Genetic Association Analysis and Selection Indices for Yield Attributing Traits in Available Chilli (Capsicum annuum L.) Genotypes

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Abstract The present investigation was conducted with 30 chilli genotypes at the experimental field of Regional Spices Research Centre, BARI, Gazipur to assess the genetic association and selection indices among yield and important yield attributing traits. Fruit length, fruit weight, 100 seed weight and fruits/plant showed significant and positive correlation with yield/plant both at genotypic and phenotypic level. Path coefficient analysis revealed that fruits/plant had maximum positive direct effect on yield. Besides fruits/plant; fruit weight, fruit length and number of primary branches/plant also contributed positive direct effect to yield. Selection indices were constructed through the discriminate functions using five characters. Highest relative efficiency was found for fruit weight +fruits/plant +yield/plant comparable to other combinations of characters. This research indicated that the selection of high yielding chilli genotypes based on these three characters might be more efficient. Biplot analysis was also performed to find out superior genotypes.

Keywords Chilli; Genotypic correlation; Path analysis; Selection index; Biplot

Introduction

Chilli (Capsicum annuum L.) (2n = 24) belongs to Solanaceae family, a dicotyledonous flowering plant grown worldwide, with different names in English, such as hot pepper, chilli pepper and bell pepper etc., (Knapp et al., 2004; Hunziker, 2001). It is one of the most popular vegetables originated from South and Central America (Bahurupe et al., 2013). It is a self-pollinated crop but 2 to 96% out-crossing was observed under open pollination (AVRDC, 2000).

Chilli is an important commercial crop all over the world. Green fruits of chilli are used as vegetable whereas ripe dried fruits as spice because of its pungency and pleasant flavors (Hasan et al., 2014). It is inseparably involved with almost every Bangladeshi cuisine and its demand is increasing day by day owing to its pungency, appealing color and flavor (Hasan et al., 2015). A rich diversity of chilli exists due to diverse geo climatic regions of Bangladesh (Hasanuzzaman and Golam, 2011).

Despite having a rich diversity, the production of chili is decreasing day by day. In Bangladesh, the total production of chilli in was 1.45 mt/ha during 2010-11, but this production was reduced to 1.3 and 1.09 mt/ha during 2011-12 and 2011-13 respectively (BBS, 2013). The lack of improved genotypes is the prime cause of low production. Assurance of production of chilli in a large scale is feasible only by means of breeding programmes.

Character association and cause effect analysis are pre-requisites for improvement of any trait of a crop through selection (Krishnaveni et al., 2006). The correlation coefficient analysis measures the interactive relationship between different traits and it resolves the component traits on which selection can be relied upon the effect of improvement (Ajjapplavara, 2005). Assessing the direct and indirect effects of each component towards yield through path coefficient analysis would help in identifying the reliable characters contributing to yield. It is too laborious to consider all the yield contributing characters at a time, hence, the breeder requires adequate
knowledge on selection index analysis. Selection indices are useful in understanding the extent of improvement that can be used in breeding programmes to improve yield by combination of characters (Basavaraj and Sheriff, 1992). This method has been successfully followed by various researchers in various crops such as Habib et al. (2007) in rice, Deb and Khaleque (2007) in chickpea, Ferdous (2010) in spring wheat, Akter et al. (2013) in rice, Sarker et al. (2013) in chickpea and Bashar et al. (2015) in eggplant.

1 Results and Discussion
1.1 Character association

The genotypic and phenotypic correlation coefficients were analyzed and presented in Table 1. Fruits per plant, fruit weight and 100 seed weight had significant and positive correlation with yield per plant both at genotypic and phenotypic level. Hence yield per plant can be improved by selecting the genotypes with more number of fruits per plant, fruit weight and 100 seed weight. The high correlation between fruits per plant and yield have been reported by several workers viz., Pandit et al. (2014), Luitel et al. (2013), Ullah et al. (2011), Jabeen et al. (2009), Islam and Singh (2009), Krishna et al. (2007). Negative correlations were found for plant height, days to first flowering, days to 50% flowering, days to fruit maturity and pedicel length with yield.

