

Genetic diversity evaluation of Cumin (*Cuminum cyminum* L.) based on phenotypic characteristics

Alireza Bahraminejad¹, Ghasem Mohammadi-Nejad^{*2}, Mihdzar Abdul Khadir³

¹Crop Science Department, Agricultural Faculty, University of Putra Malaysia, P.O.B. 43400 UPM, Serdang, Selangor Darul Ehsan, Malaysia

²Horticultural Research Institute, Shahid Bahonar University of Kerman, Kerman, P.O.B 76169-133-Iran

³Department of Agriculture Technology, Agricultural Faculty, University Putra Malaysia, P.O.B. 43400 UPM, Serdang, Selangor Darul Ehsan, Malaysia

*Corresponding author: Mohammadinejad@mail.uk.ac.ir

Abstract

In order to assess the genetic diversity of cumin and determine the traits effective on seed yield and cumin-aldehyde, forty nine cumin ecotypes which they are sub-populations belonged to nine populations from different provinces of Iran were evaluated based on morphological and biochemical traits. Results indicated a significant variation for all the measured traits among and within populations derived from different provinces. Kerman and Esfahan populations showed the best performance based on the phenotypic data, while Yazd had almost the lowest levels of traits. Correlation analysis showed number of seed per umbel and umbel per plant had highest relationship with seed yield. Path analysis also demonstrated that number of umbel per plant and number of seed per umbel had the most direct effects on seed yield and were identified as the most effective factors on seed yield. Cumin aldehyde was mostly correlated by number of umbel per plant. The present study showed that different qualitative characteristics such as seeds with light color and without trichome and leaves without trichome, alternate and large pods of Petiole tend to produce high seed yield. Pattern analysis of different populations based on first two main principal components categorized the measured genotypes in to three groups: Pars, Northern_Khorasan, Golestan, Semnan and Yazd (Group1), Southern_Khorasan and Khorasan_Razavi (Group2) Kerman and Esfahan (Group3), which the third group are high yielding genotypes with different genetic background can be advised for cultivation and breeding programs. So the available genetic diversity among the Iranian cumin populations can be lead to produce high yielding population of cumin.

Keywords: Cumin; Genetic diversity; phenotypic assay.

Introduction

Cumin (*Cuminum cyminum* L.) a herbaceous, annual and medicinal which is one of the most important export crops for countries such as India, Iran and some other Asian countries (Kafie et al., 2002). Economic value of cumin is the numerous uses of the seeds as a drug and spicy for about a thousand years ago. It is regarded as part of food culture in West Asia, a predominant habitat of this plant. Therefore, trade and consumption of the crop is almost limited to natural areas that produce it (Avatar et al., 1991). The areas of production create numerous business opportunities because the planting operations of cumin require many human resources, thus create employment prospects in those regions. Cumin yield components include number of umbel per plant, number of seeds per umbel and 1000-seed weight. The number of umbel per plant explained alone about 96% of yield variation. (Amin Poor et al., 1995). Different regions of cumin adaptation can vary in terms of yield and genetic components due to variation in genetic characteristics and ecological influence. Therefore, geographical and genetic diversity play a related role in cumin characteristics (Jangir et

al., 1996). Cumin is allogam due to its protandery nature (Sihag 2001). One significant advantage of cumin which was compared to other crops is its high harvest index; an increase in this index in terms of agronomy can increase production of other parameters in cumin (Kafie, 1992). Cumin aldehyde is a major merger in the composition of cumin essence with chemical formula C₁₀H₁₂O (Para Iso Propel Benzaldehyde, molecular weight of 148.13 g) and it constitutes 63% of the total essence (Guenther, 1975). Cumin aldehyde has a powerful dour and is used only in traces in compounding synthetic floral perfumes such as cassie (Agarwal et al., 2010). Plant genetic diversity is created over thousands of years in nature to remain stable. Masses of native plants are germplasm for appropriate eugenics programs. It is imperative that researchers tirelessly work and provide information on Gene banks collection, identification, and evaluation for the protection of gene pool and plant masses. Agriculture and food production also depends on the use of plant genotypes. Conventional methods based on selection of desirable genotypes have modified crops during the past

