



Selection for High Yielding and Stemphylium Blight Resistant Lentil (*Lens culinaris* Medikus) Genotype based on Principle Component and Selection Indices

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ABSTRACT

Background: Lentil (*Lens culinaris* medikus.) is one of the most important nutritious rabi pulse crops in. The fungal pathogen *Stemphylium botryosum*, which causes stemphylium blight, has gained attention recently and is responsible for 62% of crop loss in many countries, including India. This current study was conducted to assess the lentil germplasm in preparation for a future breeding project, taking into account the crop's relevance in relation to the disease's severity as well as a number of other desired variables like yield and quality attributes.

Methods: The study was undertaken in the Instructional farm of UBKV, Pundibari during the *rabi* season of 2019-20 and 2020-21 with forty lentil germplasm to select distinguished high yielding genotype for resistance against Stemphylium blight. The field experiment was conducted by following by alpha lattice design with three replications. Statistical analysis was carried out using PB Tools v. 1.3 software.

Result: Principle component analysis based selection indexing were performed considering 20% selection intensity and all the 18 traits under study were considered to compute selection indices, viz., days to 50% flowering, plant height, days to 90% maturity, primary branches plant⁻¹, secondary branches plant⁻¹, pods plant⁻¹, seeds pod⁻¹, pod weight plant⁻¹, 100 seed weight, yield plant⁻¹, harvest index, area under disease progress curve, change in phenol, change in OD phenol, polyphenol oxidase, seed iron, seed zinc and seed protein content in matured seeds. The genotype IC241061 was identified with the highest smith index score which could be used in future for resistance breeding.

Key words: Principle component analysis, Selection indices, Stemphylium blight, Lentil, Smith index.

INTRODUCTION

Lentil (*Lens culinaris* Medik.), an important pulses crop of the world, stands as the second-most significant pulse crop in terms of acreage, production and consumer preference (Bahl *et al.*, 1993). In India the states of Uttar Pradesh, Madhya Pradesh, West Bengal and Bihar account for nearly 95% of the land dedicated to the crop and it is one of the most nutrient-rich *rabi* pulse crops consumed primarily as dal. However, the production of the crop seems to be declining each year owing to a number of constraints viz., limited genetic resources, vulnerability to diseases, smaller areas and due to delay in sowing.

Susceptibility to disease is one of the major constraints, Stemphylium blight, caused by fungal pathogen *Stemphylium botryosum* being one of them which during epidemic can cause a total failure of the crop (Taylor *et al.* 2007). It is therefore crucial to estimate genetic and phenotypic parameters of the available resources to ascertain such parameters as heritability and expected response to selection that will direct the future breeding programme.

The selection index can effectively aid in the identification of potential genotype/s when several parameters are considered at once. In addition to conventional selection techniques employed for population development, breeders may use selection indices to aid in

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the simultaneous selection of several characteristics too (Smith, 1936). Besides selection indices offer useful guidance on how to combine characters (Banziger and Lafitte, 1997). Several other researchers have successfully employed selection indices as a selection criterion in their breeding work for other crops (Vikram and Roy, 2003; Xie *et al.*, 1998 and Dolan *et al.*, 1996).

Considering the above-mentioned factors, the present investigation was carried out to assess the genetic diversity among the lentil genotypes using principal component analysis and to identify the lentil genotype/s for yield and attributing traits using selection index (Hazel, 1943).

MATERIALS AND METHODS

The present study was conducted in the Agricultural Instruction Farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar under *terai* agro-climatic region of West Bengal located at 26°24'09.1"N latitude and 89°23'08.3"E longitude and 43 m above mean sea level. A

total of forty lentil germplasm including two checks, viz., WBL77 and IPL220 were used in the experiment carried out during *rabi* season of 2019-20 and 2020-21 (Table 1).

