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Selection of Parents through Genetic Diversity Studies for Improvement of Yield and Yield Components in Mungbean (*Vigna radiata* L. Wilczek)

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ABSTRACT

The present investigation was undertaken to select the parents through genetic divergence studies in thirty one mungbean genotypes for sixteen morpho-physiological traits by using Mahalanobis D^2 statistic. The genotypes were grouped into ten clusters. Cluster one was largest with nineteen genotypes followed by cluster II with four genotypes. The clusters III, IV, V, VI, VII, VIII, IX and X possessed one genotype each. Cluster I had maximum intra-cluster distance while inter-cluster distance was highest between clusters VII and X. Based on mean performance and divergence studies it was concluded that, hybridization between genotypes belonging to different clusters *viz.,* PUSA VISHAL x EC 396117 (cluster VII x cluster X), ASHA x EC 396117 (cluster III x cluster X), LGG 450 x EC 396117 (cluster I x cluster X), KM 122 x EC 396117 (cluster I x cluster X), MGG 347 x EC 396117 (cluster I x cluster X) and MGG 295 x EC 396117 (cluster VI x cluster X) could be suggested for the exploitation of transgressive segregants for both yield as well as yield components. Chlorophyll content contributed relatively maximum towards genetic divergence followed by relative injury, days to 50% flowering, days to maturity and seed yield.

Key words : D^2 analysis, Genetic divergence, Morpho-physiological traits, Mungbean.

Among the wide array of pulses cultivated in India, mungbean holds key position and has established itself as highly valuable short duration crop having many desirable characters like high protein content, wider adoptability, low input requirement and ability to improve soil fertility by fixing the atmospheric nitrogen in symbiotic association with rhizobium bacteria. However, the productivity in mungbean is being hampered by different biotic and abiotic stresses. Among which drought could be considered as the major one. Hence, there is an immediate need to breed the mungbean cultivars with high yield and drought tolerance. To initiate the improvement programme with the existing mungbean varieties, the selection of suitable diverse parents for hybridization is an important step for getting desired recombinants in the segregating generations. The availability of transgressive segregants in any breeding programme depends upon the diversity between the parents involved (Gupta and Singh, 1970). Multivariate analysis by means of Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence at genotypic level. The D^2 analysis classifies the genotypes into homogeneous groups or clusters with the little diversity within cluster while, diversity between two clusters is usually high. Thus, representative genotypes from diverse clusters can be earmarked for utilization in hybridization programme depending upon breeding objective. Therefore the present investigation was planned to assess the genetic divergence among thirty one genotypes of mungbean considering sixteen morpho-physiological traits to develop varieties with high yield and yield components.

MATERIAL AND METHODS

The experimental material for the present investigation consisted of thirty one mungbean genotypes obtained from Regional Agricultural Research Station, Lam, Guntur and Agricultural Research Station, Madira. The experiment was conducted in randomized block design (RBD) with three replications during *rabi,* 2013-14 at wet land farm, Sri Venkateswara Agricultural College, Tirupati. The inter and intra- row spacing adapted was 30cm x 10cm. Each genotype was sown in three rows of 3m length and observations were recorded on five randomly selected plants without border effect of each genotype in each replication for characters *viz.,* plant height (cm), number of clusters per plant, number of pods per cluster,

Table 1. Cluster composition of thirty one mungbean genotypes.

Cluster No.	No. of genotypes	Genotypes
I	19	AKM 9904, LGG 460, GIVT 203, PM 110, COGG 974, KM 122, LGG 410, TM 96-2, MGG 347, PUSA 9531, MH-3-18, LGG 528, LGG 407, WGG 37, RMG 492, KM-8-657, VG-6197A, LGG 450, WGG 2
II	4	TLM 7, VG-7098A, MH 565, IPM-02-19
III	1	ASHA
IV	1	ML 267
V	1	MGG 350
VI	1	MGG 295
VII	1	PUSA VISHAL
VIII	1	ML 145
IX	1	IPM-02-03
X	1	EC 396117

