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Research Article

Agronomic traits of twenty-one resistant, semi-resistant and susceptible chickpea genotypes to blight disease

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Abstract

Introduction: Blight caused by *Ascochyta rabiei* is the most destructive disease of chickpea worldwide. Identification of agronomic and morphological properties of disease-resistant cultivars is necessary to set up a suitable chickpea breeding program. **Materials and Methods:** Twelve agronomic and morphological properties of 21 resistant, semi-resistant, and susceptible chickpea genotypes were investigated in a field experiment in a randomized complete block design with six replications in one agronomic year in western Iran. **Results:** All genotypes were divided into three main clusters based on the UPGMA dendrogram. The lowest yielding genotypes were located in cluster II and IDDMAR-2012-32 genotype was susceptible to disease and desi-type in this cluster. The genotypes with the highest yield were placed in cluster III, and the genotype Gebres 419-2 was resistant to the disease and the desi-type in this cluster. Among the Kabuli-type genotypes, ILC482 was included in cluster III as a high-yielding and semi-disease-resistant cultivar, and yielding-low FLIp-02-65C and FLIp-01-164C lines along with disease resistance were included in cluster I. **Conclusion:** Gebres 419-2 can be crossed with FLIp-02-65C or FLIp-01-164C to produce robust, high-yielding Kabuli chickpea varieties with large seeds.

Key words: Genetic Divergence, Hybrid, Kabuli Type

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خصوصیات زراعی بیست و یک ژنوتیپ نخود مقاوم، نیمه مقاوم و حساس به بیماری سوختگی

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چکیده

مقدمه: سوختگی ناشی از *Ascochyta rabiei* مخرب‌ترین بیماری نخود در جهان است. شناسایی صفتهای زراعی و شکل شناختی رقمهای مقاوم به بیماری برای تنظیم یک برنامه مناسب اصلاح نخود ضروری است. **مواد و روش‌ها:** دوازده صفت زراعی و شکل شناختی ۲۱ ژنوتیپ نخود مقاوم، نیمه مقاوم و حساس به بیماری در یک آزمایش مزرعه‌ای در قالب طرح بلوک‌های کامل تصادفی با شش تکرار در یک سال زراعی در غرب ایران بررسی شد. **یافته‌ها:** همه ژنوتیپ‌ها بر اساس تجزیه خوشه‌ای روش جفت گروه بدون وزن با میانگین حسابی به سه خوشه اصلی تقسیم شدند. ژنوتیپ‌های با پایین‌ترین عملکرد درخوشه II قرار گرفتند و ژنوتیپ IDDMAR-2012-32 حساس به بیماری و نوع دسی در این خوشه بود. ژنوتیپ‌های با بالاترین عملکرد درخوشه III قرار گرفتند و ژنوتیپ Gebres 419- 2 مقاوم به بیماری و نوع دسی در این خوشه بود. همچنین در بین ژنوتیپهای نوع کابلی، ILC482 به عنوان رقم پرمحصول و نیمه مقاوم به بیماری در خوشه III قرار گرفت و لاین‌های FLIp-02-65C و FLIp-01-164C با عملکرد پایین همراه با مقاومت به بیماری در خوشه I قرار گرفتند. **نتیجه‌گیری:** Gebres 419-2 را می‌توان با FLIp-02-65C یا FLIp-01-164C تلاقی داد تا گونه‌های نخود کابلی مقاوم و پرمحصول و با دانه‌های درشت ایجاد کرد.

