

Agro-Morphological Characterization of *Vicia faba* L. Accessions in the Kingdom of Saudi Arabia

Zia Amjad, Salem S. Alghamdi

Abstract—The study was conducted at the student educational farm at the College of Food and Agriculture in the Kingdom of Saudi Arabia. The aim of study was to characterize 154 *Vicia faba* L. accessions using agro-morphological traits based on The International Union for the Protection of New Varieties of Plants (UPOV) and The International Board for Plant Genetic Resources (IBPGR) descriptors. This research is significant as it contributes to the understanding of the genetic diversity and potential yield of *V. faba* in Saudi Arabia. In the study, 24 agro-morphological characters including 11 quantitative and 13 qualitative were observed for genetic variation. All the results were analyzed using multivariate analysis i.e., principal component analysis (PCA). First, six principal components (PC) had eigenvalues greater than one; accounted for 72% of available *V. faba* genetic diversity. However, first three components revealed more than 10% of genetic diversity each i.e., 22.36%, 15.86% and 10.89% respectively. PCA distributed the *V. faba* accessions into different groups based on their performance for the characters under observation. PC-1, which represented 22.36% of the genetic diversity, was positively associated with stipule spot pigmentation, intensity of streaks, pod degree of curvature and to some extent with 100 seed weight. PC-2 covered 15.86 of the genetic diversity and showed positive association for average seed weight per plant, pod length, number of seeds per plant, 100 seed weight, stipule spot pigmentation, intensity of streaks (same as in PC-1) and to some extent for pod degree of curvature and number of pods per plant. PC-3 revealed 10.89% of genetic diversity and expressed positive association for number of pods per plant and number of leaflets per plant. This study contributes to the understanding of the genetic diversity and potential yield of *V. faba* in the Kingdom of Saudi Arabia. By establishing a core collection of *V. faba*, the research provides a valuable resource for future conservation and utilization of this crop worldwide.

Keywords—Agro-morphological characterization, genetic diversity, core collection, PCA, *Vicia faba* L.

I. INTRODUCTION

FABA bean (*Vicia faba* L.) is an important food and forage legume crop. It is generally grown for its edible seeds (beans), these seeds have a high nutritional value as they are full of protein and other important nutritional constituents such as starch. It is being consumed as a part of daily diet e.g., as a part of breakfast meal, it is very popular in Arabic world. It is homegrown and can easily be processed on farm. It is also grown as a cover crop, as a fodder crop and as a green manure crop as it can add nitrogen to soil by nitrogen fixing bacteria. Small seeded cultivars are usually used in animal feed e.g., horse bean. The plant has an erect stem that bears branches with compound leaves. The seeds are small to large in size. The pods

are usually arising from the axils of leaves. It can also tolerate slight freezing. *V. faba* is native to North Africa and West Asia and can survive in climates with winter spells. It belongs to family Fabaceae, subfamily Faboideae, genus and species *V. faba*. It contains diploid chromosome number of 12. It is also known as broad bean, fava bean, field bean, horse bean or tic bean. Saudi Arabia is among the top importer countries of *V. faba*, had imported 33702 tons in 2008, amounting 704 US dollars/ton [1]. Yield instability has been of greatest concern for this crop [2]. The production of this crop in the Kingdom is extremely low perhaps due to the less emphasis on research for improved varieties while the per capita need is escalating [3].

During the previous years, this crop has been facing many pitfalls like lack of improved varieties, lack of adoption of better production technology, diseases and insect pest problems and yield instability due to inefficient varieties/ cultivars due to the loss of their vigor being the main reasons for its declining cultivation, thus the yield potential of existing varieties is low [4], [5]. Plant genetic resources play a very important role for the improvement of a particular crop, lack of proper characterization or evaluation of available germplasm followed by its improper utilization are some of the causes of its declining gene pool vigor. Breeding improvement is only possible if we carefully characterize and evaluate available accessions for their unique parameters like high yield [6]. This unique gene pool serves as the most important crop improvement tool [7], [8].

Historical data suggest that only cultivated forms of this crop are available, wild ancestors have not been discovered or become extinct; it could be because of having a complex genome, a relatively high percentage of cross-pollination and stability issues that significantly hamper the genetic improvement of the crop worldwide. The morphological variability of species is largely based on differences in morphological traits, like seed shape, seed size, seed hilum color, flower color and number of stems per plant, which are important for breeding improvement [9]. Detection of genetic diversity based on morphological traits is important for accessions identity and protection for future utilization. Seed shape, seed weight, time to flower and plant height has been used for a long time to evaluate the collections, and significant differences in these agronomic traits have been observed [10]. Scientists had observed that days to flowering and maturity, number of pods, number of seeds per plant are considered in genetic behavior of *V. faba* genotypes and all genotypes showed

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significant differences for these traits [11].

Given the limited genetic diversity within the *V. faba* genetic pool, it becomes crucial to focus on the agro-morphological aspects of this crop. This approach could enable the selection of superior *V. faba* genotypes [12]. Since there are no wild ancestors, interspecific crosses among *V. faba* are challenging, and there is a reliance on natural or mutagenic lines, further emphasizing the need for phenotyping. The lack of well-characterized faba cultivars is a significant constraint on its dry seed production [13]. The aim of this study is threefold: 1) to screen and identify high-yielding *V. faba* cultivars suitable for cultivation in Saudi Arabia, 2) to establish a core collection of *V. faba* future conservation and utilization worldwide, and 3) to assess the genetic variability of *V. faba* accessions. This research is significant as it contributes to the understanding of the genetic diversity and potential yield of *V. faba* in Saudi Arabia. This would favor the future conservation and utilization in the Kingdom of Saudi Arabia.

