

Research Article

Genetic variability and association studies in Napier grass (*Pennisetum purpureum* schumach.) for green fodder yield and quality traits

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Abstract

Thirty five Napier grass (*Pennisetum purpureum* Schumach.) genotypes were evaluated for character association study during *Kharif* 2013 at Forage Research Farm, Punjab Agricultural University, Ludhiana. The genotypes were analysed for genetic variability, correlation and path coefficients. The genotypes were significantly different for all the characters, which indicated scope for further genetic studies. High heritability along with high genetic advance was recorded for plant height, leaf length, leaf width, stem girth, number of leaves, crude protein, acid detergent fibre, dry matter yield and green fodder yield indicating the predominance of additive effects in the inheritance of these characters. The phenotypic coefficients of variation (PCV) were invariably higher than their corresponding genotypic coefficient of variation (GCV) thereby suggesting the environmental influence. High estimates of GCV and PCV were observed for leaf length, number of leaves/plant, number of tillers/plant, leaf stem ratio, dry matter yield and green fodder yield, suggesting that selection based on these characters would facilitate successful isolation of desirable types. Traits like plant height, leaf length, leaf width, stem girth, number of leaves per plant and dry matter yield had positive and significant correlation at genotypic as well as phenotypic level with green fodder yield and the selection based on these traits will result in improving the green fodder yield in Napier grass. Most of the yield contributing traits like plant height, leaf width, stems girth and dry matter yield as well as the quality trait neutral detergent fibre exhibited positive direct effect on green fodder yield.

Key words

Variability, Green fodder yield, Crude Protein, Correlation and path coefficient

Introduction

Napier grass or elephant grass (*Pennisetum purpureum* Schum.) is one of the most productive biomass plants in tropical and subtropical climates and it is an important forage and bioenergy crop. It is an important crop for dairy production in tropics. It is the forage of choice not only in the tropics but worldwide, due to its desirable traits such as drought tolerance and wide adaptability to soil conditions. It has high forage production potential coupled with high biomass and is of multicut nature that usually provides 5-8 cuts/year. Furthermore, it has an excellent regeneration potential along with its perennial growth behavior which makes it highly favorable among the dairy farmers. Plant breeding and selection in Napier grass has primarily been aimed at improving different agronomic traits such as disease resistance, yield, nutritional quality, growth habit (dwarfing), palatability and abiotic stress tolerance.

The efficiency of a breeding program depends primarily on the direction and magnitude of the association between the yield and yield components and on the relative importance of each factor to forage yield. The knowledge about association between yield and yield components facilitates the choice of suitable breeding method to be applied for improving the crops *per se*. Path analysis has been used by plant breeders to assist for identifying useful selectable traits (Dewey and Lu, 1959). Partitioning of the correlation

coefficient into its components, one component being the path coefficient that measures the direct effect of a predictor variable upon its response variable; the second component being the indirect effects of a predictor variable on the response variable through another predictor variable is the advantage of path analysis (Dewey and Lu, 1959). This technique is beneficial in determining the direct influence of one variable on another, and also separates the correlation coefficient into its components (Dewey and Lu 1959). An attempt was, therefore, made to estimate the extent of variability for different yield contributing traits, magnitude and direction of association among different characters both at genotypic and phenotypic levels. In view of this, the present investigation was carried out with the objective of assessing the nature and magnitude of genetic variability prevalent among the Napier grass genotypes tested along with the nature of characters association amongst the various yield contributing traits and quality parameters. In this study, an attempt was made to study the direct and indirect effects of some important forage yield components on forage yield of Napier grass by correlation and path coefficient analysis. The results might be capable in developing the selection criteria in further studies in order to increase the selection efficiency in Napier grass breeding programme.

Materials and Methods

The experiment was conducted during *Kharif* 2013 at Forage Research Farm, Punjab Agricultural University, Ludhiana with thirty five genotypes and the material was grown in randomized complete block design (RBD), where each entry was accommodated in 3 x 3 sq. m. plot size containing 5 rows of 3 m length with inter row and plant to plant spacing of 60 cm with three replications. Recommended package of practices to raise a good crop were followed. Observations were recorded on five competitive and healthy plants selected randomly from each entry on nine quantitative variables *viz.*, plant height, leaf length, leaf width, stem girth, number of leaves/plant, number of tillers/plant, leaf stem ratio, crude protein, *in vitro* dry matter digestibility, acid detergent fibre and neutral detergent fibre, dry matter yield and green fodder yield. The data were analysed for variability, divergence, correlation and path coefficient study. Genotypic and phenotypic coefficients of correlation were calculated from genotypic and phenotypic covariances and variances as described by Singh and Chaudhry (1977) and Johnson *et al.* (1955). Direct and indirect effects were calculated by the path coefficient analysis as suggested by Dewey and Lu (1959) at both phenotypic and genotypic levels. Genotypic and phenotypic coefficients were calculated using the formulae as used by Burton and De Vane (1953) and Johnson *et al.* (1955). Heritability in broad sense was estimated as suggested by Burton (1952). The expected genetic advance at 5% selection intensity was calculated by the formula as used by Johnson *et al.* (1955).