The statistical design namely alpha lattice implied with three replications for field experiment. The crop was raised by following the standard cultural methods with a plant-to-plant and row-to-row distance of 10 cm and 30 cm respectively in each plot measuring 2 m×1.5 m. The morphological observations were made on five randomly selected plants in each each replication. Characters viz., days to 50% flowering (DF), plant height (PH), days to 90% maturity (DOM), primary branches plant⁻¹ (PBPP), secondary branches plant⁻¹ (SBPP), pods plant⁻¹ (PODPL), seed pod⁻¹ (SPP), pod weight plant⁻¹ (PODWT), 100 seed weight (HSW), yield plant⁻¹ (YPP) and harvest index (HI) were measured as per DUS descriptors. For biochemical analysis random sampling was performed for each replication for characters change in phenol (CP), change in OD phenol (CODP), polyphenol oxidase (PPO), seed

Table 1: List of lentil genotypes.

Sl. no.	Name of genotypes	Sl. no.	Name of genotypes	Sl. no.	Name of genotypes	Sl. no.	Name of genotypes
1	IC241067	11	IC78540	21	IC199779	31	IC614827
2	IC241090	12	EC223188	22	IC78486	32	IC201778
3	IC241119	13	IC78518	23	EC225484	33	EC223219
4	IC241072	14	IC78547	24	IC241071	34	EC267544
5	IC565035	15	WBL77	25	IC78513	35	EC267563
6	IC241082	16	IC78454	26	IC610426	36	EC267598
7	IC78535	17	IC78462	27	IC241097	37	EC267604
8	IC78531	18	EC33920	28	IC241061	38	EC267636
9	EC16391	19	EC223244	29	IC620839	39	IC78408
10	IC78545	20	EC225486	30	IC544556	40	IPL220

Table 2: The direction of selection and their weightage.

Characters	Weightage	Direction of selection
Days to 50% flowering	0.84	+
Plant height	0.63	+
Days to 90% maturity	0.89	+
Primary branches plant ⁻¹	0.50	+
Secondary branches plant ⁻¹	0.69	+
Pods plant ⁻¹	1.00	+
Seed pod ⁻¹	0.34	+
Pod weight plant ⁻¹	0.76	+
100 seed weight	0.74	+
Yield plant ⁻¹	0.77	+
Harvest index	0.65	+
AUDPC	0.00	-
Change in phenol	0.52	+
Change in OD phenol	0.30	+
Polyphenol oxidase	0.73	+
Seed iron	0.62	+
Seed zinc	0.99	+
Seed protein	0.31	+