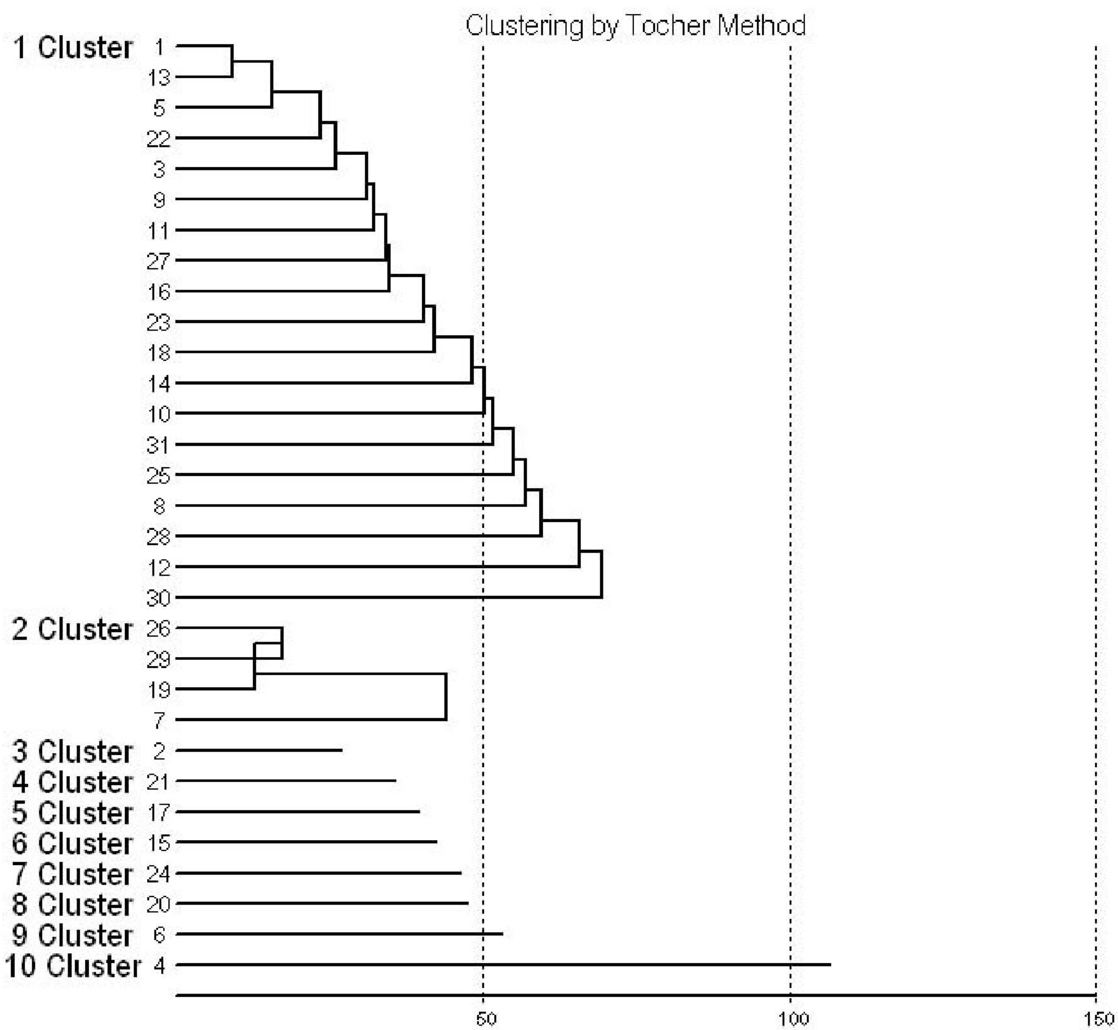

Fig 1. Dendrogram of thirty one mungbean genotypes obtained through Tocher's method of classification.

