

Association studies on soybean [*Glycine max* (L.) Merrill] germplasm accessions for yield and yield attributing traits

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ABSTRACT

The experiment was conducted to evaluate 135 soybean genotypes in order to determine the genetic variability, heritability, genetic advance, correlation, and path analysis for ten quantitative characters. Analysis of variance showed the existence of significant differences among all the traits except the number of branches per plant and the number of seeds per pod. High heritability accompanied by high genetic advance was observed in plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, hundred seed weight, and single plant yield suggested selection from these characters could be effective for future crop improvement program. Based on the association analysis characters like the number of pods per plant, plant height, number of clusters per plant, number of branches per plant, number of seeds per plant, and hundred seed weight were observed to be highly correlated with yield and hence these characters should be given more consideration in breeding for higher grain yield in soybean.

Keywords- Soybean, Variability, Correlation, Path analysis

INTRODUCTION

Soybean (*Glycine max* L. Merrill) is a self-pollinated crop with a natural outcrossing rate of 0.03–6.32 percent [1]. The soybean is indigenous to northeast Asia, particularly China. World soybean production was estimated as 385.527 million tonnes. Brazil ranks first in soybean production followed by the United States, Argentina, China and India [2]. Production in India accounts for 12.04 million tonnes cultivated under 11.45 million hectares with average productivity of 1051 kg/ha. Madhya Pradesh is the soybean bowl of India, contributing more than 89 percent of the country's soybean production, followed by Maharashtra and Rajasthan [3]. The area and productivity of soybean is low when compared to other legume crops in India and therefore a step has to be taken to improve the seed yield. Increasing seed yield requires the presence of variability and hence variability is studied. Again, along with variability, the inheritance must be studied to assess the heritability of the characters. The heritability estimates provide a measure of the transmission of character from one generation to the next, as the consistency in the performance of the selection depends on the heritable portion of the variability. Thus, heritability and genetic advance as percent of the mean are estimated together to find the heritability nature of selected genotypes.

Seed yield is a complex character and is influenced by many environmental factors when cultivated hence it is not efficient for selection. It is therefore important for a plant breeder to identify the characteristics that are associated with the seed yield and that character could be used for the selection. Association between traits were crucial to breeding work as it helps to perform indirect selection for a quantitative trait especially yield, usually hard to be selected, by another directly correlated trait of higher genetic gain [4]. Hence, the present study was undertaken to analyze and to find the magnitude and nature of variation among 135 soybean genotypes with respect to various yield-contributing traits and the association between yield and its contributing traits in soybean by correlation and path coefficient analysis.

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Materials and methods

The research work was carried out during rabi, 2021-22 at the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore. The experimental materials consisted of 135 soybean germplasm accession including the five check varieties viz., NRC 132, NRC 142, NRC 147, MACS 1460, and CO (Soy) 3 is given in (Table 1) and were sown in an augmented block design II with a 3m row length and spacing of 30cm between the rows and 10cm within the rows. The recommended fertilizers and cultural practices were followed to raise the crop. Observations were recorded on five randomly selected plants in each genotype for days to fifty percent flowering, days to maturity, plant

height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, hundred seed weight and single plant yield. The mean data was used to estimate genetic variability, heritability and genetic advance. The phenotypic and genotypic coefficient of variability (PCV and GCV) was computed according to the method suggested [5] and heritability (h^2) as suggested [6]. The mean data was also subjected to analyze correlation and path analysis using the TNAU STAT software.

Result and Discussion

Variability studies

Genetic variability study is the basis for selection of genotypes for the future breeding program. Results from the analysis of variance (Table 2) showed that a highly significant difference exists among all genotypes in terms of all traits measured except the number of branches per plant and the number of seeds per pod. The variability parameters viz., phenotypic variation, genotypic variation, phenotypic coefficient of variation, genotypic coefficient variation, heritability, genetic advance, and genetic advance as percent of mean for ten quantitative traits is given in Table 3.