Table 3: PCA loadings for selection index in lentil genotypes.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
DF	0.080	-0.217	0.226	-0.067	0.589	-0.206	0.114	0.181	-0.014	0.476	0.156
PH	0.174	0.116	-0.424	-0.066	0.282	0.281	-0.012	-0.211	0.044	0.154	0.521
DOM	0.151	0.060	0.047	0.467	0.530	0.101	-0.028	0.087	-0.241	-0.189	-0.259
PBPP	0.405	-0.004	0.106	-0.157	-0.031	-0.153	-0.137	-0.195	-0.006	-0.124	0.082
SBPP	0.268	0.119	-0.228	0.161	0.114	-0.099	0.090	-0.370	0.686	0.013	-0.317
PODPL	0.393	0.170	0.147	0.067	-0.104	0.085	-0.182	0.131	-0.072	0.042	-0.100
SPP	-0.004	-0.033	0.458	-0.010	-0.051	-0.115	0.190	-0.736	-0.293	0.134	0.009
PODWT	0.443	0.136	0.120	-0.067	-0.109	-0.002	0.021	0.205	-0.070	0.089	0.008
HSW	-0.115	0.366	-0.217	0.346	-0.073	-0.175	0.106	-0.024	-0.181	0.094	0.418
Yield	0.436	0.161	0.113	-0.064	-0.109	-0.017	0.037	0.194	-0.085	0.044	0.010
HI	0.184	0.132	-0.104	-0.216	-0.046	0.050	0.779	0.044	-0.076	-0.153	0.041
AUDPC	0.208	-0.402	-0.242	0.235	0.097	-0.007	0.017	-0.184	-0.214	-0.065	-0.093
CHP	-0.139	0.402	0.235	-0.241	0.227	-0.153	-0.137	-0.003	0.270	0.195	0.005
CHODP	-0.077	0.441	0.082	-0.133	0.306	0.012	-0.162	-0.135	-0.169	-0.557	0.031
PPO	0.072	0.020	0.347	0.574	-0.221	-0.016	-0.047	0.015	0.259	-0.045	0.397
Fe	-0.043	0.274	-0.011	0.068	-0.102	0.636	-0.082	-0.145	-0.160	0.456	-0.260
Zn	-0.136	-0.068	0.368	0.098	0.134	0.455	0.375	0.123	0.271	-0.187	0.047
Protein	-0.150	0.314	-0.111	0.262	-0.047	-0.381	0.272	0.108	-0.116	0.200	-0.326
SD	2.06	1.60	1.38	1.20	1.17	1.16	1.02	0.92	0.78	0.77	0.71
PV (%)	23.66	14.22	10.53	7.95	7.55	7.45	5.74	4.68	3.34	3.28	2.79
CPV (%)	23.66	37.88	48.41	56.35	63.90	71.35	77.08	81.77	85.15	88.43	91.23
	PC12	PC13	PC14	PC15	PC16	PC17	PC18				
DF	-0.028	0.159	0.016	-0.278	-0.031	0.308	0.075				
PH	-0.358	-0.125	0.227	0.170	0.083	-0.197	-0.049				
DOM	0.281	-0.291	0.065	0.126	0.273	-0.180	-0.040				
PBPP	-0.104	0.140	-0.474	0.170	0.609	0.189	0.081				
SBPP	0.150	0.154	0.104	-0.186	-0.053	0.043	0.001				
PODPL	-0.037	0.140	0.409	0.492	-0.239	0.463	0.057				
SPP	0.039	0.006	0.238	0.045	-0.044	-0.165	-0.055				
PODWT	0.003	0.084	-0.074	-0.208	-0.094	-0.239	-0.760				
HSW	0.460	0.429	-0.142	0.070	-0.029	0.042	0.006				
Yield	0.002	0.082	0.028	-0.209	-0.124	-0.500	0.624				
HI	0.135	-0.363	-0.079	0.011	-0.052	0.291	0.044				
AUDPC	-0.173	0.067	-0.472	0.149	-0.547	-0.011	0.022				
CHP	0.103	-0.292	-0.368	0.400	-0.285	-0.167	-0.007				
CHODP	-0.240	0.139	-0.016	-0.365	-0.221	0.195	0.007				
PPO	-0.205	-0.384	-0.094	-0.198	-0.060	0.158	0.036				
Fe	-0.001	-0.031	-0.272	-0.232	0.056	0.193	0.072				
Zn	-0.150	0.468	-0.098	0.243	0.032	-0.168	-0.022				
PROT	-0.603	0.072	0.002	0.101	0.146	-0.063	-0.017				
SD	0.65	0.62	0.58	0.44	0.37	0.30	0.08				
PV (%)	2.34	2.17	1.87	1.10	0.77	0.49	0.03				
CPV (%)	93.57	95.73	97.60	98.70	99.47	99.97	100.00				

DF= Days to 50% flowering, PH= Plant height (cm), DOM= Days to 90% maturity, PBPP= Primary branches plant⁻¹, SBPP= Secondary branches plant⁻¹, PODPL= Pods plant⁻¹, SPP= Seeds pod⁻¹, PODWT= Pod weight plant⁻¹, HSW= 100 seed weight (g), Yield= Yield plant⁻¹ (g), HI= Harvest index (%), AUDPC= Area under disease progress curve.

CHP= Change in phenol (mg g⁻¹), CHODP= Change in OD phenol (mg COE g⁻¹), PPO= Polyphenol oxidase (abs min⁻¹ g⁻¹), Fe= Seed iron= (mg kg⁻¹), Zn= Seed zinc (mg kg⁻¹), Protein= Seed protein (g 100 g⁻¹).

SD= Standard deviation, PV= Proportion of variance, CPV= Cumulative proportion of variance.

Table 4: Lentil genotypes identified with high selection index score.