Results and Discussion

Estimates of genetic variability: The extent of variability and heritability of the characters among the genotypes is the basic source for the exploitation of superior potentiality of genotypes. Genetic variability study helps to know about the nature and extent of variability attributable to different cases, sensitive nature of the crop to the environmental influences, heritability of the characters and genetic advance that can be realized in practical breeding. The analysis of variance in the present study showed highly significant differences among the genotypes for all the characters studied, indicating the presence of adequate variability in the experimental material of Napier grass. This variation indicated the scope of selection for these traits in further breeding programme. Similar result for plant height and number of tillers per plant has been reported by Sowmiya (2012) and Sathya (2014) in pearl millet.

It is evident from the range of mean values for different traits among the genotypes evaluated (Table 1) that these had diverse genetic background. The traits like plant height (185.0 – 223.0 cm), leaf length (65.0 – 115.0 cm), leaf

width (4.2 – 7.1cm), number of leaves per plant (75.0 – 192.8), number of tillers per plant (14.5 – 56.7), leaf stem ratio (0.35 – 0.80), dry matter yield (10.2 – 22.0) and green fodder yield (42.0 – 110.0) had wide range of mean values. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2) and genetic advance as percent of mean (GA) (Table 1) revealed that GCV and PCV values were invariably higher for most of the traits except number of leaves/plant, stem girth, *in-vitro* dry matter digestibility, acid detergent fibre and neutral detergent fibre indicating that these traits are primarily controlled by the genetic parameters rather than environment effect alone. Also high estimates of GCV and PCV were observed for leaf length, number of tillers/plant, leaf stem ratio, dry matter yield and green fodder yield, suggesting that selection based on these characters would facilitate successful isolation of desirable types. Concomitant findings for crude fibre content were reported by Suthamathi and Dorairaj (1997) in Napier grass. However, the genetic variability together with heritability estimates would give a better idea on the amount of genetic advance (GA) expected from selection (Burton 1952). Stem girth along with the three quality parameters evaluated *viz.*, *in-vitro* dry matter digestibility, acid detergent fibre and neutral detergent fibre had low GCV values indicating little scope for improvement in these traits in the material studied.

High h^2 along with high GA was recorded for plant height, leaf length, leaf width, stem girth, number of tillers per plant, crude protein, acid detergent fibre, dry matter yield and green fodder yield. The obtained results were in accordance with the results on number of leaves per plant by Suthamathi and Dorairaj (1997) in Napier grass. Heritability along with phenotypic variance and the severity of selection provide estimableness of genetic advance or responding to the selection which is very useful in the selection of promising lines (Johnson *et al.*, 1955). Traits having high h^2 and high GA are supposed to be under control of additive genes; hence, these can be improved by selection based on phenotypic performance (Singh *et al.*, 2005). Number of leaves had lowest h^2 (13.41) followed by leaf stem ratio (29.84), and hence it is difficult to improve these traits by phenotype guided selection. Traits like *in-vitro* dry matter digestibility, neutral detergent fibre had high h^2 but low values of GA suggesting the involvement of non-additive gene action in their inheritance. Traits like leaf length, stem girth, number of tillers per plant, dry matter yield and green fodder yield exhibited high h^2 coupled with high PCV suggesting greater scope for selection of these traits on phenotypic basis.

Genotypic and phenotypic correlation coefficients: Fodder yield is a complex character controlled by several components which reflect positive and negative effects on this trait. It is important to note that whenever two traits are correlated, selecting for one would ensure selection for the other trait, therefore selecting for the best of the traits that correlated with yield in this study would result in increased yields. Association between green yield, plant height and number of tillers per plant was also reported by Santosh *et al*, 2017. Thus, for achieving rational improvement in fodder yield and its components, knowledge on mechanism of association, cause and effect relationship provides a basis for formulating suitable selection methods for the yield components.