Single plant yield ranges from 2.09 – 37.32g. A maximum single plant yield (37.32g) was observed in PK 1146. In a previous study, it was reported that the genotypes MACS 1460, EC 18736 and PK 1038 showed high values for single plant yield [7]. The phenotypic coefficient of variation was higher than the genotypic coefficient of variance for all the ten traits. PCV and GCV for ten quantitative traits were represented in bar chart (Figure 1). Highest phenotypic coefficient of variation and genotypic coefficient of variance was observed in single plant yield as 45.36 and 42.42 respectively. The lowest phenotypic and genotypic variation was observed in days to maturity as 5.51 and 5.49 respectively. The maximum difference between phenotypic and genotypic variation was observed in single plant yield whereas the minimum difference was observed in days to maturity. High PCV and GCV was observed in plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and single plant yield. A similar result on plant height and number of pods per plant was reported [8, 9] for the number of branches per plant [10,11] for number of clusters per plant [12] and for hundred seed weight [13, 14]. High PCV and GCV in single plant yield were reported [15]. Moderate PCV and GCV were observed in hundred seed weights. Similar results were also reported [9], [16], and [17]. Low PCV and GCV were observed in days to fifty percent flowering and days to maturity. Similar results on days to fifty percent flowering and days to maturity were reported [14-15].

Heritability and genetic advance as percent of mean expressed in percent for ten traits in 135 soybean germplasm accessions were depicted in bar chart in Figure 2. High heritability and high genetic advance as percent mean was observed in plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, hundred seed weight, and single plant yield. This showed that these traits exhibit additive gene action and could be used for selection. Similar results on plant height, number of branches per plant and number of pods per plant were reported [16] and along with the number of clusters per plant [11]. The same results on a number of seeds per plant was

reported [18]. A similar finding on hundred seed weight and single plant yield was reported [14] and [9]. Days to fifty percent flowering and days to maturity showed high heritability and moderate genetic advance as per cent mean indicates the presence of both additive and non-additive gene action for these traits. Similar findings on days to fifty percent flowering and days to maturity had been reported [19] and [20].

Correlation coefficient analysis

The phenotypic correlation for ten quantitative traits is given in Table 3. The phenotypic correlation coefficient of seed yield was positive and significant with days to fifty percent flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, and hundred seed weight at 1 percent level. A similar results were obtained on days to fifty percent flowering, plant height [4] and along with a number of pods per plant and a number of branches per plant [21] and along with a number of pods per plant [22]. However, single-plant yield showed positive and significant association with a number of seeds per plant.

Inter correlation among the yield attributing traits was given in the Table 3. Days to fifty per cent flowering showed a positive and significant correlation with days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster and number of pods per plant. Plant height showed a positive and significant association with number of branches per plant, number of clusters per plant, number of pods per plant. Positive and significant association between plant height and the number of pods per plant was reported [4], [23] and [24]. The number of branches per plant showed positive and significant association with number of clusters per plant and number of pods per plant. A positive and significant association of number of clusters per plant was observed with a number of pods per cluster and a number of pods per plant. Similar findings were reported [11].

The character with positive association can be raised through indirect selection for the corresponding trait in a breeding program. Intercorrelated traits contributing to yield can also be selected indirectly for breeding programme. In terms of the present study, days to fifty per cent flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per plant and hundred seed weight were positively associated with single plant yield and therefore these traits except days to fifty percent could be used for yield improvement breeding work.

Path coefficient analysis

The results of the path coefficient analysis for ten quantitative traits were given in Table 4 and Figure 3. The present study on path analysis revealed that a number of pods per plant had the highest and most direct effect on the single plant yield. Similar findings of high direct effect of number of pods per plant were reported [24-25]. A number of seeds per pod and hundred seed weight were observed to have moderate and positive direct effect on single plant yield. Previous studies reported same results of a number of seeds per pod on yield [26-27]. A number of clusters per plant had a positive and low direct effect on single plant yield. The remaining traits viz., days to fifty per cent flowering, days to maturity, plant height, number of branches per plant and number of pods per cluster were observed to have negligible direct effect on single plant yield.

Days to fifty percent flowering have a moderate and positive indirect effect on single plant yield through a number of pods

per plant and similar results were reported [27]. Plant height, number of branches per plant, number of clusters per plant and number of pods per cluster had positive and high indirect effects on single plant yield via the number of pods per plant. A similar result of the number of branches per plant on yield was reported [4]. Days to fifty percent flowering, plant height, number of branches per plant and number of pods per plant had low and positive indirect effects on single plant yield via number of clusters per plant.