Genotype	DF	PH	DOM	PBPP	SBPP	PODPL	SPP	PODWT	HSW	Yield	HI	Smith index
IC241061	51.17	37.97	111.83	1.83	6.80	45.30	1.67	1.57	2.80	1.33	42.30	0.77
IC614827	52.33	37.33	109.50	2.10	5.55	83.54	1.77	2.94	1.82	2.48	30.33	0.77
IC78486	55.00	34.04	109.83	2.40	5.83	80.66	1.73	3.58	1.73	2.62	38.10	0.73
IC544556	52.00	39.20	111.33	1.90	5.07	65.48	1.87	2.11	1.73	1.81	43.99	0.65
IC241071	51.67	34.47	108.83	1.90	4.63	58.70	1.70	2.62	1.76	2.27	44.85	0.62
IC201778	52.17	37.56	113.00	2.17	5.67	50.71	1.83	2.15	2.71	1.82	35.23	0.56
IC241097	64.00	37.79	114.83	2.03	5.57	61.59	1.73	2.23	1.75	1.84	35.25	0.51
IC241067	49.50	41.71	106.83	2.00	6.33	35.70	1.80	1.88	2.08	1.62	45.94	0.45
Mean of selected individuals	53.48	37.51	110.75	2.04	5.68	60.21	1.76	2.38	2.05	1.97	39.5	-
Means of all individuals	52.64	35.14	108.29	1.98	5.25	46.8	1.77	1.84	1.96	1.51	35.38	-
Selection differential	0.84	2.37	2.46	0.07	0.43	13.41	-0.01	0.54	0.09	0.46	4.11	-
Expected genetic gain for 20%	-0.47	0.46	0.67	0.02	0.05	11.67	0.01	0.36	0.04	0.30	1.25	-
Genotype	AUDPC	CHP	CHODP	PPO	Fe	Zn	Protein					
IC241061	253.67	22.89	2.38	3.60	115.37	62.40	29.28					
IC614827	158.33	23.45	1.89	4.98	129.18	55.03	20.71					
IC78486	360.08	14.42	0.86	5.25	108.13	58.61	20.15					
IC544556	345.50	4.86	0.60	3.32	130.18	79.80	25.79					
IC241071	210.00	19.27	2.00	4.78	118.58	71.40	25.72					
IC201778	346.33	9.03	1.94	2.13	111.00	41.35	27.09					
IC241097	433.00	9.97	0.90	2.18	87.89	59.59	20.15					
IC241067	280.67	17.84	1.05	4.57	118.33	64.37	21.09					
Mean of selected individuals	298.45	15.22	1.45	3.85	114.83	61.57	23.75					
Means of all individuals	312.94	13.38	1.15	3.42	103.74	59.06	23.10					
Selection differential	-14.49	1.84	0.3	0.43	11.09	2.51	0.65					
Expected genetic gain for 20%	-62.85	3.45	0.25	0.5	15.91	5.62	0.18					

DF= Days to 50% flowering, PH= Plant height (cm), DOM= Days to 90% maturity, PBPP= Primary branches plant⁻¹, SBPP= Secondary branches plant⁻¹, PODPL= Pods plant⁻¹, SPP= Seeds pod⁻¹, PODWT= Pod weight plant⁻¹, HSW= 100 seed weight (g), Yield= Yield plant⁻¹ (g), HI= Harvest index(%).

AUDPC= Area under disease progress curve, CHP= Change in phenol (mg g⁻¹), CHODP= Change in OD phenol (mg COE g⁻¹), PPO= Polyphenol oxidase (abs min⁻¹ g⁻¹), Fe= Seed iron= (mg kg⁻¹), Zn= Seed zinc (mg kg⁻¹), Protein= Seed protein (g 100 g⁻¹).

iron (Fe), seed zinc (Zn) and seed protein (SP) content the former three being important biochemical parameters in disease reaction. The percent disease index (PDI) based on disease scoring against Stemphylium blight was done after (Hashemi *et al.*, 2005) assessing the disease severity from initiation till the maturity of the crop. Area Under Disease Progress Curve (AUDPC) was also calculated to ascertain the spread of the disease.

The direction of selection and their weightage has been presented in Table 2 where, the scale 0.00 to 1.00 has been used. Under the present experiment, 20% of selection intensity was considered. Principal component analysis (PCA) was carried out using R v 4.1.1 software using the mean data for the traits and characters contributing the most towards variability were identified through PCA (Jolliffe 2002). Hence based on the PCA loadings the weightage was applied and rescaling of derived values for the traits was done following mini-max normalization formula:

$$x' = \frac{x - \min(x)}{\max(x) - \min(x)}$$

Where,

x' = original value.

x' = normalized value.