Table 2. Intra cluster (diagonal) and inter-cluster distances for ten clusters in mungbean.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	ClusterIX	ClusterX
Cluster I	54.81 (7.40)	108.24 (10.40)	83.15 (9.12)	96.34 (9.82)	76.96 (8.77)	77.50 (8.80)	83.69 (9.15)	89.56 (9.46)	106.17 (10.30)	272.85 (16.52)
Cluster II		38.95 (6.24)	180.24 (13.43)	102.52 (10.13)	101.28 (10.06)	87.92 (9.38)	108.94 (10.44)	97.17 (9.86)	98.82 (9.94)	149.32 (12.22)
Cluster III			0.00 (0.00)	146.38 (12.10)	104.26 (10.21)	103.18 (10.16)	98.57 (9.93)	83.68 (9.15)	108.65 (10.42)	282.40 (16.80)
Cluster IV				0.00 (0.00)	91.38 (9.56)	146.54 (12.11)	128.75 (11.35)	186.65 (13.66)	61.54 (7.84)	241.70 (15.55)
Cluster V					0.00 (0.00)	98.44 (9.92)	118.63 (10.89)	67.14 (8.19)	106.87 (10.34)	227.43 (15.08)
Cluster VI						0.00 (0.00)	139.16 (11.80)	80.96 (9.00)	102.44 (10.12)	258.21 (16.07)
Cluster VII							0.00 (0.00)	87.77 (9.37)	153.68 (12.40)	287.03 (16.94)
Cluster VIII								0.00 (0.00)	148.11 (12.17)	202.85 (14.24)
Cluster IX									0.00 (0.00)	184.34 (13.58)
Cluster X										0.00 (0.00)

Table 3. Contribution of different quantitative characters to diversity in mungbean.

S. No.	Character	Times ranked first	Contribution (%)
1.	Days to 50% flowering	63	13.55%
2.	Days to maturity	32	6.88%
3.	Plant height (cm)	13	2.80%
4.	No. of clusters/ plant	20	4.30%
5.	No. of pods/ cluster	2	0.43%
6.	No. of pods/ plant	0	0.00%
7.	No. of seeds/ pod	3	0.65%
8.	100 seed weight (g)	30	6.45%
9.	Harvest index (%)	20	4.30%
10.	SCMR	2	0.43%
11.	Relative Water Content (%)	20	4.30%
12.	Relative Injury (%)	90	19.35%
13.	CSI	26	5.59%
14.	Specific leaf area (cm^2 g^{-1})	17	3.66%
15.	Chlorophyll content (mg g^{-1})	96	20.65%
16.	Seed Yield (g)	31	6.67%

Table 4. Mean performance of the clusters with respect to different characters

Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of clusters/ plant	No. of pods/ cluster	No. of pods/ plant	No. of Seeds/ pod	100 seed weight (g)	Harvest Index (%)	SCMR	RWC (%)	Relative injury (%)	Chloro-phyll Stability index	Specific leaf area (cm^2 g^{-1})	Chloro-phyll content	Seed yield/ plant (g)
Cluster I	37.21	62.39	51.29	9.19	3.40	30.85	12.03	3.83	43.40	51.95	85.97	67.05	62.05	183.39	2.42	10.12
Cluster II	32.83	58.25	41.62	7.02	3.45	24.27	11.28	4.12	45.48	49.07	85.76	73.12	68.50	191.01	1.86	8.46
Cluster III	39.00	63.00	48.47	7.93	3.21	25.73	11.73	3.99	39.62	52.23	84.71	38.17	52.98	140.26	2.42	8.47
Cluster IV	33.67	63.33	42.33	8.53	3.49	29.67	12.93	3.68	45.84	53.97	83.04	72.59	54.37	166.24	3.22	9.18
Cluster V	35.00	64.00	52.47	11.40	3.12	35.60	12.00	3.74	44.57	55.20	79.26	60.02	76.08	176.01	2.10	10.76
Cluster VI	38.67	60.00	43.93	8.67	2.85	27.53	11.90	3.93	46.88	50.77	83.36	69.32	70.38	156.74	1.58	9.27
Cluster VII	36.00	60.33	55.00	7.13	3.48	27.13	11.43	3.54	36.15	45.53	81.43	55.70	64.10	218.42	2.53	6.86
Cluster VIII	34.67	60.00	48.53	9.27	3.43	31.20	11.77	3.88	39.31	51.83	86.90	52.14	69.89	175.41	1.12	9.60
Cluster IX	32.67	57.33	43.33	8.20	3.41	27.47	12.60	4.08	46.45	54.63	88.07	54.47	61.82	123.40	2.98	9.02
Cluster X	31.00	56.67	33.93	6.20	3.48	20.07	11.07	6.35	41.99	55.57	90.39	64.79	61.29	153.14	1.68	8.35