Table 1 Correlation between yield and yield components at genotypic and phenotypic level.

| Character | PB/P | SB/P | DFFL | D50%F | DFM | FD(mm) | FL(cm) | FPL(cm) | FW(gm) | F/P | 100SW | Y/P |
|-----------|------|------|------|-------|-----|--------|--------|---------|--------|-----|-------|-----|
| PH (cm)   | 0.072| 0.27 | 0.094| 0.11  | -0.142| 0.135  | -0.24  | -0.015  | -0.062 | -0.02| 0.009 | -0.128|
| PB/P      | 0.959**| 0.033| -0.053| -0.22| -0.112| -0.317*| -0.225 | -0.013  | -0.046 | -0.017| 0.006 | -0.105|
| SB/P      | 0.553**| -0.003| -0.089| -0.227| -0.089| -0.242 | -0.161 | -0.236 | 0.22   | 0.167 | 0.06  |
| DFL       | 0.868**| 0.637**| -0.26| -0.212| -0.043| -0.536**| 0.029  | -0.433**| -0.299 | 0.112 |
| D50%F     | 0.826**| 0.626**| -0.253| -0.196| -0.052| -0.507**| 0.023  | -0.412**| -0.281 | 0.121 |
| DFM       | 0.736**| -0.168| -0.374*| 0.009| -0.522**| -0.157| -0.459**| -0.409**| 0.281 |
| F         | 0.718**| -0.167| -0.322*| -0.016| -0.476**| -0.138| -0.432**| -0.362*| 0.197 |
| FD(mm)    | 0.347**| -0.346*| 0.22 | 0.033 | 0.328* | 0.296*|
| FL (cm)   | 0.474**| 0.25 | 0.028 | 0.346* | 0.342*|
| FPL (cm)  | 0.435**| 0.22 | 0.105 | -0.272 | 0.125 | -0.107|
| FW(gm)    | 0.102 | -0.225 | 0.118 | -0.072 | 0.187 | 0.458** | 0.463**|
| F/P       | 0.056| 0.691**| 0.059| 0.698**| 0.339*|
| 100SW     | 0.323*|

Note: PH= Plant height, PB/P= No. of primary branches/plant, SB/P= No. of secondary branches/plant, DFFL= Days to first flowering, D50%F= Days to 50% flowering, DFM = Days to fruit maturity, FD= Fruit diameter, FL= Fruit length, FW= Fruit weight, F/P= Fruits/plant, 100SW= 100 seed weight, Y/P= Yield/plant

** = Significant at 1% level of probability, * = Significant at 5% level of probability

1.2 Path analysis

In the present study, path analysis was worked out to find out the direct and indirect effect of 12 traits on fruit yield per plant (Table 2). Path analysis revealed that fruits per plant and fruit weight had high direct effect on yield.
hence selection can be made directly by using these characters (Figure 1). Similar result was observed by several workers Verma et al. (2014), Yatung et al. (2014), Krishnamurthy et al. (2013), Kumari et al. (2011), Sarkar et al. (2009), Farhad et al. (2008) and Kulkarni (2006). Other characters like days to first flowering, fruit diameter and fruit pedicel length had direct negative effect. Thus, increase of yield per plant through direct selection for these traits should be avoided whereas indirect selection should be more appropriate to apply. Although days to 50% flowering and days to fruit maturity showed direct positive effects on yield/plant but its genotypic and phenotypic correlation was negative indicating that these two traits would not be reliable criteria for improving yield/plant. However, high positive indirect effect of number of secondary branches/plant via number of primary branches/plant resulted in significant positive correlation with fruit yield at genotypic level. Thus, selection for the above traits can be made indirectly through number of secondary branches/plant and number of primary branches/plant.

