

**AGROECOLOGICAL VARIABILITY OF SEED PROTEIN
CONTENT IN CHICKPEA (*Cicer arietinum* L.) GENETIC RESOURCES**

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ABSTRACT: *The study evaluated variation in seed protein content among 30 chickpea (*Cicer arietinum* L.) genetic resources grown under three agroecological conditions of Uzbekistan: Andijan, Surkhandarya, and Tashkent. Field observations collected in 2025 were analyzed to compare protein concentration and selected yield-related traits. Mean seed protein content was 24.18%, 24.07%, and 23.93% in Andijan, Surkhandarya, and Tashkent, respectively, indicating relatively small environmental differences for this nutritional trait. Considerable genotypic variation was observed. K-1492 (Xosildor) had the highest mean protein content (27.72%), followed by K-1486 (Sahro-1) (26.78%) and K-16747 (25.91%). K-1492 also showed the highest mean grain yield (23.67 centners ha⁻¹), indicating a favorable combination of productivity and nutritional value. Grain yield showed positive associations with seed protein content ($r=0.294$), seeds per plant ($r=0.392$), and pods per plant ($r=0.390$). These results demonstrate the value of chickpea genetic resources for identifying materials combining high yield and improved seed quality. The selected genotypes may be useful as parental or starting materials in breeding programs targeting productive and nutritionally valuable chickpea cultivars adapted to diverse environments.*

Keywords: *chickpea; genetic resources; seed protein; agroecological variation; grain yield; breeding.*

1. INTRODUCTION

Chickpea is an important pulse crop and a major source of dietary protein. Its genetic resources provide variation for yield, adaptation, seed quality and resilience traits, making systematic characterization an important component of breeding programs [1,2]. The use of diverse germplasm is especially relevant where production environments differ in temperature, water availability and soil conditions.

Seed protein concentration is an important quality trait because improvement of chickpea productivity should be accompanied by preservation or enhancement of nutritional value. However, protein expression may vary among genotypes and environments. Therefore, evaluation of germplasm across contrasting locations can help identify materials that combine desirable agronomic performance with nutritional quality.

Recent multi-environment studies have emphasized the importance of genotype $\times$ environment interaction when selecting elite chickpea materials. AMMI and GGE biplot analyses can separate mean performance from stability and identify genotypes suited to broad or specific adaptation [3]. Phenology and reproductive traits are also important determinants of adaptation and yield formation [4].

The objective of this preliminary study was to characterize seed protein variability in 30 chickpea genetic resources tested in three regions of Uzbekistan and to identify genotypes combining comparatively high protein concentration with favorable yield performance.

2. MATERIALS AND METHODS

Thirty chickpea genetic resources were evaluated during 2025 in three agroecological environments: Andijan, Surkhandarya and Tashkent. The field dataset included replicated observations. The evaluated material included the standard cultivar Yulduz and genetic resource entries such as K-1492 (Xosildor), K-1486 (Sahro-1), K-16748, K-1301, K-16756, K-6814, K-16747 and Polvon.

The present conference thesis focuses on seed protein concentration (%), while grain yield, pods per plant, and seeds per plant were used as complementary

traits. Means and standard deviations were calculated for each environment and genotype. Pearson correlation coefficients were calculated from plot-level observations.

All values reported here were calculated directly from the supplied 2025 field spreadsheet; the present work is a preliminary characterization rather than a final stability classification.

3. RESULTS

Mean seed protein concentration was $24.18 \pm 1.49\%$ in Andijan, $24.07 \pm 2.03\%$ in Surkhandarya, and $23.93 \pm 1.47\%$ in Tashkent. Thus, environmental means were relatively close, while genotype-level differences were more pronounced.

