria	6	1.7a	5.57a	3.3a	3.52
	Morocco	6	2.19a	3.99ab	3.27a	3.15
	Italy	6	1.79a	4.09ab	3.59a	3.16
	Stressful Italy	3	1.88a	3.98ab	3.95a	3.27
Lines from PS	Algeria	3	2.19a	5.95a	3.46a	3.87
	Morocco	3	2.07a	4.15ab	3.21a	3.14
	Italy	3	1.59a	3.85ab	3.41a	2.95
EP	Algeria	1	1.96a	4.54ab	3.67a	3.39
	Morocco	1	2.85a	3.76b	3.77a	3.46
	Italy	1	1.88a	4.33ab	3.2a	3.13
Parent cultivars	Varieties	3	1.98a	4.46ab	3.67a	3.37
Aviron (Control)	Variety	1	2.49a	5.34ab	3.75a	3.86
LSD ($P < 0.05$)			0.16	0.01*	0.93	

Table 4 Pea dry grain yield, and protein content of inbred lines (GS and PS), evolutionary populations (EP), parent cultivars, and control variety targeted to regions of Algeria, Morocco and Italy (data averaged across three test years)

Targete region of selection	Grain yield (tones/ha)			Mean protein content* (%)
	Min	Mean	Max	
Algerian selection lines	3.08	3.64	3.98	27.54
Italian selection lines	2.16	3.17	4.04	28.11
Moroccan selection lines	2.87	3.20	3.68	26.33
Average of total lines	2.7	3.32	3.9	27.40
Average of EP	2.9	3.25	3.46	27.78
Average total (lines + EP)	2.8	3.31	3.68	27.44
Average of parent cultivars	3.36	3.55	3.78	27.20
Control variety	/	3.86	/	22.30^{R}
LSD for genotype (*p* value < – 0,05)	0.0191680 *			
LSD for Environment (*p* value < – 0,05)	0.011*			
LSD for interaction (*p* value < – 0,05)	0.00026 ***			

* Data from the 2021–2022 agricultural season; ^{R}: data characteristic of the variety

Table 5 Analysis of variance of main effects and interactions for pea grain yield

Source of variation	Degrees of freedom (df)	Sum of squares (SS)	Mean Squares (MS)	F value (F)	Probability (> F)	Variabilty explaines (%)
Repetition	6	102.97	17.161	193,296	< 2.2e-16 ***	
Environments (Years)	2	361.95	180.974	10.5456	0.011 *	50.261
Genotypes (GEN)	36	52	1.444	1.6269	0.019 *	7.221
GE interactions	72	120.64	1.676	1.8873	0.000 ***	16.752
GE interaction contribution						
IPCA1	37	86.857	2.347	2.64	0	77
IPCA2	35	26.002	0.743	0.84	0.725	23
Residuals	209	185.55	0.888			25.766

highly significant explaining 0.49 of variance component. This justifies the use of the AMMI analysis. IPCA1 explained 77% of the total variation in GEI effects, indicating that this first component is highly informative and captures a large portion of the differences observed in grain yield across the different environments.

The graphical representation in Fig. 2 shows the x and y axes of the AMMI 1 biplot. The most stable genotypes (Table 6) were: evpop_IT, KI_41, AI_L155, evpop_AL, AI_L231, AI_S118, KI_L61, and KA_S127. These genotypes are located near the center of the coordinate system, with coordinate values close to zero, indicating stable performance across environments. The genotypes KI_S92, KI_S8, and AI_S6 displayed the highest grain yields but were positioned farther from the center (Fig. 2).

The Genotype Selection Index (GSI) allows for the transparent ranking of genotypes based on their overall selection value. Genotypes with the lowest GSI values (Table 6), representing a compromise between high yield and stability, were AI_S118, AI_L155, the control variety AVIRON, evpop_AL, KI_S8, and KI_41. These genotypes are located to the right of the vertical line (Fig. 2), which represents the overall mean yield across all genotypes. Among the top 5 genotypes identified in this study (Table 7), three belong to Algerian selections (AI_S118, KI_S8, and evpop_AL), highlighting their good adaptation to their target selection environments. In addition to these genotypes, the control variety AVIRON and the Moroccan genotype KI_41 also showed good performance.