Table 2 Path coefficient analysis (direct and indirect effect of yield component on yield at genotypic and phenotypic level)

| Character | PH(cm) | PB/P | SB/P | DFPL | DS50%F | DFM | FD(mm) | FL(cm) | FPL(cm) | FW(gm) | F/P | 100SW | Correlation with yield |
|-----------|--------|------|------|-------|--------|-----|--------|--------|---------|--------|-----|--------|-----------------------|
| PH(cm)    | 0.0905 | 0.0302 | -0.0555 | -0.0343 | 0.0481 | -0.0273 | -0.0043 | -0.1101 | 0.0023 | -0.05 | -0.0175 | 0.0005 | -0.128 |
|           | 0.0351 | 0.0033 | 0.0062 | -0.0159 | 0.0302 | -0.0038 | -0.0053 | -0.0408 | 0.0003 | -0.0302 | -0.0142 | 0.0001 | -0.105 |
| PB/P      | 0.0065 | 0.4204 | -0.197 | -0.0123 | -0.0233 | -0.0422 | 0.0335 | -0.1451 | 0.0362 | -0.2028 | 0.226 | 0.0122 | 0.082 |
|           | 0.0254 | 0.4029 | -0.2055 | 0.0098 | -0.0826 | -0.042 | 0.0553 | -0.0301 | 0.0438 | -0.0214 | 0.2412 | 0.003 | 0.349 |
| SB/P      | 0.0124 | 0.0333 | 0.0697 | 0.0033 | -0.0364 | -0.0047 | 0.0066 | -0.0004 | 0.0004 | -0.0421 | 0.0924 | -0.0003 | 0.121 |
| DFL       | 0.0085 | 0.014 | 0.0055 | -0.3672 | 0.3814 | 0.1223 | 0.0082 | -0.0969 | 0.007 | 0.4328 | 0.0252 | 0.0254 | 0.299 |
|           | 0.0034 | -0.0002 | 0.0165 | 0.2012 | 0.0187 | 0.011 | -0.0355 | 0.0012 | 0.3329 | 0.0194 | 0.0059 | -0.281 |
| D50%F     | 0.0099 | -0.0223 | 0.0387 | -0.3188 | 0.4393 | 0.1414 | 0.0053 | -0.1715 | 0.0015 | -0.4217 | 0.1347 | 0.027 | -0.409 |
|           | 0.0044 | 0.0004 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.1136 | 0.0136 | -0.3126 | 0.0854 | 0.0004 | 0.061 |
| DFM       | 0.0039 | 0.014 | 0.0002 | 0.0320 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
|           | 0.0057 | 0.0004 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
| FD(mm)    | 0.0122 | 0.0071 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
|           | 0.0013 | 0.0046 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
| FL(cm)    | 0.0057 | 0.0004 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
|           | 0.0013 | 0.0046 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
| FPL(cm)   | 0.0122 | 0.0071 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
|           | 0.0013 | 0.0046 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
| FW(gm)    | 0.0057 | 0.0004 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
|           | 0.0013 | 0.0046 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
| 100SW     | 0.0087 | 0.0004 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |
|           | 0.0013 | 0.0046 | 0.0004 | 0.0004 | 0.0004 | -0.0039 | 0.0364 | -0.0008 | 0.0008 | 0.0364 | 0.0136 | -0.3126 | 0.061 |

Note: Residual effect, at genotypic level: 0.2998, at phenotypic level: 0.3366

The residual effect of the present study was 0.2998 for genotypic level and 0.3366 for phenotypic level indicating that the characters studied contributed 70.02% of the yield at genotypic level and 66.34% at phenotypic level. It is recommended that maximum attention should be paid on the above characters for selecting chilli genotypes with higher yield. It is also suggested that further study should be made with more characters to find
out other traits which contribute rest of the percentage of the yield.

Figure 1 Path diagram of different yield contributing characters on yield at genotypic level
Note: PH= Plant height, PB/P= No. of primary branches/plant, SB/P= No. of secondary branches/plant, DFFL= Days to first flowering, D50%F= Days to 50% flowering, DFM = Days to fruit maturity, FD= Fruit diameter, FL= Fruit length, FW= Fruit weight, F/P= Fruits/plant, 100SW= 100 seed weight, Y/P= Yield/plant

1.3 Selection index
Selection indices were constructed through discriminant function involving the yield/plant as an independent variable index and four yield components which had positive correlation and positive direct effect on yield at genotypic level. The expected genetic gain in yield and the relative efficiencies of different selection indices, individually and in different combinations are shown in Table 3. The individual trait index, fruit weight had the highest relative efficiency (114.69%) indicated the importance of this trait as yield attribute. This finding was further confirmed by the fact that whenever fruit weight was added to or it replaced other traits in a selection index, the efficiency of such index was tremendously improved. The minimum genetic gain 0.55 and 0.58 and the minimum relative efficiencies 48.51% and 50.91% were obtained by the indices having single traits, viz., primary branches/plant and fruit length, respectively. Furthermore, when primary branches/plant was added to or it replaced another character in a selection index, the relative efficiency of such an index was drastically reduced. Therefore, it could be concluded that primary branches/plant is an inefficient selection criterion for the improvement of yield.

