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Discriminant function analysis and construction of selection indices in mulberry silkworm, *B. mori* L.

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Abstract

Background: *Silkworms are well known industrial insects which produce natural silk. Over the years in the silk industry, it is of main focus to increase the profit of silk products and other sectors by the progressive improvement of economic traits like egg and cocoon production. Improvement of these traits are very important for yield. There are several thousand silkworm strains are available all over the world and various breeding programmes are going on to ensure the highest yield of silk produces.*

Materials and Methods: *In this prospective study, selection indices were constructed from discriminant function selection for different combinations with nine quantitative characters in 65 varieties of mulberry silkworm, B. mori L. to identify the characters which may be useful during selection breeding.*

Results: *The negative expected gain of TEL, EHP, SPL, FL, FS and ECY reflected that if it is not a complete character for higher yield rather it depends on other component characters for higher yield and suggested that discriminant function selection was superior to straight selection. When a single character was considered in a selection index a gain of 26427.88%, 4350.86% and 1221.04% is possible when selection will be based on SW, CW and MLW respectively. In the same time the selection indices comprised MLW, CW and SW gave the maximum efficiency among the various indices constructed from discriminant function selection.*

Conclusion: *To boost up the silk production, selection on the basis of the characters viz. SW, CW and MLW would appear to be most effective for the improvement of silk yield in mulberry silkworm.*

Key Words: *Selection indices, Discriminant function, Bombyx mori*

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I. Introduction

Yield by itself is probably not an adequate criterion of economic worth as because yield is a quantitative character and is associated with other component characters which are influenced to varying degree by the fluctuations in the environmental conditions [1,2]. Hence, selection based on that premise could easily lead to develop unsatisfactory result [3]. A complete satisfactory criterion based on discriminant function technique would be more desirable when a combination of two or more characters with yield is studied in a selection index. The characters that show high positive genotypic correlation with yield may serve as basis for selection [4]. Moreover, the use of selection index technique would serve a two-fold purpose in such a breeding programme, namely, to bring about genetic progress simultaneously in several characters and to improve the silk yield through selection for relatively more heritable ancillary characters. The technique of discriminant function analysis first evolved by Fisher (1936) and adopted for selection programme by Smith (1936) [5,6].

In selection breeding experiment a breeder generally faces problem of selecting a component character or a number of components which will give maximum genetic advance through selection. In this respect, a number of workers have applied the method of discriminant function on different crops and animals of economic importance such as Bhide (1963) in wheat [7]; Sen et al. (1976) in *Autheraea mylitta* [8]*;* Rahman (1984) in *Philosamia ricini* [9]; Nahar (1997) in sugarcane [10]; Sarker (2005) in Blackgram [11]; and Mirhosseini et al. (2005), Sarker (2005), Singh and Kumar (2008), Seidavi et al. (2009), and Seidavi (2010) in *Bombyx mori* [9-15]. They showed that discriminant function selection is superior over straight selection. The present study was therefore, undertaken to construct of a suitable selection index for higher silk yield using nine selected quantitative characters employing 65 varieties of *B. mori.*

II. Materials And Methods

The material for the present investigation comprised of sixty five multivoltine (indigenous, developed and exotic) and bivoltine (developed and exotic) varieties of mulberry silkworm *Bombyx mori* L., collected from the Germplasm Bank of the Bangladesh Sericulture Research and Training Institute, Rajshahi. The varieties were:

