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Chemical and morphological characteristics of common bean seed and evaluating genetic advance in commercial classes

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ABSTRACT

Common bean (*Phaseolus vulagris* L.) is a nutritionally important food crop with prospective health benefits in the world. The current study was evaluated the chemical components, morphological characteristics, and genetic advance of 22 common bean cultivars/lines seeds from three commercial classes (white, red, pinto beans) adapted to different climates of Iran. The results showed significant variations among 22 common bean cultivars/lines for all studied seed traits. The commercial group comparisons showed that pinto beans were the best in terms of seed morphological characteristics but red beans were superior for seed protein percentage and zinc content. White beans had high amounts of iron, calcium and magnesium, and also presented high amounts of starch and uronic acid as anti-nutritional factors. Among the chemical components, crude fat had the highest genetic and phenotypic coefficients of variation, whereas starch percentage showed the lowest values. The genetic advance over the mean ranged from 6.73% (starch percentage) to 66.31% (100-seed weight), and high heritability was estimated for calcium content (0.99). AND1007 Line demonstrated the high seed protein, iron and zinc contents. To confirm the results, a genotype-by-trait biplot was done. These results could help to achieve a common bean cultivar with a high amount of nutritional value of seeds and appropriate seed characteristics with a low amount of anti-nutritional factors.

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Introduction

Common bean (*Phaseolus vulgaris* L.), as the major grain legume with global production of 30.4 million tons in 2020, is called a source of protein for poor people, because of its high protein content (17-30%) which it can fill the lack of meat in a healthy diet and deliver the almost same ingredients to the body (1-4). Bean while being a good source of protein, is a rich source of minerals such as iron and zinc (5), therefore, consuming of common bean has related to a decreased risk for a wide variety of diseases such as cancer, diabetes and cardiovascular diseases (6). Different ecotypes of common bean showed hypoglycaemic activity, which means they might reduce the absorption of carbohydrates with less negative effects than drugs (7). Besides the valuable nutritious composition, one of the biggest problems for the bean is protein digestibility due to its chemical structure and other anti-nutritional factors such as lectins, phytate, tannin, uronic acid and resistant starch (2, 8). They affect alteration of the gastrointestinal transit time and cause digest problems (9-11), however, these anti-nutritional factors have some health benefits including reducing the risks for aging-related diseases (12).

Anino et al. (2019) investigated the content of nutrients and non-nutrient phytochemicals in three varieties of common bean (red haricot, pinto and yellow kidney bean), and milk extracts of them. Their results showed that all three varieties contained high seed protein, carbohydrates, fiber and minerals (P, Fe, Zn, and Ca) (12). Alves et al. (2019) claimed that flour made from the common bean is an important source of protein and dietary fiber. The levels of phenolic compounds were higher in the unhulled flour, and flour made from the Manteigao cultivar had a higher phenolic compound content and antioxidant capacity than the Carioca cultivar (13). In another study, Twenty-nine legumes were assessed for their nutritional and phytochemical compositions which the

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highest zinc (3.56mg/100g) and the highest carotenoids (8.29–20.95µg/g) were found in red bean (14). De Barros and Prudencio (2016) with an evaluation of the physical and chemical characteristics of some internal Brazilian and external markets of the common bean demonstrated that the Saracura variety was a good option for both industrial and domestic use (15). Diaz-Batalla et al. (2006) showed that Mexican common bean seeds are an important source of dietary fiber, flavonols, phenolic acids, galacto-oligosaccharides, and phytic acid (16).

Recently, GGE biplot for genotype-by-trait interaction studies become popular in plant breeding programs, because it provides useful information about genetic diversity and interaction patterns between genotypes and traits (17). Therefore, the obtained results could be considered by the GT biplot method.

It seems determination of the nutritional value of common bean cultivars adapted to different climates is an important strategy. This study was carried out to investigate ten chemical traits and four morphological characteristics of seeds on 22 common bean cultivars adapted to different climates of Iran. The contribution of all these traits in seed quality would provide valuable information for breeding programs.

Materials and methods

Plant materials

Twenty-two cultivars/lines of common bean (white, red, and pinto bean) received from Khomein Bean Research National Station, Markazi province, Iran (Table 1) were cultivated in a randomized complete block design with two replications in a research greenhouse (22-24°C), Razi University, Kermanshah, Iran. Twenty seeds were planted in two rows in each plot with an intra-rows spacing of 20 cm and 50 cm inter-row spacing.

