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# Selecting Parents for Hybridization with Multivariate Analysis Approach to Improve Country Bean (*Dolichos lablab* L.) Yield

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### A b s t r a c t

Twenty-six genotypes of Country bean (*Dolichos lablab* L.) were evaluated using $D^2$ and principal component analysis (PCA). The genotypes were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur. The study was undertaken at Sher-e-Bangla Agricultural University Farm, Dhaka to select suitable donor parents for improved breeding of Country bean. Principal component analysis (PCA) revealed that the first two axes accounted for 66.72% of the total variation among the fourteen characters studied. The highest intra-cluster distance was found in cluster IV and the lowest in cluster I. Among five clusters, the highest inter-cluster distance was observed between cluster I and cluster II and the lowest between cluster III and cluster IV. Considering all the characters the G7 (BD-8832), G6 (BD-7985), G13 (BD-8034) and G26 (BD-8816) were selected for future breeding programme.

**Keyword:** Country bean, principal component analysis, Principal coordinates analysis and genotypes.

## Introduction

Lablab bean [*Dolichos lablab* L. (Sweet)], commonly known as 'Seem' or Country bean, hyacinth bean, is an indigenous vegetable of Indo-Bangladesh region (Ahmed, 1976). It is a self-pollinated crop and belongs to the family leguminosae, sub-family papilionaceae. This crop is grown in a few countries like Bangladesh, India, Philippines, Malaysia, Japan, Egypt and Sudan. Some people believe that this crop is originated in Africa (Mozumder *et al.,* 1996).

The present nutritional situation of Bangladesh is a matter of great concern. The prime nutritional problem of the country is that of protein-energy malnutrition. Most of our people are suffering from malnutrition. There are two sources of protein, viz. animal and plant protein. Leguminous crops play an important role to meet up the protein deficiency problem. Pulses and bean contain 20-30% protein on a dry weight basis which is nearly three times that in most cereals. Vegetables can play an important role in human nutrition. It is of economic importance for seed and pod in Bangladesh. It is a nutritional vegetable. Its green pods provide good amount of protein in addition to vitamins and minerals (Gopalan *et al.*, 1982). One hundred grams of young pods contain

83% water, 4.50 g protein, 10.00 g carbohydrate, 1.00 g fat, 2.00 g fiber, 0.05 mg thiamine, 0.01 mg riboflavin and little amount of vitamin C. The dry seed contains 8% water, 25.00 g protein. 60.00 g carbohydrate, 0.80 g fat, 1.40 g fiber, 100 IU of vitamin A, 0.50 mg thiamine, 0.10 mg riboflavin, 1.80 mg niacin and slight amount of vitamin C (Mozumder *et al.,* 1996). In Bangladesh India and some other countries, the young pods developed unripe seeds are used as vegetables and the ripe seeds are used as pulse. Both the pod and seeds are delicious and are liked by all Bangladeshi people. This crop has the potential to reducing the protein deficiency of our people (Main, 1989). People, in Bangladesh consume 104 g vegetable per head per day (Anonymous, 1991) but the minimum requirement is 200 g (Mozumder *et al.,* 1996). Massive production of country bean can fulfill the minimum requirement of vegetables and also the protein requirement. It is grown on approximately 25910 ha across the country during the winter season, yielding an average of 8.85 t of fresh pods per ha for a total yield of about 228000 t (BBS 2023). It is comparatively lower than other developed country and the main reason behind this are use of low yielding local indigenous cultivars, unavailability of locally developed high yielding variety and low management

practices. So important objective of country beans breeding programs in Bangladesh and other countries should be to increasing the genetic potential of yield, tolerance to biotic and abiotic stress.

