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Full Length Research Paper

The use of reproductive vigor descriptors in studying genetic variability in nine Tunisian faba bean *(Vicia faba* L.*)* populations

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A collection of nine Tunisian faba bean (*Vicia faba*) populations belonging to three botanical classes (*Var. minor*, *var. equina* and *var. major*) was evaluated using twenty seven agro-morphological traits. Analysis of variance, correlation coefficients and principal components analysis (PCA) were performed based on MVSP 3.13 program. Significant differences between populations were noted for most agro-morphological traits in four main groups. The first group, positively correlated to the two axes, is represented by 'Bachaar' belonging to *V. faba. var. minor*, the second group, including *V. faba. var. minor* population ('Massri' and 'Badï'), is positively correlated to the PC1 and negatively correlated to the PC2 while the third group, is composed of two *V. faba var. major* ('Malti' and 'Batata') and were positively and negatively correlated to the PC2 and PC1, respectively. Finally, the fourth group negatively correlated to the two axes, gathers the remaining population ('Chahbi', 'Chemlali', 'Aguadulce' and 'Super Aguadulce'). The dendrogram based on Nei's genetic distance of the 9 populations using UPGMA method, show some genetic drift between populations.

Key words: Faba bean, agromorphological traits, principal components analysis, UPGMA method.

INTRODUCTION

Faba bean *(Vicia faba L.)* is a grain legume cultivated for multiple usages because of its high nutritional value and its ability to grow over a wide range of climatic and soil conditions (Bond et al., 1980; Lawes et al., 1983). They are excellent source of protein, which ranges from 27 to 34% (Duc, 1997; Haciseferogullari et al., 2003) depending on their genotypes. Most of these proteins include globulins (79%), albumins (7%) and glutelins (6%) (Hossain and Mortuza, 2006). Based on differences in seed weight, shape and size, Muratova, (1931) cited four botanical varieties; *V. faba paucijuga* (particular shape), *V. faba major* (more than 2.0 g per seed), *V. faba equina* (0.45 to 1.1 g per seed) and *V. faba minor* (0.2 to 0.5 g per seed).

Genetic variability of faba bean is quite large (Polignano et al., 1985). The great part of variability may be due to the presence of intermediate crossing system between autogamy and allogamy (Picard, 1979; Hanelt and Mettin, 1989). Indeed, *V. faba* is partially insect-cross pollinated crop, so the pollinators can carry out both self-pollinations by the tripping process when they trip the flower and out crossing, when they visit other plants flowers (Nadal et al, 2003). In Mediterranean region, faba bean is especially self- and cross pollinated by diverse solitary bees (Bond and Kirby, 1999).

Knowledge of genetic variation and relationships between accessions or genotypes is important as it helps to (1) Understand the genetic variability available and its potential use in breeding programs, (2) offer evidence of the evolutionary forces shaping the genotypic diversities, and (3) choose genotypes to be given priority for conservation (Thormann et al., 1994). For the genetic improvement of yield, which is the product of several contributing traits, information on the direct and indirect influences of these traits is a basic requirement.

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Table 1. Populations' common name, origins/pedigree and botanical class.

Populations' common name	Origins/pedigree	Botanical class
Malti	Local population	Major
Batata	Local big seeded landrace collected from Bousalem (Tunisia)	Major
Chahbi	S83182-22/New Mammoth x Local Tunisian faba bean	Major
Super aguadulce	Commercial variety	Equina
Aguadulce	Commercial variety	Equina
Chemlali	Local population	Equina
Badï	Bulk selection from Tunisian POL3	Minor
Bachaar	FLIP84-59FB x S82166	Minor
Massri	Local small seeded landrace collected from Bousalem (Tunisia)	Minor

This study is carried out to compare the performance of nine Tunisian faba bean populations regarding: (1) Their yield components and (2) Their potential selection criteria for yield improvement. In order to approach the best classification of these populations, both UPGMA and Principal Component Analysis were evaluated.

MATERIALS AND METHODS

Plant material

Nine Tunisian populations of *V. faba L.* derived from self-crossing, were cultivated under white insect proof to prevent out-cross pollination. These populations were kindly received from the laboratory of leguminous of the National Institute of Agronomic research of Tunisia. They belong to the three botanical classes of *V. faba* (*major, equina* and *minor*) (Table 1).

Experimental design

The study was conducted in the field during two growing seasons (2006 and 2007) at Bou Salem (located in the north of Tunisia). The experiment was laid out in a randomised block design with three replications. Each entry consisted of a 5 plants row distant of 50 cm. Twenty seven agro-morphological traits, taken during plant cycle and based on the faba bean descriptors (IBGR/ICARDA, 1985) were assigned. These agro-morphological traits were related to the plant growth, plant fertility and yield components (Table 2).