King Saud University Riyadh 24°.72" North and 46°.62" East, with an average rainfall, temperature and humidity as given in Fig. 1.

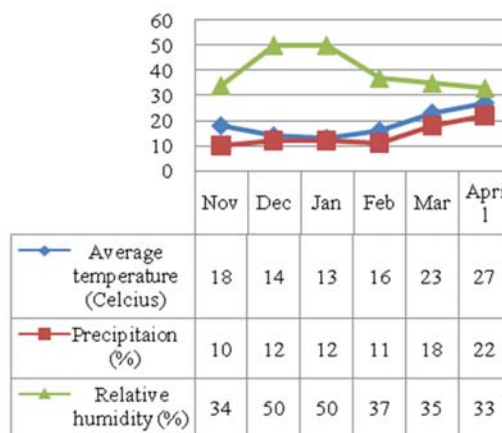


Fig. 1 Average temperature, precipitation and relative humidity [24]

II. MATERIAL AND METHODS

This experiment was carried out at the Educational Farm,

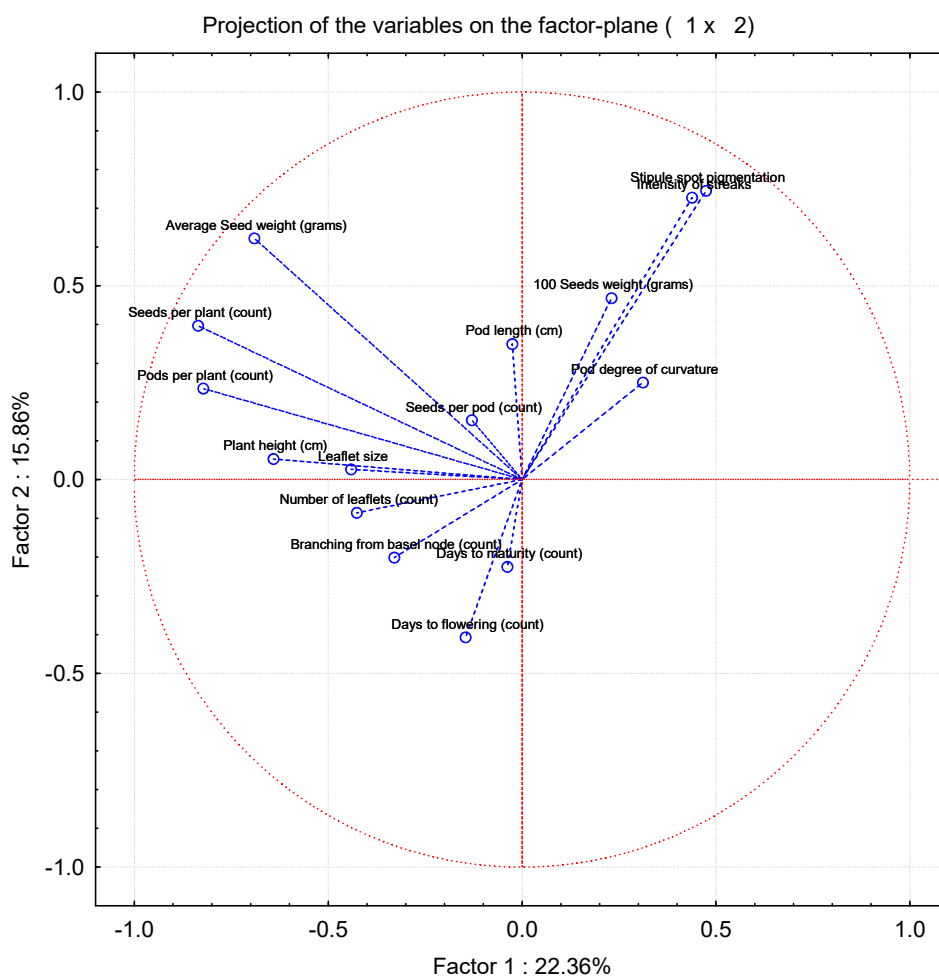


Fig. 2 Projection of the variables on the factor-plane (1x2)