Table 1. Twenty-two varieties and lines of common bean used in the study

No	Cultivar/line	Type	No	Cultivar/line	Type
1	Jules	White	12	Goli	Red
2	Daneshkade	White	13	Derakhshan	Red
3	Dehghan	White	14	Akhtar	Red
4	Wa4531	White	15	Sayad	Red
5	74-Emersun	White	16	G169	Red
6	G11867	White	17	G14088	Pinto
7	Wa2662	White	18	Araucano	Pinto
8	Cifem Cabe	White	19	COS16	Pinto
9	AND1007	Red	20	G01437	Pinto
10	Naz	Red	21	Talash	Pinto
11	D81083	Red	22	Taylor	Pinto

Soil test

Because the chemical compounds of the seeds are influenced by both genetic and environmental conditions, then a soil test was done for obtaining better results (18). To determine the physicochemical characteristics of the soil, composite soil samples were randomly selected from four different points of the greenhouse surfaces. After transferring the sample to the laboratory, they were passed from a two-millimeter sieve. properties such as saturated mud pH (19), soil electrical conductivity (EC) (20), soil texture (21), soil organic carbon (22), calcium carbonate titration (23), absorbable phosphorus and potassium (24), DTPA soil test for zinc, iron, manganese, and copper (25), soil cations exchange capacity (CEC) (26) and soil bulk density (27) were measured. The results of the soil test were shown in Table 2.

Table 2. The physicochemical characteristics of the research greenhouse soil

Sample	Depth (cm)	FC (%)	PWP (%)	CEC (meq/100g)	pH	EC (dS/m)	OC (%)	Total Nitrogen (%)	Phosphorus (ppm)	Potassium (ppm)	Sand (%)	Silt (%)	Clay (%)	Soil Texture
1	0-30	-	-	-	7.21	1.8	1.18	0.16	11.10	234	37	45	18	Loam
2	0-30	-	-	-	7.14	1.9	1.22	0.17	11.53	225	24	45	31	Clay Loam
3	0-30	-	-	-	7.22	1.4	1.15	0.16	11.32	233	32	42	26	Loam
4	0-30	-	-	-	7.21	1.4	1.07	0.15	11.40	212	27	46	27	Loam
mean	0-30	28	15	18	7.19	1.6	1.15	0.164	11.33	226	30	44.5	25.5	Loam

FC: Field Capacity; PWP: Permanent Wilting Point; CEC: Cation-Exchange Capacity; EC: Electrical Conductivity; OC: Organic Carbon

Seed morphological characteristics

Four different seed characteristics consist of seed number per pod, 100 seed weight (by CAS Scale CA), and seed size (length and width by Brown & Sharpe 599 Series Vernier Caliper) were measured (28).

Seed chemical analysis

The measured chemical compounds were mineral ash content by A. O. A. C. method (29, 30), crude protein by Kjeldahl method (VELP Scientifica Srl, Italy) (31), crude fat by Soxhlet extraction method (32), total soluble sugar percentage (MyBioSource, USA)(33), starch percentage (34), iron and zinc contents by atomic absorption spectrometric determination (35), calcium and magnesium by titration complexometry technique (36), and uronic acid by Enzymatic Uronic Acid Assay Kit (Libios, France) (37).

Data analysis

Normality test, correlation and cluster analyses were done by SPSS software ver. 16.0. Analysis of variance was carried out by SAS software ver. 9.1. The comparison of the mean test was performed by SPSS software ver. 16.0, using least significant difference (LSD). Cluster analysis was done for grouping cultivars/lines by the UPGM method. To estimate variability among cultivars/lines and to determine genetic and environmental effects on different traits, genetic parameters such as genotypic variance (VG), phenotypic variance (VP), genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (H2bs), genetic advance (GA), and genetic advance over mean (GAM) were evaluated (38, 39). Genotype-by-trait (GT) biplot analysis was conducted to compare and define common bean varieties/lines based on multiple traits by GGE biplot software version 4.1.

Results and discussion

Evaluation of differences among common bean cultivars/lines in the term of the measured characteristics

The analysis of variance results showed the significant differences between 22 cultivars/lines of common bean for all the measured seed traits (Table 3). Group comparisons were performed between white, pinto and red beans. Contrast 1 is a comparison of white with red bean, contrast 2 is white with pinto bean and contrast 3 is red with the pinto bean. Except for seed number per pod in contrast 1 and ash content in all contrast, significant differences were observed in all contrasts for the investigated traits.