Results indicated that all the yield contributing traits except leaf stem ratio, acid detergent fibre and neutral detergent fibre had positive and significant correlation at genotypic as well as phenotypic level with green fodder yield (Table 2) and the selection based on these traits will result in improving the green fodder yield in Napier. On the contrary, leaf stem ratio and two other quality traits evaluated *viz.*, acid detergent fibre and neutral detergent fibre exhibited a negative and significant correlation with green fodder yield and dry matter yield as well, whereas crude protein did not exhibit significant correlation (positive or negative) with green fodder yield. Traits like plant height, leaf length, leaf width, stem girth and number of leaves/plant, number of tillers/plant showed positive and highly significant correlation amongst each other but exhibited negative and highly significant correlation with quality parameters *viz.*; neutral detergent fibre, acid detergent fibre and crude protein. Highest value of positive and significant correlation was observed between green fodder yield and number of leaves/plant (0.9406, 0.9343) closely followed by green fodder yield and plant height (0.8995, 0.8828) whereas acid detergent fibre and crude protein (-0.8708, -0.8506) exhibited highest value of negative and significant correlation.

Amongst the four quality parameters under study only *in-vitro* dry matter digestibility exhibited positive and significant correlation with dry matter yield and green fodder yield whereas the other two traits *viz.*, acid detergent fibre and neutral detergent fibre exhibited negative and significant correlation with dry matter yield and green fodder yield. There are no published reports on association study between forage quality traits and other fodder yield contributing traits in Napier, therefore, our study, for the first time, shed the light on association behaviour between forage quality and other fodder yield contributing traits.

Path coefficient analysis for direct and indirect effects on green fodder yield

Partitioning of the total correlation coefficient into direct and indirect effects for green fodder yield showed a positive direct effect of many yield contributing traits except leaf length (Table 3). Amongst quality traits only crude protein and neutral detergent fibre had positive direct effect on green fodder yield whereas other two quality traits *viz.*, *in vitro* dry matter digestibility and acid detergent fibre had negative direct effect that deluded the positive and direct effect of earlier traits on green fodder yield. Many other studies have also reported that the dry forage yield/ plant is significantly and positively associated with green fodder yield and yield components such as plant height, number of leaves/plant, and stem diameter. Thus, the improvements in characters such as plant height, number of leaves/plant, and stem diameter will help to improve fodder yield both directly and indirectly. The positive indirect effects were contributed through most of the yield contributing traits except leaf length and stem girth (Table 3). Out of the four quality traits evaluated crude protein and neutral detergent fibre had positive whereas *in vitro* dry matter digestibility and acid detergent fibre had negative indirect effects on green fodder yield. Positive and significant genotypic correlation values of traits *viz.*, plant height, leaf width, stem girth, number of leaves/plant, number of tillers per plant and dry matter yield with green fodder yield and their positive direct effect values on green fodder yield indicated a true picture of association between these traits.

Selection for taller plants with more number of broader and longer leaves with thicker stem and having high tillering ability will be significant for the improvement of green fodder yield in the Napier grass genotypes under study. At the same time progress in breeding for enhanced green fodder yield may be adversely affected by selection for quality traits like leaf stem ratio, neutral detergent fibre and acid detergent fibre due to a strong negative association of these traits with green fodder yield.

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Table 1. Estimates of genetic parameters for different traits in Napier genotypes

| Characters | Range | h^2 (%) | GA (%) | PCV | GCV | GM |
|--------------|---------------|-----------|--------|-------|-------|-------|
| PH | 185.0 – 223.0 | 94.57 | 29.12 | 16.26 | 15.18 | 179.1 |
| LL | 65.0 – 115.0 | 94.50 | 40.10 | 22.45 | 21.72 | 74.1 |
| LW | 4.2 – 7.1 | 90.40 | 27.41 | 14.35 | 13.71 | 5.3 |
| SG | 1.5 - 3.1 | 71.33 | 24.41 | 13.88 | 12.45 | 1.8 |
| NOL | 75.0 – 192.8 | 13.41 | 32.11 | 8.59 | 5.88 | 88.9 |
| NOT | 14.5 - 56.7 | 32.24 | 20.78 | 32.47 | 18.45 | 22.3 |
| LSR | 0.35 – 0.80 | 29.84 | 17.45 | 32.31 | 17.63 | 0.45 |
| CP | 6.2- 10.8 | 90.05 | 24.15 | 12.40 | 11.19 | 7.2 |
| IVDMD | 50.1 - 59.5 | 91.74 | 12.71 | 6.64 | 6.12 | 52.2 |
| ADF | 38.9 - 51.6 | 74.42 | 25.89 | 12.05 | 12.00 | 40.1 |
| NDF | 50.1 - 62.6 | 71.47 | 9.12 | 5.74 | 5.41 | 54.3 |
| DMY | 10.2 - 22.0 | 96.44 | 86.11 | 48.48 | 42.17 | 16.8 |
| GFY | 42.0 - 110.0 | 98.18 | 78.51 | 39.73 | 36.12 | 75.2 |