There are several cultivars of country bean which are traditionally cultivated in our country but there is no recommended variety. Farmers cultivate the country bean from their own seeds. Therefore, it is necessary to develop superior varieties of country bean for commercial cultivation in our country. So, improvement of the crop is urgent now for our agriculture. Hybridization is one of the major tools for achieving variability aiming at the improvement of a crop. Genetic diversity is a useful tool in quantifying the degree of divergence in a biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra and inter-cluster levels (Jatasara and Paroda, 1978). Cluster analysis is also carried out to detect divergent parents for hybridization purposes and to attain meaningful group constellations of a collection of genotypes. Considering the availability of genetic variability, its scope of yield improvement and export potential, the present investigation was undertaken to search suitable diverse germplasm as suitable parents for future breeding program of country bean.

## Materials and Methods

The investigation was carried out at the experimental field (23°77'N latitude and 90°33'E longitude: altitude was 8.6 meter above the sea level) of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28. Twenty-six genotypes of Country beans were used for the present research work. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur. (Table 1). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The genotypes were distributed into the pit of each block of the prepared layout of the experiment. The Twenty-six genotypes of the experiment were assigned at random into pits of each replication. The distance maintained spacing pit to pit 3 m. The distance maintained between blocks was 1 m.

**Table 1.** Name and origin of twenty-six genotypes of country bean used in the present study.

| Sl.No. | Genotypes No. | BARI ACC Number | Origin |
|---|---|---|---|
| 1 | G1 | BD-8737 | PGRC, BARI |
| 2 | G2 | BD-1816 | PGRC, BARI |
| 3 | G3 | BD-808 | PGRC, BARI |
| 4 | G4 | BD-8312 | PGRC, BARI |
| 5 | G5 | BD-7978 | PGRC, BARI |
| 6 | G6 | BD-7985 | PGRC, BARI |
| 7 | G7 | BD-8832 | PGRC, BARI |
| 8 | G8 | BD-1805 | PGRC, BARI |
| 9 | G9 | BD-7995 | PGRC, BARI |
| 10 | G10 | BD-7977 | PGRC, BARI |
| 11 | G11 | BD-7998 | PGRC, BARI |
| 12 | G12 | BD-113 | PGRC, BARI |
| 13 | G13 | BD-8034 | PGRC, BARI |
| 14 | G14 | BD-130 | PGRC, BARI |
| 15 | G15 | BD-7999 | PGRC, BARI |
| 16 | G16 | BD-8027 | PGRC, BARI |
| 17 | G17 | BD-137 | PGRC, BARI |
| 18 | G18 | BD-8001 | PGRC, BARI |
| 19 | G19 | BD-1830 | PGRC, BARI |
| 20 | G20 | BD-132 | PGRC, BARI |
| 21 | G21 | BD-1809 | PGRC, BARI |
| 22 | G22 | BD-8729 | PGRC, BARI |
| 23 | G23 | BD-8813 | PGRC, BARI |
| 24 | G24 | BD-7988 | PGRC, BARI |
| 25 | G25 | BD-6 | PGRC, BARI |
| 26 | G26 | BD-8816 | PGRC, BARI |

Here, PGRC = Plant Genetic Resources Centre, BARI = Bangladesh Agricultural Research Institute

Data were recorded on Inflorescence characteristics (Days to first flowering, Days to first fruiting, Number of inflorescence per plant, Number of flower per inflorescence, Number of pod per inflorescence, Inflorescence length) and Fruit characteristics **(**Pod length (cm), Pod breadth (cm), Pod weight (g), Seed length (mm), Seed width (mm), Number of pod per plant, Pod yield per plant (g)). The genetic diversity among the genotypes was assessed by general distance ($D^2$) statistic and its auxiliary analyses. The parent's selection in hybridization programme based on Mahalanobis's $D^2$ statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Data were subjected to both univariate and multivariate analysis. Under multivariate analysis Principal Component Analysis (PCO), Principal Coordinate Analysis (PCA), Cluster Analysis (CA) and Canonical Vector Analysis were done by using GENSTAT 5.5 program.