Table1. List of 49 studied cumin ecotypes/sub-populations from 9 different provinces in Iran

Sample No	Populations	Sub-Populations /Ecotypes	Sample No	Populations	Sub-Populations /Ecotypes	Sample No	Populations	Sub-Populations /Ecotypes
1	Pars	Sarvestan	18	Kerman	Kooh-banan	35	Semnan	Shahmirzad
2	Pars	Sepidan	19	Kerman	Mahan	36	Semnan	Sorkheh
3	Pars	Sivand	20	Kerman	Ravar	37	Semnan	Ivanaki
4	Pars	Estahban	21	Kerman	Rafsanjan	38	Semnan	Kalateh
5	Yazd	Ardekan	22	Kerman	Sirjan	39	Northern- Khorasan	Esfarayen
6	Yazd	Bafq	23	Kerman	Zarand	40	Northern- Khorasan	Shirvan
7	Yazd	Sadoq	24	Southern- Khorasan	Qaen	41	Northern- Khorasan	Bojnord
8	Yazd	Khatam	25	Southern- Khorasan	Nahbandan	42	Northern- Khorasan	Baneh
9	Yazd	Sadroea	26	Southern- Khorasan	Birjand	43	Khorasan-Razavi	Gonabad
10	Golestan	Maraveh-Tapeh	27	Southern- Khorasan	Sarayan	44	Khorasan-Razavi	Ferdows
11	Golestan	Aq-Qala	28	Southern- Khorasan	Darmian	45	Khorasan-Razavi	Torbat-Heidareh
12	Golestan	Jat	29	Esfahan	Feridan	46	Khorasan-Razavi	Torbat-Jam
13	Golestan	Gonbad	30	Esfahan	Semirom	47	Khorasan-Razavi	Kashmar
14	Kerman	Baft	31	Esfahan	Ardestan	48	Khorasan-Razavi	Taybad
15	Kerman	Bardsir	32	Esfahan	Naien	49	Khorasan-Razavi	Bardsekan
16	Kerman	Chatrood	33	Esfahan	Khansar			
17	Kerman	Joopar	34	Esfahan	Natanz			

Table2. Analysis of Variance Based on Lattice Procedure

S.O.V	DF	Mean of Square						
		Seed length (mm)	No. Umbel/plant	No. Seed /Umbel	1000-Seed weight (gr)	Biological Yield (gr/m ²)	Seed yield (gr/m ²)	Cumin –aldehyde (ml)
Replication	1	0.02205	1.7245	0.09184	0.00921	0.6547	11864	0.02296
Block within Replication	12	0.3261	23.1888	19.7466	0.6087	506708	619609	0.3793
Adjusted Treat	48	0.3571**	14.706**	14.3259**	0.4933**	280395.12**	396218.11**	0.331**
Between Populations	8	1.9378**	79.4742**	81.1838**	2.8470**	1140533.649**	2299264.63**	1.784**
Within Populations	40	0.0410**	1.7531**	0.9541**	0.0225**	108367.418**	15608.80**	0.041**
Intra Block Error	36	0.1010	2.3753	3.5125	0.1390	35596	79332	0.09095

decades and this has created awareness of the diversity of population and the first prerequisite step in improve plants (Avatar et al., 1991). Most studies are carried on cumin, mainly on its essential oil, medicinal properties and aspects of agronomy (Kafie et al., 1992), tissue culture (Valizadeh et al., 2005) and cytogenetic studies (Nadernejad et al., 2001). The plant breeding aspect of cumin is quite new due to limited research work conducted in that area. The collection of cumin genetic materials in different areas where the plants grow will undoubtedly shed light on the diversity and classification of the plant. Therefore, this study seeks to evaluate and determine the genetic diversity of native masses of cumin under optimum conditions. Furthermore, it investigates the traits or characteristics of cumin under different environmental conditions and make available high correlation the between yield and content of cumin- aldehyde (Koli et al., 2000). The comparison of accession groups based on traits verified that it is possible to find out contrasting group based on the traits for improving genetic materials in breeding programs (Aghaee et al., 2010). The object of this research was comprehensive study of genetic diversity of cumin in Iran, in order to determine the performance of genotypes based on different traits using biometrical approaches.

