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Selection of Promising Erect Chickpea (Cicer Arietinum L.) Germplasm Accessions Based on Biometric Indicators

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Abstract: This article presents the results of a study conducted under weakly saline soil conditions using collected chickpea (Cicer arietinum L.) samples. High-yielding chickpea accessions such as FLIP 98-189c (25.5 t/ha), FLIP 98-140c (32.6 t/ha), FLIP 98-116c (26.6 t/ha), and FLIP 98-183c (25.7 t/ha) were identified and recommended for breeding purposes. Accessions FLIP 98-121c, FLIP 97-25c, FLIP 98-183c, and FLIP 98-189c demonstrated superior performance in terms of 1000-grain weight and are recommended as initial sources for breeding programs.

Keywords: Chickpea, germplasm, correlation, yield, yield components, factor analysis.

Introduction: Chickpea is among the most significant leguminous crops, valued for its high content of protein, carbohydrates, and fiber, and it plays a vital role in the food industry. As a drought-tolerant legume, chickpea also enhances soil fertility. Although it is primarily cultivated in drylands, recent efforts have aimed to grow chickpea on arable lands susceptible to waterlogging and salinization. For this purpose, breeding programs tailored to regional agro-climatic conditions are essential, focusing on scientifically grounded selection of initial genetic sources.

Yield remains the primary trait for selecting varieties suitable for specific environmental conditions. Although it is a complex quantitative trait influenced by both genotype and environment, high yield under natural local conditions reflects a genotype's adaptability. Additionally, productivity depends on yield components.

In the Syrdarya region’s weakly saline soils, when chickpea varieties such as “Uzbekistan-32” (control), FLIP 98-140c, FLIP 98-1116c, FLIP 98-152c, and FLIP 98-183c were planted in the autumn using various row spacings (60×10×1, 60×15×1, 60×20×1), the highest number of pods, grains, and grain mass was observed in the 60×20×1 planting pattern. However, decreasing plant spacing led to fewer grains per plant and an increase in individual grain size. All chickpea samples exceeded the control in 1000-grain weight (69–128 g) [6; 71–75].

According to O. Soipov [13; 22], planting larger seed fractions resulted in an additional 1.5 t/ha grain yield (a 27.4% increase), and even higher fractions led to a 2.1 t/ha yield increase (29.5%). In saline, irrigated lands of the Syrdarya region, chickpea seeds ("Malhotra" variety) were fractionated into very small to very large sizes. For quality seed material, an 8.0 mm sieve is recommended [3; 262–264].

Previous studies have shown that grain length and width are largely genotype-dependent, while grain mass is influenced by the environment. Larger grain fractions improve seed quality and germination—by 13–18% in soybean and 10–11% in chickpea. A weak correlation exists between grain length and thickness, while a strong correlation exists between width and thickness, with a weak positive correlation between seed mass and germination [3; 262–264; 4; 28–33].

Chickpea productivity is also influenced by external conditions and agronomic practices. According to Z.K. Yuldasheva, yields reached 28.7–31.0 t/ha in autumn and 26.8–27.0 t/ha in spring, depending on row spacing. "Uzbekistan-32" achieved 36–37 c/ha, "Yulduz" 31.1–32.4 c/ha, and "Lazzat" 26.8–27.8 c/ha. The highest yields occurred in wider row spacings and when the “Uzbekistan-32” variety was planted in double rows spaced at 60 cm [16; 32–33].

It was observed that dense plantings (60×10×1) led to higher yields in accessions FLIP 98-140c (25–36.1 c/ha) and FLIP 98-1116c (25.4–39 c/ha) [9; 22; 11; 172–174].

G.K. Mirsharipova (2010), Z.K. Yuldasheva (2002), and A.A. Abdiev (2008) confirmed that the height of the lower pods is lower in early-sown and densely planted chickpeas compared to late or sparse plantings [1; 9; 15; 41–56].

These findings demonstrate that quantitative traits vary with genotype and environment. Therefore, applying statistical methods—particularly factor analysis—is essential for identifying promising germplasm adapted to local conditions [2; 23–25; 3; 243–245].

In addition, detailed studies of saline soils in the Mirzachul region have provided insights into their characteristics and recommendations for improving their fertility [17; 18]. Using factor analysis, it was determined that the vetch variety Mirzachul-1 exhibits salinity tolerance [4; 4–7].

Objective

To identify promising erect chickpea genotypes suitable for the soil and climatic conditions of the Syrdarya region.

METHODS

The study involved 25 chickpea accessions, with “Uzbekistan-32” used as the control. All accessions were planted in a 60×10×1 pattern. Phenological observations and biometric measurements were conducted according to the manual published by the Cotton Research Institute [12; 15–140], and primary data were analyzed using a statistical software program [14; 65–107; 5; 45–100].