Table 1. List of soybean genotypes used in the study

| Sl. No | Genotypes | Sl. No | Genotypes | Sl. No | Genotypes |
|--------|------------|--------|----------------|--------|--------------|
| 1. | CLARK | 46. | MACS 1148 | 91. | NRC 43 |
| 2. | CO 1 | 47. | MACS 1188 | 92. | VLS 53 |
| 3. | CO 2 | 48. | MACS 1238 | 93. | VLS 69 |
| 4. | CSB 0804 | 49. | MACS 1254 | 94. | PK 1158 |
| 5. | CSB 0806 | 50. | MACS 1259 | 95. | PK 1223 |
| 6. | CSB 0808 | 51. | MACS 1281 | 96. | PK 1243 |
| 7. | CSB 0809 | 52. | MACS 145 | 97. | MAUS 59 |
| 8. | CSB 0810 | 53. | MACS 565 | 98. | MAUS 60 |
| 9. | CSB 0811 | 54. | MACS 610 | 99. | MAUS 61 |
| 10. | EC 18678 | 55. | MACS 629 | 100. | NRC 44 |
| 11. | EC 18736 | 56. | MACS 693 | 101. | NRC 45 |
| 12. | JS 20-01 | 57. | MACS 694 | 102. | NRC 46 |
| 13. | JS 20-09 | 58. | MACS 715 | 103. | NRC 76 |
| 14. | JS 76119 | 59. | MACS 798 | 104. | NRC 78 |
| 15. | JS 76-1194 | 60. | MACS 94-2 | 105. | NRC 79 |
| 16. | JS 87-12 | 61. | MACS 985 | 106. | NRC 80-1 |
| 17. | JS 89-24 | 62. | MAUS 109 | 107. | NRC 82 |
| 18. | JS 90-21 | 63. | MAUS 144 | 108. | NRC 84 |
| 19. | JS 90-29 | 64. | MAUS 17 | 109. | NRC 95-06-03 |
| 20. | JS 92-22 | 65. | MAUS 2 | 110. | VLS 70 |
| 21. | JS 95-60 | 66. | MAUS 20 | 111. | VLS 75 |
| 22. | JS 95-98 | 67. | MAUS 311 | 112. | WC 37 |
| 23. | JS 97-52 | 68. | MAUS 34 | 113. | WC 67 |
| 24. | JS 98-21 | 69. | MAUS 39 | 114. | PK 1000 |
| 25. | JS 98-61 | 70. | MAUS 414 | 115. | PK 1303 |
| 26. | JS 98-63 | 71. | MAUS 417 | 116. | PK 25 |
| 27. | JS 98-68 | 72. | MAUS 52-1 | 117. | PK 257 |
| 28. | JS 99-12 | 73. | MAUS 55 | 118. | PK 258 |
| 29. | JS 99-128 | 74. | JS(SH) 2001-04 | 119. | PK 727 |
| 30. | JS 99-72 | 75. | JS(SH) 2002-14 | 120. | PK 768 |

| | | | | | |
|---------------------------|-------------|-----|----------------------------|------|------------|
| 31. | JS 99-76 | 76. | JS(SH) 8554 | 121. | PK 1011 |
| 32. | JS 99-77 | 77. | JS(SH) 89-2 | 122. | PK 1014 |
| 33. | JS 99-83 | 78. | MAUS 65 | 123. | PK 1024 |
| 34. | JS(SH)18608 | 79. | MAUS 68 | 124. | PK 1028 |
| 35. | JS(SH)89-49 | 80. | MAUS 71-07 | 125. | PK 1038 |
| 36. | JS(SH)90-91 | 81. | MAUS 81 | 126. | PK 1125 |
| 37. | JS(SH)91-93 | 82. | NRC 2006-M-6 | 127. | PK 1146 |
| 38. | JS(SH)92-46 | 83. | NRC 2007-G-1-13 | 128. | PK 1225 |
| 39. | JS(SH)93-37 | 84. | NRC 2007-I-3 | 129. | PK 701 |
| 40. | JS(SH)93-44 | 85. | NRC 2007-K-7-2 | 130. | PK 7247 |
| 41. | JS(SH)99-14 | 86. | NRC 21 | 131. | NRC 132 |
| 42. | MACS 1039 | 87. | NRC 25 | 132. | NRC 142 |
| 43. | MACS 1126 | 88. | NRC 29 | 133. | NRC 147 |
| 44. | MACS 1139 | 89. | NRC 34 | 134. | MACS 1460 |
| 45. | MACS 1140 | 90. | NRC 42 | 135. | CO (Soy) 3 |
| Source of variance | | | Mean sum of squares | | |

