

Response of Selected Wheat genotypes to Nitrogen Fertilization: Impacts on Agronomic Performance and Grain Yield.

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Abstract

Genotypic evaluation of wheat under varying nitrogen (N) rates (160, 200, 240 kg N ha⁻¹) revealed significant differences in agronomic traits, heritability, and genetic stability. Wheat genotypes NSP(P1) and NSP(P2) demonstrated superior performance, achieving the highest grain yields (6308.88 – **6180.64** kg ha⁻¹) and elevated numbers of spikes/m² (402–436) and grains per spike (48–54) under optimal N. Thousand-grain weight was highest in SWP1 (41.7 g) and NSP(P1) (39.0 g). Across all traits, the 240 kg N ha⁻¹ rate achieved the greatest mean values: yield (**5480.68** kg ha⁻¹), spikes (397 m²), grains per spike (47.5), and grain weight (38.8 g). Genetic variance consistently exceeded environmental variance, producing high broad-sense heritability estimates ranging from 52.6% (grains/spike) to 86.5% (grain yield)—and exceptionally high genetic stability indices (85–95%), indicating uniform morphological response across environments and N levels. These findings confirm robust genetic control over key yield components and highlight the potential for genotype × N interactions, particularly pronounced in NSP(P1). The observed genotype responsiveness and high heritability underline the potential to breed N-efficient, high-yielding wheat cultivars, aligning with best practices in nitrogen use efficiency research under different sowing dates and variable climates.

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops worldwide, providing nearly 20% of the global population's caloric and protein intake [1]. As the global population continues to grow, enhancing wheat productivity remains a major challenge, particularly under varying environmental and agronomic constraints such as soil fertility, water scarcity, and climate variability. Among these, nitrogen (N) availability plays a pivotal role in determining wheat growth, development, and grain yield [2].

Nitrogen is the most yield-limiting nutrient in wheat production systems and significantly influences key yield components such as the number of spikes per unit area, grains per spike, and thousand kernel weight [3].

Adequate nitrogen fertilization enhances vegetative growth, chlorophyll content, and photosynthetic efficiency, ultimately improving biomass accumulation and grain filling. However, excessive or poorly managed N fertilization may lead to lodging, delayed maturity, and environmental pollution through leaching or gaseous emissions [4]. Therefore, optimizing nitrogen use efficiency (NUE) is essential to achieving high yield while minimizing environmental risks.

The genetic potential of wheat genotypes plays a critical role in how plants respond to nitrogen availability. Genotypic variation in NUE is well-documented, with some cultivars displaying higher adaptability and productivity under limited nitrogen conditions [5]. Breeding efforts have increasingly focused on

developing nitrogen-efficient varieties capable of maintaining yield stability across diverse nitrogen regimes. Selection techniques such as mass selection and trait-specific breeding have been applied to isolate lines with superior performance for seed weight, spike number, and grain number [6]. Incorporating these traits into breeding programs could enhance resilience and productivity under suboptimal nutrient conditions.

Several studies have reported positive correlations between nitrogen application and wheat yield components. For example, Aryan et al. [7] observed that increasing nitrogen levels improved the number of spikes and grain number per spike. Similarly, Stefanova-Dobreva & Muhova [8] reported significant increases in thousand-kernel weight and overall grain yield with higher nitrogen doses. However, the degree of response to nitrogen is often genotype-dependent, and understanding these genotype-by-nitrogen interactions is crucial for targeted cultivar recommendations [9].

Recent breeding approaches have leveraged quantitative selection from segregating populations to develop improved wheat lines. Progenies derived from introduced genetic materials and evaluated for specific agronomic traits, such as seed weight (SW), number of kernels per spike (NKS), and number of spikes per plant (NSP), offer potential for enhanced performance under varying nitrogen inputs. Such targeted selection allows the accumulation of favorable alleles for yield-determining traits, providing a robust genetic base for developing nitrogen-efficient cultivars [9].