number of pods per plant, number of seeds per pod, hundred seed weight (g), harvest index (%), SPAD Chlorophyll Meter Reading (SCMR), relative water content (%), relative injury (%), chlorophyll stability index, specific leaf area (cm^2 g^{-1}), chlorophyll content (mg g^{-1}) and seed yield per plant (g). However, the data for days to 50% flowering and days to maturity were recorded on plot basis. The data were statistically analyzed to study the diversity by Mahalanobis D^2 statistic as per the method suggested by Mahalanobis (1936) and the genotypes were grouped into different clusters by following Tocher's method as suggested by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) showed significant differences among the genotypes for all the characters which revealed the presence of notable genetic variability among 31 mungbean genotypes. Then these data were used for genetic diversity analysis. The estimated V-statistics was also found significant. Based on the D^2 analysis, all the genotypes were grouped into ten different clusters (Table 1 and Fig. 1). Cluster I was the largest with 19 genotypes and cluster II had four genotypes. The clusters III, IV, V, VI, VII, VIII, IX and X possessed one genotype each *i.e.* mono-genotypic clusters. Clustering pattern indicated that the genotypes originating from different geographical regions grouped together into different clusters showing no parallelism between genetic diversity and geographical distribution. Similar findings were also reported by Gupta and Singh (1970), Natarajan *et al.* (1988), Naidu and Satyanarayana (1991) and Raje and Rao (2001). This implies that the seletion of parents for hybridization based on geographical origin would be arbitrary.

The intra-cluster distance was minimum for cluster II (38.95) and maximum for cluster I (54.81), while it was zero for cluster III, cluster IV, cluster V, cluster VI, cluster VII, cluster VIII, cluster IX and cluster X as these clusters consisted of only single genotype (Table 2). The highest intra-cluster distance in cluster I indicates the presence of considerable genetic diversity among the nineteen genotypes within the cluster. The inter-cluster distance was minimum between cluster IV and IX (61.54) followed by cluster V and VIII (67.14), cluster I and V (76.96) and cluster I and VI (77.50), indicating a close relationship and similar magnitude for most of the characters of the genotypes in these

Table 5. Mean performance of thirty one genotypes of mungbean for sixteen characters