Table 3. Analysis of variance for the seed measured traits in 22 common bean genotypes

		Mean Squares						
S.O.V	DF	Seed number per pod	100 seed weight	Seed length	Seed width	Ash	Protein%	Fat%
Replication	1	0.2031	0.2341	0.2327	0.0769	0.323	0.178	0.014
Genotype	21	0.5475**	459.65**	7.0018**	1.8940**	0.777**	11.43**	0.319**
Contrast1	1	0.002^{ns}	435.3**	7.86**	4.08**	0.0030^{ns}	42.55**	1.24**
Contrast2	1	1.508**	2586.2**	15.9**	19.15**	0.009 ^{ns}	21.60**	0.15**
Contrast3	1	1.540**	994.6**	1.9**	6.27**	0.004 ^{ns}	114.2**	2.01**
Experimental Error	21	0.0717	0.4334	0.1616	0.1856	0.003	0.104	0.015
CV%	-	7.83	1.41	2.90	4.92	2.54	1.44	7.36

Contrast1: White with red, Contrast2: White with pinto, Contrast3: red with pinto; <ns> and <**> means non-significant and significant at 0.01 level of probability, respectively.

		Mean Squares						
S.O.V	DF	Soluble sugar%	Starch%	Iron	Zinc	Calcium	Magnesium	Uronic Acid%
Replication	1	0.001	0.010	0.002	0.051	1.454	0.204	0.0006
Genotype	21	0.751**	4.604**	2.711**	0.267**	2190.7**	626.9**	0.072**
Contrast1	1	12.5**	84.37**	3.69**	0.18**	36382**	7595**	0.94**
Contrast2	1	3.01**	15.20**	35.8**	0.49**	17617**	768**	0.07**
Contrast3	1	2.37**	21.20**	17.7**	1.20**	1923**	2806**	0.39**
Experimental Error	21	0.028	0.025	0.103	0.023	7.549	6.490	0.004
CV%	-	1.63	0.35	4.67	5.20	1.62	1.62	5.55

Contrast1: White with red, Contrast2: White with pinto, Contrast3: red with pinto; <ns> and <**> means non-significant and significant at 0.01 level of probability, respectively.

The mean comparisons of 22 cultivars/lines for the seed morphological and chemical characteristics demonstrated that cultivar Araucano had the highest means for all the seed characteristics (Table 4). The highest amount of ash content belonged to COS16 and G11867 lines. The highest amount of seed protein was found in AND1007, Sayad and D81083 genotypes. Line G01437 presented the greatest values of fat percentage and uronic acid. Jules cultivar had the most amounts of soluble sugar percentage and starch. Goli cultivar and AND1007 line simultaneously revealed the greatest amounts of iron and zinc. Derakhshan had the highest amount of magnesium (Table 4).

Table 4. Mean comparisons of 22 common bean cultivars/lines for the measured seed characteristics

cultivars/lines	SNPP	SW (g)	SL (mm)	SWTH (mm)	Ash (g/5g)	PR (%)	Fat (%)	SS (%)	Starch (%)	Iron (mg/100g)	Zinc (mg/100g)	Ca (mg/100g)	Mg (mg/100g)	UA (%)
Jules	4.24	30.53	13.00	8.25	0.24	20.1	1.75	11.33	47.99	7.57	2.5	235.5	179.5	1.45
Daneshkade	3.05	32.56	12.60	7.95	0.23	21.8	2.05	11.24	47.21	8.24	2.6	213.5	175.0	1.40
Dehghan	3.92	25.51	12.35	7.45	0.24	21.1	1.65	11.04	47.71	6.75	3.2	222.5	186.5	0.97
Wa4531	2.89	53.62	14.55	8.20	0.23	22.8	2.15	11.03	47.00	7.67	2.8	196.5	171.0	1.32
74-Emersun	2.87	41.16	12.80	8.40	0.24	22.1	1.80	11.07	45.95	8.13	2.7	206.5	148.0	1.38
G11867	2.81	36.35	13.85	8.20	0.26	25.0	2.15	10.56	47.17	8.16	3.0	185.0	174.5	1.42
Wa2662	3.21	48.05	14.90	8.75	0.24	22.8	1.75	11.50	46.51	7.41	3.1	204.0	177.5	1.43
Cifem Cabe	3.36	41.54	10.60	7.03	0.24	20.2	1.15	10.73	47.52	8.21	3.4	200.0	158.0	1.31
AND1007	3.18	65.49	14.85	9.45	0.22	26.9	1.45	10.24	43.36	8.06	3.8	129.0	160.5	0.98
Naz	2.90	28.42	12.45	8.85	0.23	23.2	1.45	10.01	44.37	6.51	2.9	159.0	126.5	1.04
D81083	3.77	60.73	17.40	9.35	0.24	26.4	1.45	9.51	43.89	6.97	2.5	142.5	128.5	1.04
Goli	3.47	35.60	11.60	7.80	0.23	25.2	1.35	9.63	43.59	7.87	3.7	129.0	146.5	1.00
Akhtar	3.42	54.49	15.65	9.85	0.21	22.1	1.45	10.13	44.45	6.02	3.3	128.5	129.0	1.03
Derakhshan	2.46	56.60	16.03	8.95	0.20	22.5	1.45	9.66	43.68	6.71	3.2	142.5	155.5	0.97
Sayad	3.20	30.37	12.60	8.10	0.22	26.5	1.50	9.63	43.85	7.96	3.0	132.0	142.5	0.97
G169	3.92	36.64	12.00	7.70	0.23	21.4	1.30	9.67	43.90	6.60	2.9	161.5	134.5	0.89
G14088	3.56	57.72	12.85	10.35	0.22	21.1	1.50	10.22	45.07	4.60	2.8	150.5	168.0	1.18
Araucano	4.26	84.37	17.20	10.45	0.21	17.8	1.50	10.66	46.23	4.48	2.5	173.0	149.0	1.37
COS16	3.68	46.32	13.70	9.10	0.25	20.7	1.80	10.71	45.99	6.09	2.6	164.0	159.5	1.33
G01437	3.08	45.05	12.38	8.40	0.23	20.3	2.75	10.64	45.17	5.37	2.6	156.5	150.5	1.31
Talash	3.52	43.56	15.25	9.35	0.24	19.7	2.45	10.21	46.43	6.84	3.0	156.5	166.0	1.15
Taylor	4.46	71.50	16.25	10.55	0.22	21.5	1.65	9.95	44.97	5.51	2.9	143.0	171.0	1.02
Maximum	4.46	84.37	17.40	10.55	0.26	26.9	2.75	11.47	47.99	8.24	3.8	235.5	186.5	1.45
Minimum	2.46	25.51	10.60	7.03	0.20	17.8	1.15	9.51	43.36	4.48	2.5	128.5	126.5	0.89
Mean	3.42	46.64	13.85	8.74	0.23	22.3	1.70	10.43	45.55	6.90	3.0	169.5	157.1	1.18
LSD 5%	0.57	1.35	0.84	0.88	0.02	0.7	0.25	0.34	0.32	0.65	0.3	5.6	5.1	0.14