In this study, the expected genetic gain and the relative efficiency of the index was increased with the increase in the number of characters involved except in few cases. The selection index involving all the five characters exhibited the highest expected genetic gain (2.7) and the maximum relative efficiency (236.47%).

Among two character combinations, the maximum efficiency was obtained (183.91%) based on fruit weight+ yield/plant. When three characters were included in the selection index, maximum relative efficiency over selection for yield was obtained (215.51%) for the index based on fruit weight+ fruits/plant+ yield/plant. Another combinations as fruit length +fruit weight +yield/plant had also showed higher relative efficiency.

Considering four characters, maximum relative efficiency was obtained (235.04%) in combination of fruit length +fruit weight+ fruits/plant+ yield/plant. The other combination as primary branches/plant + fruit length +fruit weight+ yield/plant had also higher efficiency over selection for grain yield/plant.
Table 3 Construction of selection indices in 30 chilli genotypes

| Selection index | Expected genetic gain | Relative efficiency over direct selection (%) |
|-----------------|-----------------------|-----------------------------------------------|
| I₅=0.8890x5     | 1.14                  | 100                                           |
| I₁=0.7837x1     | 0.55                  | 48.51                                         |
| I₃=0.8853x2     | 0.58                  | 50.91                                         |
| I₄=0.9548x3     | 1.31                  | 114.69                                        |
| I₅=0.8890x4     | 0.84                  | 73.52                                         |
| I₁=0.7078x1+0.8014x2 | 0.68             | 59.84                                         |
| I₁=0.7845x1+0.9233x3 | 1.29             | 113.17                                        |
| I₄=0.5136x1+0.8857x4 | 1.11             | 97.29                                         |
| I₂=2.1870x1+0.8879x5 | 1.3              | 114.16                                        |
| I₂=0.8963x2+0.9898x3 | 1.55             | 135.96                                        |
| I₄=0.7491x2+0.8895x4 | 1.03             | 90.70                                         |
| I₅=4.4896x2+0.8760x5 | 1.44             | 125.81                                        |
| I₁=0.3128x3+0.8855x4 | 1.42             | 124.72                                        |
| I₁=3.4505x3+0.8812x5 | 2.1              | 183.91                                        |
| I₁=0.8629x4+0.8925x5 | 1.83             | 160.07                                        |
| I₁=0.7227x1+0.8214x2+0.9619x3 | 1.48       | 129.52                                        |
| I₁=1.4420x1+0.8305x2+0.8861x4 | 1.19       | 104.52                                        |
| I₁=3.3320x1+5.0712x2+0.8728x5 | 1.51       | 132.28                                        |
| I₄=1.4099x1+0.4141x3+0.8830x4 | 1.48       | 130.06                                        |
| I₂=2.7310x1+2.9381x3+0.8772x5 | 2.11       | 184.81                                        |
| I₁=3.1893x1+0.8372x4+0.8971x5 | 1.99       | 174.26                                        |
| I₄=0.8947x2+0.3483x3+0.8855x4 | 1.66       | 145.32                                        |
| I₄=4.4305x2+1.9659x3+0.8712x5 | 2.35       | 205.89                                        |
| I₅=4.4790x2+0.9049x4+0.8707x5 | 2.03       | 178.00                                        |
| I₂=1.5114x3+0.8813x4+0.8852x5 | 2.46       | 215.51                                        |
| I₁=1.374x1+0.9434x2+0.4302x3+0.8831x4 | 1.66   | 145.31                                        |
| I₁=3.8557x1+5.0746x2+2.8598x3+0.8625x5 | 2.32   | 203.37                                        |
| I₁=4.1372x1+5.1203x2+0.8762x4+0.8731x5 | 2.14   | 187.24                                        |
| I₁=3.3204x1+2.2290x3+0.8774x4+0.8810x5 | 2.51   | 220.19                                        |
| I₁=4.6650x2+2.6264x3+0.9619x4+0.8482x5 | 2.68   | 235.04                                        |
| I₁=4.5383x1+5.5173x2+3.9688x3+0.9749x4+0.8331x5 | 2.7    | 236.47                                        |