1. Nistari	14. BSR-3 (p)	27. BSR-95/10(P)	40. Bipul	53. Ziangsu (P)
2. Nistari (P)	15. BSR-3 (m)	28. BSR-95/14(P)	41. BSRI-83/1	54. Dong 34(M)
3. Nistari (M)	16. BSR-10 (m)	29. BSR-95/22(P)	42. BSRI-83/2	55. Dong 34 (P)
4. Nistari L	17. Nistid white (P)	30. BSR-98/1(P)	43. BSRI-83/3	56. BV (M)
5. Nistari G	18. BSR-JB	31. BSR-98/2(P)	44. BSRI-85/1	57. BV (P)
6. ISK	19. BSR-IM(P)	32. BSR2000/1 (GM)	45. BSRI-85/2	58. RB (M)
7. MBY- 011S (P)	20. BSR-(GL)	33. BSR-02/1(M)	46. BSRI-85/3	59. RB (P)
8. BN P	21. BSR-92/2(P)	34. BSR-02/2(P)	47. BSRI-J	60. RB-001 (M)
9. BN (M)	22. BSR-92/5(P)	35. BSR-02/3	48. Urboshi-1	61. RB-001 (P)
10. NN-7B (P)	23. BSR-92/7(P)	36. BSR-03/1	49. Urboshi-4	62. RB-111
11. NM-7B (M)	24. BSR-92/8(P)	37.BSR-03/2	50. BSRI-801	63. RB-112
12. BSR-1 white (p)	25. BSR-92/14(P)	38. O_5	51. BSRI-802	64. RB-SB (M)
13. BSR-1 white (m)	26. BSR-92/16(P)	39. R_1S_1	52. Ziangsu 12-J	65. RB-SP (P)

The eggs of these varieties were brushed (3dfls for each genotype) in a randomized design with three replications each. The rearing was conducted in the rearing house No. 2 of the BSRTI, Rajshahi. Scientific technology of silkworm rearing was followed according to Rahman (1983) [16]. Data recorded for this study were: Total number of eggs laid per female (TEL), egg hatching percentage (EHP), mature larval weight (MLW), surviving percentage of larvae (SPL), cocoon weight (CW), shell weight (SW), Length of filament (FL), size of filament (FS) and estimated cocoon yield out of 100 dfls (ECY). The coefficients b_1, b_2 .... b_n were used in discriminant function selection technique. The phenotypic and genotypic variances and covariances as obtained were used for constructing the discriminant function using different character combinations according to the method as developed by [6]. Estimated cocoon yield out of 100 dfls was also included as one of the independent characters as suggested by [3]. The expected genetic advance from straight selection [GA(S)] and from discriminant function [GA(D)] was calculated as follows:

$GA(S) = (Z/P) \times (g_{yy})/(t_{yy})^{1/2}$ and

$GA(D) = (Z/P) \times (b_{1g1y} + b_{2g2y})^{1/2}$

Where,

Z/P = The selection differential in standard units, for the present study, it was 2.06 at 5% level of selection (Lush, 1949).

g_{yy} and t_{yy} = The genotypic and phenotypic variances of character,

$b_1, b_2, \ldots b_n$ = The relative weights for character

$g_{1y}, g_{2y}, \ldots g_{ny}$ = The genotypic covariances of independent character with y.

The expected genetic gain from the discriminant function over straight selection was calculated for all the functions as shown below:

Expected gain (%) = [GA(D)/GA(S)-1] × 100

III. Results And Discussion

Selection indices (Character combinations) and expected gain in percent over straight selection for expected cocoon yield out of 100 dfls are presented in Table 1. This table showed that SW, MLW and CW expressed positive genetic gain alone over the straight selection for silkworm. The negative expected gain of TEL, EHP, SPL, FL, FS and ECY reflected that they are not complete character for higher yield rather they depend on other component characters for higher yield and suggested that discriminant function selection was superior to straight selection.

A fairly large value for expected gain was obtained when large numbers of characters were included in the discriminant functions. This table showed that the maximum genetic gain of 322.36% was obtained where MLW, CW, SW, FL, FS and ECY were included in the discriminant function. This value was followed by 109.99% GA where EHP, SW and FL were included in the discriminant function. The next value in the ranking of GA was 101.65% where EHP, SW and FS were included in the discriminant function. The next lower value of GA was 100.80% (EHP, SW and ECY). Rahman (1983) in *P. ricini* reported that selection index containing CW and SW gave higher efficiency than the indices lacking other characters [9]. Sen et al. (1976) in *Antheraea mylitta* found that indices containing shell weight gave higher efficiency [8].

In plants inclusion of yield per plant has been emphasized in selection indices in a number of crop plants [17-19]. In practice it is not possible to use many characters in selection programme and thus one would prefer to use a discriminant function which would give maximum possible genetic advance by using a minimum number of characters. In the present investigation selection indices comprising greater number of characters showed high efficiency but the selection indices comprised MLW, CW and SW gave the maximum efficiency among the various indices constructed from discriminant function selection.