SNPP: Seed number per pod; SW: 100-Seed weight; SL: Seed length; SWTH: Seed width, PR: Protein; SS: Soluble Sugar; Ca: Calcium; Mg: Magnesium; UA: Uronic Acid

Jules cultivar as a white-seeded genotype, having indeterminate and type III growth habit, presented the high amounts of seed number per pod (4.24), soluble sugar (11.33%), starch (47.99%), calcium (235.5 mg/100g) and uronic acid (1.45%). Chilean cultivar Araucano, a pinto-seeded cultivar, had great values of seed number per pod (4.26), 100 seed weight (84.37 g), seed length (17.20 mm), seed width (10.45 mm) and uronic acid (1.40%).

Among these cultivars and lines, the AND1007 line is a large red-seeded breeding line, having indeterminate, type II growth habit, belonging to the Andean gene pool (40). This line could be used as a high qualitative seed having genotype for the breeding programs.

The Results of group mean comparisons between white, pinto and red beans showed that white beans had higher amounts of ash (0.24 g/5 g), sugar (11.06%), starch (47.13%), iron (7.76 mg/100 g), calcium (207.94 mg/100 g), magnesium (171.25 mg/100 g) and uronic acid (1.33%) than the other two groups (Table 5). Pinto beans showed more values of seed number per pod (3.77), 100 seed weight (53.63 g), seed length (14.22 mm), seed width (9.48 mm) and fat (1.95%). In the red beans were observed greater amounts of seed protein (24.26%) and zinc (3.14 mg/100 g). These results were in agreement with the results of Koehler et al. (1987), in which white beans had higher amounts of iron (7.86 mg/100 g), calcium (196 mg/100 g), and magnesium (165 mg/100 g) (41). Also in a study by Jannat et al. (2019), red beans seed had the highest protein content among others with an average of 23% protein (42). Hasanzadeh et al. (2019) also showed that the highest amounts of protein were related to red beans (24%) and the highest amounts of sugar (12.7%) and starch (45%) belonged to white beans (43).