PH= plant height (cm), leaf length=LL (cm), LW= Leaf width (cm), SG= stem girth (cm), NOL= Number of leaves/plant, NOT= number of Tillers/plant, LSR= Leaf stem ratio, CP= Crude Protein (%), IVDMD= *In Vitro* Dry Matter Digestibility, ADF= Acid Detergent Fibre (%), NDF= Neutral Detergent Fibre (%), DMY= Dry matter yield (kg/plot), GFY= Green fodder yield (kg/plot). h^2 = heritability (broad sense); PCV= Phenotypic coefficient of variability; CV= Genotypic coefficient of variability; GA (%)= Genetic advance as percentage of mean; GM= grand mean



Table 2. Genotypic and phenotypic correlation coefficients among various traits of Napier genotypes

| Characters | | PH | LL | LW | SG | NOL | NOT | LSR | CP | IVDMD | ADF | NDF | DMY |
|------------|---|----------|----------|-----------|----------|----------|---------|----------|----------|----------|---------|----------|----------|
| LL | G | 0.913** | | | | | | | | | | | |
| | P | 0.896** | | | | | | | | | | | |
| LW | G | 0.521** | 0.864** | | | | | | | | | | |
| | P | 0.506** | 0.844** | | | | | | | | | | |
| SG | G | 0.778** | 0.963** | 0.347** | | | | | | | | | |
| | P | 0.671** | 0.942** | 0.392** | | | | | | | | | |
| NOL | G | 0.598** | 0.714** | 0.277** | 0.929** | | | | | | | | |
| | P | 0.534** | 0.692** | 0.134* | 0.734** | | | | | | | | |
| NOT | G | 0.133* | 0.497** | 0.151** | 0.802** | 0.513** | | | | | | | |
| | P | 0.131* | 0.374** | 0.031 | 0.521** | 0.327** | | | | | | | |
| LSR | G | -0.306** | -0.078 | -0.592** | -0.373** | -0.235** | -0.176* | | | | | | |
| | P | -0.175* | -0.037 | -0.395** | -0.073 | 0.100 | 0.030 | | | | | | |
| CP% | G | 0.079 | -0.05 | -0.697** | 0.388** | 0.591** | 0.008 | -0.125* | | | | | |
| | P | 0.072 | -0.049 | -0.642** | 0.337** | 0.249** | 0.073 | -0.066 | | | | | |
| IVDMD | G | 0.341** | 0.305** | -0.417** | 0.746** | 0.835** | 0.307** | -0.240** | 0.781** | | | | |
| | P | 0.329** | 0.3017** | -0.4176** | 0.683** | 0.502** | 0.191* | -0.031 | 0.732** | | | | |
| ADF | G | -0.193* | 0.1152* | 0.056 | -0.336** | -0.520** | -0.033 | 0.725** | -0.871** | -0.797** | | | |
| | P | -0.188* | 0.1163* | 0.050 | -0.255** | -0.091 | -0.069 | 0.544** | -0.851** | -0.789** | | | |
| NDF | G | 0.046 | 0.2551** | 0.087 | -0.141* | -0.039 | -0.153* | 0.370** | -0.784** | -0.645** | 0.892** | | |
| | P | 0.043 | 0.2519** | 0.079 | -0.101 | -0.107 | -0.042 | 0.254** | -0.755** | -0.633** | 0.885** | | |
| DMY | G | 0.878** | 0.9753** | 0.443** | 0.914** | 0.945** | 0.081 | -0.170* | 0.052 | 0.474** | -0.177* | -0.227** | |
| | P | 0.849** | 0.9361** | 0.412** | 0.811** | 0.497** | 0.096 | -0.016 | 0.019 | 0.467** | -0.165* | -0.214** | |
| GFY | G | 0.899** | 0.9025** | 0.491** | 0.919** | 0.941** | 0.115* | -0.242** | 0.008 | 0.446** | -0.155* | -0.171* | 0.877** |
| | P | 0.8828** | 0.9008** | 0.468** | 0.843** | 0.934** | 0.134* | -0.070 | -0.009 | 0.442** | -0.149* | -0.167* | 0.868s** |