Statistical analysis

Analysis of variance and correlation coefficients were calculated to determine associations between the traits measured. The Principal Component Analysis was made based on the centred and standardized varieties using measured data with MVSP 3.13 software (Kovach, 1993).

To group the populations based on morphological dissimilarity, cluster analysis was conducted on the Euclidean distance matrix with the Unweighted Pair Group Method based on Arithmetic Averages (UPGMA).

RESULTS

A highly and significant variation ($p < 0.01$) was found among faba bean populations for most morphological traits, a significant ($p < 0.05$) variation of plant height at maturity, petal length and style length. No significant variation was found for the number of stems per plant at flowering. The range of the measurements and their averages for all the agro- morphological parameters are shown in Table 3.

Matrix of correlation (Table 4) showed different level of significance between traits. Moderately high positive associations were detected among traits. To avoid spurious significant results due to examining a large number of correlations, only correlation with $p < 0.01$ are given. Therefore, positives correlations were detected between nodes number until first flower (Nbnf1) and seed number per fructufal nodes (Ngrnfr), leaflet length (Longf) and leaflet width (Larf), leaflet width (Larf) and average length of fresh pods (LgGs), date of flowering (Fl) and number of stems per plant at flowering (Ntgp), petal length (Lgpl) and plant height at flowering (HFl), ovary length (LgOv) and average length of fresh pods (LgGs), style length (LgSty) and average length of fresh pods (LgGs), plant height at flowering (HFl) and average number of seeds per pod at maturity (Ngrgs), total inflorescence (InfTot) and total number of flower (NbflTot), total number of flower (NbflTot) and plant height at maturity (HF), average length of fresh pods (LgGs) and seed length (LgGr), number of stems per plant at flowering (Ntgp) and number of fructufal stems per plants at maturity (Ntgfrp), number of fructufal nodes on the primary stem at maturity (Nnfrtp) and number of pods per fructufal node at maturity time (Ngsnfr), number of fructufal nodes per plant at maturity (Nnfrp) and number of pods per plant at maturity (NgsP), number of pods per plant at maturity (NgsP) and number of pods per primary stem at maturity time (NgsTp), number of pods per primary stem at maturity (NgsTp) and average number of seeds per plant at maturity (Ngrp), average number of seeds per plant at maturity (Ngrp) and seed number per fructufal nodes (Ngrnfr), average number of seeds per pod at maturity (Ngrgs) and seed number per fructufal nodes (Ngrnfr), seed yield per plant at maturity (RdtP) and 100 seeds weight at maturity (P100), 100 seeds weight at maturity (P100) and seed length (LgGr); seed

Table 2. Agromorphological traits studied for the nine faba bean populations.

Agromorphological traits	Abbreviation	Trait
Plant growth	Longf	Leaflet length
	Larf	Leaflet width
	Nbnf1	Nodes number until first flower
	HFl	Plant height (cm)at flowering
	LgGs	Average length (cm) of fresh pods
	HF	Plant height (cm)at at maturity
	LgGr	Seed length
	lrGr	Seed width
Plant fertility	NtgPFl	Number of stems per plant at flowering
	Fl	Flowering date
	InfTot	Total inflorescence
	nbfl Tot	Total number of flower
	Lgpl	Petal length
	LgOv	Ovary Lengths
	LgSty	Style lengths
	Nnfrtp	Number of fructufal nodes on the primary stem at maturity
	Nnfrpl	Number of fructufal nodes per plant at maturity
	Ntgp	Number of stems per plants at maturity
	Ntgfrp	Number of fructufal stems per plants at maturity
	Ngsnfr	Number of pods per fructufal node
	NgsP	Number of pods per plant
	NgsTp	Number of pods per primary stem
Yield components	Ngrp	Average number of seeds per plant
	Ngrgs	Average number of seeds per pod
	Ngrnfr	Seed number per fructufal nodes
	RdtP	Seed yield per plant
	P100F	100 seed weight

length (LgGr) and seed width (lrGr). Negatives correlations were observed with: Nodes number until first flower (nbnf1) and leaflet width (Larf), leaflet length (Longf) and number of pods per plant at maturity (NgsP), leaflet width (Larf) and flowering date (Fl), flowering date (Fl) and average length of fresh pods (LgGs), ovary lengths (LgOv) and number of fructufal nodes on the primary stem at maturity (Nnfrtp), plant height at flowering (HFl) and number of fructufal nodes on the primary stem at maturity (Nnfrtp), total number of flowers (NbflTot) and number of stems per plant at flowering (Ntgp), average length of fresh pods (LgGs) and number of pods per fructufal node at maturity (Ngsnfr), number of fructufal stems per plants at maturity (Ntgfrp) and number of fructufal nodes on the primary stem at maturity (Nnfrtp), number of fructufal nodes on the primary stem at maturity (Nnfrtp) and seed length (LgGr), number of pods per fructufal node at maturity (Ngsnfr) and seed length (LgGr).