Table 5. The commercial group means for the seed chemical and morphological characteristics in 22 common bean cultivars/lines

	SNPP	SW (g)	SL (mm)	SWTH (mm)	Ash (g/5g)	PR (%)	Fat (%)	SS (%)	Starch (%)	Iron (mg/100g)	Zinc (mg/100g)	Ca (mg/100g)	Mg (mg/100g)	UA (%)
White	3.29	38.66	13.08	8.03	0.24	21.95	1.79	11.06	47.13	7.76	2.99	207.94	171.25	1.33
Pinto	3.77	53.63	14.22	9.48	0.22	20.38	1.95	10.44	45.76	5.73	2.72	162.25	163.16	1.23
Red	3.29	46.04	14.07	8.74	0.22	24.26	1.40	9.81	43.88	7.19	3.14	140.50	140.44	0.99

SNPP: Seed number per pod; SW: 100-Seed weight; SL: Seed length; SWTH: Seed width, PR: Protein; SS: Soluble Sugar; Ca: Calcium; Mg: Magnesium; UA: Uronic Acid

Estimation of genetic variability parameters

The genetic coefficient of variation (GCV) for the 14 traits ranged from 3.32 to 32.48%. PCV values were higher than GCV for all traits studied, which indicated a low influence of environment on the expression of the trait. Among the chemical components, fat showed the highest GCV (22.93%) and PCV (24.03%), whereas starch showed the lowest GCV (3.32%) and PCV values (3.33%) (Table6). Genetic advance over mean ranged from 6.73% (starch) to 66.31% (100-Seed weight). Broad-sense heritability values ranged from 0.76 to 0.99 for all traits. Seed in pod showed the lowest heritability values (0.76), and 100-Seed weight, ash, and calcium traits showed heritabilities above 0.99. High heritability (0.99) and genetic advance (67.61) for calcium were found among the common bean cultivars/lines (Table 6). Estimation of genetic variability parameters results revealed little difference between genotypic and phenotypic variances for all the traits. This result could be because the experiment was performed in an environment and the genotype x environment interaction was not estimated.

Table 6. Mean, range, and genetic variability components for the seed chemical and morphological characteristics among 22 common bean cultivars/lines

Trait	Range	Mean	Vg	Vp	GCV (%)	PCV (%)	H^2_{bs}	GA	GAM (%)
Seed number per pod	2.46-4.46	3.42	0.2379	0.31	14.26	16.23	0.76	0.87	25.43
100-Seed weight (g)	25.51-84.37	46.64	229.69	230.04	32.48	32.51	0.99	30.93	66.31
Seed length (mm)	10.60-17.40	13.85	3.42	3.58	13.35	13.66	0.95	3.70	26.71
Seed width (mm)	7.03-10.55	8.74	0.85	1.04	10.57	11.66	0.82	1.72	19.67
Ash (%)	4.0-5.2	4.6	0.39	0.39	13.52	13.57	0.99	1.27	27.60
Protein (%)	17.8-26.9	22.3	5.66	5.77	10.67	10.76	0.98	4.84	21.70
Fat (%)	1.15-2.75	1.70	0.15	0.17	22.93	24.03	0.91	0.76	44.70
Soluble sugar (%)	9.51-11.47	10.43	0.36	0.39	5.76	5.98	0.92	1.18	11.31
Starch (%)	43.36-47.99	45.55	2.29	2.31	3.32	3.33	0.98	3.07	6.73
Iron (mg/100g)	4.48-8.24	6.90	1.30	1.41	16.54	17.19	0.92	2.24	32.46
Zinc (mg/100g)	2.5-3.8	3.0	0.12	0.15	11.64	12.69	0.84	0.65	21.66
Calcium (mg/100g)	128.5-235.5	169.5	1091.58	1099.17	19.49	19.55	0.99	67.61	39.88
Magnesium(mg/100g)	126.5-186.5	157.1	310.21	316.70	11.21	11.32	0.97	35.55	22.62
Uronic Acid (%)	0.89-1.45	1.18	0.034	0.04	15.62	16.51	0.89	0.35	29.66

VG: genotypic variance; VP: phenotypic variance; GCV: genetic coefficient of variation; PCV: phenotypic coefficient of variation; H^2bs: broad-sense heritability; GA: genetic advance; GAM: genetic advance over mean

Evaluation of relationships among the measured characteristics

The results of correlation analysis showed the positive significant correlation of ash percentage with 100 seed weight, seed width and calcium content, and the negative significant correlation with soluble sugar, starch percentage and uronic acid (Table 7). Ash, as the residue of incomplete burning and one of the components in the analysis of biological materials, had positive significant correlations with 100 seed weight, seed width and calcium content. Because ash contains mineral contents like calcium, it is clear that different weights and sizes of seed can affect seed ash amounts (44).

Seed protein percentage had the negative significant correlations with soluble sugar percentage, starch percentage and calcium content, and the positive significant correlations with zinc and iron contents (Table 7). There is a possible genetic linkage on chromosomes between the inheritance of iron content and seed protein percentage (45) and even zinc content in the common bean genome. A study on legumes demonstrated that an increase in calcium content reduces the amount of protein (46).