## Results and Discussions
### Principal component analysis (PCA)

Analysis of variance showed significant variations among the tested genotypes for all the characters studied indicating a wide genotypic variation among the genotypes. The principal component analysis produced first three Eigen values of principal component axes for coordination of genotypes in which the first two axes accounted for 66.72% of the total variation (Table 2). On the basis of principal axes I and II, a two dimension chart (Z1-Z2) of the genotypes are presented in Figure 1. As per the scattered diagram the genotypes were apparently distributed into five clusters.
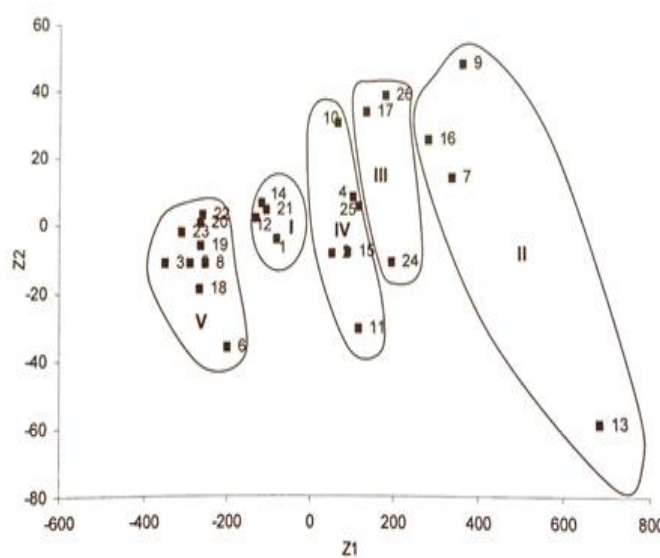


**Figure 1.** Scattered diagram of twenty-six country bean genotypes superimpose cluster.

**Table 2.** Eigen values and present contribution of 13 yield contributing characters of twenty-six country bean genotype.

| Characters | Eigen value | % contribution | Cumulative variation |
|---|---|---|---|
| Days to 1st flowering | 5.340 | 31.02 | 31.02 |
| Days to 1st fruiting | 3.414 | 19.83 | 50.85 |
| No. of inflorescence/plant | 2.733 | 15.87 | 66.72 |
| No. of flower/ Inflorercence | 2.204 | 12.80 | 79.52 |
| No. of pod/ Inflorercence | 1.169 | 6.79 | 86.31 |
| Inflorercence length (cm) | 1.013 | 5.89 | 92.20 |
| Pod length (cm) | 0.502 | 2.92 | 95.12 |
| Pod width (cm) | 0.406 | 2.36 | 97.48 |
| Pod weight (g/pod) | 0.231 | 1.34 | 98.82 |
| Seed length (mm) | 0.129 | 0.75 | 99.57 |
| Seed width (mm) | 0.047 | 0.27 | 99.84 |
| No. of pods/plant | 0.028 | 0.16 | 100.00 |
| Pods yield/plant (g) | 0.000 | 0.00 | 100.00 |

**Principal coordinates analysis (PCO)**

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotypes G3 and G13 (2.108) followed by G13 and G22 (1.958) and the lowest distance was observed (0.387) between genotypes G12 and G18 followed by the distance (0.391) between genotypes G4 and G17 (Table 3). The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 26 genotypes of country bean. The highest intra-cluster distance was recorded in cluster IV (1.091) containing six genotypes BD-1816, BD-8312, BD-7977, BD-7998, BD-7999, BD-6. The lowest intra-cluster distance was observed in cluster 1 (0.85) having four genotypes viz. BD- 8737 and BD-113, BD-130 and BD-1809. It favored to decide that intra-group diversity was the highest in cluster IV and the lowest in cluster I. Cluster II having four genotypes viz. BD-8832, BD-7995, BD-8034, BD-8027 and had an intra-cluster distance 1.066. Cluster III having three genotypes viz. BD-137, BD-7988, BD-8816 and had an intra-cluster distance 0.945. The cluster V consisted nine genotypes viz. BD-808, BD-7978, BD-7985, BD-1805, BD-8001, BD-1830, BD-132, BD-8729, BD- 8813 and had the intra-cluster distance 0.979 (Table 4).