Note: x₁=Primary branches/plant, x₂= Fruit length (cm), x₃= Fruit weight (gm), x₄= Fruits/plant, x₅= Yield/plant (gm)

In the present study, selection index based on five characters gave maximum genetic gain and high efficiency over straight selection but it is tedious and time consuming for a plant breeder to choose all characters for improving yield. Keeping eyes on saving time and labour in a selection programme, it would be desirable to choose a few characters. Hence, an efficient plant breeder feel like including as minimum as possible the characters at a time to achieve as maximum as possible the genetic gain. In this present investigation, selection index (I₃₄₅) based on three characters (fruit weight+ fruits/plant+ yield/plant) showing genetic gain (2.46%) and relative efficiency (215.51%) is more desirable and practically possible to use than those based on four or more characters.
1.4 Improvement based on index score

Successful hybrid breeding programme depends on judicious selection of suitable parents with important traits. So, it is essential to identify the diverse genotypes for best character combination which may give the better heterotic response for yield improvement. Utilizing the best selection index \( I_{345} \) (fruit weight + fruits/plant + yield/plant), the relative genetic score of each genotype was determined (Table 4). It was found that the genotypes Surjomukhi, Bindumorich, Golmorich and BARI morich -2 were superior among all the 30 genotypes having excellent combination of attributes. Alam et al. (2014), Singh et al. (2013), Gupta et al. (2012) and Ferdous et al. (2010) selected best genotypes based on selection score.

Table 4 Selection of genotypes based on the best selection index \( X_3 + X_4 + X_5 \) with mean value and relative genetic score

| Genotype code | Fruit weight (gm) | Fruits/plant | Yield/plant (gm) | Selection score |
|---------------|-------------------|--------------|------------------|----------------|
| G1            | 1.62              | 116.50       | 188.58           | 272.06         |
| G2            | 1.94              | 114.50       | 224.12           | 302.23         |
| G3            | 2.63              | 82.00        | 215.64           | 267.14         |
| G4            | 1.52              | 74.50        | 112.33           | 167.38         |
| G5            | 1.70              | 144.00       | 243.21           | 344.77         |
| G6            | 9.11              | 33.50        | 307.41           | 315.42         |
| G7            | 3.81              | 97.50        | 371.83           | 420.85         |
| G8            | 2.42              | 138.00       | 334.22           | 421.14         |
| G9            | 0.93              | 86.50        | 79.44            | 147.95         |
| G10           | 2.63              | 88.50        | 233.46           | 288.63         |
| G11           | 1.88              | 64.50        | 121.21           | 166.99         |
| G12           | 1.37              | 83.50        | 114.45           | 176.97         |
| G13           | 2.74              | 111.00       | 302.38           | 369.65         |
| G14           | 2.92              | 70.50        | 202.67           | 245.95         |
| G15           | 1.37              | 93.50        | 125.97           | 195.97         |
| G16           | 1.36              | 107.50       | 147.24           | 227.13         |
| G17           | 1.17              | 69.00        | 81.01            | 134.28         |
| G18           | 1.85              | 117.00       | 214.99           | 296.22         |
| G19           | 3.25              | 125.00       | 406.88           | 475.25         |
| G20           | 2.05              | 87.00        | 175.22           | 234.87         |
| G21           | 1.71              | 130.00       | 221.49           | 313.22         |
| G22           | 2.03              | 80.50        | 163.58           | 218.82         |
| G23           | 1.87              | 82.00        | 154.38           | 211.76         |
| G24           | 3.68              | 93.00        | 345.86           | 393.69         |
| G25           | 3.49              | 177.00       | 617.13           | 707.58         |
| G26           | 1.44              | 106.00       | 156.14           | 233.81         |
| G27           | 1.77              | 258.00       | 459.47           | 636.79         |
| G28           | 2.33              | 139.00       | 321.55           | 410.68         |
| G29           | 2.75              | 180.00       | 492.51           | 598.78         |
| G30           | 1.18              | 59.00        | 69.38            | 115.20         |
Superior genotypes were easily identified through biplot analysis (Figure 2). The genotype closer to the arrow mark refers ideal genotype. Genotype G25 was situated in second concentric circle and was also close to arrow mark indicating most superior genotype followed by G29, G27 and G19. Figure 3 showed mean performance of selected genotypes.