واژگان کلیدی: تیپ کابلی، تنوع ژنتیکی، هیبرید

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Introduction مقدمه

Chickpea (*Cicer arietinum* L.) is the third most important pulse crop after the common bean *Phaseolus vulgaris* L. and field pea *Pisum sativum* L. (Gaure, et al. 2010). It is a major source of protein for humans in semi-arid tropical areas and plays a crucial role in maintaining soil fertility, particularly in dry rainy areas (Choudhary et al. 2012). Chickpea blight caused by *Ascochyta rabiei* (Pass.) Labrousse is the most destructive foliar disease of chickpeas in several countries (Pande et al. 2005). Chickpea blight can cause significant losses (5 to 100%) worldwide (Haware 1998). Various aspects of this disease such as epidemiology, severity, pathogenicity, life cycle, resistance breeding, chemical and cultural control measures have been studied worldwide; however, it still poses a threat to the chickpea crop (Mohamed et al. 2009). The breeding of resistant chickpea varieties is very difficult due to the large differences in the pathogenicity of *A. rabiei* isolates (Ali et al. 2009). Aggressiveness in *A. rabiei* populations (Chen et al. 2004; Chongo et al. 2004) and resistance differ among chickpea varieties (Cho et al. 2004; Udupa and Baum 2003). Aggressive isolates of *A. rabeii* seriously affect some chickpea cultivars that are resistant to less aggressive isolates under the same conditions. In addition, resistance is reduced once plants enter the flowering and pod stages (Chongo and Gossen 2001; Singh and Reddy 1993). Advanced plant breeding and agricultural cultivation systems have limited the genetic base of cultivated chickpeas. Therefore, new sources of variation should be explored to develop superior hybrids and also cultivars that can withstand the biotic and abiotic stresses in chickpea breeding programs (Janghel et al. 2020). The identification and characterization of chickpea cultivars using agromorphological traits and molecular markers seems necessary for their effective use and conservation. Studies on chickpeas show marked genetic variation for number of secondary branches per plant and pods per plant, biomass, seed yield, harvest index (Malik et al. 2009), and days to flowering and maturity (Bakhsh et al. 2003). A clear variation was also observed for seed shape and coat color, growth habit (Qureshi et al. 2004), number of primary and secondary branches per plant, plant height, pods per plant and biomass yield (Aslamshad et al. 2009). We evaluated the chickpea *Ascochyta* rot-resistant genotypes that are poorly used as parents in chickpea breeding programs. Such germplasm acts as a source of alternative genetic pools for improving cultivars. We performed agromorphological characterization of 21 chickpea genotypes, including *Ascochyta rabiei* resistance and susceptibility testing genotypes, to assess their potential use in the breeding program.

Materials and Methods مواد و روش‌ها

Twenty-one chickpea genotypes (consisting of 15 Ascochyta blight (AB) resistant and 6 susceptible) were obtained from the gene banks of the Research Center for Agriculture and Natural Resources, Kurdistan and Ilam University. Table 1 shows some information including genotype names and their responses. Field experiments were conducted at the Ilam University farm (46°25′22″E, 33°38′15″N) at an elevation of 1427 m above sea level, located in the upper midland zone with semi-humid climate with silty clay soil. An

جدول ۱. لیست مشخصات ژنوتیپ‌های مورد استفاده در این مطالعه.

Table 1. The list of genotypes used in the present study in details.

Genotype No.	Genotype	Type	Reaction
1	FLIp-02-65C	Kabuli	Resistant
2	FLIp-01-164C	Kabuli	Resistant
3	IDDUR-2012-12	desi	Semi resistant
4	FLIP-97-178C	Kabuli	Semi resistant
5	ILC533	Kabuli	Susceptible
6	FLIP-05-157C	Kabuli	Semi resistant
7	IDDMAR-2012-32	desi	Susceptible
8	FLIP-05-156C	Kabuli	Semi resistant
9	FLIP-85-05C	Kabuli	Resistance
10	ILC482	Kabuli	Semi resistant
11	Pirouz	desi	Susceptible
12	IDDSAL-2012-02	desi	Semi resistant
13	Bivanij	Kabuli	Susceptible
14	ILC482	Kabuli	Semi resistant
15	IDDMAR-2012-08	desi	Semi resistant
16	IDDSAL-2012-10	desi	Susceptible
17	Kaka	desi	Susceptible
18	IDDUR-2012-16	desi	Semi resistant
19	Gebres 419-1	desi	Resistant
20	Gebres 419-2	desi	Resistant
21	Karaj 41-1	desi	Semi resistant

annual rainfall of 655.4 mm and an average annual temperature of 13.63 °C are reported for this region. The experiment was conducted from October 2019 to June 2020 as a dry farming in a randomized complete block design with 6 replicates. In each replication, seeds were sown at a distance of 7 cm in three rows with 2.5 m long with a distance of 0.5 m from each other.

The numbers of nodes in the main stems, the number of sub branches, flowers and leaves, as well as the length of the pod and seed shape were recorded. Data on days to 50% flowering, days to 50% pod formation and days to 50% maturity in each row were recorded. The other traits such as number of seeds per plant, number of pods per plant, 100-seed weight, plant height and seed yield of five plants randomly selected from the middle of each row were recorded. Data were subjected to analysis of variance (ANOVA) using SAS Statistical Software Ver. 9.2 (SAS Institute Inc. 2013). A randomized complete block design was used for analysis of variance, and Duncan's multiple range post-hoc tests were used for comparisons of means. Descriptive statistics such as minimum and maximum values, mean, range, coefficient of variation, standard error and standard deviation were applied using MINITAB 16 software. Cluster analysis (to group evaluated genotypes according to Ward's method (Ward 1963) was determined by MINITAB 16 software.