Materials and methods

Plant Materials and growing conditions

In this study forty nine cumin ecotypes which they are sub-populations belonged to nine populations from different provinces of Iran that has the biggest variation for cumin were laid out in a simple lattice design with two replications in the Agricultural Research field in Zarand-Kerman (30°, 48', 39" N, 56°, 34', 2" E and 1651 AMSL) in 2005-2006 (Table 1). The genotypes were planted in plots of 4 m long. There was 50 cm row spacing and the distance between plants was 5 cm. All experimental plots were treated uniformly. Plants were harvested after removal of edge effect, for measuring the traits 20 plants were selected randomly.

Studied traits

Plants were harvested after removal of edge effect, 20 plants were selected randomly. The measured quantitative traits were including: seed length, number of umbel per plant, number of seed per umbel, 1000 - seed weight, biological yield, seed yield and cumin-aldehyde that was obtained by super heat- water distillation method. The scored qualitative traits were seed and leaf color, presence of wool on seed, trichoma on leaves, shape petiole and phyllotaxy.

Statistical analysis

Analysis of variance between and within populations, Correlation analysis of traits, as well as multiple linear regressions was performed by SAS ver 9.1. Path analysis for partitioning of yield components correlations on seed yield and cumin aldehyde in to direct and indirect effects was done by Path software. Factor analysis and cluster analysis was carried out using SPSS ver 10. Pattern analysis which is made from combining the result of clustering and coordinate analysis was done by Excel.

Results and discussion

The relative lattice efficiency was higher than randomized complete block design, as a result analysis of variance was executed using simple lattice for all traits and a very significant difference was observed between treatments. Analysis of variance of the traits showed that there was very significant difference between genotypes of different traits. Finally, inter and intra variation between traits was executed. Analysis of variance between and within populations showed highly significant difference for all the measured traits (Table 2). According to the result of mean comparison for the populations derived from different provinces, nine populations were compared based on the measured traits, Kerman and Esfahan Populations exhibited highest average number of umbel per plant, while Yazd population had the lowest average. The average number of seeds per umbel in Kerman and Esfahan populations was highest and the lowest was seen in Khorasan_Razavi. On average, higher 1000-seed weight was obtained from Kerman and Esfahan, while the lowest obtained from Khorasan_Razavi population. The highest mean seed yield and cumin-aldehyde was from Kerman and Esfahan Populations, while Khorasan_Razavi and Yazd showed the lowest average (Table 3). In order to evaluate genotype distribution pattern in each province separately, multivariate analysis was performed, that take generally information about evolution of Cumin plants in different regions of each provinces and the rate of relationship between the plants in the provinces.

Regression modeling of seed yield, biological yield and cumin- aldehyde in each population

The total traits number of umbel per plant, number of seeds per umbel and seed length in Pars and Golestan populations demonstrated 86 and 99 percent of linear changes, respectively. There was not an efficient linear model to represent seed yield linear variation based on yield components in the populations Kerman and Khorasan_Razavi. In Northern_Khorasan and Semnan populations 96.8 and 90.2 percent of linear changes of seed yield was explained by umbel per plant, seed number per umbel, 1000-seed weight respectively. However, the number of umbel per plant, number seed per umbel, 1000-seed weight and seed length in Southern_Khorasan population showed 97.2 percent of linear changes. In Esfahan Population 73 percent of linear changes of seed yield was explained by umbel per plant, seed number per umbel, 100-seed weight. Regression model of seed yield in Yazd population was explained 94.3 percent by seed length (Table 4). Since there is a significant genetic diversity for biological yield, so the total traits of number of umbel per plant, seed number per umbel and seed yield in Khorasan_Razavi population exhibited 66.1 percent of linear change in biological yield. Seed yield and seed length in Pars Population showed 48.3 percent of its linear change for biological yield in Kerman and Yazd demonstrated insufficiency in the linear model with linear change based on the components. 1000-seed weight, seed length and seed yield were included in the regression model of Semnan population with R² equal to 0.58 for biological yield. In Populations of Southern_Khorasan and Semnan seed yield showed 60 and 58 percent of their linear changes for biological yield respectively.