Soluble sugar percentage demonstrated the positive significant correlations with contents of calcium, magnesium and uronic acid percentage, and high negative significant correlations with ash content, seed protein percentage and starch percentage (Table 7). Uronic acids are sugars whose terminal carbon's hydroxyl group has been oxidized to a carboxylic acid (45). Therefore increasing the amount of soluble sugar enhances the amount of uronic acid (47).

The starch percentage had positive and significant correlations with calcium and magnesium contents, whilst had the negative and significant correlations with ash, protein and soluble sugar percentages (Table 7). Starch reserves in the cotyledon of common bean (48). Each time seed needs soluble sugar, amylase increases in the cotyledon as starch starts to decline, therefore a correlation between percentages of soluble sugar and starch will be negative (49). De Barros and Prudencio (2016) reported the positive significant correlations between starch percentage with calcium and magnesium contents, which were in agreement with the current study results (15). According to the results of Moraghan and Grafton (2001), the calcium content had a significant and negative correlation with 100 seed weight and seed length (50).

The negative significant correlations were observed between seed iron content with seed number per pod, 100 seed weight and seed width. Seed iron content also had a positive significant correlation with seed protein percentage. A positive non-significant correlation was observed between contents of iron and zinc in seed (r=0.34). It therefore could be concluded that smaller and lighter seeds have more iron content. The obtained results were according to the results of Blair et al (2009) (51).

Table 7. Pearson correlation coefficients between the seed chemical and morphological characteristics in 22 common bean cultivars/lines

Traits	SNPP	SW	SL	SWTH	Ash	Pr	Fat	SS	Starch	Iron	Zinc	Ca	Mg	UA
SP	1.00													
SW	0.26	1.00												
SL	0.18	0.77**	1.00											
SWTH	0.31	0.79**	0.74**	1.00										
Ash	0.07	0.47*	0.35	0.42*	1.00									
Pr	-0.39	-0.12	0.04	-0.12	-0.04	1.00								
Fat	-0.22	-0.14	-0.01	-0.05	-0.31	-0.24	1.00							
SS	-0.02	-0.17	-0.18	-0.24	-0.48*	-0.43*	0.40	1.00						
Starch	0.13	-0.26	-0.20	-0.31	-0.6**	-0.54**	0.40	-0.84**	1.00					
Iron	-0.45*	-0.53*	-0.35	-0.69**	0.39	0.53**	-0.02	0.19	0.17	1.00				
Zinc	-0.23	-0.03	-0.15	-0.16	0.25	0.43*	-0.38	-0.28	-0.34	0.34	1.00			
Ca	0.05	-0.44*	-0.48*	-0.39	0.57**	-0.42*	0.24	0.86**	0.88**	0.31	-0.36	1.00		
Mg	0.10	-0.09	-0.08	-0.13	0.34	-0.25	0.39	0.66**	0.70**	0.16	-0.01	0.61**	1.00	
UA	-0.09	-0.01	-0.06	-0.08	-0.45*	-0.40	0.18	0.81**	0.11	0.11	-0.48*	0.67**	0.46*	1.00

* Correlation is significant at the 0.05 level (2-tailed); ** Correlation is significant at the 0.01 level (2-tailed). Abbreviations are: SNPP: Seed number per pod; SW: 100-Seed weight; SL: Seed length; SWTH: Seed width, PR: Protein; SS: Soluble Sugar; Ca: Calcium; Mg: Magnesium; UA: Uronic Acid

The similarity of cultivars/lines on the base of measured characteristics

Cluster analysis using the UPGMA method classified 22 common bean cultivars/lines into three groups (Figure 1). The first group consists of Goli, Sayad, Akhtar, Naz, Talash, Derakhshan, Taylor cultivars, and D81081, G169, COS16, G01437, G14088 and AND1007 lines. The genotypes with high amounts of seed protein (22.86%) and zinc (2.999 mg/100 g) were located in the first group (Table 8). The second group consists of Chilean cultivar Araucano with high values for seed number per pod (4.275), 100 seed weight (84.37 g), seed length (17.20 mm), seed width (10.45 mm) and uronic acid (1.37 mg/100g). The cultivars of Jules, Dehghan, Daneshkadeh, 74-Emersun, Cifem Cabe and lines of Wa4531, Wa2662 and G11867 were classified in the third group. The cultivars/lines of third group demonstrated the high values of ash (0.237 g/5 g), fat percentage (1.793%), soluble sugar percentage (11.05%), starch percentage (47.13%), iron (7.764 mg/100 g), calcium (207.9 mg/100 g) and magnesium (171.2 mg/100 g).