Results یافته‌ها

Variation in Morphological Traits: The field experiment showed a variation in all assessed traits of the chickpea genotypes resistance and susceptibility to AB (Table 2). All characteristics showed a significant difference at the 1% level of probability. A wide

جدول ۲. میانگین مربعات تجزیه واریانس ۱۲ صفت رشدی ۲۱ ژنوتیپ نخود.

Table 2. Mean squares of analysis of variance for 12 growth traits among 21 chickpea genotypes.

Source of variation	Mean square						
	Flower length	Leaf length	Plant height	Number of nodes in the main stem	Number of sub-branches	Number of pods/plant	Seed yield
Block	0.049	0.11	41.06	9.92	0.019	48.97	3.86
Genotype	0.026**	0.13**	226.46**	8.60**	0.15**	111.2**	2.8**
Error	0.0085	0.019	62.13	2.44	0.045	12.09	1.06
CV%	8.54	12.00	22.29	7.78	16.51	28.84	15.6

Source of variation	Mean square				
	100-seed weight	Days to flowering	Days to podding	Days to maturity	Number of seeds/plant
Block	1847.14	41.57	202.42	15.32	0.025
Genotype	386.18**	20.28**	192.04ns	42.39**	0.19**
Error	36.86	4.96	205.97	12.38	0.037
CV%	23.49	1.34	8.29	1.69	15.02

ns,* and ** are non-significant, significant at 5% and significant at 1% probability level respectively.

جدول ۳. آماره‌های توصیفی خصوصیات زراعی-ریختی ۲۱ ژنوتیپ نخود.

Table 3. Descriptive statics for agro-morphological characters of 21 chickpea genotypes.

Traits	Mean	SE Mean	St. Dev.	Coef. Var. (%)	Min.	Max.
Days to flowering	165.32	0.401	1.84	1.11	162.83	169.83
Days to podding	173.19	1.23	5.66	3.27	148.67	176.00
Days to maturity	207.94	0.580	2.66	1.28	203.17	214.83
100-seed weight (gr)	25.84	1.75	8.02	35.72	14.49	39.43
Seed yield (gr)	43.25	1.78	8.14	18.83	30.16	57.04
Plant height (cm)	35.35	1.34	6.14	17.38	23.60	48.22
Number of nodes in the main stem	20.07	0.26	1.20	5.97	16.27	21.47
Number of pods/plant	12.05	0.94	4.31	31.05	6.57	21.67
Number of seeds/plant	1.28	0.03	0.16	12.25	1.07	1.70
Number of sub-branches	1.73	0.097	0.45	25.83	1.20	3.30
Leaf length (cm)	1.15	0.033	0.15	12.93	0.98	1.438
Flower length (cm)	1.73	0.097	0.45	25.83	1.21	3.308

SE: standard error, St.Dev.: Standard deviation, Coef.Va.: coefficient of variation

variation was observed for all characteristics, as evidenced by a clear difference between the minimum and maximum values. The 100 seed weight showed the highest coefficient of variation (35.72%) while the lowest was found for days to 50% flowering (1.11%) (Table 3).

The earliest flowering genotype was IDDUR-2012-16 (162.83 days), while FLIp-01-164C (169.83 days) was the last genotype to flower. The shortest maturity time was 203.17 days for the Karaj 41-1 cultivar, while the longest maturity time was 214.83 days for the FLIP-05-157C cultivar. The cultivar FLIp-01-164C yielded the lowest number of pods/plant (6.57), while the maximum number of pods/plant was recorded for the cultivar Kaka (21.67). Cultivar IDDMAR-2012-32 was the shortest (23.60 cm) and cultivar Gebres 419-1 was the tallest (48.22 cm). The lowest number of seeds/pod was recorded for the cultivar Karaj 41-1 (1.07 seeds) and the highest number for the cultivar Kaka (1.7 seeds). The yield ranged from 30.16 g for the IDDMAR-2012-32 cultivar to 57.04 g for the Gebres 419-2 cultivar. The Gebres 419-2 cultivar had the shortest pod period (148.67 days), while the IDDSAL-2012-10 cultivar had the longest (176 days). The shortest pod length (15.3 cm) was observed in genotype IDDMAR-2012-08 and the longest (33.7 cm) in genotype FLIP-05-156C. The Kaka cultivar had the fewest secondary branches/plants (1.2) and FLIP-05-156C had the highest (3.3). The shortest leaf length (0.98 cm) belongs to genotype IDDMAR-2012-08 and the longest leaf length (1.43 cm) to genotype FLIP-85-05C. Genotype IDDMAR-2012-32 had the shortest flower length (0.93 cm) and genotype IDDSAL-2012-10 the longest (1.18 cm). 100-seed weight ranges from 14.49g for cultivar Kaka to 39.43g for cultivar FLIp-01-164C. The lowest number of nods per primary branch observed in the IDDMAR-2012-32 cultivar (16.27), while the highest number of buds (21.47) was recorded in the Bivanij cultivar (Table 4).