Table 3. Comparison of measured traits mean in Cumin populations.

Populations	Seed length (mm)	N.Umbel /plant	N.Seed /umbel	1000-seed weigh (gr)	Biological yield (gr/m ²)	Seed yield (gr/m ²)	Cumin-aldehyde (ml)
Pars	5.4 ^{ed}	19.5 ^c	9.75 ^c	3.6 ^c	1022.6 ^a	777.34 ^c	2.42 ^d
Yazd	5.18 ^{ef}	17.60 ^{ed}	11.20 ^b	3.90 ^b	1063.1 ^a	710.14 ^{cd}	2.02 ^e
Golestan	5.61 ^{cb}	19.13 ^c	8.50 ^d	3.50 ^c	1033.8 ^a	487.15 ^{ef}	2.17 ^e
Kerman	4.52 ^{cd}	24.35 ^a	13.75 ^a	4.42 ^a	288.7 ^b	1540.28 ^a	2.96 ^{ab}
Southern-Khorasan	5.46 ^g	18.60 ^{cd}	7.90 ^d	3.28 ^d	1056.3 ^a	489.45 ^{ef}	2.72 ^c
Esfahan	5.35 ^{ed}	22.90 ^b	13.30 ^a	4.10 ^b	1111.5 ^a	1294.07 ^b	3.10 ^a
Semnan	5.76 ^{ab}	19.38 ^c	10.50 ^{bc}	3.30 ^d	1030.2 ^a	606.90 ^{ed}	2.20 ^e
Northern- Khorasan	5.00 ^f	16.63 ^e	11.13 ^b	3.63 ^c	1049.6 ^a	544.40 ^e	2.13 ^e
Khorasan- Razavi	5.86 ^a	19.63 ^c	6.52 ^e	3.03 ^e	989.8 ^a	395.29 ^f	2.85 ^{bc}

Note: Mean follow by similar letters in each column are not significantly different

Table 4. Regression Model of seed yield for each population

Population	Constant	Seed length (mm)	No. Umbel/Plant	No. seed/umbel	1000-Seed Weight (gr)	Biological yield (gr/m ²)	Cumin-aldehyde (ml)	R ²
Pars	6431.79	-274.65	-	-	-393.85	-	457.80	.86
Yazd	612.96	-	-20.58	-21.68	-	-	321.32	.943
Golestan	12298.55	-	-	-86.71	-	-10.71	-	.99
Kerman	-1398.65	1110.73	-60.86	-	-	-.29	-553.61	.344
Southern-Khorasan	3643.36	-	34.08	40.62	-1037.48	-	-285.33	.972
Esfahan	1401.84	-	-3.65	3.89	-31.12	-	16.31	.73
Northern-Khorasan	11370.09	43.81	-	-1.97	47.89	-10.91	42.34	.968
Semnan	-5753.50	-21.88	1.11	3.01	-34.50	6.15	31.64	.902
Khorasan-Razavi	242.27	-	5.59	2.86	-	.02	-	.641

In Esfahan population the number of umbel per plant and 1000-seed weight demonstrated 59.5 percent of linear changes in biological yield. Length of seed, number of seed per umbel and seed yield in Golestan population also showed 99.6 percent of biological yield (Table 5). Seed yield of Northern_Khorasan and Khorasan_Razavi populations explained 54.2 and 51.2 percent of linear changes, respectively in Cumin- aldehyde. There is no efficient linear model for Cumin-aldehyde variation in populations of Semnan and Kerman. In the Number of umbel per plant, seed length, 1000- seed weight, biological yield and seed yield, 95.2 percent of linear changes of Cumin-aldehyde were demonstrated in Yazd population. The number of seed per umbel, 1000- seed weight and seed yield, were entered in the model and demonstrated 94.8 percent of Cumin-aldehyde linear changes Golestan population. In Southern_Khorasan population the number of umbel per plant, number of seed per umbel, 1000-seed weight and seed yield justified 83.6 percent of linear changes. The number of umbel per plant, number of seed per umbel and seed yield showed 88.6 percent R² in the linear model in Pars population However seed length alone in Esfahan population justified 52.7 percent