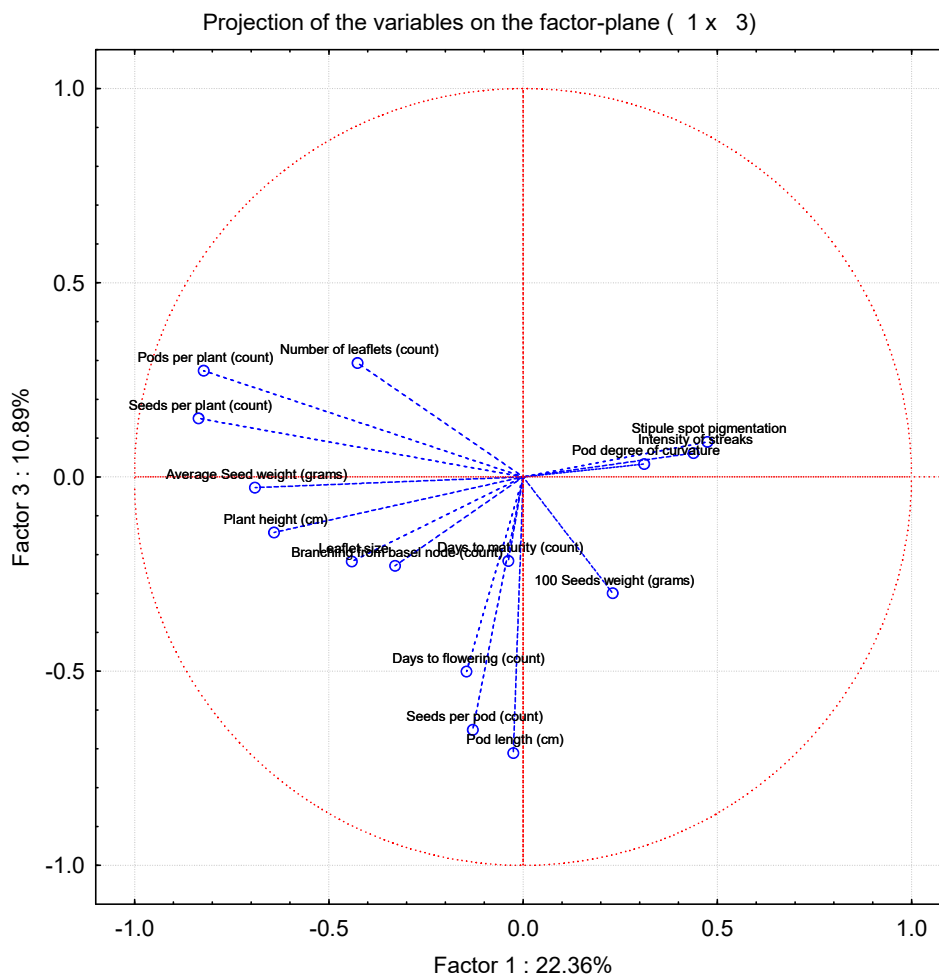


Fig. 3 Projection of the variables on the factor-plane (1x3)

A total of 154 *V. faba* accessions were grown in the field according to Randomized Complete Block Design (RCBD) layout. Plant to plant and row to row distance were maintained at 20 cm and 60 cm respectively to allow uniform exposure to all the inputs. These were in isolated fields to avoid out crossing. Plants were nourished properly and all other cultural practices were kept optimum in order to have a good health and vigor of plants. Five plants per accession were maintained per row. Soil preparation was done and *V. faba* nodule forming bacteria were inoculated in order to initiate root nodulation [14]. Irrigation schedule was maintained as per requirement in early days it was kept at 7 days interval while later increased based on crop need. Hoeing was performed at 15 days interval in order to avoid any competition with main crop (*V. faba*) [15]. Rouging was performed in order to remove off-type plants, thus genetic purity for each accession was maintained [15]. Control measures were adopted and these insect pests were controlled successfully.

The data were recorded for 24 agro-morphological characters, including 11 quantitative and 13 qualitative traits, according to the UPOV and the IBPGR descriptors for *V. faba*. Multivariate analysis, specifically PCA, was used to analyze the data and determine the genetic diversity within the *V. faba* accessions [16], [17]. The data for agro-morphological traits were used for characterization and primary evaluation of *V. faba* accessions. A total of 154 *V. faba* accessions was used in this study. Seeds for these genotypes were obtained from the legume research unit Department of Plant Production, College of Food and Agriculture King Saud University. Accessions with their names and origin are listed in Table I. All the qualitative and qualitative characters were considered for substantial agro-morphological variation for the *V. faba* accessions. Mean values and descriptor scores for both quantitative and qualitative characters were taken into consideration to perform the analysis of variance and PCA using statistical software Minitab-15. Cluster analysis was performed in order to estimate the agro-morphological variation. Results obtained were used to evaluate and characterize the *V. faba* accessions [18]-[22].