In Iraq and similar semi-arid regions, wheat productivity is often constrained by

inconsistent nitrogen availability and variable rainfall. Introducing and evaluating genetically diverse lines under controlled nitrogen regimes provides valuable insights into adaptive performance and nitrogen responsiveness. Previous studies in these environments have highlighted the importance of matching genotype to agronomic practices to ensure maximum resource use efficiency [10]. This study aimed to evaluate selected wheat genotypes derived from mass selection under different nitrogen rates

Materials and methods .

A field experiment was conducted in the fields of Saqlawiyah city – Al-Anbar Governorate, with the aim of developing a high-yielding varieties with Gene recombination by using Reciprocal Recurrent Selection from the use of two segregation genotypes (F₃). This experiment including eight genotypes with control (Ipa99) produced by hybridization and selection. (4 cycle selection) from two segregating F₃ populations (designated as **Progeny P1** and **Progeny P2**) and that were introduced from the United States. Seeds were sown using the **single seed method**, which ensures equal representation of genotypes and maintains genetic integrity across generations. From each progeny, plants were selected based on three agronomic traits: **Seed Weight (SW)**, **Number of Kernels per Spike (NKS)** and **Number of Spikes per Plant (NSP)**. This trait-specific selection was conducted on mature plants, and representative individuals were used to form the first selection cycle (S1). These were then advanced (4) selection cycles, by using selection with intensity (10%) and resulting genotypes in table (1)

Table.1.The name of selected wheat genotypes and their parents

Number	Genotypes	Details
1	Progeny p1	Segregation F3 (introduced variety)
2	Progeny p2	Segregation F3(introduced variety)
3	Swp1	Selected of seed weight from progeny p1
4	NKS p1	Selected of kernels per spike from progeny p1
5	NSP (P1)	Selected of number spikes per plants from progeny p1
6	SW p2	Selected of seed weight from progeny p2
7	NKSp2	Selected of number kernels per spike
8	NSP (P2)	Number of spikes per plants
9	IPAA99	Local variety (control)

Experimental Design and Fertilization Treatments

The genotypes were sown under three nitrogen fertilization levels: **160 kg N ha⁻¹, 200 kg N ha⁻¹, 240 kg N ha⁻¹**. The **Nitrogen** was applied in two time. the first one at sowing and the last in the tillering stage. The study followed a **factorial arrangement** in a **randomized complete block design (RCBD)** with three replicates. All agronomic practices including irrigation, weed control, and pest management and the traits were taken after harvest and the following;

- 1- **Number of Spikes per Square Meter (NS)** – Measured by counting the total number of productive spikes within a fixed 1 m² area in each plot.
- 2- **Number of Grains per Spike (NKS)** – Determined by randomly selecting and threshing spikes from each plot and averaging the grain count

- 3- **Thousand Grain Weight (g)** – Measured by weighing a sample of 1000 fully developed grains from each plot
- 4- **Grain Yield (kg ha⁻¹)** – Calculated by harvesting the central rows in each plot, threshing, and extrapolating the grain weight to a per-hectare basis.

Statistical Analysis

All data were subjected to analysis of variance (ANOVA) using appropriate statistical software. Least Significant Difference (LSD) tests at the 0.05 level of significance were used to determine the statistical differences among treatment mean.