Cluster analysis: Chickpea genotypes were clustered using 12 traits that differed significantly between genotypes. The genotypes were classified into three classes (Fig. 1). In terms of the traits considered, members of one cluster were more closely related than those in other clusters. Similarly, accessions in non-significant distance clusters may have closer relationships with each other compared to those with significant distance. The first cluster contained the genotypes FLIP-01-164C, FLIP-02-65C, FLIP-97-178C, FLIP-05-156C, FLIP-05-157C, FLIP-85-05C and ILC482; the second contained the genotypes IDDUR-2012-12, ILC533, IDDMAR-2012-32, Pirouz, IDDSAL-2012-02, IDDMAR-2012-08, IDDSAL- 2012-10, Kaka and IDDUR-2012-16 and the Bivanij, ILC482, Gebres 419-1, Gebres 419-2 and Karaj 41-1 genotypes belonged to the third cluster. Cluster I included high-yielding genotypes, Kabuli type, and resistance to *A. rabiei*. Average yield, height, pod length, 100-seed weight, leaf length, number of secondary branches and day to germination showed an increase compared to the overall average. This group was found to have the lowest seed/pod count and the lowest pod/plant count, while the highest 100-seed weight was recorded for this group (Table 5). Cluster II included genotypes characterized by low yield potential and susceptible to *A. rabei*. These accessions had the shortest pod formation period and the highest number of

جدول ۴. مقایسه میانگین ۱۲ صفت زراعی-ریختی ۲۱ ژنوتیپ نخود

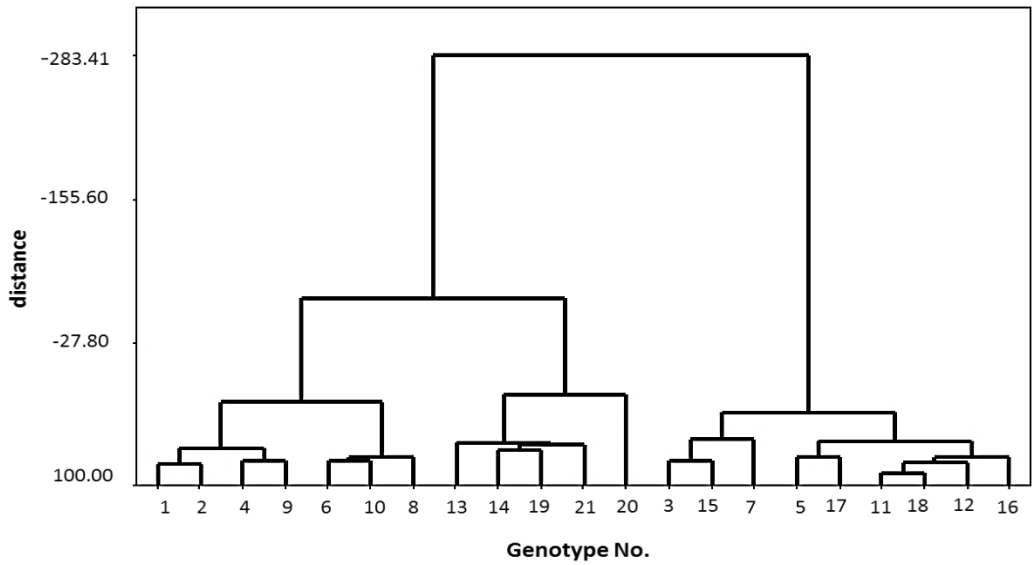
Table 4. Mean comparison of 12 agro-morphological traits in 21 chickpea genotypes