Table 8. The mean of cluster groups for the measured traits in 22 common bean cultivars/lines

	SNPP	SW (g)	SL (mm)	SWT (mm)	Ash (g/5g)	PR (%)	Fat (%)	SS (%)	Starch (%)	Iron (mg/100g)	Zinc (mg/100g)	Ca (mg/100g)	Mg (mg/100g)	UA (%)
1st Group	3.427	48.65	14.07	9.060	0.223	22.86	1.642	10.01	44.51	6.543	2.999	145.6	149.1	1.06
2nd Group	4.275	84.37	17.20	10.45	0.210	17.80	1.500	10.65	46.22	4.480	2.500	173.0	149.0	1.37
3rd Group	3.291	38.66	13.08	8.028	0.237	21.95	1.793	11.05	47.13	7.764	2.893	207.9	171.2	1.33

SNPP: Seed number per pod; SW: 100-Seed weight; SL: Seed length; SWTH: Seed width, PR: Protein; SS: Soluble Sugar; Ca: Calcium; Mg: Magnesium; UA: Uronic Acid

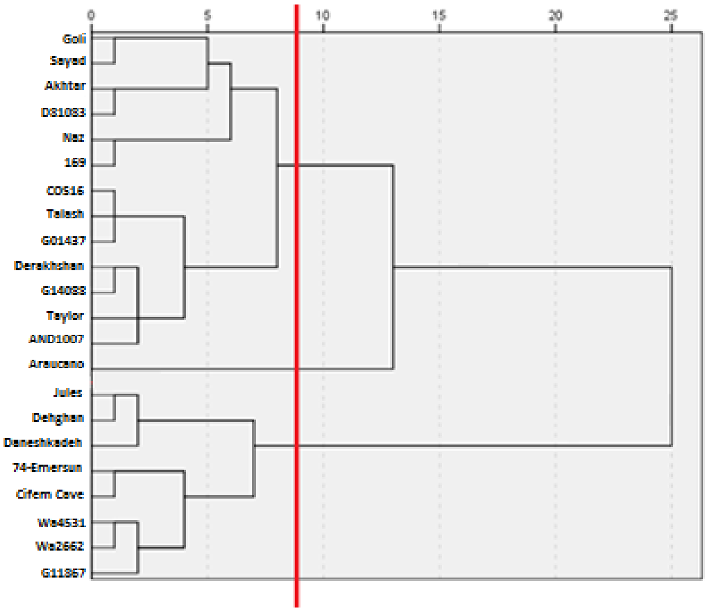

Figure 1. The diagram of the cluster analysis by UPGMA method for 22 common bean cultivars/lines

GT biplot analysis

The results of GT biplot analysis showed that the first and the second principal component accounted for 38.4% and 23.7%, respectively, and they explained a total of 62.1% of the total changes (fig. 2). According to this diagram, genotypes number 5 (74-Emersun), 1 (Jules), 21 (Talash), 12 (Goli), 9 (AND1007) and 18 (Araucano), which are located at the vertices of the polygon, are the superior genotypes for the studied traits. Genotype 5 (74-Emersun) has the highest values for 100 seed weight (SW), seed length (SL), and seed width (SWth). Genotype 1 (Jules) showed the highest amounts in terms of ash, fat, calcium (Ca), magnesium (Mg), starch, sugar and uronic acid (UA). Genotype 21 (Talash) also had the highest amount of iron (Fe) and genotypes 12 (Goli) and 9 (AND1007) had the highest amounts of seed protein (Pr) and zinc (Zn). No related traits were observed around genotype 18 (Araucano).

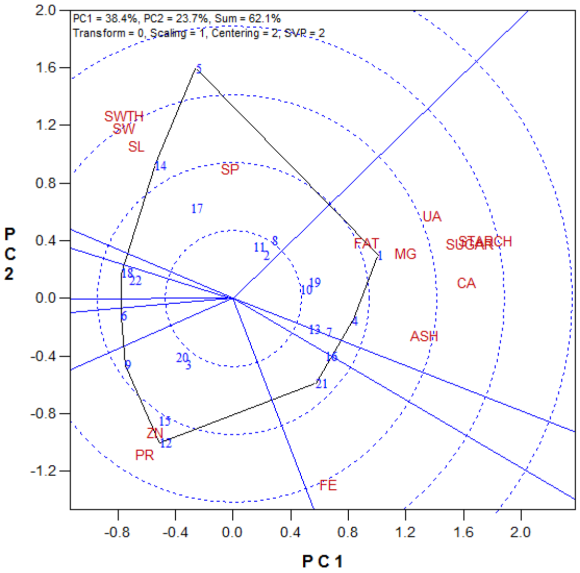

Figure 2. The GT biplot polygon for superior common bean cultivar/lines selection; (SP=Seed in Pod; SW=Seed Weight; SL=Seed Length; SWTH=Seed Width; Pr=Protein; Fe=Iron; Zn=Zinc; Ca=Calcium; Mg=Magnesium; UA=Uronic Acid)