Results and discussion

Number of Spikes per Square Meter (NS)

The results presented in Table 1 revealed significant differences among wheat genotypes in the number of spikes per square meter under varying nitrogen levels. The genotypes NKS P2 and NSP(P1) recorded the highest spike densities, with 410.69 and 401.29 spikes/m², respectively. In contrast, Progeny P2 showed the lowest spike density at 301.16 spikes/m². Nitrogen supply significantly influenced spike number. The application of 240 kg N/ha resulted in the highest average spike count (397.33 spikes/m²), compared to 336.50 spikes/m² under 160 kg N/ha. This increase is attributed to enhanced tillering with higher nitrogen input (Aryan et al., 2024). A significant interaction between genotype and nitrogen level was observed. For example, NSP(P1) at 240 kg N/ha produced 436.67 spikes/m², while

Progeny P1 at 150 kg N/ha yielded only 264.42 spikes/m². This suggests that higher nitrogen levels may improve spike production in certain genotypes [11]. According to Table 6, genetic variance exceeded environmental variance at 160 and 200 kg N/ha, resulting in high heritability estimates of 82.45%, 82.83%, and 60.90%, respectively. These findings align with previous research [1]. The genetic stability index was also high—91.9%, 89.9%, and 89.04%—indicating homogeneity in phenotypic and genotypic coefficients of variation (P.C.V. and G.C.V.). At 160 kg N/ha, P.C.V. and G.C.V. were 12.24% and 11.23%, respectively; at 200 kg N/ha, 7.45% and 6.68%; and again at 200 kg N/ha, 9.65% and 7.62%. These results further confirm the consistency reported by Al- Al-essawi and Abed [1].

Table 2. The effect of selected genotypes of wheat and N- rates and their infraction on the number of spikes per mater square.

Genotypes	N-rates kg N ha ⁻¹			Mean
	160	200	240	
Progeny p 1	264.42	312.5	344.53	307.15
progeny p2	280.34	298.32	326.28	301.6
SW p1	325.25	360.33	386.34	347.30
NKS P1	340.21	394.62	414.20	383.03
NSP(P1)	367.88	402.34	436.67	402.29
SW p2	343.44	370.56	423.56	379.18
NKS P2	388.77	413.65	429.67	410.69
NSP(P2)	372.87	399.44	421.89	398.06
Ipaa 99	345.32	368.90	392.76	368.99
LSD 0.005	12.78			

Mean	336.50	368.05	397.33	
LSD 0.005	4.54			

Number of Grains per Spike (NKS)

Table 1 revealed statistically significant differences among wheat genotypes in grain number per spike (NKS) across nitrogen treatments. Genotypes NKS P2 and NSP(P2) exhibited the highest values, with 50.85 and 48.10 grains per spike, respectively, whereas SWP1 had the lowest count at 38.73 grains per spike. Nitrogen supply also had a significant impact. At 240 kg N/ha, the mean NKS reached 47.50 grains/spike, compared to only 37.78 grains/spike under 160 kg N/ha. This increase likely reflects enhanced photosynthetic activity induced by higher nitrogen levels [12]. A notable genotype $\times$ nitrogen interaction was observed: NSP(P1) at 240 kg N/ha produced 54.0 grains per spike, while Progeny P2 at 150 kg N/ha yielded just 35.00 grains per spike. This underscores the potential for modern cultivars to maximize spike fertility under increased nitrogen regimes [13].

Genetic analysis (Table 6) showed genetic variance exceeded environmental variance at 160, 200, and 240 kg N/ha, with heritability estimates of 58.75%, 82.83%, and 52.62%, respectively. The results consist with Al- Al-essawi and Abed [1]. The genetic stability index was similarly high—94.67%, 94.25%, and 92.45% across the three nitrogen levels—indicating uniformity between phenotypic and genotypic coefficients of variation (P.C.V. and G.C.V.). Specifically, at 160 kg N/ha⁻¹ (6.6% ,6.03%) at 200 kg N/ha⁻¹ ,6.00, 5.01%) and at 240 kg N/ha⁻¹ (16.78% ,11.70%). The results were consistent with stability measures reported by Al- Al-essawi and

Table 3. The effect of selected genotypes of wheat and N- rates and their infraction on the number of grains per spike

Genotypes	N-rates kg N ha⁻¹			Mean
	160	200	240	
Progeny 1	35.60	40.23	44.3	40.04
progeny 2	35.00	42.34	40.65	39.33
SW p1	36.79	40.54	38.88	38.73
NKS P1	38.00	43.22	46.12	42.44
NSP(P1)	39.01	42.07	48.34	43.14
SW p	38.00	44.05	50.24	44.09

NKS P2	44.23	50.32	58.02	50.85
NSP(P2)	42.23	48.08	54.0	48.10
Ipa 99	40.21	44.08	47.02	43.77
LSD 0.005	3.67			
Mean	37.78	43.88	47.50	
LSD 0.005	2.10			

Thousand Grain Weight (gm).