**Table 3.** Ten highest and ten lowest inter genotypic distance among the twenty-six country bean genotypes.

| Sl. No. | Genotypic combination | Distances |
|---|---|---|
| | *A. 10 highest inter genotypic distance* | |
| 1 | BD-8034 - BD-808 (G$_{13}$ – G$_3$) | 2.108 |
| 2 | BD-8729 - BD-8034 (G$_{22}$ – G$_{13}$) | 1.958 |
| 3 | BD-6 - BD-1809 (G$_{25}$ – G$_{21}$) | 1.914 |
| 4 | BD-8832 - BD-808 (G$_7$ – G$_3$) | 1.910 |
| 5 | BD-6 - BD-7985 (G$_{25}$ – G$_6$) | 1.861 |
| 6 | BD-132 - BD-8034 (G$_{20}$ – G$_{13}$) | 1.859 |
| 7 | BD-8813 - BD-8034 (G$_{23}$ – G$_{13}$) | 1.849 |
| 8 | BD-7995-BD-808 (G$_9$ – G$_3$) | 1.835 |
| 9 | BD-6 - BD-808 (G$_{25}$ – G$_3$) | 1.806 |
| 10 | BD-7977-BD-7985 (G$_{10}$ – G$_6$) | 1.804 |
| | *B. 10 lowest inter genotypic distance* | |
| 1 | BD-8001 - BD-113 (G$_{18}$ – G$_{12}$) | 0.387 |
| 2 | BD-137-BD-8312 (G$_{17}$ – G$_4$) | 0.391 |
| 3 | BD-8813-BD-132 (G$_{23}$ – G$_{20}$) | 0.395 |
| 4 | BD-1830-BD-113 (G$_{19}$ – G$_{12}$) | 0.418 |
| 5 | BD-8729-BD-808 (G$_{22}$ – G$_3$) | 0.456 |
| 6 | BD-8813-BD-1830 (G$_{23}$ – G$_{19}$) | 0.462 |
| 7 | BD-113-BD-8312 (G$_{12}$ – G$_4$) | 0.476 |
| 8 | BD-8027-BD-7999 (G$_{16}$ – G$_{15}$) | 0.487 |
| 9 | BD-7999-BD-8312 (G$_{15}$ – G$_4$) | 0.495 |
| 10 | BD-1830-BD-7978 (G$_{19}$ – G$_5$) | 0.515 |

**Table 4.** Distribution of twenty-six country bean genotypes in five clusters.

| Cluster | Members | No. of genotypes | Designation |
|---|---|---|---|
| 1 | 4 | 1, 12, 14, 21 | BD-8737, BD-113, BD-130, BD-1809 |
| 2 | 4 | 7, 9, 13, 16 | BD-8832, BD-7995, 8034, BD-8027 |
| 3 | 3 | 17, 24, 26 | BD-BD-137, BD-7988, BD-8816 |
| 4 | 6 | 2, 4, 10, 11, 15, 25 | BD-1816, BD-8312, BD- 7977, BD-7998, BD-7999, BD-6 |
| 5 | 9 | 3, 5, 6, 8, 18, 19, 20, 22, 23 | BD-808, BD-7978, BD-7985, BD-1805, BD-8001, BD- 1830, BD-132, BD-8729, BD-8813 |

**Non-hierarchical clustering**

The computations from covariance matrix gave non-hierarchical clustering among twenty-six genotypes of country bean and grouped them into five clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. Table 4 represents the clusters occupied by 26 genotypes of country bean. It explains that cluster V contained the highest number of genotypes nine, cluster IV constitute by six genotypes, cluster III constitute by three genotypes and cluster II constitute by four genotypes and cluster I having four genotypes. Cluster V was composed of BD-808, BD-7978, BD-7985, BD-1805, BD-8001, BD-1830, BD-132, BD-8729, BD-8813.The genotypes of cluster V are collected from Plant Genetic Resource Centre, BARI, Gazipur. Cluster mean for 13 traits are presented in (Table 5). From the Table 5, it was observed that the mean value of cluster V ranked first for pod width (3.07). Among 13 characters cluster III produced the maximum cluster mean for the five characters viz. inflorescence length (31.67), pod length (10.67), pod weight (8.15), seed length (13.05) and seed width (9.32). Similarly, cluster I ranked the first for days to first flowering (54.25), days to first fruiting (65.75). Cluster II had the highest cluster mean value was achieved for three characters viz. inflorescence per plant (37.50), pods per plant (171.50), pod yield per plant (1297.99).