When a single character was considered in a selection index a gain of 26427.88% is possible when selection will be based on SW only. Single character selection with CW and MLW also gave 4350.86% and

1221.04% respectively. Sen et al. (1976) and Rahman (1984) found little efficiency in single character in discriminant function selection in *Antheraea mylitta* and *P. ricini* respectively [8,9].

Since observed gains do not always agree with those expected, the claimed advantages of selection indices based on expected gain need to be confirmed in practice. Before initiating a selection programme it is important for a breeder to know whether or not the discriminant function is superior to straight selection, even on the basis of expected gain in the material under study. For practical purposes many characters in a function are too much to use in selection programme. Therefore, it is always preferable to use a discriminant function containing a minimum number of characters which may lead to maximum genetic advance.

Table 1. Expected gain in percent of expected cocoon yield out of 100 dfls from the use of various selection indices in *Bombyx mori*. Index which showed high value is shown only.

Selection index	EG% (Expected Gain)	Selection index	EG% (Expected Gain)
x_1 (TEL)	-76.81	$x_2 + x_6 + x_9$	100.80
x_2 (EHP)	-9.21	$x_2 + x_8 + x_9$	64.99
x_3 (MLW)	1221.04	x1 + x2 + x3 + x6	14.81
x_4 (SPL)	-40.43	x1 + x2 + x3 + x7	19.51
x_5 (CW)	4350.86	x1 + x2 + x4 + x6	15.47
x_6 (SW)	26427.88	x1 + x2 + x4 + x7	20.14
x_7 (FL)	-87.93	x1 + x2 + x5 + x6	18.34
x_8 (FS)	-1812.13	x1 + x2 + x5 + x7	22.91
x_9 (ECY)	-44.74	x1 + x2 + x6 + x7	29.50
$x_1 + x_6$	11.37	x1 + x2 + x6 + x8	15.49
$x_1 + x_7$	16.21	x1 + x2 + x6 + x9	13.99
$x_2 + x_8$	69.42	x1 + x2 + x7 + x8	20.16
$x_3 + x_8$	66.65	x1 + x2 + x7 + x9	18.72
$x_4 + x_8$	64.44	x1 + x3 + x4 + x6	16.24
$x_8 + x_9$	69.59	x1 + x3 + x4 + x7	20.88
$x_1 + x_2 + x_6$	12.71	x1 + x3 + x5 + x6	19.09
$x_1 + x_2 + x_7$	17.49	x1 + x3 + x5 + x7	23.62
$x_1 + x_3 + x_6$	13.49	x1 + x3 + x6 + x7	30.18
$x_1 + x_3 + x_7$	18.24	x1 + x3 + x6 + x8	16.26
$x_1 + x_4 + x_6$	14.16	x1 + x3 + x6 + x9	14.77
$x_1 + x_4 + x_7$	18.89	x1 + x3 + x7 + x8	20.90