Gen.	Plant height (cm)	Number of nodes in the main stem	Number of sub-branches	Number of pods/ plant	Seed yield (gr)
1	40.06abcd	19.46a	1.33bc	8.7fg	36.03bc
2	43.29ab	20.23a	1.12bc	6.56g	48.02abc
3	31.53bcde	20.83a	1.08c	12.13cdefg	47.01abc
4	43.23ab	19.46a	1.38bc	6.68g	42.94abc
5	34.40abcde	18.66a	1.19bc	14.3bcdef	30.94bc
6	37.05abcde	19.03a	1.25bc	8.13fg	51.74abc
7	23.06e	16.26a	1.48ab	11.1cdefg	30.16c
8	34.74abcde	20.03a	1.77a	8.63fg	52.43abc
9	41.53abc	20.56a	1.25bc	9.5efg	48.75abc
10	38.81abcd	20.53a	1.42bc	10.3cdefg	55.89ab
11	28.8cde	21.06a	1.27bc	19.2ab	43.11abc
12	26.87de	18.9a	1.33bc	16.06abcd	40.7abc
13	37.43abcde	21.46a	1.33bc	9.5efg	52.26abc
14	38.17abcd	20.40a	1.31bc	12.2cdefg	55.37abc
15	28.56cde	20.06a	1.26bc	15.23bcde	37.21bc
16	30.22bcde	21.43a	1.26bc	18.43ab	43.47abc
17	34.34abcde	21.36a	1.08c	21.66a	32.89bc
18	29.58bcde	20.7a	1.34bc	16.5abc	39.76abc
19	48.21a	21.03a	1.15bc	9.56efg	54.79abc
20	36.33abcde	20.16a	1.25bc	13.10defg	57.042a
21	35.49abcde	19.8a	1.11bc	8.4fg	45.49abc

	100-seed weight (gr)	Days to flowering	Days to podding	Days to maturity	Number of seeds/ plant	Flower length (cm)	Leaf length (cm)
1	35.12ab	169.33ab	174.83a	209.0abcd	1.33bcd	1.12abcd	1.38abc
2	39.43a	169.83a	175.0a	209.0abcd	1.2cd	1.13abcd	1.34abc
3	19.51efgh	165.83bcd	175.16a	205.50cd	1.38bcd	1.006bcde	0.99f
4	36.81ab	167.33abc	174.83a	209.0abcd	1.15cd	1.073abcde	1.25abcd
5	18.08fgh	164.66cd	173.83a	206.66bcd	1.36bcd	0.93e	1.01ef
6	35.40ab	164.33cd	174.66a	214.83a	1.15cd	1.046abcde	1.21abcdef
7	22.64defgh	166.00abcd	174.16a	209.0abcd	1.15cd	1.013abcde	1.00f
8	33.57abc	166.83abcd	173.83a	209.0abcd	1.16cd	0.99cde	1.21abcdef
9	32.7abcd	166.33abcd	174.33a	212.5ab	1.10d	1.07abcde	1.43a
10	29.29abcde	164.83cd	174.83a	210.16abc	1.31bcd	1.10abcd	1.12cdef
11	19.12efgh	163.83cd	174.50a	206.66bcd	1.23cd	1.136abcd	1.00f
12	14.91h	163.5cd	173.66a	205.50cd	1.58ab	1.04abcde	1.006ef
13	24.09cdefg	164.50cd	174.0a	209.0abcd	1.36bcd	1.05abcde	1.15bcdef
14	28.83bcde	164.66cd	173.50a	207.83bcd	1.28bcd	1.13abcd	1.24abcde
15	16.99gh	163.66cd	173.50a	204.33cd	1.2cd	1.10abcd	0.97f
16	17.16fgh	165.33cd	176.0a	205.50cd	1.25bcd	1.18a	1.03def
17	14.48h	163.33cd	174.33a	207.83bcd	1.7a	1.09a	1.01def
18	17.73fgh	16.83d	173.5a	206.66bcd	1.46abc	1.17ab	0.99f
19	27.65bcdef	165.83	174.66a	209.0abcd	1.21cd	1.12abcd	1.27abc
20	27.23bcdef	164.50cd	148.66b	206.66bcd	1.26bcd	0.98de	1.29abc
21	32.13abcd	164.33cd	175.16a	203.16d	1.06d	1.16abc	1.37ab

Mean numbers annotated with the same letter are not significantly different in ANOVA and LSD test ($P \leq 0.05$).

seeds/pods and pods/plants. These genotypes showed the shortest maturation time and yield, 100-seed weight, height and pod length (Table 5). Cluster III contained early-maturing accessions that were resistant or semi-resistant to AB, with the exception of Beanie as susceptible. The highest yield, longest pod length and longest flower length were observed in these genotypes, while they had the shortest period of pod formation (Table 5).