**Table 5.** Cluster mean of 13 characters of twenty six country bean genotypes.

| Characters | I | II | III | IV | V |
|---|---|---|---|---|---|
| Days to 1st flowering | 54.25 | 46.25 | 46.00 | 51.50 | 50.22 |
| Days to 1st fruiting | 65.75 | 59.50 | 52.00 | 61.67 | 59.33 |
| No. of Inflorercence/plant | 28.00 | 37.50 | 29.00 | 28.00 | 27.22 |
| No. of flower/ Inflorercence | 9.00 | 10.25 | 11.00 | 12.00 | 11.67 |
| No. of pod/ Inflorercence | 5.00 | 7.00 | 7.67 | 8.17 | 7.89 |
| Inflorercence length (cm) | 25.85 | 21.00 | 31.67 | 20.43 | 27.11 |
| Pod length (cm) | 9.60 | 10.25 | 10.67 | 9.60 | 7.13 |
| Pod width (cm) | 2.40 | 1.83 | 2.50 | 2.18 | 3.07 |
| Pod weight (g/pod) | 6.44 | 7.97 | 8.15 | 6.88 | 5.31 |
| Seed length (mm) | 12.56 | 12.26 | 13.05 | 12.58 | 11.36 |
| Seed width (mm) | 8.36 | 8.11 | 9.32 | 8.96 | 8.80 |
| No. of pods/plant | 125.75 | 171.50 | 137.00 | 149.67 | 121.44 |
| Pods yield/plant (g) | 808.47 | 1297.99 | 1087.3 | 1011.45 | 640.68 |

## Canonical variate analysis

Canonical variate analysis was done to compute the inter-cluster Mahalanobis's D² values. Statistical distances represent the index of genetic diversity among the clusters. The highest inter-cluster distance was observed (Table 6 and Figure 2) between cluster II and cluster V (43.76) followed by between cluster I and cluster II (33.12) and between cluster III and cluster V (30.05). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum of segregating population if parents chosen from these distant clusters are used for hybridization program. However, the highest inter-cluster distance was observed between clusters II and V indicated the genotypes in these clusters were far diverged than those of other clusters. Similarly, the lowest inter-cluster distance was observed between the cluster III and cluster IV (6.32). Moderate or intermediate distance was found between cluster II and cluster IV (19.57). On the other, the highest intra-cluster distance was found in cluster IV (1.091) followed by cluster II (1.066).
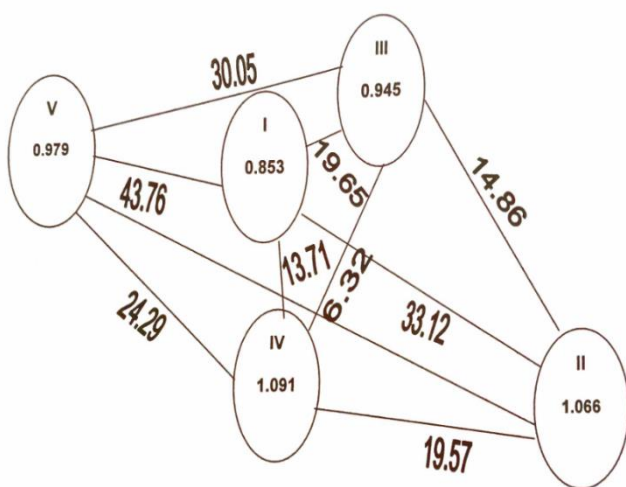


**Figure 2.** Diagram showing intra-and inter-cluster distances of twenty six genotypes of country bean.

The lowest intra-cluster distance was observed between in cluster I (0.853). The inter cluster distances were found much higher than the intra cluster distances suggesting wider genetic diversity existed among the genotype of different groups Result of different multivariate analysis were superimposed in figure 2 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another.