In order to describe and gain a better understanding of variance sources among faba bean populations, Principal Component Analysis (PCA) was carried out. Based on eigenvalues of the order of 1.7 as was suggested by Tomassone et al. (1993), the PCA grouped variables were divided into three components, which explained 74.61% of the total variation. The two first axes were considered as they elucidate the maximum simple variation (33.55 and 25.14% of the total variation respectively) with the cumulative variation of 58.69%. Consequently, we had chosen them to discuss traits variation.

Loading variables and the PCA scores were also calculated (Table 5 and Figure 1). The PC1 accounted for 33.55% of the variation and showed the largest loading values with phenological, morphological and yield-related traits; leaflet width (larf), flowering date (Fl), petal length (Lgpl), ovary length (LgOv), style length (LgSty), plant height at flowering (HFl), average length of fresh pods (LgGs), number of fructufal stems per plants at maturity (Ntgfrp), number of fructufal nodes on the primary stem at maturity (Nnfrtp), number of pods per fructufal node at maturity (Ngsnfr), average number of seeds per pod at maturity (Ngrgs), seed number per fructufal nodes (Ngrnfr), 100 seeds weight (g) at maturity (P100F), seed length (LgGr) and seed width (lrGr), whereas, the PC2 accounted for 25.14% of the variation which shared the rest loading values with phenological, morphological and yield-related traits: Nodes number until first flower

Table 3. Range (maximum and minimum values), averages and variance of the twenty seven agromorphologial parameters.

Trait	Max	Min	Average	Variance	MS	F_{ob}
Longf	7.79	6.20	6.70	0.053	0.37	16.50**
Larf	3.77	3.30	3.77	0.066	0.17	13.83**
nbnf1	9.81	5.13	7.92	0.152	4.26	18.81**
HFl	52.75	38.65	43.30	0.084	41.65	42.27**
LgGs	19.91	7.81	14.12	0.309	61.18	145.11**
HF	102.44	85.81	94.60	0.034	19.63	3.03*
LgGr	3	1.21	2.008	0.288	1.08	225.01**
lrGr	2.13	0.93	1.437	0.283	0.53	591.10**
NtgPFl	5.50	3.81	4.,61	0.077	0.09	0.77ns
Fl	89.25	82.56	85.06	0.031	22.28	522.09**
InfTot	13.81	9.94	11.80	0.093	3.06	7.41**
nbfl Tot	36.13	26.38	31.12	0.086	6.73	6.73**
Lgpl	6.08	3.16	3.64	0.146	0.51	2.91*
LgOv	1.99	1.66	1.78	0.047	0.02	24.66**
LgSty	0.43	0.34	0.38	0.057	0.001	3.08*
Nnfrtp	8.63	3.94	6.13	0.261	8.09	67.15**
Nnfrpl	19.69	8.63	13.04	0.265	36.90	40.45**
Ntgp	7.38	4.31	5.32	0.124	0.99	5.15**
Ntgfrp	5.75	4.06	4.65	0.102	0.54	5.62**
Ngsnfr	1.47	1.01	1.12	0.1	0.03	9.57**
NgsP	25.75	8.75	14.71	0.339	74.56	32.31**
NgsTp	14	4.44	7.50	0.447	35.72	80.91**
Ngrp	95.31	31.06	59.59	0.328	1193.97	54.57**
Ngrgs	5.31	2.81	4.01	0.164	1.31	30.47**
Ngrnfr	4.87	3.18	4.87	0.274	5.25	21.70**
RdtP	58.75	27.88	43.32	0.202	236.91	67.91**
P100F	218.32	57.32	122.12	0.447	9658.49	921.95**

(nbnf1), leaflet length (Longf), number of stems per plant at flowering (NtgPFl), total inflorescence (InfTot), total number of flower (Nbfl Tot), plant height at maturity (HF), number of stems per plant at flowering (Ntgp), number of fructufal nodes per plant at maturity (Nnfrpl), number of pods per plant at maturity (NgsP), number of pods per primary stem at maturity (NgsTp), average number of seeds per plant at maturity (Ngrp) and seed yield per plant at maturity (RdtP).