شکل ۱. نمودار دندوگرام رابطه بین ۲۱ ژنوتیپ نخود بر اساس ۱۲ صفت زراعی- ریختی.

Figure 1. The dendrogram showing relationship among 21 chickpea genotypes using 12 agro-morphological traits.

جدول ۵. میانگین ۱۲ صفت زراعی-ریختی برای سه گروه شناسایی شده در تجزیه خوشه‌ای ۲۱ ژنوتیپ نخود.

Table 5. Mean values of 12 agro-morphological characters for three groups revealed by cluster analysis among 21 chickpea genotypes.

Character	Cluster I	Cluster II	Cluster III
Days to flowering	1.66	1.64	1.64
Days to podding	1.74	1.74	1.69
Days to maturity	2.10	2.06	2.07
100-seed weight (gr)	34.62	17.81	27.98
Seed yield (gr)	45.11	36.95	51.98
Plant height (cm)	39.82	29.76	39.13
Number of nodes in the main stem	19.90	19.92	20.57
Number of pods/plant	8.38	16.07	9.96
Number of seeds/ pod	1.20	1.37	1.24
Number of sub-branches	1.93	1.65	1.56
Leaf length (cm)	1.26	1.00	1.26
Flower length (cm)	1.00	3.37	1.08

Discussion بحث

For all 21 chickpea genotypes, all traits showed highly significant variations. Significant differences were found among the evaluated genotypes in 100-seed weight Significant differences in 100-seed weight were found between the evaluated genotypes. These results agreed with the results of Qureshi et al. (2004), Khan et al. (2011), Tesfamichael et al. 2015, and Malik et al. (2009), who found significant differences in 100-seed weight in the germplasm of chickpeas. The available resistant sources are insufficient for breeding purposes, so new sources of resistance should be identified to maintain chickpea production (Kanouni et al. 2011; Rani et al. 2020).

The genotypes were divided into three different clusters. The cultivar IDDMAR-2012-32 genotype (Desi-type) in cluster II had the lowest yield and the lowest susceptibility to AB. The highest yielding AB resistance genotype, Gebres 419-2 (Desi-type), located in cluster III. Bivanij (Desi-type), a high-yielding cultivar with the highest susceptibility to AB, belonged to cluster III. However, the Kabuli types, ILC482, the high-yielding semi-resistant to AB, belonged to cluster III and FLIp-02-65C, FLIp-01-164C, the low-yielding types resistant to AB, belonged to cluster I.

Desi seeds are small and dark with thicker seed coats and are generally used after hulling. The Kabuli-type is light-colored with big seeds and thinner seed coats, and is commonly used as whole seeds in Western Asia and the Mediterranean, where Kabuli is widespread. Possible genes causing disease resistance, agronomic traits, and traits distinguishing the desi and Kabuli were recognized (Varshney et al. 2013) and the variation at molecular level has been recorded by a Desi × Kabuli cross (Bharadwaj et al. 2011). Thus, Gebres 419-2 can be crossed with FLIp-02-65C or FLIp-01-164C to develop AB resistant Kabuli chickpea cultivars with high yielding traits and big seeds for export purpose (Srivastava et al. 2016).

Conclusion نتیجه‌گیری

The presence of greater agromorphological diversity in the chickpea collections may imply the opportunity to improve the crop as well as the need to conserve diversity. Our results indicated that the level of genetic variation in the chickpea accessions remained fairly constant. Information on current genetic diversity allows for the classification of our existing germplasm into different groups, which appears important for chickpea hybrid/crossbreeding programs.

Authors' contribution

Conceptualization of research (Shina Soleyman Nejad); Designing of the experiments (Zahra Tahmasebi(; Contribution of experimental materials (Ali Asherf Mehrabi and Homayoun Kanouni); Execution of field/lab experiments and data collection (Shina Soleyman Nejad); Analysis of data and interpretation (Shina Soleyman Nejad and Zahra Tahmasebi(; Preparation of the manuscript (Zahra Tahmasebi).

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