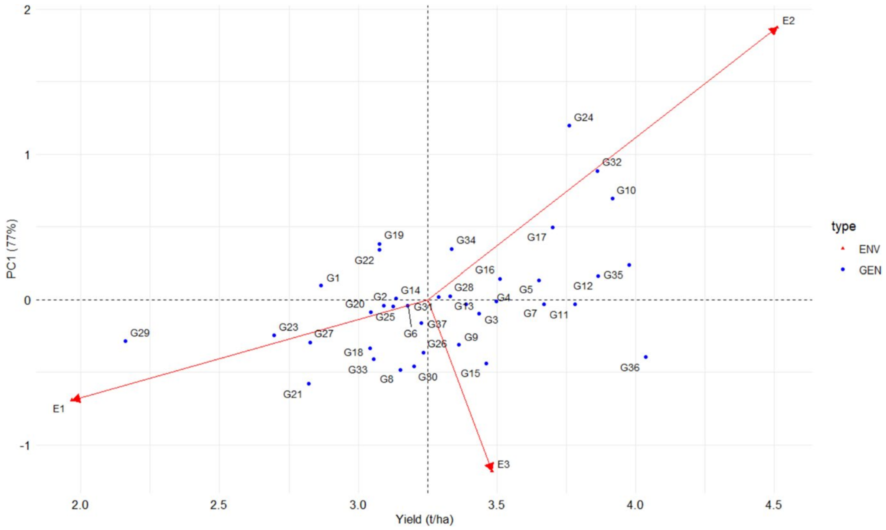

Fig. 2 Biplot for the Interaction Principal Component Axis 1 (IPCA1) and the average grain yield of pea genotypes. The vertical line at the center of the biplot represents the overall mean

The AI_S118 selection, a line derived from GS, ranked first, outperforming the AI_L155 line, which was also derived from GS. The evolutionary population evpop_AL, ranked second, further illustrates the potential of evolutionary breeding approaches, where genotypes naturally adapt to environmental conditions over time. Finally, although PS ranked behind GS and EP in overall performance, it successfully identified 2 interesting genotypes: KI_S8, an Algerian selection, and KI_41, a Moroccan selection**.** These results highlight the complementarity of different breeding methods while emphasizing the superiority of GS for improving performance under a subhumid environment characterized by a highly variable annual rainfall distribution.

Although the second principal component (PC2) is not statistically significant according to the AMMI analysis, the PC1 × PC2 biplot is presented to visualize the distribution of genotypes and environments. PC1, which accounts for a large proportion of the yield variation, serves as the main basis for interpretation.

The AMMI2 biplot uses distances from the origin to provide information on the degree of interaction exhibited by genotypes across environments, or vice versa. Environments with high IPCA1 and IPCA2 scores have a significant impact on genotype stability, as highlighted in several studies, notably by Voltas et al. (2002). In contrast, environments with low IPCA1 and IPCA2 scores have a limited influence on genotype-environment interaction.

Regarding grain yield, the genotypes KI_S184, KA_S106, and KA_L247 showed a spatial distribution deviating from the central region and were strongly correlated with the agricultural seasons 2021–2022, 2022–2023, and 2023–2024, respectively (Fig. 3).

The 2022–2023 and 2023–2024 seasons, characterized by longer vectors, exhibited higher levels of interaction and a greater ability to discriminate among genotypes in relation to grain yield, compared to the 2021–2022 season, which had a shorter vector and thus lower variability in interaction effects.

Discussion

The strong significance of the environment (agricultural season) effect on grain yield can be mainly attributed to variations in precipitation observed during the crop cycle. In contrast, temperature fluctuations were relatively minor compared to rainfall, suggesting that temperature was not a major source of environmental variation. A favorable distribution of rainfall, supporting both growth and grain production, was recorded during the second agricultural season. (Tack and Holt 2016) emphasized that climatic conditions are among the main factors contributing to maize yield variability. Moreover, several studies (Bueckert et al. 2015; Jiang et al. 2019; Osorio et al. 2022) have established a significant correlation between heat stress and flower abortion, which

Table 6 Mean pea grain yield, AMMI analysis, of the 37 genotypes tested across three environments