Subsequently the selection index for each genotype was computed and they were ranked based on all the characters including the morphological and biochemical with derived index values. To calculate the selection index PB Tools v. 1.3 software was used.

RESULTS AND DISCUSSION

The analysis revealed significant differences among the studied genotypes for all the characters in conformity with similar findings by (Vanave *et al* 2019, Akter *et al* 2020 Ahmed *et al* 2021 and Satpathy and Debnath 2020).

The principle component analysis identified seven PCs having eigen value more than 1 accounting for a cumulative proportion more than 77.08% of the total variation. The PC with eigen value more than 1 are designed to be used in selection indices (Mattjik *et al* 2011) due to the variance being readily explained. The characters viz., primary branches plant⁻¹ (0.405), pods plant⁻¹ (0.393), pod weight plant⁻¹ (0.443), showed high eigen vector values in PC1 while in PC2 100 seed weight (0.366), change in phenol content (0.402), change in OD phenol (0.441) and seed protein revealed highest loading value. In PC3 the characters viz; seeds pod⁻¹ (0.458), polyphenol oxidase (0.347) and seed zinc content (0.368) showed maximum loading value with days to 90% maturity (0.467) and 100 seed weight (0.346) showing maximum weightage in PC4. Whereas plant height (0.281) showed maximum weightage in PC6 harvest index(0.779) showed the same in PC7 (Table 3). Similar such reports on principal component analysis in lentil have been made by Pratap *et al.*, 2014, Siahsar *et al* 2010, Crippa *et al* 2009, Cristobal *et al.*, 2014,

Kumar and Solanki, 2014 and Mahmood *et al.*, 2019 among the others.

The smith index values calculated based on PCA loadings varied from -1.15 (IC241072) to 0.77 (IC241061 and IC614827) for the studied germplasm and eight lentil genotypes were identified with highest selection index value with a selection intensity of 20% as presented in Table 4. The selection differential for the studied characters was estimated by subtracting the value of mean of each character for all individual from the mean of selected individuals which revealed that the characters pods plant⁻¹ (13.41) had the highest selection differential followed by seed iron content (11.09) and harvest index (4.11). The characters AUDPC (-14.49) and days to 50% flowering (-0.47) were found to have negative selection differential values and thus were also likely to fit in the improvement goals in the sense that disease and flowering traits are favourable in negative direction. The study further revealed that the expected genetic gain for the selected genotypes were maximum for seed iron content (15.91) followed by pods plant⁻¹(11.67) and seed zinc content (5.62) and the minimum genetic gain was noted for AUDPC (-62.85) followed by seeds pod⁻¹ (0.01) and primary branches plant⁻¹ (0.02). (Pavithra and Vengadessan, 2020) in an experiment with 48 genotypes of rice similarly studied on principal component analysis (PCA) and selection index with the objective to select discriminating rice genotypes for drought tolerance and likewise reported a PCA based reduction of the 12 traits into six traits viz., days to 50 per cent flowering, plant height, panicle length, grains per panicle, grain yield and stress percentage across the environments. They further computed selection index with the economic weights derived from PCA found the genotype IET-27693 with high index score for drought tolerance. The use of stress tolerance index and PCA was similarly considered effective in the formation of the selection index on salinity screening in rice by Farid *et al.* (2021).

CONCLUSION

Selection index for the studied genotypes was computed based on the relative weight of the 18 characters towards the corresponding principal component axis and the rescaled PCA loadings for all the characters towards corresponding principal component axes were used to calculate the selected index score (smith index) for the lentil genotypes which revealed that the genotype IC241061 and IC614827 had the highest smith index value (0.77) while the genotype IC241072 had the lowest smith index value (-1.15). Eight lentil genotypes were identified with highest smith index value based on all the characters with 20% selection intensity and seed iron content and AUDPC had the highest (15.91) and the lowest (-62.85) expected genetic gain respectively. Selection based on the above can thus be fruitful to develop superior genotype with high yielding potential and resistance to the disease Stemphylium blight as well along with such qualitative traits as high seed protein, zinc and iron content.

Conflict of interest

All authors declared that there is no conflict of interest.

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