Considering the plot defined by the PC1 and PC2 and taking into account their projection on the third plan (PC3), four groups of characters can be distinguished. Two groups are positively correlated to the first axis; the first one, composed of total inflorescence (InfTot), total number of flour (nbfl tot), number of fructufal nodes per plant at maturity (Nnfrpl) and flowering date (Fl), and is also positively correlated to the second one. The second group including number of pods per fructufal node at maturity (Ngsnfr) is negatively correlated to axis two. The two other groups are negatively correlated to the first axis. However, this group composed of average number of seeds per plant at maturity time (Ngrp), number of pods per primary stem at maturity time (NgsTp), number of pods per plant at maturity time (NgsP), seed yield per plant at maturity time (RdtP), plant height at maturity time(HF), number of fructufal stems per plants at maturity time (Ntgfrp), seed number per fructufal nodes (Ngrnfr), nodes number until first flower nbnf1, 100 seed weight at maturity time (P100F), seed length (LgGr), seed width (lrGr), average length of fresh pods (LgGs), lengths of the style (LgSty) and is positively correlated to axis two, in contrast of variables number of fructufal stems per plants at maturity time (NtgPFl), number of stems per plant at flowering time (Ntgp), average number of seeds per pod at maturity time (Ngrgs), petal length (Lgpl), plant height at flowering (HFl), lengths of the ovary (LgOv), leaflet length (Longf) and leaflet width (Larf) which represent the fourth group is negatively correlated to axis two.

A clear separation of *V. faba* populations was observed and four main groups can be distinguished (Figure 2). The first group positively correlated to the two axes is represented by Bachar and it belongs to *V. faba* var. minor. The second group which include the *V. faba* var. minor population (Massri and Badï) is positively correlated to the PC1 and negatively correlated to the PC2.

Table 4. Correlations between agromorphological traits.

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14
V1	1													
V2	-0.21	1												
V3	**-0.37***	**0.64***	1											
V4	0.07	-0.39*	**-0.51***	1										
V5	-0.05	0.50	0.39*	-0.22	1									
V6	0.01	0.51*	0.52*	-0.43*	0.42*	1								
V7	-0.03	0.23	0.35*	-0.18	0.42*	0.32	1							
V8	-0.11	0.55*	0.49*	-0.08	**0.46***	0.62*	0.46*	1						
V9	-0.09	0.19	0.12	-0.10	0.37*	0.01	0.02	-0.06	1					
V10	0.21	-0.14	-0.18	0.25	0.06	-0.24	0.20	-0.05	-0.14	1				
V11	0.18	-0.17	-0.18	**0.50***	0.12	-0.16	0.25	0.23	-0.12	**0.83***	1			
V12	0.01	0.37*	**0.65***	**-0.72***	0.43	**0.63***	**0.55***	0.54*	-0.01	-0.12	-0.10	1		
V13	0.03	-0.16	-0.10	0.22	0.19	0.14	0.04	0.23	-0.08	0.43*	**0.52***	-0.01	1	
V14	-0.07	-0.15	-0.01	**-0.50***	-0.10	-0.01	-0.11	-0.32	-0.01	-0.27	**-0.41***	0.19	0.13	1
V15	-0.03	-0.08	-0.03	-0.19	0.07	0.12	-0.15	0.06	-0.02	0.02	0.01	0.12	0.20	**0.42***
V16	-0.22	-0.20	-0.13	0.40*	-0.26	**-0.51***	-0.19	**-0.40***	0.02	0.04	-0.05	-0.52*	0.14	-0.25
V17	-0.23	-0.28	-0.01	0.03	-0.17	-0.39*	0.06	-0.24	0.03	0.28	0.28	-0.04	0.04	0.04
V18	-0.09	-0.16	-0.33	0.65*	-0.24	-0.51*	-0.30	-0.32	0.04	0.18	0.14	**-0.72***	0.01	-0.29
V19	0.33	**-0.43***	-0.17	-0.01	-0.09	-0.25	0.10	-0.23	-0.04	0.53*	0.43**	0.05	0.21	0.02
V20	0.53*	-0.35	-0.35	0.03	-0.01	-0.13	0.01	-0.16	-0.10	0.49*	0.37*	-0.01	0.20	-0.12
V21	0.42*	-0.15	-0.02	-0.03	0.02	-0.09	0.15	-0.01	-0.17	0.48*	0.35*	0.18	0.11	-0.20
V22	0.22	0.55*	0.43*	-0.17	0.45*	0.55*	0.24	**0.59***	0.05	-0.02	0.05	0.44*	0.03	-0.25
V23	**0.57***	0.25	0.17	-0.16	0.31	0.36*	0.18	0.34	-0.12	0.23	0.13	0.36*	0.08	-0.31
V24	-0.17	-0.14	0.16	-0.21	0.04	-0.22	0.26	-0.10	0.03	0.40*	0.23	0.23	0.08	-0.14
V25	0.11	-0.15	0.23	-0.59*	0.15	0.36*	0.35*	0.19	-0.02	0.06	0.07	0.74*	0.20	0.30
V26	0.11	-0.07	0.26	-0.62*	0.19	0.45*	0.35*	0.25	-0.02	-0.01	0.02	**0.75***	0.17	0.29
V27	0.10	-0.07	0.25	-0.61*	0.19	0.39*	0.37*	0.21	0.02	0.05	0.06	0.72*	0.17	0.29
	V15	**V16**	**V17**	**V18**	**V19**	**V20**	**V21**	**V22**	**V23**	**V24**	**V25**	**V26**	**V27**	**V15**
V15	1													
V16	**-0.44***	1												
V17	-0.09	0.37*	1											
V18	-0.27	**0.43***	-0.07	1										
V19	0.03	0.05	**0.70***	-0.08	1									
V20	0.12	-0.01	0.42*	-0.13	**0.80***	1								
V21	-0.03	0.09	0.52*	-0.18	0.78*	**0.83***	1							
V22	0.01	-0.18	-0.19	-0.37*	-0.08	0.14	0.29	1						
V23	-0.01	-0.26	-0.30	-0.23	0.19	0.45*	**0.62***	**0.59***	1					
V24	-0.05	0.32*	0.63*	-0.08	0.59*	0.41*	0.53*	-0.15	0.08	1				
V25	0.27	-0.52*	0.17	-0.65*	0.40*	0.28	0.25	-0.03	0.18	**0.40***	1			
V26	0.24	**-0.58***	0.11	**-0.67***	0.34	0.25	0.22	0.01	0.20	0.31	**0.98***	1		
V27	0.21	-0.55	0.17	-0.64*	0.40*	0.27	0.24	-0.04	0.16	0.37*	0.98*	**0.98***	1	