Selection	Genotype	Graph code	Type of selection	Mean grain yield (t/ha)	ASV	rASV	rYSI	rGSI
Algerian selected lines	AI_L15	G3	GS	3.435	0,667	16	14	10
	AI_S118	G7	GS	3.669	0,177	6	9	1
	KA_L250	G22	GS	3.076	1,136	24	29	22
	KA_S106	G24	GS	3.761	4,019	37	7	19
	KI_S125	G32	GS	3.863	2,973	36	5	16
	KI_S78	G34	GS	3.337	1,167	25	17	17
	AI_S6	G10	PS	3.916	2,325	35	3	14
	KA_156	G17	PS	3.701	1,664	33	8	16
	KI_S8	G35	PS	3.976	0,798	18	2	4
Moroccan selected lines	AI_S144	G8	GS	3.153	1,618	32	24	24
	KA_L10	G19	GS	3.077	1,371	28	28	24
	KA_S127	G25	GS	3.125	0,244	8	26	11
	KI_S184	G33	GS	3.055	1,426	29	30	26
	AI_S260	G9	GS	3.362	1,029	22	16	14
	KI_S94	G37	GS	3.227	0,591	14	21	12
	KI_41	G28	PS	3.330	0,090	2	18	4
	AI_41	G1	PS	2.866	0,521	12	33	20
	KA_S7	G26	PS	3.234	1,222	26	20	21
Italian and stressful Italian selected lines	KI_L166	G30	GS_IT	3.201	1,537	31	22	22
	AI_L155	G4	GS_IT	3.498	0,091	3	12	1
	KI_L61	G31	GS_IT	3.289	0,182	7	19	7
	AI_L104	G2	GS_IT	3.092	0,391	10	27	13
	KA_L72	G23	GS_IT	2.697	0,826	19	36	23
	KI_S92	G36	GS_SIT	4.036	1,342	27	1	9
	AI_L231	G6	GS_SIT	3.179	0,139	5	23	9
	KA_L247	G21	GS_SIT	2.82	2,028	34	35	27
	KA_L175	G20	GS_IT + SIT	3.044	0,303	9	31	15
	AI_L23	G5	PS	3.652	0,682	17	10	8
	KI_L16	G29	PS	2.161	0,995	20	37	25
	KA_28	G18	PS	3.043	1,123	23	32	23
Evolutionary populations	evpop_AL	G13	Evolutionary	3.389	0,126	4	15	3
	evpop_IT	G14	Evolutionary	3.137	0,084	1	25	7
	evpop_MO	G15	Evolutionary	3.462	1,500	30	13	18
Parents	ATTIKA	G11	Variety	3.782	0,642	15	6	5
	ISARD	G16	Variety	3.511	0,497	11	11	6
	KASPA	G27	Variety	2.826	1,028	21	34	23
Control variety	AVIRON	G12	Variety	3.865	0,552	13	4	2

GS Genotypic selection, *PS* Phenotypic selection, *GS_IT* Genotypic selection Italy, *GS_SIT* Genotypic selection stressful Italy, *ASV* AMMI stability value, *rASV* rank of AMMI stability value, *rYSI* rank of yield stability index, *rGSI* rank of genotype selection index

ultimately leads to reduced grain yield. Inadequate rainfall further exacerbates this phenomenon (Jiang et al. 2019). According to (Ray et al. 2015), about 60% of agricultural production variability worldwide can be attributed to the effects of temperature, precipitation, and their interactions. (Daba et al. 2023) reported a yield reduction ranging from 80 to 87% in less favorable environments compared to optimal ones. Our results, along with previous studies, clearly indicate that temperature and precipitation

Table 7 Top Five High-Yielding and Stable Genotypes, with Key Agronomic Traits, Evaluated across Three Years in Mediterranean Environments (2021–2024)

Targeted region of selection	Genotype	Type of selection	Grain yield (tonnes/ha)	Stabilité (rASV)	Straw yield (tonnes/ha)	Onset of flowering (days)	Height (cm)	Protein content* (%)
Algerian selected lines	KI_S8	PS	3.98^{a}	Low (18)	8.73^{a}	84.7^{abc}	68.9^{bcdefg}	$28,22^{abcdefgh}$
Italian selected lines	AI_L155	GS IT	3.5^{ab}	Very high (3)	$6.84^{abcdefg}$	90.9^{efghi}	69.3^{bcdefg}	$26,63^{cdefgh}$
Moroccan selected lines	KI_41	PS	3.33^{ab}	Very high (2)	5.23^{cdefgh}	88.2^{cdefg}	54.2^{hijk}	$27,94^{abcdefgh}$
Algerian selected lines	AI_S118	GS	3.67^{ab}	High (6)	$5.47^{bcdefgh}$	87.8^{cdef}	$63.2^{defghij}$	$26,35^{efgh}$
Evolutionary population (EP)	EP AL	Evolutionary	3.39^{ab}	High (4)	$6.56^{abcdefgh}$	88^{cdefg}	$66.5^{bcdefgh}$	$28,02^{abcdefgh}$