$x_1 + x_5 + x_6$	17.07	x1 + x3 + x7 + x9	19.46
$x_1 + x_5 + x_7$	21.68	x1 + x4 + x5 + x6	19.73
$x_1 + x_6 + x_7$	28.33	x1 + x4 + x5 + x7	24.24
$x_1 + x_6 + x_8$	14.18	x1 + x4 + x6 + x7	30.76
$x_1 + x_6 + x_9$	12.67	x1 + x4 + x6 + x8	16.91
$x_1 + x_7 + x_8$	18.90	x1 + x4 + x6 + x9	15.43
$x_1 + x_7 + x_9$	17.45	x1 + x4 + x7 + x8	21.53
$x_2 + x_6 + x_7$	109.99	x1 + x4 + x7 + x9	20.10
$x_2 + x_6 + x_8$	101.65	x1 + x5 + x6 + x7	33.31
$x_1 + x_5 + x_6 + x_8$	19.75	$x_1 + x_2 + x_5 + x_7 + x_9$	24.08
$x_1 + x_5 + x_6 + x_9$	18.30	$x_1 + x_2 + x_6 + x_7 + x_8$	31.93
$x_1 + x_5 + x_7 + x_8$	24.26	$x_1 + x_2 + x_6 + x_7 + x_9$	30.61
$x_1 + x_5 + x_7 + x_9$	22.86	$x_1 + x_2 + x_6 + x_8 + x_9$	16.74
$x_1 + x_6 + x_7 + x_8$	30.78	$x_1 + x_2 + x_7 + x_8 + x_9$	21.36
$x_1 + x_6 + x_7 + x_9$	29.46	$x_1 + x_3 + x_4 + x_5 + x_6$	21.71
$x_1 + x_6 + x_8 + x_9$	15.45	$x_1 + x_3 + x_4 + x_5 + x_7$	26.15
$x_1 + x_7 + x_8 + x_9$	20.12	$x_1 + x_3 + x_4 + x_6 + x_7$	32.58
$x_1 + x_2 + x_3 + x_4 + x_6$	17.52	$x_1 + x_3 + x_4 + x_6 + x_8$	18.94
$x_1 + x_2 + x_3 + x_4 + x_7$	22.12	$x_1 + x_3 + x_4 + x_6 + x_9$	17.48
$x_1 + x_2 + x_3 + x_4 + x_8$	7.15	$x_1 + x_3 + x_4 + x_7 + x_8$	23.48
$x_1 + x_2 + x_3 + x_5 + x_6$	20.34	$x_1 + x_3 + x_4 + x_7 + x_9$	22.07
$x_1 + x_2 + x_3 + x_5 + x_7$	24.83	$x_1 + x_3 + x_5 + x_6 + x_7$	35.09
$x_1 + x_2 + x_3 + x_5 + x_8$	10.24	$x_1 + x_3 + x_5 + x_6 + x_8$	21.72
$x_1 + x_2 + x_3 + x_6 + x_7$	31.33	$x_1 + x_3 + x_5 + x_6 + x_9$	20.30
$x_1 + x_2 + x_3 + x_6 + x_8$	17.54	$x_1 + x_3 + x_5 + x_7 + x_8$	26.16
$x_1 + x_2 + x_3 + x_6 + x_9$	16.07	$x_1 + x_3 + x_5 + x_7 + x_9$	24.79
$x_1 + x_2 + x_3 + x_7 + x_8$	22.13	$x_1 + x_3 + x_5 + x_7 + x_8$	32.59
$x_1 + x_2 + x_3 + x_7 + x_9$	20.72	$x_1 + x_3 + x_5 + x_7 + x_9$	31.29
$x_1 + x_2 + x_4 + x_5 + x_6$	20.98	$x_1 + x_3 + x_5 + x_8 + x_9$	17.50
$x_1 + x_2 + x_4 + x_5 + x_7$	25.44	$x_1 + x_3 + x_7 + x_8 + x_9$	22.09
$x_1 + x_2 + x_4 + x_6 + x_7$	31.91	$x_1 + x_4 + x_5 + x_6 + x_7$	35.65
$x_1 + x_2 + x_4 + x_6 + x_8$	18.19	$x_1 + x_4 + x_5 + x_6 + x_8$	22.35
$x_1 + x_2 + x_4 + x_6 + x_9$	16.72	$x_1 + x_4 + x_5 + x_6 + x_9$	20.93
$x_1 + x_2 + x_4 + x_7 + x_8$	22.76	$x_1 + x_4 + x_5 + x_7 + x_8$	26.77