Figure 2 Selection of genotypes based on the best selection index (X3 + X4 + X5) with mean value and relative genetic score using Biplot method
Note: FW= Fruit weight, FP= Fruits/plant, YP= Yield/plant, SSc= Selection Score

![Biplot Analysis](image1)

Figure 3 Mean performance of superior genotypes according to best characters combination

Table 5 Chilli genotypes used in the experiment

| Genotype code | Name of the genotype | Place of collection | Genotype code | Name of the genotype | Place of collection |
|---------------|----------------------|---------------------|---------------|----------------------|---------------------|
| G1            | Potuakhali           | Potuakhali          | G16           | Co613                | Comilla             |
| G2            | Co525-3              | Unknown             | G17           | Tsu Buka             | Japan               |
| G3            | Bodorgonj morich     | Rangpur             | G18           | BARI morich-3        | BARI                |
| G4            | Co611-1              | Gazipur             | G19           | BARI morich-2        | BARI                |
| G5            | Co525-1              | Magura              | G20           | Co610                | Unknown             |
| G6            | Ruba bhutan          | Bhutan              | G21           | Ramgar               | Khagrachhori        |
| G7            | BARI morich-1        | BARI                | G22           | Ramnagar laxmi 20    | Laxmipur            |
| G8            | Co611-2              | Gazipur             | G23           | Moheshkhali          | Cox'sbazar          |
| G9            | Co621-2              | Noakhali            | G24           | Balughuri            | Jamalpur            |
| G10           | Co525-2              | Magura              | G25           | Surjomukhi           | Unknown             |
| G11           | Halda morich         | Khagrachhori        | G26           | Dosmina               | Jessore             |
| G12           | Current morich       | Dinajpur            | G27           | Bindu morich         | Manikgonj           |
| G13           | Co620                | Gazipur             | G28           | BARI-1 X 610         | BARI                |
| G14           | Cox'sbazar morich    | Cox'sbazar          | G29           | Golmorich            | Kustia              |
| G15           | Co446                | Magura              | G30           | Boot morich          | Unknown             |

2 Materials and Methods
2.1 Experimental materials
The materials for present investigation comprising of thirty genotypes of chilli (*Capsicum annuum* L.) were
collected from different parts of Bangladesh (Table 5).

2.2 Field experiment
The research work was conducted at the Regional Spices Research Centre of Bangladesh Agricultural Research Institute (BARI) Joydebpur, Gazipur, during the period from December 2013 to May 2014. The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (Anon., 1988). The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replications. The genotypes were randomly allotted in each block. Each replication contained 30 genotypes having 50 cm x 50 cm spacing. The unit plot size was 2 m length and 1 m breadth. Block to block distance was 50 cm. The recommended manure and fertilizer doses were cow dung: 10 ton/ha, urea: 210 kg/ha, TSP: 330 kg/ha, MP: 200 kg/ha, gypsum: 110 kg/ha. Necessary intercultural operations were done during the crop period for proper growth and development of the plants. Each plot was covered with water hyacinth in the dry month to conserve the soil moisture.

2.3 Statistical analysis
Raw data were used to calculate the correlation and path analysis by Indostat 9.1 software. Genotypic and phenotypic variance - covariance matrix with economic weight were used to analyze the expected genetic gain for individual character and combination of characters in order to construct selection indices by the package “plant breeding” of R-3.1.1 software according to the formula given by Singh and Chaudhary (1985).

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