Table 2. Analysis of variance for the quantitative traits among soybean germplasm accession

| Source of variance | Mean sum of squares | | | | | |
|---|---------------------|-----------|---------|-----------|--------------------|-------|
| | Block | Treatment | Checks | Genotypes | Check vs Genotypes | Error |
| Degrees of freedom | 4 | 134 | 4 | 129 | 1 | 16 |
| Days to fifty per cent flowering | 42.05 | 12.12** | 72.34 | 9.98 | 46.96 | 0.22 |
| Days to maturity | 69.19 | 33.04** | 229.04 | 26.57 | 83.69 | 0.17 |
| Plant height | 77.73 | 149.96** | 377.82 | 143.30 | 98.07 | 0.48 |
| Number of branches per plant | 2.16 | 1.66 | 2.76 | 1.63 | 1.28 | 0.16 |
| Number of clusters per plant | 74.01 | 88.87** | 105.34 | 88.46 | 75.26 | 0.84 |
| Number of pods per cluster | 0.95 | 0.99 | 3.70 | 0.91 | 0.77 | 0.13 |
| Number of pods per plant | 8.18 | 1074.43** | 2539.54 | 1037.33 | 0.01 | 8.49 |
| Number of seeds per pod | 0.54 | 0.50 | 1.50 | 0.47 | 0.24 | 0.10 |
| Hundred seed weight | 0.77 | 4.50** | 9.22 | 4.38 | 0.54 | 0.22 |
| Single plant yield | 22.00 | 84.07 | 281.99 | 78.54 | 6.87 | 9.87 |

Table 3. Correlation coefficient for yield and yield attributing traits in the soybean germplasm accessions

| | DFD | DM | PH | NBP | NCP | NPC | NPP | NSP | HSW | SPY |
|-----|----------|----------|----------|-----|-----|-----|-----|-----|-----|-----|
| DFD | 1 | | | | | | | | | |
| DM | 0.6126** | 1 | | | | | | | | |
| PH | 0.5672** | 0.3464** | 1 | | | | | | | |
| NBP | 0.5435** | 0.2329** | 0.5594** | 1 | | | | | | |

| | | | | | | | | | | |
|-----|----------|---------|----------|----------|----------|----------|----------|---------|----------|---|
| NCP | 0.5367** | 0.0811 | 0.6397** | 0.7758** | 1 | | | | | |
| NPC | 0.1690* | 0.0597 | 0.1622 | 0.1298 | 0.2727** | 1 | | | | |
| NPP | 0.4670** | 0.0414 | 0.5802** | 0.6260** | 0.8375** | 0.5386** | 1 | | | |
| NSP | -0.0730 | -0.0482 | -0.1135 | 0.0276 | -0.0817 | -0.0579 | -0.1676 | 1 | | |
| HSW | -0.0216 | -0.0551 | -0.1864* | 0.0754 | 0.0282 | 0.1079 | -0.0414 | -0.0416 | 1 | |
| SPY | 0.3866** | 0.0524 | 0.3648** | 0.5855** | 0.6907** | 0.4146** | 0.7056** | 0.2192* | 0.3439** | 1 |

*Significance at 5% level **Significance at 1% level

| | | | | | |
|------------|---|----------------------------------|------------|---|----------------------------|
| DFD | - | Days to fifty per cent flowering | NPC | - | Number of pods per cluster |
| DM | - | Days to maturity | NPP | - | Number of pods per plant |
| PH | - | Plant height (cm) | NSP | - | Number of seeds per pod |
| NBP | - | Number of branches per plant | HSW | - | Hundred seed weight (g) |
| NCP | - | Number of clusters per plant | SPY | - | Single plant yield (g) |