Selection index	**EG% (Expected Gain)**
$x_1 + x_2 + x_4 + x_7 + x_9$	21.35
$x_1 + x_2 + x_5 + x_6 + x_7$	34.43
$x_1 + x_2 + x_5 + x_6 + x_8$	20.99
$x_1 + x_2 + x_5 + x_6 + x_9$	19.56
$x_1 + x_2 + x_5 + x_7 + x_8$	25.46
$x_1 + x_5 + x_6 + x_7 + x_8$	35.67
$x_1 + x_5 + x_6 + x_7 + x_9$	34.39
$x_1 + x_5 + x_6 + x_8 + x_9$	20.95
$x_1 + x_5 + x_7 + x_8 + x_9$	25.42
$x_1 + x_6 + x_7 + x_8 + x_9$	31.89
$x_1 + x_2 + x_3 + x_4 + x_5 + x_6$	22.93
$x_1 + x_2 + x_3 + x_4 + x_5 + x_7$	27.33
$x_1 + x_2 + x_3 + x_4 + x_5 + x_8$	13.06
$x_1 + x_2 + x_3 + x_4 + x_6 + x_7$	33.71
$x_1 + x_2 + x_3 + x_4 + x_6 + x_8$	20.19
$x_1 + x_2 + x_3 + x_4 + x_6 + x_9$	18.75
$x_1 + x_2 + x_3 + x_4 + x_7 + x_8$	24.69
$x_1 + x_2 + x_3 + x_4 + x_7 + x_9$	23.30
$x_1 + x_2 + x_3 + x_5 + x_6 + x_7$	36.19
$x_1 + x_2 + x_3 + x_5 + x_6 + x_8$	22.95
$x_1 + x_2 + x_3 + x_5 + x_6 + x_9$	21.54
$x_1 + x_2 + x_3 + x_5 + x_7 + x_8$	27.35
$x_1 + x_2 + x_3 + x_5 + x_7 + x_9$	25.99
$x_1 + x_2 + x_3 + x_6 + x_7 + x_8$	33.72
$x_1 + x_2 + x_3 + x_6 + x_7 + x_9$	32.43
$x_1 + x_2 + x_3 + x_6 + x_8 + x_9$	18.77
$x_1 + x_2 + x_3 + x_7 + x_8 + x_9$	23.32
$x_1 + x_2 + x_4 + x_5 + x_6 + x_7$	36.75
$x_1 + x_2 + x_4 + x_5 + x_6 + x_8$	23.57
$x_1 + x_2 + x_4 + x_5 + x_6 + x_9$	22.17
$x_1 + x_2 + x_4 + x_5 + x_7 + x_8$	27.95
$x_1 + x_2 + x_4 + x_5 + x_7 + x_9$	26.59
$x_1 + x_2 + x_4 + x_5 + x_8 + x_9$	12.23
$x_1 + x_2 + x_4 + x_6 + x_7 + x_8$	34.29
$x_1 + x_2 + x_4 + x_6 + x_7 + x_9$	33.00
$x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_9$	24.11
$x_1 + x_2 + x_3 + x_4 + x_5 + x_7 + x_8$	29.80
$x_1 + x_2 + x_3 + x_4 + x_5 + x_7 + x_9$	28.47
$x_1 + x_2 + x_3 + x_4 + x_5 + x_8 + x_9$	14.33
$x_1 + x_2 + x_3 + x_4 + x_6 + x_7 + x_8$	36.06
$x_1 + x_2 + x_3 + x_4 + x_6 + x_7 + x_9$	34.79
$x_1 + x_2 + x_3 + x_4 + x_6 + x_8 + x_9$	21.39
$x_1 + x_2 + x_3 + x_4 + x_7 + x_8 + x_9$	25.85
$x_1 + x_2 + x_3 + x_5 + x_6 + x_7 + x_8$	38.50
$x_1 + x_2 + x_3 + x_5 + x_6 + x_7 + x_9$	37.26
$x_1 + x_2 + x_3 + x_5 + x_6 + x_8 + x_9$	24.13
$x_1 + x_2 + x_3 + x_5 + x_7 + x_8 + x_9$	28.48
$x_1 + x_2 + x_3 + x_6 + x_7 + x_8 + x_9$	34.80
$x_1 + x_2 + x_4 + x_5 + x_6 + x_7 + x_8$	39.05
$x_1 + x_2 + x_4 + x_5 + x_6 + x_7 + x_9$	37.81
$x_1 + x_2 + x_4 + x_5 + x_6 + x_8 + x_9$	24.74
$x_1 + x_2 + x_4 + x_5 + x_7 + x_8 + x_9$	29.08
$x_1 + x_2 + x_4 + x_6 + x_7 + x_8 +$	35.37