V1, Nodes number until first flower (nbnf1); V2, leaflet length (Longf); V3, leaflet width (Larf); V4, date of flowering (Fl); V5, petal length (Lgpl); V6, lengths of the ovary (LgOv); V7, lengths of the style (LgSty); V8, plant height at flowering (HFl); V9, number of stems per plant at flowering time (NtgPFl); V10, total of inflorescence (InfTot); V11, total number of flour (NbflTot); V12: average length of fresh pods (LgGs); V13, plant height at maturity time (HF); V14, number of stems per plant at flowering time (Ntgp); V15, number of fructufal stems per plants at maturity time (Ntgfrp); V16, number of fructufal nodes on the primary stem at maturity time (Nnfrtp); V17, number of fructufal nodes per plant at maturity time (Nnfrp); V18, number of pods per fructufal node at maturity time (Ngsnfr); V19, number of pods per plant at maturity time (NgsP); V20, number of pods per primary stem at maturity time (NgsTp); V21, average number of seeds per plant at maturity time (Ngrp); V22, average number of seeds per pod at maturity time (Ngrgs); V23, seed number per fructufal nodes (Ngrnfr); V34, seed yield per plant (g) at maturity time (RdtP); V25, 100 seed weight (g) at maturity time (P100); V26, seed length (LgGr); V27, seed width (lrGr).

Table 5. PCA variable loadings

Variable	Axis 1	Axis 2
nf1		
Longf		0.174
larf	-0.246	-0.192
Fl	0.306	
Lgpl	-0.278	
LgOv	-0.290	
LgSty	-0.255	
HFl	-0.282	
NtgPFl		
InfTot		-0.190
nbfl TOT		0.322
LgGs	-0.316	0.321
HF		
Ntgp		0.222
Ntgfrp	-0.097	-0.099
Nnfrtp	0.233	
Nnfrpl		
Ngsnfr	0.293	0.227
NgsP		
NgsTp		0.361
Ngrp		0.34
Ngrgs	-0.188	0.333
Ngrnfr	-0.162	
RdtP		
P100F	-0.233	0.298
LgGr	-0.252	
lrGr	-0.238	

The third group is composed of two *V. faba* var. major (Malti and Batata) and are positively correlated to the PC 2 and negatively correlated to the PC 1. The fourth group, which is negatively correlated to the two axes, gathered the most populated number (Chahbi, Chemlali, Aguadulce and Super Aguadulce). The dendrogram based on (Nei, 1978) genetic distance of the agro morphological data using UPGMA method assigned the different populations into three groups (Figure 3). The first cluster includes Malti and Batata, belonging to the *major* faba bean type and these populations in the first cluster had low to moderate means for all traits. The second group included Massri, Badï and Bacha, these populations belong to the *minor* faba bean. In this cluster Massri and Badï showed the highest similarity. Nevertheless, Chahbi population which belong to *major* faba bean, is gathered with the three *equina* faba bean populations tested in our study (aguadulce, super aguadulce and chemlali) corresponding with the third and the latest group.

