Biplot Analysis for Evaluation of Tolerance in some Bean (*Phaseolus vulgaris* L.) Genotypes to *Bean Common Mosaic Virus* (BCMV)

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Abstract—The common bean is the most important grain legume for direct human consumption in the world and BCMV is one of the world's most serious bean diseases that can reduce yield and quality of harvested product. To determine the best tolerance index to BCMV and recognize tolerant genotypes, 2 experiments were conducted in field conditions. Twenty five common bean genotypes were sown in 2 separate RCB design with 3 replications under contamination and non-contamination conditions. On the basis of the results of indices correlations GMP, MP and HARM were determined as the most suitable tolerance indices. The results of principle components analysis indicated 2 first components totally explained 98.52% of variations among data. The first and second components were named potential yield and stress susceptible respectively. Based on the results of BCMV tolerance indices assessment and biplot analysis WA8563-4, WA8563-2 and Cardinal were the genotypes that exhibited potential seed yield under contamination and non-contamination conditions.

Keywords—*Phaseolus vulgaris*, BCMV, principle components analysis, biplot analysis, tolerance

I. INTRODUCTION

COMMON bean (*Paseolus vulgaris* L.) is one of the major food legumes produced. Its production is very important in north, central and south America, eastern Africa, eastern Asia and south eastern Europe [1] Bean common mosaic virus (BCMV) can reduce the seed yield as much as 80 percent [2]. Strategies for the management of viral diseases normally include control of vector population using insecticides, use of virus-free propagating material, appropriate cultural practices and use of resistant cultivars. However, each of the above methods has its own drawback [3]. Puttaraju *et al*(2004) [4] reported that number of pods per plant, number of seeds per plant and 100-seed weight were significantly reduced in plants infected by BCMV during primary to third trifoliate leaf stages. Castillo-Urquiza *et al*.(2006) [5] showed single infection of 'Ouro Negro' and 'Novirex' beans by BRMV(Bean rugose mosaic virus) caused a reduction in the total weight of pods per plant of 3.4% and 84.9% respectively. Mixed infection with BCMV caused a reduction of pod weight per plant of up to 70.1% in 'Novirex' and up to 90.8% in 'Ouro Negro'. According to Ittah (2006) [6], the relationship between disease severity and yield showed that as disease severity increased cowpea yield decreased. BCMV-BIC reduced the seed yield between 62 and 87% and CABMV(Cowpea aphid-borne mosaic virus) between 54 and 87% in some cowpea cultivars.The purpose of this study was to estimate of BCMV damage on grain yield, yield components and determine various reaction of genotypes in field conditions.

II. MATERIAL AND METHODS

This trial performed during 2006 cropping season in field conditions. 25 lines and cultivars obtained from Khomaien bean international research center. Two separate experiments (with and without infection) in the same conditions were conducted in RCB design with 25 genotypes and 3 replications. Considered virus was isolated from a research field and after biological purification was used to multiplication on susceptible seedlings. Plants were inoculated second trifoliate leaf stages and percent of apparent contamination was recorded 3 weeks after inoculation for each genotypes. ELISA test was performed to determine of amount contamination. During the course of the study, 7 phenological plant characters and 14 agro-morphological traits were recorded on the two experiments. Observations of examined characters were performed 6 plants chosen randomly from the mid-row of each plot. Data analysis was conducted by computerized statistical program SAS and STATGRAPH.

III. RESULTS AND DISCUSSION

Tolerance indices and correlation between them and seed yield in non-infected and infected conditions was showed in tables 1&2. In order to results of table 2 correlation between seed yield in non-infected and infected conditions was significant at 0.01 probability level(r=0.72). Correlation of seed yield in non-infected conditions with GMP(r=0.91), STI(r=0.69), TOL(r=0.77), MP(r=0.89) and HARM(r=0.85) was significant at 0.01 probability level too. In general, indices that have strong correlation with seed yield in two conditions introduce as the best indices (Fernandez, 1992). So here GMP, MP and HARM was introduced as the suitable indices for recognize of stable varieties in two conditions.

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TABLE I
TOLERANCE INDICES FOR BEAN VARIETIES AND LINES

Row	Genotype	Yp	Ys	GMP	STI	SSI	TOL	MP	HARM
1	Khomein-5	377/61	216/71	286/06	0/04	1/14	160/89	297/16	275/38
2	Local Khomein	1131/65	514/15	762/79	0/32	0/89	617/49	822/90	707/06
3	Daneshjo	1115/51	342/00	617/66	0/21	0/70	773/51	728/76	523/50
4	Cardinal	1571/95	992/16	1248/85	0/85	1/32	579/79	1282/06	1216/51
5	Cran 75	1591/44	849/93	1163/02	0/74	1/04	741/51	1220/69	1108/08
6	Pinto	1342/41	532/41	845/40	0/39	0/81	810/00	937/41	762/43
7	MCD4012	1342/99	856/24	1072/35	0/63	1/34	486/75	1099/62	1045/75
8	COS16	2190/74	748/34	1280/39	0/89	0/74	1442/40	1469/54	1115/60
9	Taylor	1320/59	530/07	836/66	0/38	0/81	790/52	925/33	756/49
10	Goli	1115/38	681/65	871/96	0/41	1/25	433/73	898/52	846/18
11	Naz	1235/05	631/67	883/26	0/43	1/00	603/38	933/36	835/85
12	Capsoli	2882/60	1028/79	1722/08	1/62	0/76	1853/81	1955/69	1516/38
13	D81083	1082/18	705/02	873/47	0/42	1/40	377/15	893/60	853/80
14	Sayad	1294/73	534/45	831/85	0/38	0/83	760/28	914/59	756/59
15	Derakhshan	790/10	466/09	606/84	0/20	1/19	324/01	628/09	586/31
16	Akhtar	1034/97	382/04	628/80	0/22	0/77	652/93	708/50	558/07
17	G5710	951/61	622/24	769/50	0/32	1/41	329/37	786/92	752/46
18	WA8528-9	1244/61	848/33	1027/54	0/58	1/53	396/28	1046/47	1008/95
19	WA8563-2	1446/41	1128/02	1277/33	0/89	2/21	318/39	1287/22	1267/53
20	WA8563-6	1594/28	890/32	1191/39	0/77	1/10	703/96	1242/30	1142/57
21	WA8563-4	2394/10	1845/48	2101/97	2/41	2/12	548/62	2119/79	2084/29
22	WA8563-3	1274/85	846/89	1039/07	0/59	1/45	427/96	1060/87	1017/71
23	11805	1095/68	717/73	886/79	0/43	1/41	377/95	906/70	867/32
24	Cifemcave	1378/08	703/25	984/44	0/53	0/99	674/83	1040/66	931/26
25	WA4502-1	1042/87	402/99	648/28	0/23	0/79	639/88	722/93	581/34