Table 4. Path coefficient analysis for yield and yield attributing traits

| | | DFD | DM | PH | NBP | NCP | NPC | NPP | NSP | HSW | SPY |
|---|------------|----------------|---------------|----------------|---------------|---------------|---------------|---------------|---------------|---------------|----------|
| 1 | DFD | 0.0066 | 0.0348 | -0.0253 | 0.0068 | 0.1011 | 0.0006 | 0.2958 | -0.0259 | -0.0080 | 0.3866** |
| 2 | DM | 0.0040 | 0.0569 | -0.0155 | 0.0029 | 0.0153 | 0.0002 | 0.0262 | -0.0171 | -0.0206 | 0.0524 |
| 3 | PH | 0.0037 | 0.0197 | -0.0446 | 0.0070 | 0.1206 | 0.0005 | 0.3677 | -0.0402 | -0.0696 | 0.3648** |
| 4 | NBP | 0.0036 | 0.0132 | -0.0250 | 0.0126 | 0.1462 | 0.0004 | 0.3965 | 0.0098 | 0.0281 | 0.5855** |
| 5 | NCP | 0.0035 | 0.0046 | -0.0285 | 0.0098 | 0.1885 | 0.0009 | 0.5305 | -0.0290 | 0.0105 | 0.6908** |
| 6 | NPC | 0.0011 | 0.0034 | -0.0072 | 0.0016 | 0.0514 | 0.0034 | 0.3411 | -0.0205 | 0.0403 | 0.4146** |
| 7 | NPP | 0.0031 | 0.0024 | -0.0259 | 0.0079 | 0.1578 | 0.0018 | 0.6334 | -0.0594 | -0.0155 | 0.7056** |
| 8 | NSP | -0.0005 | -0.0027 | 0.0051 | 0.0003 | -0.0154 | -0.0002 | -0.1061 | 0.3543 | -0.0155 | 0.2192** |
| 9 | HSW | -0.0001 | -0.0031 | 0.0083 | 0.0009 | 0.0053 | 0.0004 | -0.0262 | -0.0148 | 0.3712 | 0.3439** |
| | | Residue=0.4678 | | | | | | | | | |

*Significance at 5% level **Significance at 1% level

| | | | | | |
|------------|---|----------------------------------|------------|---|----------------------------|
| DFD | - | Days to fifty per cent flowering | NPC | - | Number of pods per cluster |
| DM | - | Days to maturity | NPP | - | Number of pods per plant |
| PH | - | Plant height (cm) | NSP | - | Number of seeds per pod |
| NBP | - | Number of branches per plant | HSW | - | Hundred seed weight (g) |
| NCP | - | Number of clusters per plant | SPY | - | Single plant yield (g) |

Figure 1. Bar chart depicting PCV and GCV for ten quantitative traits of soybean germplasm accessions