*=Critical value of 'r' at 5% = 0.1102, **=Critical value of 'r' at 1% = 0.2001; G= genotypic correlation coefficient; P= phenotypic correlation coefficient

PH= plant height(cm), LL = leaf length (cm), LW= leaf width (cm), SG= stem girth (cm), NOL= number of leaves/plant, NOT= number of Tillers/plant, LSR= Leaf stem ratio, CP= crude protein (%), IVDMD= *in vitro* dry matter digestibility, ADF= acid detergent fibre (%), NDF= neutral Detergent Fibre (%), DMY= Dry matter yield (kg/plot), GFY= Green fodder yield (kg/plot)



Table 3. Path coefficient analysis for direct (bold) and indirect effects on green fodder yield (kg/plot) in Napier genotypes

| Characters | PH | LL | LW | SG | NOL | NOT | LSR | CP | IVDMD | ADF | NDF | DMY | Genotypic correlation with GFY |
|--------------|---------------|---------------|--------------|---------------|---------------|---------------|---------------|---------------|---------------|----------------|---------------|---------------|--------------------------------|
| PH | 0.5401 | -0.3471 | 0.2609 | 0.531 | 0.2086 | 0.2141 | 0.0976 | 0.1399 | 0.0839 | 0.2445 | 0.1784 | 1.0112 | 0.8995** |
| LL | 0.5052 | -0.419 | 0.276 | 0.5762 | 0.2104 | 0.2194 | 0.1052 | 0.1529 | 0.1347 | 0.2133 | 0.183 | 0.9241 | 0.9025** |
| LW | 0.3857 | -0.2003 | 0.309 | 0.4171 | 0.2287 | 0.2197 | 0.0779 | 0.1646 | 0.2186 | 0.1385 | 0.2182 | 0.749 | 0.4912** |
| SG | 0.464 | -0.3268 | 0.2608 | 0.6409 | 0.2056 | 0.2273 | 0.0475 | 0.1362 | 0.0409 | 0.3351 | 0.103 | 0.8291 | 0.9186** |
| NOL | 0.5921 | -0.4834 | 0.2541 | 0.7655 | 0.2668 | 0.2388 | 0.0853 | 0.1247 | -0.0435 | 0.3618 | 0.1365 | 0.938 | 0.9406** |
| NOT | 0.2671 | 0.0308 | 0.2421 | 0.4453 | 0.2146 | 0.2404 | 0.0978 | 0.1481 | 0.1213 | 0.2366 | 0.1176 | 0.0882 | 0.1149* |
| LSR | 0.1334 | 0.3921 | 0.1717 | -0.0728 | 0.2508 | 0.2013 | 0.3314 | 0.1517 | 0.2369 | 0.035 | 0.223 | -0.1178 | -0.2424** |
| CP% | 0.2506 | 0.3773 | 0.1616 | 0.2627 | 0.2287 | 0.2066 | 0.1144 | 0.1011 | -0.0493 | 0.3796 | 0.05 | 0.3271 | 0.0075 |
| IVDMD | 0.3306 | 0.1517 | 0.1882 | 0.4206 | 0.2167 | 0.2154 | 0.0943 | 0.1055 | -0.074 | 0.42 | 0.0323 | 0.513 | 0.4463** |
| ADF% | 0.1676 | 0.2709 | 0.2331 | -0.0564 | 0.2585 | 0.2054 | 0.2635 | 0.173 | 0.3675 | -0.0621 | 0.3283 | -0.0813 | -0.1549* |
| NDF% | 0.2405 | 0.1829 | 0.2361 | 0.0294 | 0.2455 | 0.2019 | 0.2012 | 0.1695 | 0.3324 | -0.0179 | 0.3611 | -0.039 | -0.1714* |
| DMY | 0.4945 | -0.2702 | 0.2699 | 0.4945 | 0.2191 | 0.2088 | 0.1066 | 0.1353 | 0.0753 | 0.2505 | 0.1373 | 1.1601 | 0.8768** |

PH= plant height(cm), LL = leaf length (cm), LW= leaf width (cm), SG= stem girth (cm), NOL= number of leaves/plant, NOT= number of Tillers/plant, LSR= Leaf stem ratio, CP= crude protein (%), IVDMD= *in vitro* dry matter digestibility, ADF= acid detergent fibre (%), NDF= neutral Detergent Fibre (%), DMY= Dry matter yield (kg/plot), GFY= Green fodder yield (kg/plot). h^2 = heritability (broad sense); PCV= phenotypic coefficient of variability; CV= genotypic coefficient of variability; GA (%)= genetic advance as percentage of mean; GM= grand mean