TABLE I
ACCESSION NAME AND ORIGIN

Accession. No	Accession Name	Origin	Accession. No	Accession Name	Origin	Accession. No	Accession Name	Origin
1	Hassawi1	KSA	52	Ahnacya 2	ICARDA	103	FLIP06-012FB	ICARDA
2	Hassawi2	KSA	53	H4	KSA	104	FLIP06-013FB	ICARDA
3	Hassawi3	KSA	54	H7	KSA	105	FLIP06-015FB	ICARDA
4	Goff1	KSA	55	Line 9	KSA	106	FLIP08-051FB	ICARDA
5	Sudan	Sudan	56	Line 5	KSA	107	FLIP08-052FB	ICARDA
6	Gazira 1	Sudan	57	Line 22	KSA	108	FLIP08-053FB	ICARDA
7	Gazira 2	Sudan	58	HBP/So/2006	ICARDA	109	FLIP08-054FB	ICARDA
8	Giza 3	Egypt	59	HBP/SoE/2002	ICARDA	110	FLIP08-055FB	ICARDA
9	Giza 4	Egypt	60	HBP/S0G/2008	ICARDA	111	FLIP08-056FB	ICARDA
10	Giza 40	Egypt	61	HBP/SoA/2008	ICARDA	112	FLIP08-057FB	ICARDA
11	Giza 429	Egypt	62	HBP/S0A/2009	ICARDA	113	FLIP08-058FB	ICARDA
12	Giza 461	Egypt	63	HBP/S0B/2009	ICARDA	114	FLIP08-059FB	ICARDA
13	Yamani (Large seed)	Yamen	64	HBP/SoC/2009	ICARDA	115	FLIP08-060FB	ICARDA
14	Luz	Spain	65	HBP/SoD/2009	ICARDA	116	FLIP08-061FB	ICARDA
15	Pakistani	Pakistan	66	HBP/SoF/2009	ICARDA	117	FLIP08-062FB	ICARDA
16	Aquadolce (ILB 1266)	Spain	67	FLIP03-004FB	ICARDA	118	FLIP08-063FB	ICARDA
17	Kamline	Spain	68	FLIP03-005FB	ICARDA	119	FLIP08-064FB	ICARDA
18	T.W.	Sudan	69	FLIP03-006FB	ICARDA	120	FLIP08-065FB	ICARDA
19	L.56	KSA	70	FLIP03-007FB	ICARDA	121	Syrian local large	Syria
20	ILB 4347	ICARDA	71	FLIP03-008FB	ICARDA	122	Ascot	Greece
21	ILB 4358	ICARDA	72	FLIP03-013FB	ICARDA	123	WRB 1-4	UK
22	1016/752/95	Egypt	73	FLIP03-019FB	ICARDA	124	WRB 1-5	UK
23	987/255/95	Egypt	74	FLIP08-001FB	ICARDA	125	WRB 2-1	UK
24	989/306/95	Egypt	75	FLIP08-002FB	ICARDA	126	FLIP03-001FB	ICARDA
25	989/309/95	Egypt	76	FLIP08-005FB	ICARDA	127	FLIP03-002FB	ICARDA
26	H3	KSA	77	FLIP08-007FB	ICARDA	128	FLIP03-003FB	ICARDA
27	H5	KSA	78	FLIP08-009FB	ICARDA	129	FLIP03-004FB	ICARDA
28	H8	KSA	79	FLIP08-010FB	ICARDA	130	FLIP03-005FB	ICARDA
29	Sakha 1	Egypt	80	FLIP08-012FB	ICARDA	131	FLIP03-006FB	ICARDA
30	Sakha 4	Egypt	81	FLIP08-015FB	ICARDA	132	FLIP03-007FB	ICARDA
31	L.4	KSA	82	FLIP08-016FB	ICARDA	133	FLIP03-008FB	ICARDA
32	L.21	KSA	83	FLIP08-017FB	ICARDA	134	FLIP03-009FB	ICARDA
33	Giza 674	Egypt	84	FLIP08-018FB	ICARDA	135	FLIP03-010FB	ICARDA
34	Giza 714	Egypt	85	FLIP08-019FB	ICARDA	136	FLIP03-011FB	ICARDA
35	Pop. 3	KSA	86	FLIP08-026FB	ICARDA	137	FLIP03-012FB	ICARDA
36	Pop. 4	KSA	87	FLIP08-027FB	ICARDA	138	FLIP03-013FB	ICARDA
37	Cairo 7	Egypt	88	FLIP08-028FB	ICARDA	139	FLIP03-014FB	ICARDA
38	X.735		89	FLIP08-029FB	ICARDA	140	FLIP03-015FB	ICARDA
39	ILB 4338	ICARDA	90	FLIP08-030FB	ICARDA	141	FLIP03-016FB	ICARDA
40	ILB 4357	ICARDA	91	FLIP08-031FB	ICARDA	142	FLIP03-017FB	ICARDA
41	L.65	KSA	92	FLIP08-033FB	ICARDA	143	FLIP03-018FB	ICARDA
42	1013/694/95	Egypt	93	WBR 2-6	UK	144	FLIP03-019FB	ICARDA
43	1026/811/95	Egypt	94	WBR 2-7	UK	145	FLIP03-020FB	ICARDA
44	985/252/95	Egypt	95	WRB 1-2	UK	146	FLIP03-022FB	ICARDA
45	989/303/95	Egypt	96	WRB 1-3	UK	147	FLIP03-023FB	ICARDA
46	Misr 1	Egypt	97	WRB 1-5	UK	148	FLIP03-024FB	ICARDA
47	Sakha 2	Egypt	98	WRB 2-1	UK	149	FLIP03-025FB	ICARDA
48	Sakha 3	Egypt	99	WRB 3	UK	150	FLIP03-026FB	ICARDA
49	Giza 716	Egypt	100	Reina Blanca	Spain	151	FLIP03-027FB	ICARDA
50	Giza 717	Egypt	101	FLIP06-001FB	ICARDA	152	FLIP03-028FB	ICARDA
51	Giza 843	Egypt	102	FLIP06-003FB	ICARDA	153	WRB 1-3	UK
						154	WBR 2-7	UK

Projection of the cases on the factor-plane (1 x 2)
 Cases with sum of cosine square >= 0.00