DISCUSSION

In this study, we used agro-morphological traits to assess the variation among 9 Tunisian faba bean populations belonging to the three botanical class of *V. faba* (*minor, equina* and *major*). For all characters analysed, significant difference between faba bean populations were found. Substantial variation and important heterogeneity between populations were observed for phenological, morphological and yield-related traits. This result corroborates with that of Nachi and Guen (1996) and Terzopoulos et al. (2003). The existence of morphological and agronomical diversity among the faba bean populations is further substantiated by principal component analysis, which indicated that the total variation was fairly distributed across all of the agro morphological traits. Assessment of genetic variability between populations is of interest not only for their protection and registration but also for practical applications (conservation of germplasm and breeding purposes).

PCA of the characterized agro-morphological traits revealed that 74.61% of total variation can be explained by 3 principal components, comprising 33.55, 25.14 and 15.92%, respectively. Thus, the 27 agro-morphological characters were able to discriminate the nine investigated populations, with a clear separation between the three botanical classes of *V. faba* (*minor, equina* and *major)*. Knowledge of the genetics concerning interesting traits of species is very important for breeding improvement. Whereas, a breeding program commonly does not look for the genetic improvement of separated traits but for the genetic improvement of a set of traits, since it is interesting for the breeder to know how the intervention in one trait can cause alteration in others (Venkovsky and Barriga, 1992). So, plant breeders who are interested in improving many traits simultaneously must take care of the relationship existing between them. Information obtained throughout principal component analysis may assist plant breeders to identify the number of highly differentiated population for use in crossing and selection programs (Veronesi and Falcinelli, 1988). Moreover, each population exhibited different behaviour and rich phenoltypic diversity may provide valuable resources of important agronomic traits with respect to that variation, which is likely related to each botanical class.

In previous studies, agro-morphological were conducted to describe the genetic variation and the handling of local collections of faba bean in Ethiopia (Mulat, 1998), in Egypt (Bakheit and Mahdy, 1998) and Sudan (Khashmelmous, 1989). Sindhu (1985) described the genetic variation of varieties from all over the world, while Polignano et al. (1999) described the extent and patterns of the phenotypic diversity existing in a large sample of the Bari, Italy and faba bean collection.

When selecting morphological and yield traits, most researchers have used as dissimilarity coefficients the Average Taxonomic (Tatineni et al., 1996), Euclidean (Bisht et al., 1998), Standard taxonomic, Goodman and Mahalanobis distance (Beer et al., 1993) and also the Gower coefficient (Beer et al., 1993; Franco et al., 1997). Other researchers have used Multivariate methods, the