RESULTS AND DISCUSSION

Table 1 presents the biometric traits of the chickpea accessions. The average pod weight per plant was 24.9 g, ranging from 13.3 g to 41.0 g across genotypes. Similarly, pod number per plant averaged 48.5, with a minimum of 24.6 and a maximum of 80.4.

Grain weight per plant averaged 17.6 g, ranging from 4.8 g to 29.2 g. Grain number per plant ranged from 4.4 to 88.4, with an average of 51.6.

Table 1

Biometric indicators of standing pea genotypes

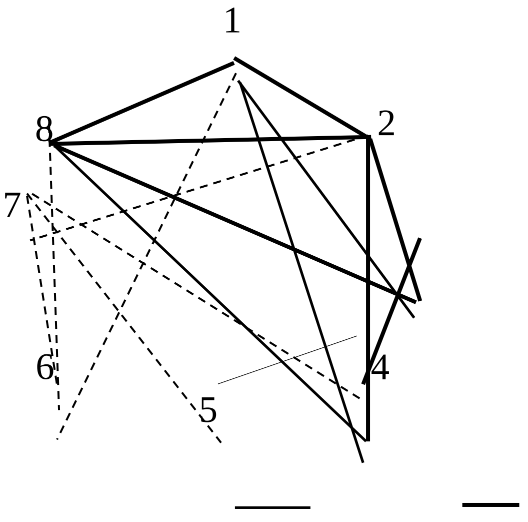
Genotypes	**On a single plant**							Productivity, ts/ha
	Legumes		Grain		Legumes A grain in one grain quantity, piece	Grain output %	1000 grain weight	
	weight, g	quantity, piece	weight, g	quantity, piece				
	1	2	3	4	**5**	**6**	**7**	**8**
Uzbekistan-32 (control)	29,4	72,3	22,6	88	1,2	77,3	258,8	22,8
FLIP 98-189c (17)	29,9	53,1	24,6	76,1	1,3	84,3	325,8	25,5
FLIP 98-189c (24)	13,4	25,2	10,6	27,2	1,1	79,1	389,5	11.0

FLIP 98-17c	25,9	54,9	10,6	27,2	1,1	73,4	302,3	17.0
FLIP 97-254c	24,9	56,9	18,7	55,8	0,9	75,1	340,2	16,7
FLIP 98-212c	27,4	57,2	20,8	65,7	1,1	75,9	351,2	17.0
FLIP 97-147c	25,5	47	19,3	54,1	1,2	75,7	355,8	17,7
FLIP 98-218c	20,2	40,9	15,3	48,5	1,75	75,7	322,6	16.0
FLIP 98-121 (62)	24,4	49,6	18,4	53,3	1,1	75,4	343,9	18,5
FLIP 98-121c (68)	24,2	39,3	16,9	40,6	1,0	69,8	474,9	15,5
FLIP 98-204c (69)	20,1	41,5	14,5	48,3	1,2	72,1	296	12,6
FLIP 97-25c	27,9	46,6	21,3	53,9	1,3	76,3	390,6	19,2
FLIP 98-197c	33.0	37	4,8	40,1	1,1	75,2	369,7	20,3
FLIP 97-32c	22,1	39,5	16,4	44,4	1,0	71,8	371,7	15,0
FLIP 98-129c	22.0	52,3	16,5	56	1,0	74	293,3	17,0
FLIP 98-107c	18,9	41,4	14,5	52,4	1,2	76,8	295,4	15,8
FLIP 98-182c	22,9	42,3	19,2	49,5	1,4	71,8	339,2	17,0
FLIP 98-201c	21,3	49,5	16,7	53,4	1,1	78,1	312,1	18,0
FLIP 97-231c	24,8	60,2	19,4	60,5	1,0	76,9	312,5	20,0
ILC-533 (106)	13,3	24,6	10,4	27,3	1,1	79,9	371,2	8,0
FLIP 98-140c	41.0	80,4	29,2	88,4	1,1	71,3	331,3	32,6
FLIP 98-116c	30,7	56,5	22,6	63	1,1	74,1	359,7	26,6
FLIP 98-152c	28,6	48,7	19,3	52,9	1,1	67,9	365,3	22,0
FLIP 98-183c	33.0	53,2	22,4	57,8	1,1	68,1	389,3	25,7
FLIP 98-116c (91)	17,2	43,1	14,5	4,4	1.0	84	340,4	17,5
Average	**24.9 ±1,3**	**48,5 ±2,5**	**17,6 ±1,0**	**51,6 ±3,7**	**1,1 ±0,01**	**75,2 ±0,8**	**344,1± 8,7**	**18,6 ±1,0**
Minimum	**13,3**	**24,6**	**4,8**	**4,4**	**0,9**	**67,9**	**258,8**	**8,0**
Maximum	**41,0**	**80,4**	**29,2**	**88,4**	**1,8**	**84,3**	**474,9**	**32,6**

The average number of grains per pod was 1.1. Grain output was 75.2%, and the 1000-grain weight averaged 344.1 g, with a range of 258.8 to 474.9 g.