Table 4 indicates significant differences among wheat genotypes regarding thousand-grain weight (TGW) under various nitrogen regimes. SWP1 and NSP(P1) exhibited the highest TGW values of 41.67 g and 39.00 g, respectively, while Progeny P2 produced the lowest, at 31.25 g. Nitrogen application significantly influenced TGW. The highest average TGW (38.84 g) was recorded at 240 kg N/ha, compared to 34.00 g at 160 kg N/ha. This improvement is likely due to elevated kernel assimilation rates driven by enhanced nitrogen supply [14]. Genotype $\times$ nitrogen interaction was also significant. Under 240 kg N/ha, SWP1 achieved 44.03 g TGW, while Progeny P2 at 150 kg N/ha had

only 29.09 g. This suggests that modern cultivars can substantially increase kernel weight with optimized nitrogen application [15]. Genetic analysis in Table 6 reveals that genetic variance surpassed environmental variance at 160, 200, and 240 kg N/ha, resulting in heritability estimates of 68.68%, 67.75%, and 67.78%, respectively—consistent with findings of Al-essawi [1]. The genetic stability index was also high across nitrogen levels—92.34%, 92.95%, and 89.76%—indicating minimal disparity between phenotypic and genotypic coefficients of variation (P.C.V, G.C.V.). Specifically, at 160 kg N/ha⁻¹: (5.68%, 3.91%) at 200 kg N/ha⁻¹: (2.54%, 1.37%) at 240 kg N/ha⁻¹: (8.96%, 7.65%). The results agree with Abed and Al-essawi [1].

Table 4. The effect of selected genotypes of wheat and N- levels and their infraction on the (1000 grains weight (gm)

Genotypes	N-levels kg N ha⁻¹			Mean
	160	200	240	
Progeny 1	33.5	35.08	36.7	35.09
progeny 2	29.09	31.6	33.08	31.25
SW p1	39.4	41	44.03	41.47
NKS P1	33.56	35,78	37.89	35.725
NSP(P1)	36.70	39.0	42.06	39.25

SW p2	34.76	37.08	43.23	38.35
NKS P2	33.12	35.65	36.89	35.22
NSP(P2)	34.86	35.88	39.76	36.83
Ipaa 99	31.05	34.4	35.96	33.80
LSD 0.005	5.21			
Mean	34.00	36.21	38.84	
LSD 0.005	1.65			

Grain yield (kg. ha⁻¹)

Table 5 demonstrates significant differences in grain yield among wheat genotypes under varying nitrogen levels. NSP(P1) and NSP(P2) produced the highest yields, at 1,508.78 and 1,489.84 kg ha⁻¹, respectively, whereas Progeny P2 recorded the lowest at 828.20 kg ha⁻¹. Nitrogen application had a pronounced effect on yield. The maximum mean yield (1,370.27 kg ha⁻¹) occurred at 240 kg N ha⁻¹, compared to 1,043.39 kg ha⁻¹ at 160 kg N ha⁻¹. This enhancement likely reflects improved kernel assimilation and increased kernel number per spike, consistent with established effects of nitrogen on wheat physiology [16]. The genotype × nitrogen interaction was also significant. For example, under 240 kg N ha⁻¹, NSP(P1) yielded 1,577.22 kg ha⁻¹, while Progeny P2 produced only 617.57 kg ha⁻¹ at the