of model linear changes (Table 6). In general, significant genetic variation was demonstrated with respect to percentage of seed, biological yield and cumin - aldehyde between different genotypes derived from different area of Iran. A good trend was seen between different populations, therefore the breeding program with the purpose for improving seed and biological yield and Cumin – aldehyde for different populations should be considered in separate strategies.

Multiple linear Regressions based on all populations

Based on the total data for all the measured populations, number of seed per plant justified 73.2 percent of seed yield linear changes and number of umbel per plant, 1000- seed weight, number of seed per umbel and seed length totally justified 89 percent of seed yield linear changes.

$$Y = -1503.968 + 88.687X_1 + 83.628X_2 + 5.628X_3 - 58.06X_4$$

Where: N. Seed / umbrella, X₂ = N.umbrella / plant, X₃ = 1000 Seed weight, X₄ = Seed length

Table 5. Regression Model of biological yield for each population

Population	Constant	Seed length (mm)	No. Umbel/plant	No. seed/umbel	1000-Seed Weight (gr)	Seed yield (gr/m ²)	R ²
Pars	1085.650	-	3.186	-1.919	-15.871	-	0.483
Yazd	1028.379	1.570	-	-	-	-0.18	0.732
Golestan	1125.527	0.308	0.523	-7.855	-	-0.75	0.996
Kerman	1320.206	-	-	-	-4.035	-0.648	0.313
Southern-Khorasan	1001.879	-	-	-	-	0.111	0.600
Esfahan	1475.033	-	-4.500	-	19.158	-	0.595
Northern-Khorasan	1069.443	3.004	-	-	5.528	-0.122	0.921
Semnan	1015.68	-	-	-	-	0.058	0.58
Khorasan-Razavi	4531.232	-	-182.368	-93.419	-	24.573	0.661

Table 6. Regression Model of Cumin – aldehyde for each population

Populations	Constant	Seed length (mm)	No. Umbel /Plant	No. seed /umbel	1000-seed weight(gr)	Biological yield (gr/m ²)	Seed yield (gr/m ²)	R ²
Pars	-1.186	-	0.54	0.50	-	-	0.03	0.886
Yazd	13.664	0.132	-0.024	-	-0.256	-0.010	-8.95	0.952
Golestan	-7.916	-	-	0.259	1.418	-	0.06	0.948
Kerman	4.455	-	-0.023	-0.069	-0.001	-	-	0.415
Southern- Korasan	12.02	-	0.109	0.120	-3.27	-	-0.003	0.836
Esfahan	0.594	0.110	-	-	-	-	-	0.527
Northern- Khorasa	8.354	-	-	-	-	-	-0.101	0.542
Semnan	3.172	-	-0.062	-	-	-	-	0.23
Khorasan-Razavi	5.783	-	-135	-	-	-	-	0.512

Table 7. Correlation coefficients of measured traits

Traits	Seed length (mm)	No. umbel (per plant)	No. seed (per umbel)	1000-seed weight (gr)	Biological yield (gr/m ²)	Seed yield (gr/m ²)	Cumin-aldehyde (ml)
Seed length (cm)	1	-0.033	-0.161**	-0.034	0.052	-0.087	0.067
No. umbel per plant	0.033	1	0.673**	0.453**	-0.7**	0.843**	0.731**
No. seed per umbel	0.161**	0.673**	1	0.453**	-0.596**	0.855**	0.374**
1000seed weight (gr)	0.034	0.453**	0.453**	1	-0.690**	0.599**	0.383**
Biological yield (gr/m ²)	0.052	-0.7**	-0.596**	-0.690**	1	-0.787**	-0.521**
Seed yield (gr/m ²)	-0.087	0.843**	0.855**	0.599**	-0.787**	1	0.632**
Cumn-aldehyde (ml)	0.067	0.731**	0.374**	0.383**	-0.521**	0.631**	1

Note: **: highly significant at 0.01 level (P<0.01).