Sl. No.	Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of clusters/ plant	No. of pods/ cluster	No. of pods/ plant	No. of Seeds/ pod	100 seed weight (g)	Harvest Index (%)	SCMR	RWC (%)	Relative injury (%)	Chlorophyll Stability index	Specific leaf area ($cm^2 g^{-1}$)	Chlorophyll content	Seed yield/ plant (g)
1.	AKM 9904	40.67	64.67	47.40	10.67	3.11	32.73	12.47	3.75	42.39	51.20	87.92	67.37	63.61	188.77	2.40	10.70
2.	Asha	39.00	63.00	48.47	7.93	3.21	25.73	11.73	3.99	39.62	52.23	84.71	38.17	52.98	140.26	2.42	8.47
3.	COGG 974	36.67	62.00	56.67	8.20	3.19	26.00	11.87	3.89	42.58	53.40	86.76	62.87	62.40	198.57	2.91	8.76
4.	EC 396117	31.00	56.67	33.93	6.20	3.48	20.07	11.07	6.34	41.99	55.57	90.39	64.79	61.29	153.14	1.68	8.35
5.	GIVT 203	36.67	63.67	57.07	9.87	3.32	33.00	11.83	3.56	43.76	51.77	84.40	60.22	58.20	182.38	2.28	10.94
6.	IPM- 02-03	32.67	57.33	43.33	8.20	3.41	27.47	12.60	4.08	46.45	54.63	88.07	54.48	61.82	123.41	2.98	9.02
7.	IPM- 02-19	33.00	57.67	47.13	6.00	3.30	20.60	11.53	4.40	44.85	51.67	87.70	51.25	61.00	194.96	2.20	7.82
8.	KM- 8-657	34.67	59.67	53.93	7.93	3.21	25.47	11.57	3.82	43.95	50.97	83.26	50.55	56.51	179.09	3.21	9.04
9.	KM 122	36.67	62.00	52.60	10.87	3.69	39.60	12.37	3.48	41.48	51.43	88.07	70.48	60.39	191.61	2.18	12.39
10.	LGG 407	36.33	61.67	46.87	10.07	3.16	31.87	12.10	3.79	43.35	50.17	86.64	85.39	71.46	183.24	2.40	9.86
11.	LGG 410	39.33	62.00	52.73	9.20	3.45	31.60	11.90	3.98	42.47	51.07	87.36	69.60	54.95	152.63	2.41	9.77
12.	LGG 450	39.67	65.67	49.20	12.00	3.87	43.53	12.80	3.61	44.85	50.17	86.60	62.40	69.04	208.84	2.28	14.02
13.	LGG 460	40.00	65.00	51.80	8.87	3.19	28.33	11.93	3.79	45.08	52.87	86.65	68.12	64.29	178.75	2.53	10.32
14.	LGG 528	36.33	62.33	57.13	9.07	3.17	28.67	12.13	3.94	45.54	53.50	81.73	64.76	55.53	163.19	3.07	9.60
15.	MGG 295	38.67	60.00	43.93	8.67	2.85	27.53	11.90	3.93	46.88	50.77	83.36	69.32	70.38	156.74	1.58	9.27
16.	MGG 347	37.33	61.67	49.27	8.40	3.43	28.80	12.43	4.01	42.42	54.77	88.74	50.53	54.50	156.61	2.55	8.80
17.	MGG 350	35.00	64.00	52.47	11.40	3.13	35.60	12.00	3.74	44.57	55.20	79.26	60.02	76.08	176.01	2.10	10.76
18.	MH-3-18	39.00	62.00	48.07	8.73	3.32	29.00	11.37	3.95	43.40	54.70	86.45	72.55	52.72	172.86	1.60	9.79
19.	MH 565	33.33	58.67	33.07	7.13	3.58	25.20	11.17	4.00	45.66	46.80	88.74	83.35	72.05	205.77	1.61	8.03
20.	ML 145	34.67	60.00	48.53	9.27	3.43	31.20	11.77	3.88	39.31	51.83	86.89	52.14	69.89	175.41	1.12	9.60
21.	ML 267	33.67	63.33	42.33	8.53	3.49	29.67	12.93	3.68	45.84	53.97	83.04	72.59	54.37	166.24	3.22	9.18
22.	PM 110	38.67	61.67	46.07	7.87	3.70	28.33	11.73	4.03	44.76	49.23	85.95	74.37	71.73	196.41	2.29	10.50
23.	PUSA 9531	36.00	62.33	53.67	9.73	3.17	30.40	11.07	3.46	41.57	52.13	85.65	56.99	38.87	184.23	2.54	9.34
24.	PUSA VISHAL	36.00	60.33	55.00	7.13	3.48	27.13	11.43	3.54	36.15	45.53	81.43	55.70	64.10	218.42	2.53	6.87
25.	RMG 492	34.33	59.67	46.33	7.67	3.80	29.20	11.63	3.60	44.41	51.20	87.44	78.19	74.35	185.52	2.27	9.88
26.	TLM 7	32.33	58.00	41.40	7.93	3.44	27.00	11.40	4.24	47.00	49.67	81.44	87.57	71.14	185.57	1.77	10.09
27.	TM 96-2	37.67	59.33	49.80	10.60	3.02	32.00	12.13	4.17	44.03	53.07	84.73	56.60	60.91	188.27	1.97	10.93
28.	VG-6197A	34.67	59.67	49.67	8.47	3.85	30.20	12.43	4.09	44.56	48.70	83.74	83.54	67.49	198.01	2.12	10.02
29.	VG-7098A	32.67	58.67	44.87	7.00	3.47	24.27	11.00	3.83	44.80	48.13	85.15	70.31	69.81	177.73	1.89	7.89
30.	WGG 2	35.67	66.67	54.07	7.93	3.24	25.53	12.63	3.89	40.63	55.83	92.21	73.47	66.89	171.50	2.49	7.78
31.	WGG 37	36.67	63.67	52.20	8.47	3.78	31.93	12.20	3.95	43.46	50.97	79.11	65.95	75.15	203.86	2.49	9.81
	General Mean	36.10	61.39	48.68	8.71	3.39	29.28	11.91	3.95	43.48	51.71	85.60	65.60	63.35	179.29	2.29	9.60
	CD at 5%	1.80	2.39	6.94	1.76	0.49	5.32	0.98	0.44	2.91	4.02	4.87	9.78	8.78	25.11	0.37	1.82
	CD at 1%	2.39	3.17	9.21	2.33	0.65	7.06	1.30	0.58	3.86	5.34	6.46	12.97	11.65	33.31	0.49	2.42
	C.V.(%)	3.05	2.38	8.71	12.31	8.86	11.10	5.05	6.80	4.09	4.75	3.47	9.10	8.47	8.55	9.91	11.58