* Data of 2021–2022

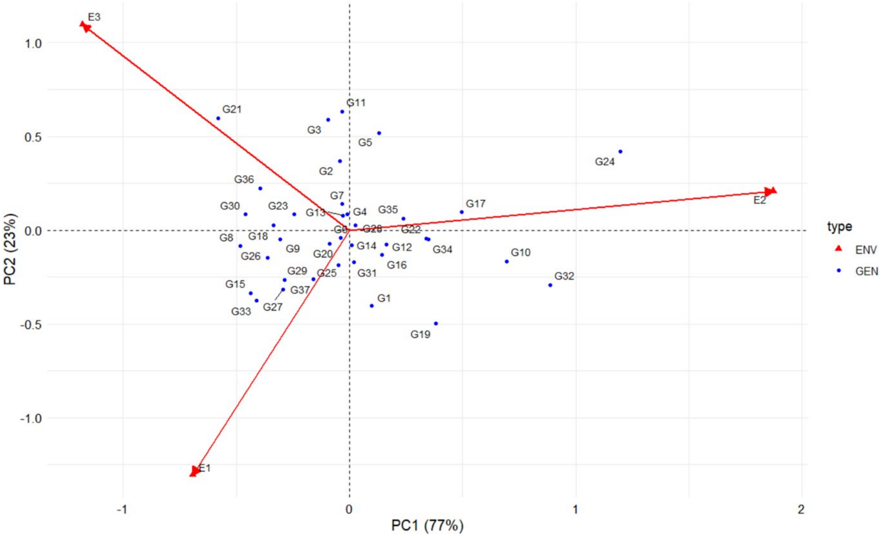

Fig. 3 Biplot of the genotype-by-environment interaction of pea genotypes grain yield across 3 environments, showing the effects of the primary and secondary components (IPCA1 and IPCA2, respectively)

significantly impact agricultural productivity, although the effect of temperature appears to be less pronounced.

The environment (agricultural season) accounted for the largest variance component (1.22) and large portion of total variability (50.26%) represented the main source of genotype variability. The distribution of genotypes highlights their diverse responses to the environmental conditions across the studied agricultural seasons. These results are consistent with the findings of (Annicchiarico and Ianucci 2008; Pecetti et al. 2019; Sellami et al. 2020; Tadesse et al. 2020; Lere et al. 2022; Yang et al. 2023; Daba et al. 2023; Annicchiarico et al. 2023; Haile and Tesfaye 2024; Kebede et al. 2024), who also observed that the environment was the principal source of variability in their studies on pea yield responses under various environmental conditions. However, (Bomma et al. 2024) reported that the genotype × environment interaction explained the greatest share of variability.

These authors also confirmed the significance of all sources of variability, namely genotype, environment, and their interaction.

Among the 37 protein pea genotypes evaluated, AI_S118, AI_L155, the control variety AVIRON, evpop_AL, KI_S8, and KI_41 emerged as the most productive and stable, with low GSI values, indicating adaptation to the sub-humid region of Algeria. The simultaneous consideration of yield and stability in selection indices, as recommended by Tadesse et al. (2023) for durum wheat in arid regions, is therefore highly relevant.

Notably, AI_S118 and AI_L155, both derived from genomic selection (GS), ranked first, outperforming AVIRON and the evolutionary population from Algiers. These findings highlight their potential for registration in sub-humid Mediterranean environments. The 2 top-ranked GS selections displayed excellent multi-year stability. Interestingly, KI_S92 despite low stability, achieved the first-highest yield, echoing Technow et al. (2014), who showed that GS can identify high-yielding genotypes with only moderate stability, especially in climates with strong inter-annual variability.