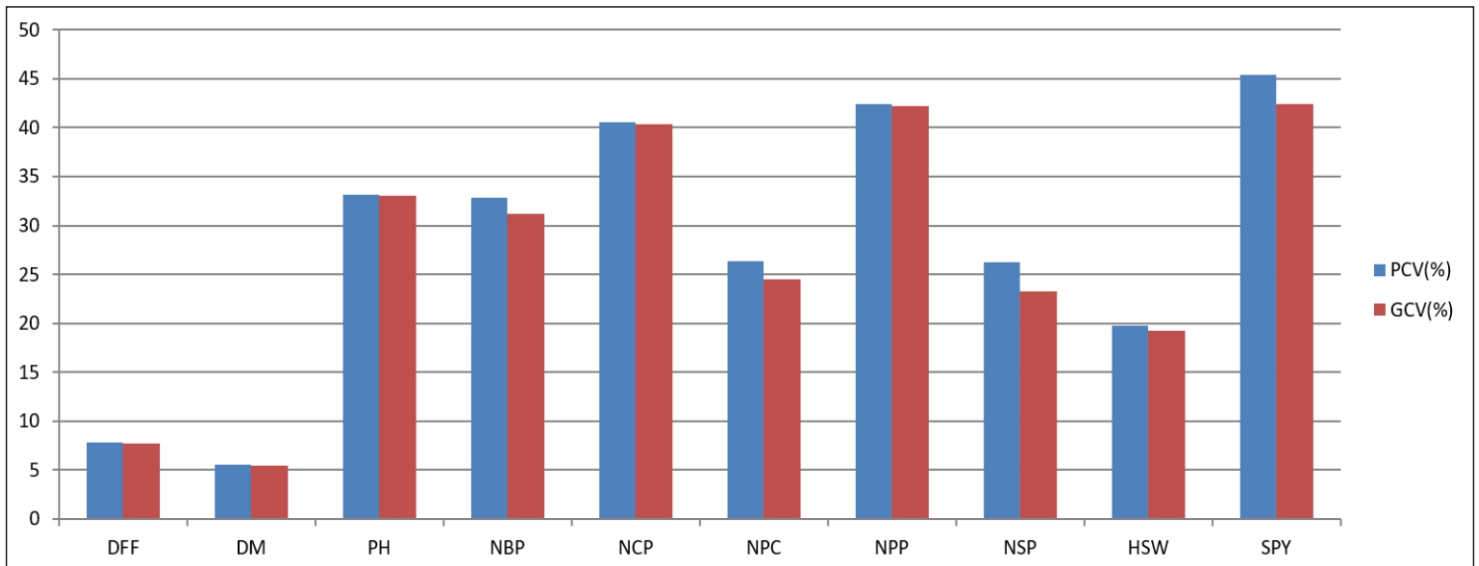


Figure 2. Bar chart depicting heritability and GAM for ten quantitative traits of soybean germplasm accessions