Yp: Genotype potential yield in non-infectsd conditions.
Ys: Genotype potential yield in infectsd conditions.

$\bar{Y}p$: Yield mean of all genotypes in non-infected conditions.

$\bar{Y}s$: Yield mean of all genotypes in non-infected conditions.

$$GMP=\sqrt{(Yp)(Ys)} \qquad STI=(Yp)(Ys)/(\bar{Y}p)^2 \qquad SSI=1-(\bar{Y}s/\bar{Y}p)/SI$$

$$SI=1-(Ys-Yp) \qquad TOL=Yp-Ys \qquad MP=(Yp+Ys)/2$$

$$HARM=2(Yp)(Ys)/Yp+Ys \qquad \bar{Y}s=720.68 \qquad \bar{Y}p=1353.70$$

Biplot is a useful implement for data analysis and assessment theoretical of structure of big matrix. For this purpose, obtained matrix from table 1 through principle components analysis was divided to 8 components. First 2 components explained 98.52 percent of data variation. In order to first (75.28) and second (23.24) components biplot was divided to four parts (Fig.1). Correlation of first component with seed yield in non-infected(r=0.37) and infected(r=0.38) conditions was significant at 0.05 probability level. Also, correlation of this component with GMP(r=0.41), STI, MP and HARM(r=0.40) indices was significant too. Therefore, first component was nominated as potential yield component. High values of this component determine tolerant genotypes with high potential yield. Correlation of second component with

SSI index was positive and significant at 0.01 probability level(r=0.64). High levels of SSI index determine unstable genotypes [7]. Second component was nominated as sensitiveness component. From this point of view, low values of second component and high values of first component consequent to selection of stable genotypes.

Therefore, biplot was divided to four parts as follows (Fig. 1)

A: High values of first component and low values of second component. This part contains of genotypes with high yield in two conditions. **Genotypes:** 21(WA8563-4), 19(WA8563-2) and 4(Cardinal).

B: High values of first and second components. This part contains of genotypes with just high yield in non-infected

TABLE II
SIMPLE CORRELATION AMONG TOLERANCE INDICES

Index	Yp	Ys	SSI	GMP	STI	TOL	MP	HARM
Yp	1/00							
Ys	0/72**	1/00						
SSI	0/05	0/69**	1/00					
GMP	0/91**	0/94**	0/44*	1/00				
STI	0/87**	0/93**	0/45*	0/97**	1/00			
TOL	0/77**	0/12	-0/55**	0/44*	0/40*	1/00		
MP	0/96**	0/89**	0/32	0/99**	0/95**	0/56**	1/00	
HARM	0/85**	0/97**	0/53**	0/99**	0/96**	0/32	0/96**	1/00

conditions. **Genotypes**: 12(Capsoli), 8(Cos16), 20(WA8563-6) and 5(Caren-75).

C: Low values of first and second components. This part contains of genotypes with median seed yield in two conditions. **Genotypes:** 1 (Khomain-5), 7 (MCD4012), 10 (Goli), 13(D81083), 15 (Derakhshan), 17 (G5710), 18 (WA8528-9), 22 (WA8563-3) and 23 (11805).

D: Low values of first component and High values of second component. This part contains of genotypes with median seed yield in non-infected conditions and low seed yield in infected conditions. **Genotypes:** 2(Local Khomain), 3(Daneshjoo),
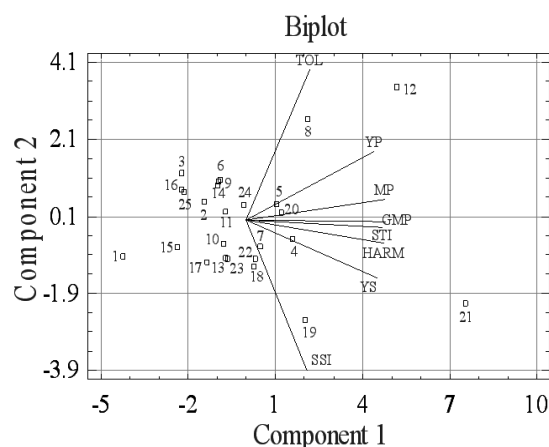
Biplot

6(Pinto), 9(Taylor), 11(Naz), 14(Sayad), 16(Akhtar), 24(Cifemcave) and 25(WA4502-1).

Fig 1 Biplot

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