Selection index	**EG% (Expected Gain)**
$x_1 + x_4 + x_5 + x_7 + x_9$	25.40
$x_1 + x_4 + x_6 + x_7 + x_8$	33.17
$x_1 + x_4 + x_6 + x_7 + x_9$	31.87
$x_1 + x_4 + x_6 + x_8 + x_8$	18.14
$x_1 + x_4 + x_7 + x_8 + x_9$	22.71
$x_1 + x_2 + x_4 + x_6 + x_8 + x_9$	19.41
$x_1 + x_2 + x_4 + x_7 + x_8 + x_9$	23.93
$x_1 + x_2 + x_5 + x_6 + x_7 + x_8$	36.77
$x_1 + x_2 + x_5 + x_6 + x_7 + x_9$	35.50
$x_1 + x_2 + x_5 + x_6 + x_8 + x_9$	22.19
$x_1 + x_2 + x_5 + x_7 + x_8 + x_9$	26.61
$x_1 + x_2 + x_6 + x_7 + x_8 + x_9$	33.02
$x_1 + x_3 + x_4 + x_5 + x_6 + x_7$	37.40
$x_1 + x_3 + x_4 + x_5 + x_6 + x_8$	24.29
$x_1 + x_3 + x_4 + x_5 + x_6 + x_9$	22.89
$x_1 + x_3 + x_4 + x_5 + x_7 + x_8$	28.64
$x_1 + x_3 + x_4 + x_5 + x_7 + x_9$	27.29
$x_1 + x_3 + x_4 + x_6 + x_7 + x_8$	34.95
$x_1 + x_3 + x_4 + x_6 + x_7 + x_9$	33.67
$x_1 + x_3 + x_4 + x_6 + x_8 + x_9$	20.15
$x_1 + x_3 + x_4 + x_7 + x_8 + x_9$	24.65
$x_1 + x_3 + x_5 + x_6 + x_7 + x_8$	37.41
$x_1 + x_3 + x_5 + x_6 + x_7 + x_9$	36.16
$x_1 + x_3 + x_5 + x_6 + x_8 + x_9$	22.91
$x_1 + x_3 + x_5 + x_7 + x_8 + x_9$	27.31
$x_1 + x_3 + x_6 + x_7 + x_8 + x_9$	33.68
$x_1 + x_4 + x_5 + x_6 + x_7 + x_8$	37.97
$x_1 + x_4 + x_5 + x_6 + x_7 + x_9$	36.71
$x_1 + x_4 + x_5 + x_6 + x_8 + x_9$	23.53
$x_1 + x_4 + x_5 + x_7 + x_8 + x_9$	27.91
$x_1 + x_4 + x_6 + x_7 + x_8 + x_9$	34.25
$x_1 + x_5 + x_6 + x_7 + x_8 + x_9$	36.73
$x_3 + x_5 + x_6 + x_7 + x_8 + x_9$	322.36
$x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7$	38.49
$x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_8$	25.49
$x_1 + x_2 + x_3 + x_4 + x_6 + x_7 + x_8 + x_9$	37.12
$x_1 + x_2 + x_3 + x_5 + x_6 + x_7 + x_8 + x_9$	39.55
$x_1 + x_2 + x_4 + x_5 + x_6 + x_7 + x_8 + x_9$	40.09
$x_1 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8 + x_9$	40.72
$x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8 + x_9$	41.79

Selection index	**EG%** **(Expected Gain)**
x_9	
$x_1 + x_2 + x_5 + x_6 + x_7 + x_8 + x_9$	37.83
$x_1 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8$	39.69
$x_1 + x_3 + x_4 + x_5 + x_6 + x_7 + x_9$	38.45
$x_1 + x_3 + x_4 + x_5 + x_6 + x_8 + x_9$	25.45
$x_1 + x_3 + x_4 + x_5 + x_7 + x_8 + x_9$	29.76
$x_1 + x_3 + x_4 + x_6 + x_7 + x_8 + x_9$	36.02
$x_1 + x_3 + x_5 + x_6 + x_7 + x_8 + x_9$	38.47
$x_1 + x_4 + x_5 + x_6 + x_7 + x_8 + x_9$	39.02
$x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8$	40.76
$x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_9$	39.53
$x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_8 + x_9$	26.64
$x_1 + x_2 + x_3 + x_4 + x_5 + x_7 + x_8 + x_9$	30.91

Selection index	**EG%** **(Expected Gain)**

IV. Conclusion

From the above results it was clear that maximum expected genetic gain may be obtained only when MLW, CW, and SW are used in the function. Therefore, selection breeding can be made on MLW, CW and SW and a considerable advancement may be achieved provided environmental factors do not limit the fuller expression of these characters.