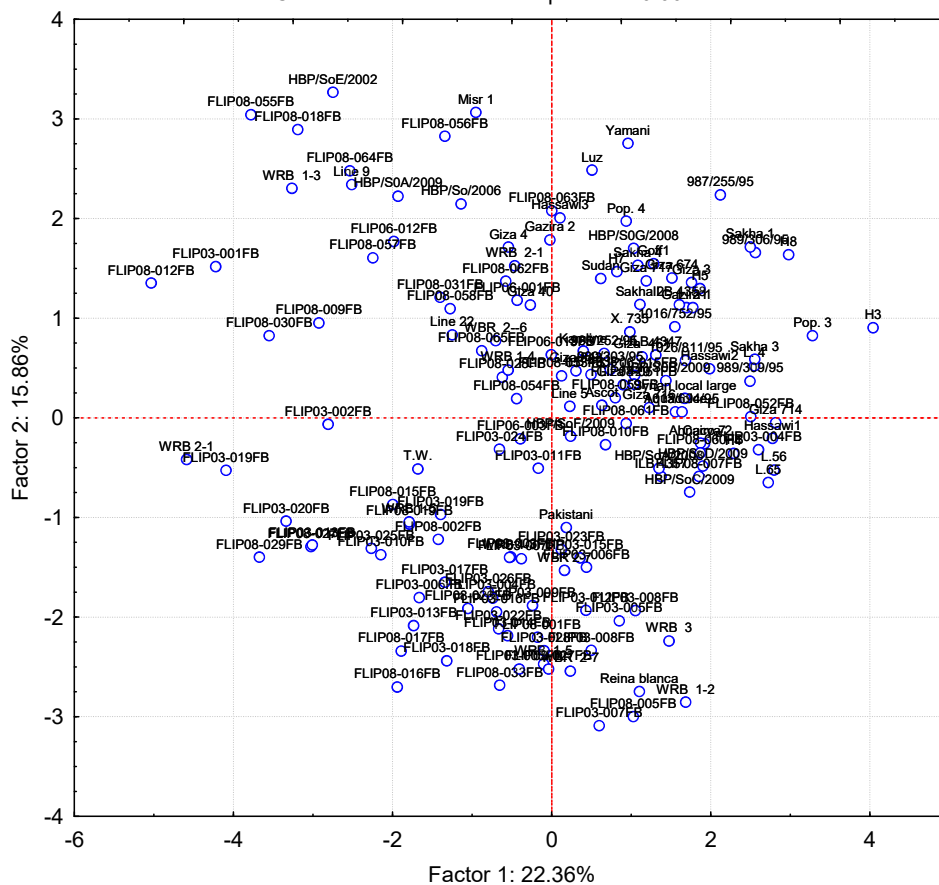


Fig. 4 Projection of the cases on the factor-plane (1x2)

III. RESULTS AND DISCUSSION

Descriptive statistics i.e., coefficient of variation and means were calculated to access the genetic variation for the *V. faba* accessions. Analysis of variance (ANOVA) showed a great range of variation for almost all the quantitative and qualitative characters under study. Basic statistical measures like mean, minimum, maximum, coefficient of variation% and standard deviation are presented in Table II.

All the quantitative (agronomic) traits except days to maturity and seeds per pod showed a significant level of variation among all the *V. faba* accessions (Tables II and III). Quantitative characters such as, branching from the basal node, plant height, pod length, average seed weight, seeds per pod, seeds per plant, pods per plant, 100 seed weight, days to flowering and the number of leaflets per leaf showed high variability for all the accessions under this study. Average seed weight showed highest degree of genetic diversity with a C.V. % of 68.97, while the lowest was recorded for days to maturity i.e., 4.16% (Table II). As far as 100 seed weight is concerned, top three genotypes with Saudi Arabian origin performed magnificently high, genotype number 28 i.e., H8 recorded

highest result for 100 seed weight i.e., 208.68 grams followed by genotype number 26 i.e., H3 and genotype number 19 i.e., L-56 with a 100 seed weight of 196.31 grams and 164.35 grams respectively. From among foreign accessions genotype number 14 i.e., Spanish Luz showed highest 100 seed weight of 164.30 grams (Fig. 7). All the qualitative characters (except pod shattering and growth habit) displayed a greater extent of variation, with non-shattering having a percentage of 99.4%, shattering with a percentage of 0.6% and determinate and indeterminate with a percentage of 1.3% and 98.7% respectively (Table II). Seed shape also represented less variability. Characters like leaflet size, flower ground color, wing petal color, stipule spot pigmentation, intensity of streaks, pod angle, hilum color, pod degree of curvature and the ground color of testa showed great extent of variation (Figs. 8-10). These results were found very promising for the screening of best *V. faba* cultivars for future utilization of this crop, not only for Saudi Arabia but also by far for the whole world. These results proved very promising for the establishment of a core collection for future conservation, utilization and accessing genetic variation for most important quantitative (agronomic) and qualitative traits.

Projection of the cases on the factor-plane (1 x 3)
 Cases with sum of cosine square >= 0.00

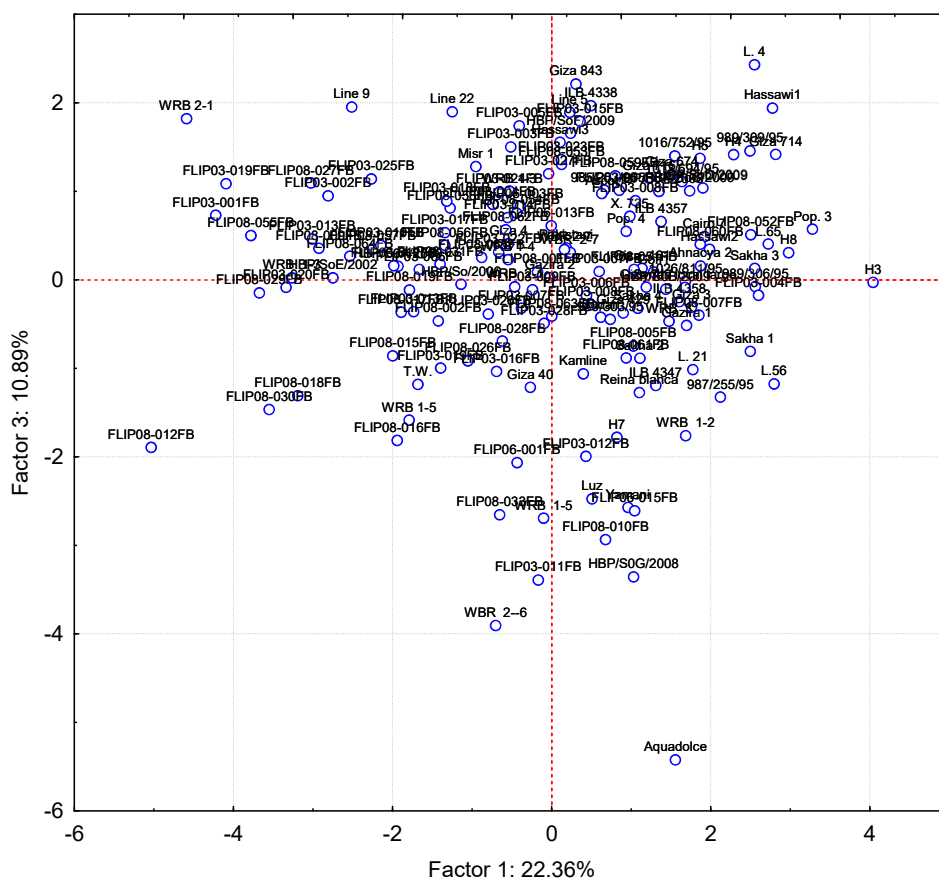


Fig. 5 Projection of the cases on the factor-plane (1x3)