**Table 6.** Average intra and inter-cluster distances of 26 country bean genotypes.

| Cluster | 1 | 2 | 3 | 4 | 5 |
|---------|-----|-----|-----|-----|-----|
| 1 | **0.853** | | | | |
| 2 | 33.12 | **1.066** | | | |
| 3 | 19.65 | 14.86 | **0.945** | | |
| 4 | 13.71 | 19.57 | 6.32 | **1.091** | |
| 5 | 10.64 | 43.76 | 30.05 | 24.29 | **0.979** |

As per scatter diagram the genotypes were apparently distributed into five clusters. It was also revealed that the genotypes of cluster II were more diverse from the genotypes of cluster V. Islam *et al.* (2004) also observed the similar result. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeding, the objective is not only high heterosis but also to achieved high-level production. In the present study the maximum distance existence between cluster II and cluster V. But considering the yield and duration crosses involving cluster II and V may be exhibit high heterosis for yield. Main and Bahl (1989) reported that the parents separated by D² values of moderate magnitude generally showed higher heterosis.

## Contribution of characters towards divergence of the genotypes

The values of Vector I and Vector II are presented in Table 7. Vector I obtained from PCA expressed that days to first fruiting (0.1421), inflorescence per plant (0.1254), flower per inflorescence (0.6813), inflorescence length (0.0546), pod length (0.8505), pod weight (10.0842), seed width (0.8215), pod per plant(0.5248) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II days to first fruiting (0.1708), inflorescence per plant (0.0513), flower per inflorescence (0.2241), pod yield per plant (0.0369) showed their important role toward genetic divergence. Negative values in both vectors for days to first flowering, pod per inflorescence, pod width and seed length had lower contribution towards the divergence.

**Table 7.** Latent vectors for 13 principal component characters of twenty-six country bean genotypes.

| Characters | Vector I | Vector II |
|-----------|----------|-----------|
| Days to 1st flowering | -0.0562 | -0.1693 |
| Days to 1st fruiting | 0.1421 | 0.1708 |
| No. of Inflorescence/plant | 0.1254 | 0.0513 |
| No. of flower/ Inflorercence | 0.6813 | 0.2241 |
| No. of pod/ Inflorercence | -0.6249 | -0.2648 |
| Inflorercence length (cm) | 0.0546 | -0.0446 |
| Pod length (cm) | 0.8505 | -0.1008 |
| Pod width (cm) | -0.3666 | -0.1802 |
| Pod weight (g/pod) | 10.0842 | -5.2361 |
| Seed length (mm) | -1.4017 | -0.0122 |
| Seed width (mm) | 0.8215 | -1.5218 |
| No. of pods/plant | 0.5248 | -0.2204 |
| Pods yield/plant (g) | -0.1505 | 0.0369 |

Selection of genetically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960; Moll *et al.,* 1962; Ramanujam *et al.*, 1974; Ghaderi *et al.*, 1984, Afroz *et al.,* 2013).
Considering the magnitude of cluster mean and agronomic performance the genotype G7 (BD-8832) for minimum days of first flowering from cluster II; G26 (BD-8816) for maximum fruit length and from cluster III; G13 (BD-8034) for maximum number of fruit per plant from cluster II and fruit width G6 (BD-7985) from cluster V were found promising. Therefore, considering group distance and other agronomic performance the inter genotypic crosses between G7 (BD-8832) and G26 (BD-8816); G6 (BD-7985) and G7 (BD-8832); G6 (BD-7985) and G26 (BD-8816) may be suggested for future hybridization program.

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**Conflict of interest**

There is ano any conflict of interest among the authors.

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