Reference

[1]. Chatterjee, S., Nagaraj, C. & Giridhar, K. in *Workshop on Biometrical Genetics Proceedings. Central Sericultural Research and Training Institute, Mysore.* 11-16.

[2]. Chatterjee, S. & Pradeep, A. Molecular markers (RAPD) associated with growth, yield, and origin of the silkworm, *Bombyx mori* L. in India. *Russ. J. Genet.* **39**, 1365-1377 (2003).

[3]. Robinson, H. & Comstock, R. E. Genotypic and phenotypic correlations in corn and their implications in selection. (North Carolina State University. Dept. of Statistics, 1950).

[4]. Punia, M., Paroda, R. & Hooda, R. Correlation and path analysis of cane yield in sugarcane. *Indian J. Genet. Plant Breed.* **43**, 109-112 (1983).

[5]. Smith, H. F. A discriminant function for plant selection. *Ann. Eugen.* **7**, 240-250 (1936).

[6]. Fisher, R. A. The use of multiple measurements in taxonomic problems. *Ann. Eugen.* **7**, 179-188 (1936).

[7]. Bhide, V. Discriminant function in wheat hybrid. *Indian Agric.* **7**, 76 (1963).

[8]. Sen, S. K., Sengupta, A. K., Das, M. G. & Jolly, M. S. Studies on the genetic variability correlations, path co-efficient analysis and discriminant functions in Antheraea mylitta D. *Indian J Seric* **15**, 9-14 (1976).

[9]. Rahman, S. *Studies on the genetic improvement of eri silkworm, Philosamia ricini. Boisd of Bangladesh*, Ph. D thesis, Department of Zoology, Rajshahi University. 419pp, (1984).

[10]. Nahar, S. *Genetic study of economically important characters and construction of selection index in sugarcane*, Ph. D. Thesis, Rajshahi University, Bangladesh, (1997).

[11]. Sarker, N. *Study of variability, path coefficient and selection index of some agronomical characters in blackgram (Vigna mungo (L.) Hepper)*, M. Sc. Thesis, University of Rajshahi, Bangladesh, (2005).

[12]. Mirhosseini, S., Ghanipoor, M., Shadparvar, A. & Etebari, K. Selection indices for cocoon traits in six commercial silkworm (*Bombyx mori* L.) lines. *The Philippine agricultural Scientist* **88**, 328-336 (2005).

[13]. Seidavi, A. Investigation on effect of individual selection based on cocoon weight on additive genetic value and selection index value in six commercial silkworm pure lines. *World J Zool* **5**, 07-14 (2010).

[14]. Seidavi, A. *et al.* Additive genetic variations and selection index changes of economic traits of the silkworm commercial pure lines against parent selection pressure. *American-Eurasian Journal of Agricultural and Environmental Science* **6**, 460-465 (2009).

[15]. Singh, H. & Kumar, N. Selection of breeding resource material of bivoltine silkworm, Bombys mori L. for breeding for high temperature tolerance. *Indian Journal of Agriculture* **47**, 20-28 (2008).

[16]. Rahman, S. Technology of mulberry silkworm rearing suitable for the climatic condition in Bangladesh. *Reshom* **1**, 71-79 (1983).

[17]. Khaleque, M., Joarder, O., Eunus, A. & Islam, A. Nature of gene interaction in the inheritance of yield and yield components in some rice crosses. *Oryza* (1979).

[18]. Paroda, R. & Joshi, A. Genetic architecture of yield and components of yield in wheat. *Indian J. Genet. Plant Breed.* **30**, 298-314 (1970).

[19]. Paul, N., Joarder, O. & Eunus, A. Variation of yield and some of its components in eight crosses of local and Indian rape varieties. *J. Asiatic Soc. Bangladesh (Sc.)* **2**, 37-42 (1976).