Productivity, a key indicator, averaged 18.6 c/ha, with the lowest being 8.0 c/ha and the highest 32.6 c/ha. The variability in performance reflects the genotypic diversity and morphological characteristics of each accession.

From the results of the initial statistical analysis of the primary data, it became clear that the genotypes of upright pea differed from each other in quantitative characteristics. This is natural. Because each collection sample is a genotype and has its own morphological characteristics and features. It is important to conduct targeted selection work among them, to select those that are important for selection. In this case, first of all, it is advisable to have complete information about each quantitative characteristic and select genotypes using them. In this case, it was determined that the correlation analysis can be used to evaluate quantitative traits and to select genotypes using them [15; 25-105-6]. This can also be seen from the data in the following figure (Figure 1). From the data in the figure, it can be seen that there is an average strong (r=0.744) correlation between the weight of pods per plant (number 1 represents the number of seeds per plant) and the number of grains per plant (2). This is natural. Because as the number of grains increases, their weight also increases.



The numbers are symbols and the lines between them represent the correlation coefficient and its level: 1. weight of pods in one plant, g; 2. number of pods, pieces; 3. grain weight in one plant, g 4- the number of grains; 5- the number of grains in one pod, piece; 6 grain output,%; 7-1000 grain weight, g; 8- yield, ts/ha

1 Figure 1. Level of correlations between quantitative traits of standing pea genotypes.

_______r=0.3-0.5; r=0.3-0.5; r=>0.7; r=-0.3-0.5.

A moderate correlation was observed between the weight of pea pods per plant (1) and the weight of grains per plant (3) (r=0.599) and the number of grains per plant (4) (r=0.683), while a strong correlation was observed between productivity (r=0.844). So, the productivity of pea genotypes depends first on pod weight, followed by the number of pods, the number of grains and its weight. A strong correlation (r=0.747, 0.759, 0.785) was observed between the number of pods per plant (2) and grain weight per plant (3), and between grain number (4) and productivity (8). The same result was found between the number of formed grains (4) per plant and productivity (8) (r=0.675).

An inverse correlation (r=-0.399) was observed between the percentage of grain in the pod (grain yield) (6) and the weight of pods per plant (1). This meant that an increase in pod weight decreased the percentage of grain in the pod. An inverse correlation (r=-0.438) was found between the 1000-grain weight (7) and the number of pods per plant (2). This meant that an increase in the number of pods led to a corresponding decrease in the 1000-grain weight.

In general, weak, medium, and strong correlations grain weight.

As we noted above, it was found that there are varying degrees of correlation between the traits of upright pea genotypes. So, since quantitative traits are correlated to varying degrees, there is a commonality in this relationship. In this case, factor analysis can be used. Factor analysis is one of the modern statistical programs, the main task of which is to divide quantitative traits into groups or factors according to the degree of correlation between them [15; 25-105-p]. Because the basis of factor analysis is correlation analysis. When traits are interconnected, they can have a common trait. We can determine this using the data in Table 2 below. From the data in the table, the factor loadings for the first factor were the highest for indicators such as the weight of pods per plant (0.882), the number of pods per plant (0.916), the weight of grains per plant (0.850), the number of grains per plant (0.878), and yield (0.909).

Table 2
Factor loadings of quantitative traits of standing pea genotypes

Signs	Factor loadings of pea symptoms			
	1	2	3	4
Weight of pods in one plant, g	0,882	-0,273	0,047	0,039
The number of dukas in one plant, pcs	0,916	0,143	-0,259	-0,112
Grain weight per plant, g	0,850	0,028	0,074	0,258
The number of grains in one plant, pcs	0,878	0,178	0,108	-0,039
The number of grains in one pod, grain	0,015	0,483	0,865	0,037
Grain output, %	-0,304	0,674	-0,305	0,587
1000 grain weight, g	-0,246	-0,814	0,227	0,456
Productivity, ts/ha	0,909	-0,081	-0,013	0,190

In this case, based on the characteristics of these traits, this factor can be called “yield.” Because the weight of pods on one plant, their weight, the number of grains, and their weight have a positive effect on yield, and there is a high correlation between them (as noted above).

A relatively high factor loading on the second factor was observed for the indicator called the proportion of grain in the pod or grain yield (0.674). This factor can be called the "proportion of grain" in the legume.