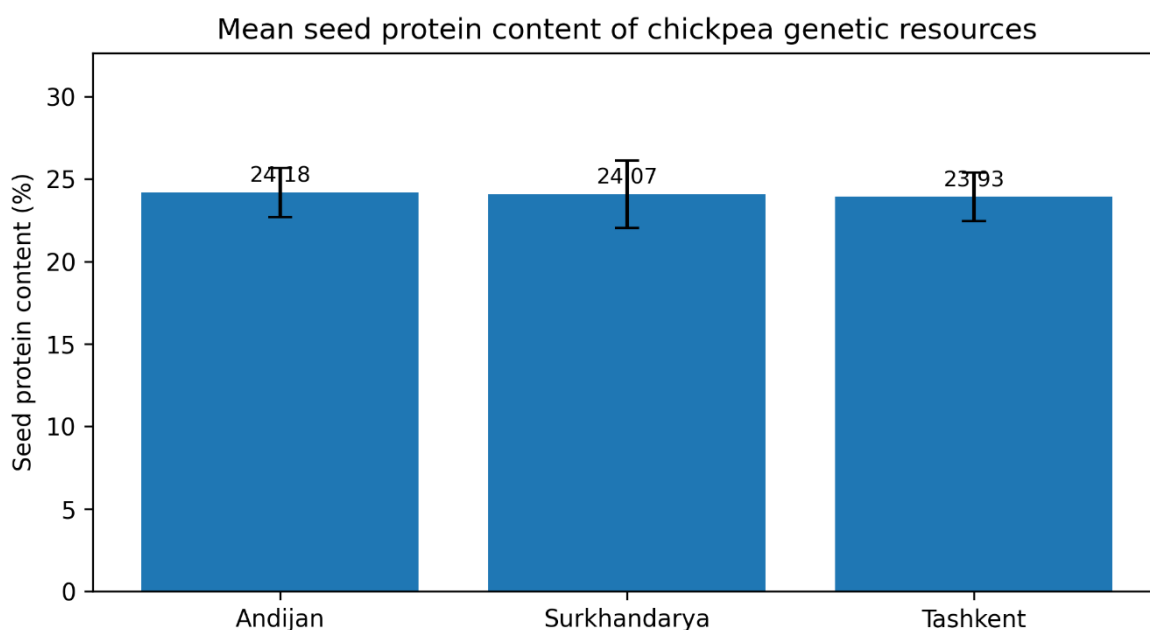


Figure 1. Mean seed protein content of chickpea genetic resources across three agroecological environments; error bars indicate SD.

Genotype	Protein (%)	Grain yield (centners ha ⁻¹)
K-1492 (Xosildor)	27.72 ± 1.23	23.67 ± 4.23
K-1486 (Sahro-1)	26.78 ± 0.96	20.90 ± 4.28
Юлдуз (СТ)	26.29 ± 1.01	15.84 ± 2.17
K-16747	25.91 ± 0.59	17.07 ± 1.55

K-240	25.37 ± 0.50	16.67 ± 5.81
K-1494	25.10 ± 0.52	14.34 ± 3.47

Table 1. Highest-protein chickpea genetic resources; values are mean ± SD across observations from the three environments.

K-1492 (Xosildor) had the highest mean protein concentration (27.72%) and the highest overall mean grain yield (23.67 centners ha⁻¹). K-1486 (Sahro-1) ranked second for protein concentration (26.78%). K-16747 also showed a high protein value (25.91%).

Grain yield was positively associated with seed protein content ($r=0.294$), seeds per plant ($r=0.392$), and pods per plant ($r=0.390$).

4. DISCUSSION

The relatively similar environmental means for protein concentration suggest that this trait was less variable among the three locations than grain yield. Nevertheless, the differences among genotypes demonstrate useful genetic variation that can be exploited to improve seed nutritional quality. Genetic resources are particularly important because they preserve allelic diversity that can be utilized in crop improvement [1,2].

K-1492 (Xosildor) was the most promising material in the present dataset because it combined the highest protein concentration with the highest mean grain yield. K-1486 (Sahro-1) and K-16747 also demonstrated favorable protein levels. Such combinations are desirable for breeding because improving productivity without compromising nutritional value is an important objective.

The positive relationship between protein concentration and grain yield was moderate, indicating that selection for yield in this material did not necessarily correspond to lower protein concentration. However, the observed correlation should be interpreted cautiously and verified using additional years and environments.

Multi-environment evaluation remains essential because genotype performance can change with environmental conditions. Recent chickpea studies have shown that significant genotype × environment interaction can affect yield and

that AMMI and GGE biplot approaches are useful for identifying high-performing and stable materials [3]. The present study therefore represents an initial screening stage rather than a final stability assessment.

Based on the available data, K-1492, K-1486 and K-16747 deserve further evaluation as potential breeding materials combining nutritional and agronomic value. Future trials should include additional years, formal stability indices and more detailed seed-quality measurements.

5. CONCLUSION

The evaluation of 30 chickpea genetic resources in Andijan, Surkhandarya and Tashkent demonstrated useful genotypic variation in seed protein concentration. K-1492 (Xosildor) showed the highest mean protein concentration (27.72%) together with the highest mean grain yield (23.67 centners ha⁻¹), making it the most promising genotype in this preliminary assessment. K-1486 (Sahro-1) and K-16747 also showed favorable protein levels. These materials can be advanced for multi-environment testing and considered as potential starting material for chickpea breeding aimed at combining productivity and nutritional quality.

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