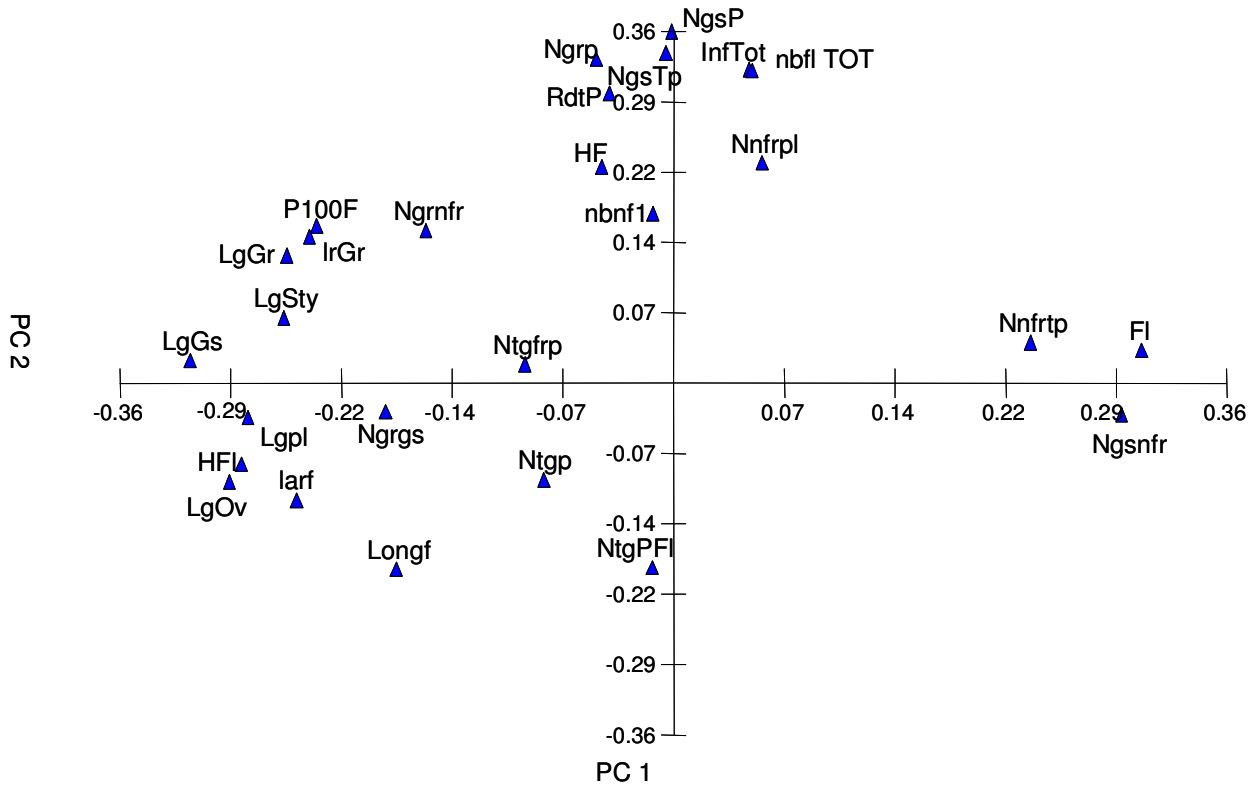

Figure 1. Principal components analysis of traits variable.

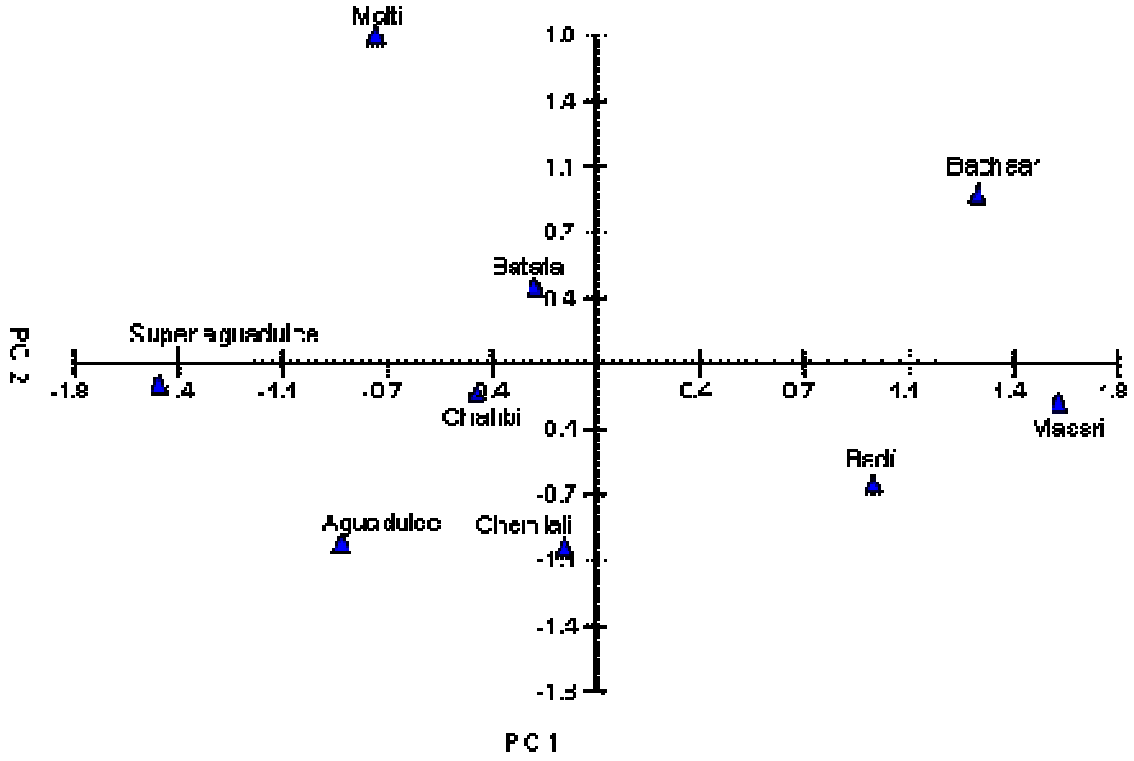

Figure 2. Principal components analysis of population's agromorphological traits. Malti (Mat); Batata (Bat); Bachaar (Bach); Massri (Mas);Badï (Badï); Chemlali(Chem); Aguadulce (Ag); Chahbi (Chah); Sag (Super Aguadulce).