lower nitrogen rate of 160 kg N ha⁻¹. This underscores the potential of modern genotypes to maximize yield under optimized nitrogen regimes [17, 18]. Genetic analysis (table 6) shows that genetic variance exceeded environmental variance across all nitrogen treatments (160, 200, and 240 kg N ha⁻¹), resulting in high heritability estimates of 86.53%, 68.71%, and 68.71%, respectively—supporting genetic yield, in line with findings by Al-Temimi & Abed [1]. The genetic stability index remained elevated across nitrogen levels (85.36%, 86.77%, and 86.60%), indicating minimal divergence between phenotypic and genotypic coefficients of variation (P.C.V. vs. G.C.V.). Specifically, at 160 kg N ha⁻¹: (14.45%, 12.47%) at 200 kg N ha⁻¹: (14.89%, 12.54%) at 240 kg N ha⁻¹: (16.78%, 11.70%). These results consist with Abed and Al-essawi [1].

Table 5. The effect of selected genotypes of wheat and N- rates and their infraction on yield (kg.ha⁻¹).

Genotypes	N-rates kg N ha ⁻¹			Mean
	160	200	240	
Progeny 1	2470.28	3640.52	4361.88	3490.87
progeny 2	2703.6	3324.84	3909.64	3312.6
SW p1	4436.12	5461.16	5909.56	5268.9
NKS P1	4328	4536.28	5646.06	4836.78
NSP(P1)	5592.00	6204.5	6308.88	6035.0
SW p2	4101.3	5509.24	5738.8	5116.44
NKS P2	4427.76	4821.6	5960.08	5069.81
NSP(P2)	5529.6	6164.24	6180.64	5958.16
Ipaas 99	3972.8	5071.44	5310.6	4784.94
LSD 0.005	166.25			
Mean	4173.17	4970.24	5480.68	4874.69
LSD 0.005	191.12			

Table .6. Some genetic parameters of nitrogen fertilization levels for some of traits in the genotypes of wheat.

Traits	Nitrogen rates 160 kg. h ⁻¹						
	σ^2_g	σ^2_e	σ^2_p	P.C.V %	G.C.V %	$h_{b.s}$ %	Stab%
Number of Spikes (NS)	29.27	6.23	35.50	12.24	11.23	82.45	91.24
Number of Grains per Spike (NKS)	18.34	12.880	31.22	6.77	6.03	58.745	94.67
Thousand Grain Weight (g)	3.40	1.45	4.95	5.68	3.91	68.68	92.34

Grain Yield (kg ha⁻¹)	32.67	5.60	38.27	14.45	12.47	86.53	85.36
Nitrogen rates 200 kg. h ⁻¹							
Traits	σ²g	σ²e	σ²p	P.C.V %	G.C.V %	h_{b.s} %	Stab%
Number of Spikes (NS)	21.56	4.57	26.03	7.45	6.89	82.83	89.90
Number of Grains per Spike (NKS)	16.89	3.60	20.29	6.00	5.01	83.22	94.25
Thousand Grain Weight (g)	2.50	0.25	3.69	2.54	1.37	67.78	92.95
Grain Yield (kg ha⁻¹)	47.89	21.87	69.76	14.89	12.54	68.71	86.77
Nitrogen rates 240 kg. h ⁻¹							
Traits	σ²g	σ²e	σ²p	P.C.V %	G.C.V %	h_{b.s} %	Stab%
Number of Spikes (NS)	14.89	9.54	24.43	9.65	7.62	60.90	89.04
Number of Grains per Spike (NKS)	23.08	20.78	43.86	8.50	5.65	52.62	92.45
Thousand Grain Weight (g)	18.89	14.05	32.94	8.96	7.45	57.34	89.76
Grain Yield (kg ha⁻¹)	67.79	23.87	81.75	16.78	11.70	82.92	86.60

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