TABLE II
 EXTENT OF VARIATION FOR QUANTITATIVE AND QUALITATIVE CHARACTERS

Characters	N	Minimum	Maximum	Range	Mean ± SD	C.V. (%)
Branching from basal node (CNT)	154	2.67	16.80	14.13	5.68 ± 2.07	36.49
Plant height (cm)	154	23.33	151.73	128.40	77.64 ± 19.11	24.61
Pod length (cm)	154	3.90	13.95	10.05	7.50 ± 1.57	20.91
Average Seed wt (g)	154	3.66	177.74	174.07	46.84 ± 32.31	68.97
Seeds per pod (CNT)	154	1.93	3.80	1.87	2.63 ± 0.33	12.44
Seeds per plant (CNT)	154	3.13	197.73	194.60	56.58 ± 34.93	61.74
Pods per plant (CNT)	154	5.67	61.67	56.00	25.45 ± 12.96	50.94
100 Seeds wt (g)	154	12.86	213.83	200.97	81.11 ± 35.81	44.14
Days to 50% flowering (CNT)	154	41.00	96.00	55.00	55.05 ± 10.30	18.71
Number of leaflets (CNT)	154	2.60	6.20	3.60	4.73 ± 0.62	13.01
Days to maturity (CNT)	154	124.00	156.00	32.00	135.44 ± 5.63	4.16

Leaflet size: large (36.4%); medium (46.1%); small (17.5%)
 Stipule spot pigmentation: absent (35.1%); present (64.9%)
 Flower ground color: pink (46.8%); violet (14.9%); white (38.3%)
 Intensity of streaks: intense (56.5%); moderate (9.7%); no streaks (33.1%); slight (0.6%)
 Wing petal color: spotted (66.2%); uniformly colored (0.6%); uniformly white (33.1%)
 Pod color: dark (brown %) (26.0%); light (yellow %) (74.0%)
 Pod angle: erect (66.9%); pendant (33.1%)
 Pod degree of curvature: medium (23.4%); strong (9.7%); very weak (5.8%); weak (61.0%)
 Hilum color: black (68.2%); light yellow (other %) (14.3%); mixed (17.5%)
 Pod shattering: non-shattering (99.4%); shattering (0.6%)
 Growth habit: determinate (1.3%); indeterminate (98.7%)
 Ground color of testa: black (0.6%); brown (9.7%); dark brown (16.9%); green (6.5%); grey (3.9%) light brown (16.2%) light green (15.6%); mixed (11.7%); yellow (18.8%)
 Seed shape: angular (11.0%); flattened (88.3%); round (0.6%)

Values within brackets are percentage

Projection of the cases on the factor-plane (2 x 3)
Cases with sum of cosine square >= 0.00

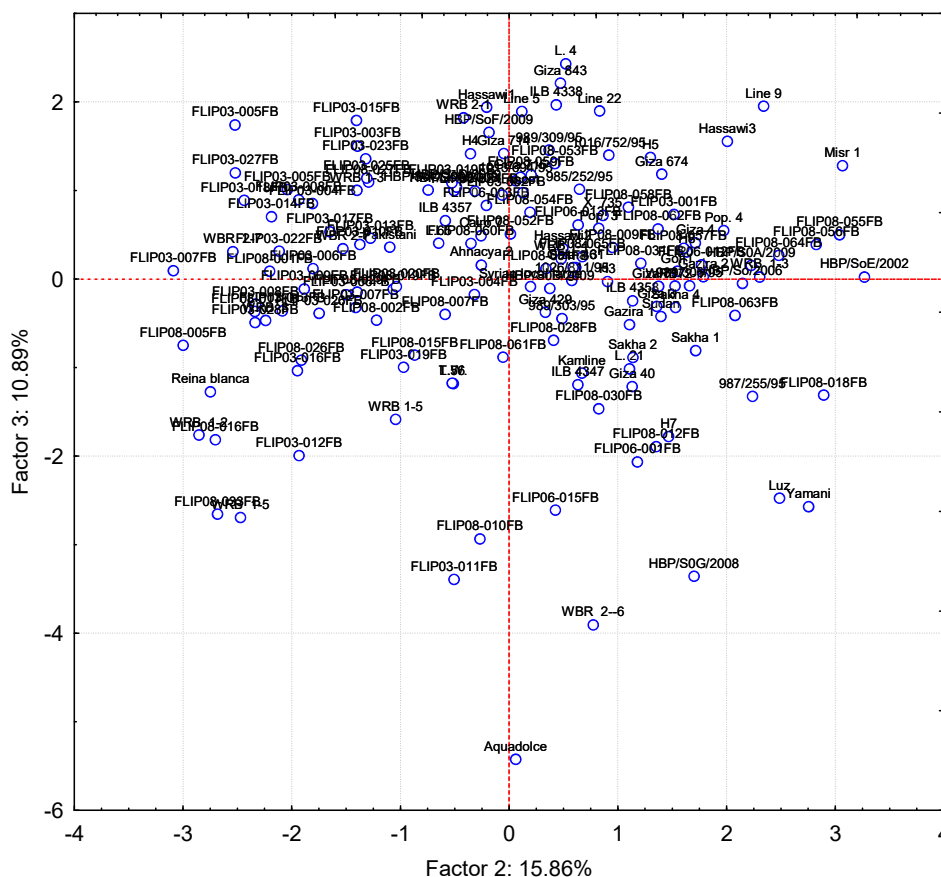


Fig. 6 Projection of the cases on the factor-plane (2x3)