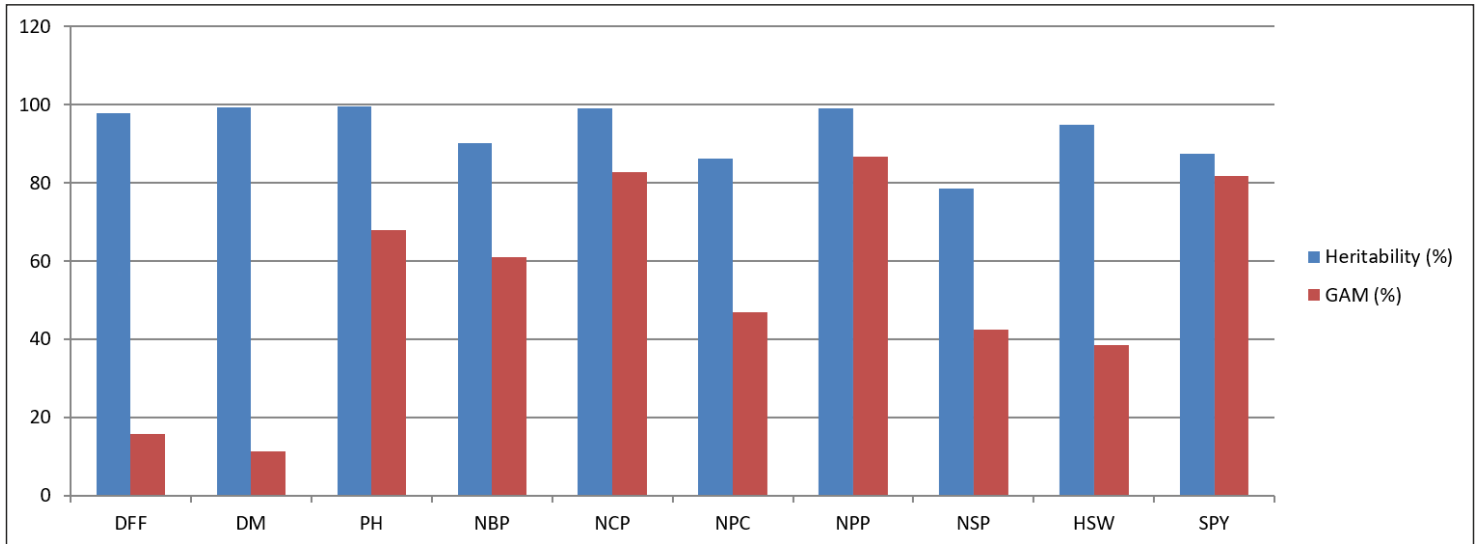
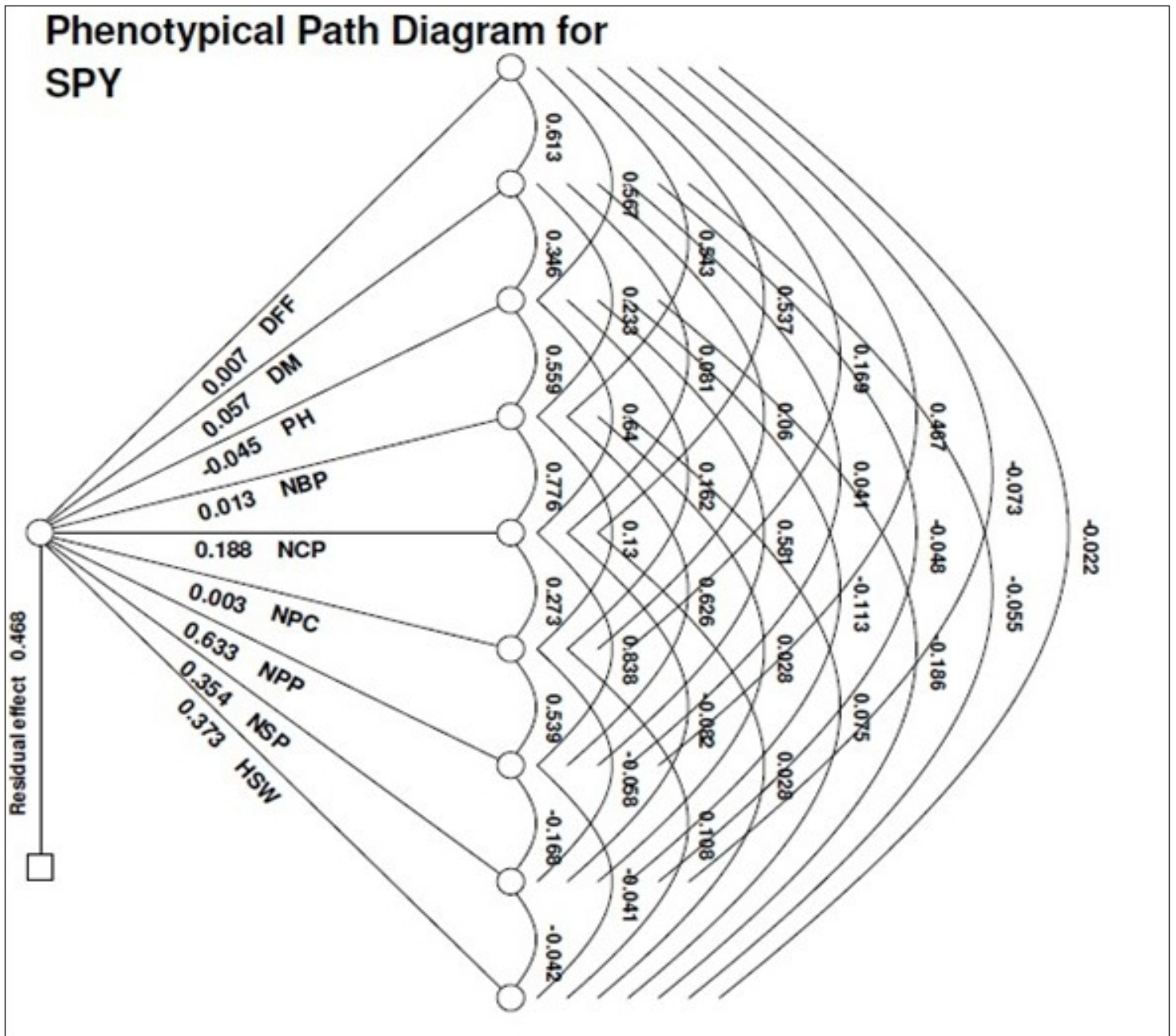


Figure 3. Path coefficient diagram for single plant yield



Conclusion

The present study showed the number of pods per plant had the maximum effect on single plant yield followed by number of clusters per plant and the number of seeds per pod. Therefore, these characters can be selected for future yield improvement breeding work.

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