clusters. The maximum inter-cluster distance was recorded between cluster VII and X (287.03) followed by cluster III and X (282.40), cluster I and X (272.85) and cluster VI and X (258.21) suggesting highest genetic divergence existing among the genotypes of these clusters and expected to give higher frequency of better transgressive segregants for high yield and drought tolerance. The inter-cluster distances were higher than the intra-cluster distances which indicate the existence of substantial diversity among the parents. Similar results were also reported by Gupta and Singh (1970) and Natarajan *et al.* (1988).

The selection and choice of parents mainly depend upon contribution of characters towards divergence. Apart from the divergence, the performance of genotypes and the character with maximum contribution towards divergence should also be given due consideration which appear as desirable for improvement. In the present study, it was observed that among all the traits, chlorophyll content (20.65%) contributed relatively maximum to genetic divergence followed by relative injury (19.35), days to 50% flowering (13.55%), days to maturity (6.88%) and seed yield (6.67%) (Table 3). Similar results were also reported by Natarajan *et al.* (1988) for days to 50% flowering; Laxmi Prasanna *et al.* (2013) for days to maturity and seed yield and Swathi (2013) for relative injury.

The cluster means of different characters help the breeder to know the performance of genotypes with better mean performance against cluster means. The cluster means for each of the sixteen characters were presented in Table 4. Considerable differences between clusters means were observed for most of the characters studied. Cluster means indicated that none of the clusters was superior for all the characters studied. Therefore, hybridization between genotypes belonging to different clusters could be suggested for development of superior genotypes.

Based on the diversity studies using the present material, maximum diversity was observed between cluster VII and X (287.03) followed by cluster III and X (282.40), cluster I and X (272.85) and cluster VI and X (258.21). Hence, to initiate breeding programme aimed for improving yield and yield components the crossing programme could be suggested between PUSA VISHAL x EC 396117 (cluster VII x cluster X), ASHA x EC 396117 (cluster III x cluster X), LGG 450 x EC 396117 (cluster I x cluster X), KM 122 x EC 396117 (cluster I x cluster X), MGG 347 x EC 396117 (cluster I x cluster X) and MGG 295 x EC 396117 (cluster VI x cluster X) for the exploitation of transgressive segregants for yield and yield components. Though, nineteen genotypes were there in the cluster I, based on mean performance for yield and yield components (Table 5) the genotypes LGG 450, KM 122, GIVT 203 and MGG 350 were showed superior performance not only for yield but also for other yield components *viz.,* pods per plant, pods per cluster, clusters per plant and seeds per pod. Hence, these genotypes were considered for yield and yield components improvement. Similarly, for improving yield as well as water use efficiency, the genotypes MGG 347, EC 396117, MGG 350, IPM-02-03 and ASHA were considered, as these genotypes were not only good in yield and yield components but also found better performance for SLA and SCMR (Table 5). Hence, the crosses from diversified clusters *viz.,* PUSA VISHAL x EC 396117 (cluster VII x cluster X), ASHA x EC 396117 (cluster III x cluster X), LGG 450 x EC 396117 (cluster I x cluster X), KM 122 x EC 396117 (cluster I x cluster X), MGG 347 x EC 396117 (cluster I x cluster X) and MGG 295 x EC 396117 (cluster VI x cluster X) could be suggested for the exploitation of transgressive segregants for yield coupled with water use efficiency.

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