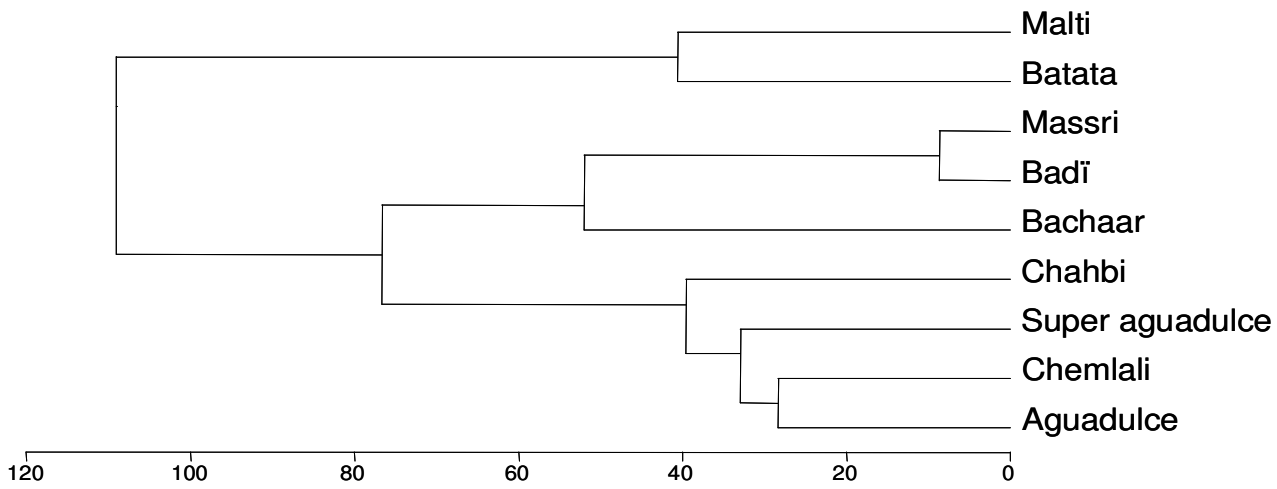

Figure 3. Euclidean distance between the 9 faba bean populations based on UPGMA method constrained distance using MVSP 3.131.

UPGMA (Huaman et al., 1999; Koutsos and Sotiriou, 2001; Tatineni et al., 1996) and the Principal Component Analysis (Grenier et al., 2001; Ortiz et al., 1998). The Neighbour-joining method and Principal Coordinate Analysis are more often applied when dealing with a two stages type of data. The use of Multivariate analysis is common in germplasm conservation to illustrate genetic diversity within the germplasm.

Complex agronomic traits are normally under polygenic control. The traits evaluated in faba bean in the present study may be grouped into three main categories; floral characters, yield distribution and yield characters, according to other authors. Agronomic traits in faba bean, as in other species, are usually complex characters determined by several interacting components, some of which are under polygenic control. This fact greatly hampers the selection process and the success of traditional breeding programs. Our results showed that seed per plant is not a stable parameter in *V. faba*, suggesting that this trait can not be critical to improve yield stability in the species. Whereas, Suso et al. (1996) and Thomson et al. (1997) has reported a stability of this trait and this can be based on the studied material.

Generally, the success of any breeding programme depends on the extent of genetic variability present on a crop and the knowledge on the correlation between yields and its component characters themselves which can improve the efficiency of selection. In this study, the increase in seed production per plant is a consequence of an increase in the number of fertile nodes per plant (r = 0.63), resulting itself in an increase in the total number of pods per plant (r = 0.70). On the contrary, the number of pods per node and the number of seeds per pod are negatively correlated (r = -0.37). Among vegetative traits, height of plants is positively affected by total inflorescence (InfTot) (r = 0.43) and total number of flowers (NbflTot) (r = 0.52). Among the characteristics that correlate directly with yield, the number of pods per plant, the number of ovules and seeds per pod and the number of branches per plant were the most important for the segregation of different studied populations. A suitable grouping of the populations is necessary in order to create core collections which have been proposed as a means for increasing the efficiency of utilization and management of germplasm collections as evidenced by (Liu et al., 1999).

Finally, the present work constitutes a first step for studying the genetic diversity of Tunisian faba bean populations. This genetic diversity will be more evidenced using molecular markers to understand the genetics and genomic organization of local varieties and this is to be of great value for breeding purposes. In fact, molecular markers have been extensively utilized for the study of genetic diversity and interspecific relationships among a number of species. Consequently, a later study using molecular markers on local faba bean populations will make a part of our research.

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