Table 8. Partitioning of correlation coefficient in to direct and indirect effect to the seed yield

	Direct effect	No .umbel/plant	No .seed/umbel	1000-seed weight	Correction coefficient With seed yield
No. umbel/plant	0.439	-	0.32	0.083	0.843
No. seed/umbel	0.475	0.295	-	0.083	0.855
1000-seed weight	0.184	0.198	0.215	-	0.599

Note: Residual=0.335

Seed Yield explained 61.9 percent of linear changes to justify biological yield, seed weight, number of seeds per umbel, umbel number per plant and seed yield explained 71.3 percent linear change to describe the biological yield.

$$Y = 1574.589 - 0.551X_1 - 9.263X_2 + 31.880X_3 - 25.60X_4$$

Where: (X1=SeedYield, X2=100 - weightseed, X3= N.seed/ umbrella, X4= N.Umb

Number of umbel per plant justified 53.4 percent of linear changes for Cumin- aldehyde and number of umbels per plant, number of seed per umbel, seed yield, biological yield and seed length traits justified 80.5 percent of model linear changes.

$$Y = 1.763 + 0.092 X_1 - 0.100X_2 - 0.001X_3 - 0.104X_4 + 9.53 \times 10^{-5} X_5$$

Where : (X1= N.Umbrella / plant, X2 = N.Seed / umbrella, X3 = Seed yield, X4 =

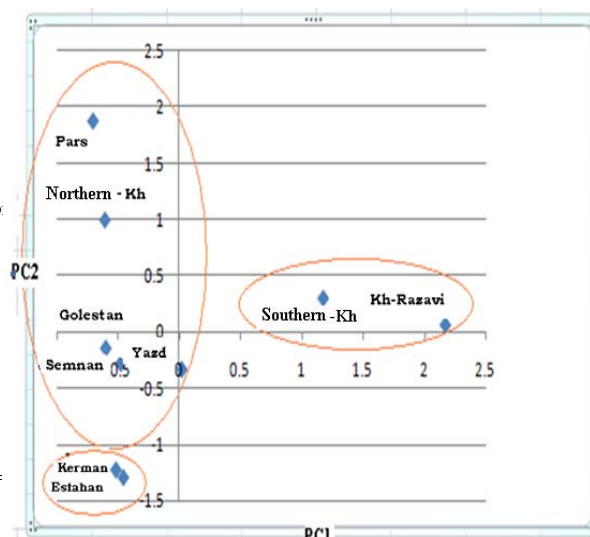


Fig1. Diagram for Pattern analysis of nine populations based on morphological traits.

Pattern analysis of studied cumin populations

Pattern analysis of different populations based on first two main principal components which justified 86 percent of the variation, categorized the measured populations in to three groups: Pars, Northern_Khorasan, Golestan, Semnan and Yazd (Group1), Southern_Khorasan and Khorasan_Razavi (Group2) Kerman and Esfahan (Group3), which the third group are high yielding genotypes with different genetic background can be advised for cultivation and breeding programs. So the available genetic diversity among the Iranian cumin population can be lead to produce high yielding cultivar of cumin (Fig1).

Correlation of traits

Correlation coefficients between the measured traits showed that seed length had only correlation with the number of seeds per umbel. Attribute number of seed per umbel was the only trait that showed correlation with all traits. Number of umbel per plant, 1000-seed weight, biological yield, seed yield and cumin-aldehyde had a significant correlation with all traits except seed length.

The number of seed per umbel and number of umbel per plant showed the highest correlation with yield and were considered as the most effective traits on yield.

Since, number of umbel per plant had most directly and highly significant effect on the cumin-aldehyde, this trait was mentioned as the most effective trait for breeding of cumin-aldehyde. The characteristic, number of umbel per plant, was effective trait in cumin breeding in term of seed yield and Cumin - aldehyde improvement. Note that seed yield had a significant positive correlation with rate of Cumin- aldehyde, while the relationship between biological yield and Cumin-aldehyde was negative (Table 7).