In the GT biplot vector display (Figure 2), for each trait, vectors are started from the origin of the biplot that reaches the trait symbols. The relationship between traits can be obtained from the angle between the vector of each trait and the vector of another trait (52). According to the GT biplot diagram (Figure 3), there was the highest correlation between 100 seed weight (SW) and seed width (SWth), and between starch and sugar due to their tangential vectors. On the other hand, there is an angle of approximately 180 degrees between the iron (Fe) vector with 100 seed weight (SW) and seed width (SWth) vectors, which indicates a high negative correlation between these traits, that is consistent with the genetic correlation coefficients (-0.53, -0.69, respectively) between these traits. Also, an angle of approximately 90 degrees can be seen between seed protein (Pr) and zinc (Zn) vectors with 100 seed weight (SW), seed length (SL) and seed width (SWth), which indicates there is no phenotypical and genotypic relationship between these traits. GT biplot vectors could be used to indicate the intensity and direction of relationships between the traits. It is completely consistent with the results of the correlation analysis (Table 7).

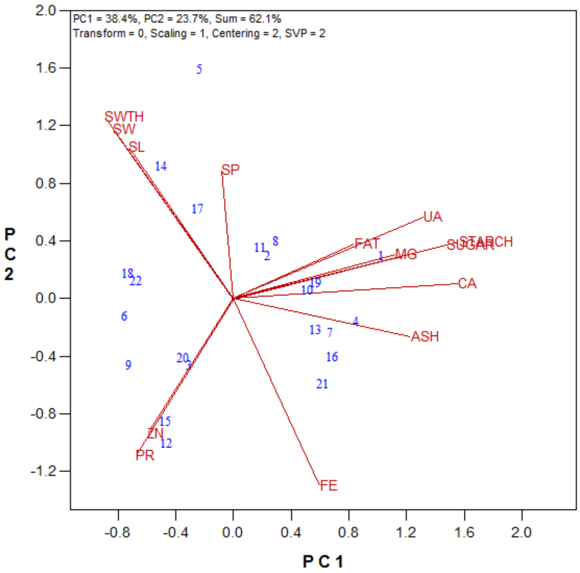

Figure 3. Biplot of correlation map of the measured traits of common bean cultivar/lines; (SP=Seed in Pod; SW=100 Seed Weight; SL=Seed Length; SWTH=Seed Width; Pr=Protein; Fe=Iron; Zn=Zinc; Ca=Calcium; Mg=Magnesium; UA=Uronic Acid)

Although the GGE biplot method was originally developed for analysing data in several environments, it can also be used to analyse all two-way tables that have an input structure in the tester, such as a two-way genotype table in trait. It should be mentioned that different traits have different units (53, 54). Therefore the unit of traits must be removed through standardization. These characteristics make the GGE biplot a powerful and comprehensive tool in quantitative genetics and plant breeding (55). In this study, this tool helps us to confirm the results of differences among common bean cultivars/lines, evaluation of relationships among the measured characteristics, and similarity of cultivars/lines based on measured characteristics.

Conclusions

In general, the studied common bean genotypes exhibited a significant amount of variation for their seed chemical components. The group comparisons demonstrated that pinto beans were the best in terms of seed morphological characteristics, but red beans are a good choice for the increasing contents of seed protein and zinc. White beans had a high amount of iron, calcium and magnesium, which are necessary mineral nutritious for a healthy diet. But besides, they have a high amount of starch and uronic acid, which are anti-nutritional factors and cause digest problems. Generally, among 22 common bean cultivars/lines, Jules cultivar presented the high amount of seed number per pod, soluble sugar, starch, calcium, and uronic acid and Chilean cultivar Araucano had the great amount of seed number per pod, 100 seed weight, seed length, seed width and uronic acid. GT biplot polygon was used to study genetic diversity and find interaction patterns between common bean cultivars/lines and the measured traits. This diversity could help us to find suitable genetic crosses to achieve a common bean with a high amount of useful nutritious and appropriate seed characteristics with a low amount of anti-nutritional factors.

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Interest conflict

There was not any conflict of interests.

Consent for publications

The author read and proved the final manuscript for publication.

Availability of data and material

All data generated during this study are included in this published article.

Authors' Contribution

All authors had equal role in study design, work, statistical analysis and manuscript writing.

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Ethics approval and consent to participate

No human or animals were used in the present research.

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