Relatively high loading on the third factor was recorded on the number of grains in one pod (0.865), while on the fourth factor it was recorded on the weight of 1000 grains (0.456).

Based on these data, the most promising genotypes of standing pea were selected. Factor loadings of each genotype were determined. These data are presented in table 3. From the data in the table, according to the first factor (recall that the first factor is productivity), genotypes such as serial number №1 (Uzbekistan-32-control) (1.473), №2 (FLIP 98-189c (0.982), №21 (FLIP 98-140c) (2.712), №22 (FLIP 98-116c) (1.018), №24 FLIP 98-183c (0.998) had high indicators in terms of factor loadings. This was the basis for recognizing these genotypes as productive genotypes. The productivity of these genotypes was 22.8 c/ha in the Uzbekistan-32 (control) variety, №2 (FLIP 98-189c -25.5 c/ha, №21 (FLIP 98-140c-32.6 , №22 (FLIP 98-116c)-26.6, and FLIP No. 24 98-183c-25.7 c/ha were found to be productive genotypes. It was also noted that these genotypes were superior to the control variety Uzbekistan-32.

According to the second factor (the proportion of grain in the ear), genotypes such as No. 2 (FLIP 98-189c (1.544), No. 8 (FLIP 98-218c) (1.579), No. 16 (FLIP 98-107c) (1.04) can be noted. The proportion of grain in the ear in these genotypes was 84.3; 75.37 and 76.8%, respectively, and differed from the others.

The third factor (number of grains per pod) showed differences in the indicators of genotypes No. 8 (FLIP 98-218c) (3.124), No. 12 (FLIP 97-25c) and No. 17 (FLIP 98-182c) (1.720). The number of grains per pod in these genotypes was 1.75; 1.3 and 1.4.

The fourth factor provided information about genotypes with high 1000-grain weight, including No. 2 (FLIP 98-189c) (2.504), No. 3 (FLIP 98-189c (0.875), No. 10 (FLIP 98-121c) (0.774), No. 12 (FLIP 97-25c) (1.363), No. 20 (ILC-533) (0.590), No. 25 (FLIP 98-116c) (1.628). The 1000-grain weight in these genotypes was 325.8 - 474.9 g.

Table 3
Factor loadings of standing pea genotypes

№	Factor loadings of genotypes				№	Factor loadings of genotypes			
	1	2	3	4		1	2	3	4
1	1,473	1,681	-0,50	-0,65	14	-0,52	-0,99	-0,22	-0,50
2	0,982	1,544	0,216	2,504	15	-0,00	0,386	-1,01	-1,35
3	-1,84	-0,17	-0,09	0,875	16	-0,52	1,04	-0,00	-0,74
4	-0,39	0,09	-0,67	-1,65	17	-0,13	0,204	1,720	-0,61
5	0,168	-0,31	-1,41	-0,30	18	-0,15	0,76	-0,65	-0,04
6	0,446	0,021	-0,26	0,259	19	0,455	0,454	-1,21	-0,15
7	0,030	0,023	0,409	0,404	20	-1,97	0,178	-0,23	0,590

8	-0,50	1,579	3,124	-0,27	21	2,712	-0,44	-0,19	0,184
9	0,048	-0,01	-0,24	0,057	22	1,018	-0,49	-0,05	0,712
10	-0,56	-2,60	0,483	0,774	23	0,463	-1,28	0,495	-0,89
11	-0,58	0,490	0,348	-1,88	24	0,998	-1,65	0,610	-0,08
12	0,190	-0,23	1,125	1,363	25	-1,24	0,620	-1,70	1,628
13	-0,53	-0,87	-0,03	-0,20					

CONCLUSIONS

1. In the collection samples of standing peas, the average weight of pods in one plant was 24.9, the number of pods was 48.5, the weight of grains was 17.6 g, and the number of grains was 51.6. The number of grains in one pod was 1.1, the share of grain in the pod was 75.2%, the weight of 1000 grains was 344.1 g, and the yield was equal to 18.6 t/h on average.

2. It was found that the correlation between pea traits is weak, medium and strong. Productivity was noted to be moderately to strongly correlated with pod number, weight, grain number and weight.

3. Among the upright pea collection samples, FLIP 98-189c (25.5 c/ha), FLIP 98-140c (32.6 c/ha), FLIP 98-116c (26.6 c/ha) and FLIP 98-183c (25.7 c/ha) were recognized as promising high-yielding genotypes, and these varieties were recommended for inclusion in the breeding process.

4. Collection samples of pea FLIP 98-121c, FLIP 97-25c, FLIP 98-183c, FLIP 98-189c were recommended as a starting source for carrying out selection work, being superior to others in terms of weight of 1000 grains.

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