Path coefficient analysis

In order to partitioning coefficient correlation of yield components and seed yield in to direct and indirect effects path coefficient analysis were used to detect the most important and effective factors on seed yield (Fig2). Number of seed per umbel and number of umbel per plant had most direct effect on seed yield (0.475 and 0.439 respectively). Also numbers of umbel and 1000-seed weight had most

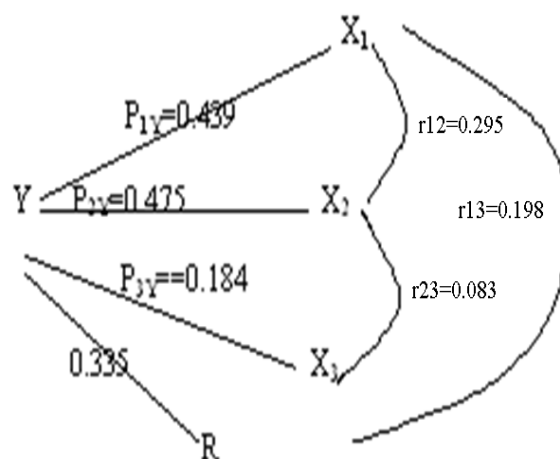


Fig2. Path analysis diagram for Description of correlation coefficient in seed yield components of Cumin X₁: No. umbel /plant, X₂ :No. seed/umbel, X₃: 1000-seed weight

indirect effect through seed number on yield. Therefore these two traits have good potential to improve seed yield through indirect selection in breeding programs. The lowest direct and indirect effects were belonged to 1000-seed weight (Table8).

Process of qualitative traits

In order to evaluate the relationship between qualitative and quantitative traits such as seed yield and other traits significance difference of quantitative traits between qualitative groups were assessed using T test. Results for seed color showed that there were significant differences between different groups of seed color in term of number of seed per plant and seed yield. Therefore it can be said that, there are linkages between genes controlling seed color and

number of seed per umbel. So it is important to select superior genotypes with dark seed color that have higher heritability than seed yield. So genotypes of bright colors have more seed. For presence or absence of wool on the seed, the result showed that there were significant differences between the different groups based on Seed yield and biological yield. It appears that there is linkage of relationship between genes controlling wool on seed and seed yield, it means selection of superior genotypes with higher seed yield can be done based on quality trait with higher heritability, so populations which have seed with wool have more seed. Results for leaves showed that there was a significant difference between different groups of leaves with or without trichome about number of seeds per umbel, number of umbel per plant and seed yield. It can be said that there are linkages between genes controlling trichome on leaf and seed number per umbel. Therefore, genotypes are containing leaves without trichome compared with trichome has more seed. Results of leaf color showed that there was a significant difference between different groups with different leaf color for number of seed and seed yield. Therefore it can be said that there are linkages between genes controlling leaf color and seed yield. So that genotypes with dark green color have more seed. Results showed that for shape petiole there was a significant difference between different groups with different shape petiole for number of seed per umbel and seed yield. So the genotypes which have petioles with a large sheath have more seed. Results for phyllotaxy showed that there was significant difference between different groups with mutual and alternate leaf for number of seed per umbel and seed yield. So that genotype with alternating leaves have more seed.

Conclusion

According to the result there is significant variation among the populations derived from different provinces and between their sub-populations (within populations). It means the available seed cumin which is under cultivation by the farmers can have different genetically background. Also there are different dispersion pattern of traits in each provinces. So the available genetic diversity among the Iranian cumin population can be lead to produce high yielding cultivar of cumin. Kerman and Esfahan populations showed the best performance based on the phenotypic data, while Yazd had almost the lowest levels of traits. Evaluation of effective traits on yield which can be used as important traits for indirect selection in cumin breeding, based on some methods showed Number of umbel per plant and number of seed per umbel has the best potential for increasing seed yield in cumin breeding. For getting the high progress of selection due to higher heritability, different qualitative characteristics such as light seed color, lack of trichome and leaves without trichome, alternate and large pods of Petiole tend to produce high seed yield.

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