Several pea-specific studies (Annicchiarico et al. 2019, 2020, 2025; ACrosta et al. 2025) have shown that GS delivers genotypes with higher yield and stability across contrasting environments, with superior selection efficiency compared to phenotypic selection (PS). While participatory and evolutionary approaches (EP) are valuable in farmer-led and low-input systems (Ceccarelli and Grando 2007), they are often slower and less targeted when addressing complex objectives such as the simultaneous improvement of yield and protein quality. However, EPs retain high genetic diversity, enabling dynamic adaptation to environmental pressures, a trait particularly valuable under climate uncertainty. The moderate stability observed for EPs in our study suggests a trade-off that can be highly beneficial for long-term breeding in marginal areas: although EPs may not achieve the highest stability indices compared with elite pure lines, their broader genetic base confers evolutive plasticity, allowing them to maintain relatively consistent yields across seasons and sites with unpredictable climatic conditions. Recent studies (Annicchiarico et al. 2025) confirm that, in Mediterranean marginal environments, EPs can perform comparably to, or even better than, elite lines selected by GS, particularly under stress-prone conditions. This moderate yet robust stability provides a buffering effect against environmental fluctuations, while offering long-term adaptive potential through on-site selection. Such findings are consistent with Ceccarelli and Grando (2020) and earlier work on dynamic populations, which indicate that the temporal consistency of EPs tends to improve over successive cycles of local adaptation. Meta-analyses of genetically heterogeneous materials, such as varietal mixtures and composite cross populations, further suggest that moderate stability can be a strategic advantage in low-input or risk-prone systems, where over-specialized cultivars may fail under unexpected stress. The combination of EPs with GS is emerging as a particularly promising strategy under high climatic variability: studies by Döring et al. (2011), Chable et al. (2014), Wolfe et al. (2008), Babalola et al. (2025), and Juliana et al. (2019) have demonstrated that applying GS within EPs can exploit intra-population variability to enhance both yield and stability, potentially outperforming fixed-line approaches in Mediterranean and semi-arid climates.

The application of genomic selection (GS) to evolutionary populations (EPs) represents a particularly promising strategy for improving crop adaptation in environments characterized by high inter-annual variability, such as Mediterranean and semi-arid regions. Unlike pure lines, EPs maintain high genetic diversity, which enables a dynamic response to environmental pressures. In this context, the study by Juliana et al. (2019) on wheat in East Africa is especially relevant. The authors demonstrated that applying GS to EPs enabled the efficient identification of genotypes adapted to fluctuating environments by exploiting intra-population variability to improve both yield performance and stability. These findings suggest that, under similar conditions, the combination of GS and EPs may outperform approaches based solely on fixed lines, by leveraging the evolutionary potential of heterogeneous populations. This strategy is particularly relevant as climatic constraints intensify under ongoing global change.

Our findings confirm the effectiveness of the genomic approach, which stood out for its stability and superior performance. This aligns with results in bread wheat under Mediterranean conditions (Sehgal et al. 2020), where GS proved particularly valuable for long-term improvement in drought-prone areas.

The authors emphasized the need for multi-year training populations to strengthen prediction models against interannual climate variability—an approach also supported by our results.

In conclusion, Agronomy researchers strive to develop stable and high-yielding crop varieties, but they face the challenges posed by GEI. Considering environmental factors and genetic characteristics is crucial to identifying high-performing varieties across various environments. The analysis of 37 grain legume genotypes revealed significant variations in their responses to different environments (Agricultural seasons), attributed to the effect of GEI. The strong contribution of the sum of squares components related to the environment (Agricultural season), observed through the AMMI model, highlights the importance of environmental factors in the variation of grain yield. Our stability and adaptability analysis based on the AMMI model revealed that the 2022–2023 agricultural season was discriminative, representative, and ideal for assessing the performance of the tested genotypes. This analysis also identified the genotypes AI_S118, AI_L155, evpop_AL, KI_S8, and KI_41, which exhibited higher grain yields than the average while showing great stability across the different agricultural seasons.

Therefore, we recommend testing these genotypes as potential candidates in a Mediterranean environment, with the aim of registering them for the subhumid region of Algeria and for similar agroecological conditions in other parts of the world. Furthermore, GS showed significant advantages over PS and EP. It is worth noting that the first two selected genotypes come from GS, demonstrating the possibility of producing high-performing genotypes through genomic methods without the need for experimental field trials. However, this preliminary conclusion requires further studies to be confirmed.

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Data availability The datasets generated during and analysed during the current study are available from the corresponding author on reasonable request.

Declarations

Conflict of interest The authors declare no competing interests.

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