TABLE III
COEFFICIENT OF VARIATION AND PROBABILITY VALUES FOR 8 AGRONOMIC DESCRIPTORS

Descriptor Name	LSD	C.V.	Prob
Branches No. (CNT)	0.997	11	**
Plant height (cm)	7.67	6.17	**
Pod length (cm)	0.692	5.74	**
Av. Seed wt (g)	12.72	16.9	**
Seeds/ pod (CNT)	0.836	19.81	Ns
Seeds/ plant (CNT)	11.4	12.54	**
Pods/ plant (CNT)	8.09	19.96	**
100 Seed wt (g)	17.12	13.19	**

LSD = least significant difference, C.V. = coefficient of variation, Prob= probability.

A. Principle Component Analysis

Multivariate analysis, specifically the PCA, classified the available accessions into nine PCs, this in turn favored ease to classify genotypes [23]. Table IV shows that the first six principal components are with eigenvalue greater than one; these accounted for 72% of the total available genetic variation for 154 *V. faba* accessions for the parameters under study, however first three components revealed more than 10% of genetic diversity each i.e., 22.36%, 15.86% and 10.89%

respectively. PCA distributed the *V. faba* accession into different groups based on their performance for different parameters. PC-1, which represented 22.36% of the genetic diversity, was positively associated with stipule spot pigmentation, intensity of streaks, pod degree of curvature and to some extent with 100 seed weight. PC-2 covered 15.86% of the accessions variation and showed positive association for average seed weight per plant, pod length, number of seeds per plant, 100 seed weight, stipule spot pigmentation, intensity of streaks and to some extent for pod degree of curvature and number of pods per plant. PC-3 revealed 10.89% of genetic diversity and expressed positive association for number of pods per plant and number of leaflets per plant. PC-4 axis was strongly associated with plant height, 100 seed weight and leaflet size. Parameters like 100 seed weight, stipule spot pigmentation, intensity of streaks, number of pods per plant, number of leaflets per plant and plant height were positively associated with more than one principal component, which showed their high discriminating ability for the characterization. Figs. 2-6 showed projection on plane for genotypes and characters.

TABLE IV
PERCENTAGE AND CUMULATIVE VARIANCES AND EIGENVECTORS ON THE FIRST TEN PRINCIPAL COMPONENTS FOR EACH CHARACTER IN 154 GENOTYPES

Parameters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	Fact.10
Eigenvalue	3.35	2.37	1.63	1.22	1.13	1.08	0.9	0.85	0.67	0.59
% Total Variance	22.361	15.86	10.89	8.16	7.51	7.22	6.03	5.64	4.49	3.95
Cumulative Eigenvalue	3.35	5.73	7.36	8.59	9.72	10.8	11.71	12.55	13.23	13.82
Cumulative %	22.36	38.22	49.12	57.28	64.78	72.01	78.04	83.68	88.17	92.11
Branches No. (CNT)	-0.33	-0.20	-0.23	0.28	0.52	0.20	0.44	-0.32	0.12	0.10
Plant height (cm)	-0.64	0.05	-0.14	0.38	0.06	0.31	-0.16	-0.15	0.23	-0.05
Pod length (cm)	-0.03	0.35	-0.71	0.10	-0.14	-0.16	0.06	0.10	0.23	0.32
Av. Seed wt. (g)	-0.69	0.62	-0.03	-0.09	0.09	-0.23	0.04	0.06	-0.11	0.02
Seeds/ pod (CNT)	-0.13	0.15	-0.65	-0.23	-0.44	0.09	0.18	0.17	0.14	-0.22
Seeds/ plant (CNT)	-0.84	0.40	0.15	-0.28	0.05	-0.05	0.01	-0.05	0.04	0.03
Pods/ plant (CNT)	-0.82	0.23	0.27	-0.30	0.05	-0.14	-0.01	-0.05	-0.06	0.03
100 Seedwt (g)	0.23	0.47	-0.30	0.43	0.19	-0.33	0.13	0.05	-0.50	-0.06
Days to flowering (CNT)	-0.15	-0.41	-0.50	-0.39	0.18	-0.04	-0.02	-0.31	-0.18	-0.41
Number of leaflets (CNT)	-0.43	-0.09	0.29	0.52	-0.18	-0.16	0.24	0.26	0.16	-0.42
Days to maturity (CNT)	-0.04	-0.23	-0.22	-0.07	0.64	-0.22	-0.38	0.49	0.21	-0.08
Leaflet size (cm ²)	-0.44	0.03	-0.22	0.34	-0.18	0.35	-0.58	-0.05	-0.25	0.00
Stipule spot pigmentation	0.47	0.74	0.09	-0.05	0.17	0.28	0.00	0.03	0.08	-0.16
Intensity of streaks	0.44	0.73	0.06	-0.09	0.19	0.35	-0.03	-0.04	0.10	-0.18
Pod degree of curvature	0.31	0.25	0.03	0.15	-0.09	-0.57	-0.31	-0.51	0.29	-0.11

Av. = Average, g = gram, wt = weight, CNT = count

Genotype	Branching from basal node (count)	Plant height (cm)	Pod length (cm)	Average Seed weight (grams)	Seeds per pod (count)	Seeds per plant (count)	Pods per plant (count)	100 Seeds weight (grams)
Gen-1	2.87	48.53	7.25	11.72	2.27	23.47	10.67	45.01
Gen-2	3.47	53.20	7.03	20.79	3.00	37.60	19.67	50.55
Gen-3	2.67	74.53	6.33	77.10	2.60	70.13	35.67	102.66
Gen-4	2.87	83.80	7.63	38.23	2.80	28.60	16.33	120.62
Gen-5	3.07	76.40	7.59	61.95	2.87	52.07	20.33	110.52
Gen-6	4.60	73.73	8.84	36.74	2.47	35.47	12.00	96.90
Gen-7	4.67	71.20	7.92	84.02	2.67	72.67	30.67	106.80
Gen-8	4.00	69.67	7.94	43.13	2.87	34.67	16.67	109.66
Gen-9	4.47	81.33	6.73	72.70	2.80	75.80	35.33	88.63
Gen-10	5.00	83.67	8.12	64.34	3.00	52.20	28.67	116.62
Gen-11	3.87	75.73	7.46	43.29	3.07	40.00	14.00	100.08
Gen-12	2.93	85.73	8.07	32.12	2.40	26.33	13.33	104.48
Gen-13	5.13	82.33	12.21	69.67	3.07	51.60	11.33	122.24
Gen-14	6.07	77.67	11.46	84.98	3.00	48.80	23.00	164.30
Gen-15	9.53	49.67	4.01	24.77	2.87	95.40	33.00	23.05
Gen-16	7.53	82.40	13.81	21.58	2.67	17.67	11.67	107.09
Gen-17	5.13	69.13	9.29	55.54	3.13	65.47	20.00	79.22
Gen-18	4.27	77.27	6.90	69.22	3.33	73.47	36.00	87.72
Gen-19	10.83	48.00	6.38	9.45	2.16	3.13	8.00	164.35
Gen-20	8.20	90.87	9.02	36.96	2.53	29.13	13.00	107.56
Gen-21	7.73	86.53	7.07	48.62	2.73	37.93	18.00	117.28
Gen-22	5.13	72.60	6.62	42.55	2.07	34.73	21.00	117.74
Gen-23	7.93	68.07	12.20	50.56	2.40	30.67	15.33	159.88
Gen-24	3.73	40.61	8.73	39.22	2.73	24.93	11.67	152.30
Gen-25	2.97	34.00	6.29	33.21	2.40	27.80	28.33	114.94
Gen-26	5.87	45.07	5.89	14.27	2.27	7.13	7.00	196.31
Gen-27	4.27	57.73	7.35	41.70	2.27	42.47	22.67	93.21
Gen-28	2.80	86.40	6.83	18.68	2.40	8.80	7.33	208.68
Gen-29	3.07	62.67	8.38	33.03	3.07	19.73	8.33	162.38
Gen-30	4.53	76.47	7.53	53.81	2.93	38.33	20.33	135.51
Gen-31	3.47	67.00	5.45	25.95	2.13	33.20	19.67	73.13
Gen-32	4.07	73.20	8.35	42.10	2.80	27.80	10.67	146.49
Gen-33	4.40	57.67	7.16	48.07	2.47	41.07	37.67	112.17
Gen-34	3.13	68.87	6.88	7.34	2.07	8.93	9.67	77.26
Gen-35	3.33	53.67	6.01	27.49	2.60	18.87	12.67	140.78
Gen-36	4.07	53.80	7.55	72.74	2.60	78.13	32.00	88.10
Gen-37	3.13	61.80	8.25	16.56	2.40	26.33	15.67	57.91
Gen-38	3.93	60.60	7.96	42.62	2.27	71.87	34.00	54.34
Gen-39	4.00	73.80	5.55	37.93	2.27	79.20	32.33	42.89
Gen-40	3.87	65.20	7.33	19.65	2.47	34.87	17.67	51.34
Gen-41	3.40	67.87	5.92	6.58	2.60	10.27	7.33	59.19

Fig. 7 Genotypes with their agronomic performance



Fig. 8 Morphological description of leaves



Fig. 9 Morphological description of seeds



Fig. 10 (a) Morphological description of flowers

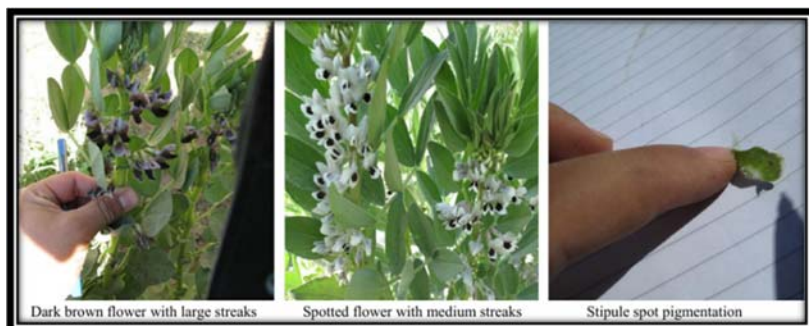


Fig. 10 (b) Morphological description of flowers

IV. CONCLUSION

In conclusion, this research identified high-yielding *V. faba* cultivars suitable for cultivation in Saudi Arabia. It also contributed to the establishment of a core collection of *V. faba*, which can be used for future conservation and utilization of the crop worldwide. The study revealed significant genetic variability among the *V. faba* accessions, providing valuable insights into the potential for improving this crop in the future.

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