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Assessment of genetic variability and character association in Tobacco (*Nicotiana tabacum* L.) genotypes

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Abstract
The present study was carried out to study yield and yield attributing traits in tobacco, to deliver information regarding the amount of variability, broad-sense heritability, genetic advance over mean and traits association. The experiment was laid out during *Rabi 2020* in an Augmented Block Design with 242 genotypes and 4 checks. The box plot analysis revealed that maximum variability for all the traits and the Analysis of variance revealed that the magnitude of the phenotypic coefficient of variance is slightly higher than the genotypic coefficient of variance for all characters studied. Furthermore, a high amount of broad-sense heritability and genetic advance over mean were observed for traits like plant height, number of leaves per plant, internode length, leaf length, leaf width, and yield. This implies that direct selection for these traits might lead to significant progress in discovering superior tobacco genotypes. The character association study revealed that yield was positively and significantly correlated with plant height, the number of leaves per plant, leaf length, leaf width, and internode length hence, selection for these traits will help improve yield.

Keywords: Tobacco genotypes, genetic variability, correlation, augmented design, box plot

Introduction

Tobacco (*Nicotiana tabacum* L.) is the world's most widely grown non-food crop. It was introduced to India by the Portuguese in 1605, which plays an important role in the country's economy. Tobacco belongs to the Solanaceae family, out of 66 species only two species *viz. N. tabacum* L. and *N. rustica* L. are under cultivation. The alternative uses of tobacco are gaining more importance nowadays, like in bio-pesticides (nicotine sulphate), pharmaceuticals (solanesol, nicotinic acid, and nicotinamide), soap, varnishes, and paints. Tobacco seed, with its high oil content and high-quality seed cake, has a lot of potential for being used in alternative ways. When compared to other vegetable oils, tobacco seed oil has the largest percentages of linoleic acid (70.6%), oleic acid (17.1%), palmitic acid (7.9%), stearic acid (3.1%), and other fatty acids. The quality of nicotine-free tobacco oil is comparable with other edible oils.

The tobacco crop improvement programme requires primarily the collection, maintenance, and evaluation of germplasm. Further crop genetic improvement requires the creation and exploitation of variability through suitable breeding procedures. It is beneficial to develop a sound breeding programme by assessing genetic variation and the degree of transmission of desirable yield attributing traits. It is important to assess variability in this regard. As a result, a plant breeder must use parameters like range, phenotypic coefficient of variation, genotypic coefficient of variation, broad-sense heritability, and genetic advance as a percent mean to evaluate variability.

Correlation analysis was performed to identify the kind and amount of relationship between a pair of characteristics. These connections help researchers to better understand on how one trait contributes to the genetic makeup of a crop's other traits. Knowledge of the relationships between economically important traits and the characters that contribute to all those traits in all combinations will aid in determining the criteria for selection and also allows for improvement in the related characters.

Materials and Methods

The experimental material comprised of 242 genotypes of tobacco collected from different

sources were evaluated at the Agricultural research station. Nipani, during *Rabi* 2020. The site of the experiment is situated in the Northern transitional zone of Karnataka at 16.2⁰ N latitude and 74.2⁰ E longitude at an altitude of 610 m above mean sea level. The experimental site receives a mean annual rainfall of 730.1 mm. The experiment was laid out in an Augmented block design with six blocks and four checks *viz.* Vedaganga-1, A-119, Bhavyashree, and NBD 209 at a spacing of 1.0 x 0.75 m. The observations were recorded for 6 characters *viz.* plant height, number of leaves per plant, internode length, leaf length, leaf width, and yield per plant. The analysis of variance for the design of the experiment was done for partitioning the variance according to the procedure given by Federer (1956) [3] and Federer (1961) [4] and the generation as well as comparison of the means of the treatments or genotypes. The data analysis was done using the *augmented RCBD* [1] package and correlation, scatter plots, and box plots were drawn using *ggally*, *ggplot2*, and *metan* packages of *Rstudio*.

Result and Discussion

Analysis of variance revealed significant differences among the genotypes for all the traits studied and indicating the presence of sufficient genetic variability for improvement of the crop (Table 1.). Table 2 and results of box plot analysis (Figure 1) show the level of variability in various genotypes concerning six traits measured in terms of range, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), amount of broad heritability (h^2bs), and estimated genetic advance as percent of mean (GAM). For all of the characters, there was a significant degree of variance. The observed phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for all the traits studied and the narrow gap between them indicates the lesser influence of environment on traits studied (Table 2). The data in the Table 2 unveiled that high GCV and PCV estimates for the traits like Number of leaves per plant (45.17 and 45.56), internode length (60.97 and 61.97), leaf width (20.77 and 20.89), and yield per hectare (47.5 and 48.22). Moderate GCV and PCV were seen for traits like Plant Height (19.33 and 19.52) and Leaf length (12.59 and 14.6). Based on the availability of sufficient variability in the genotypes tested, moderate to high GCV and PCV for these characteristics suggested ample opportunity for yield improvement in tobacco through selection. The Selection among the genotypes showing higher values of PCV and GCV will be beneficial for the improvement of the trait on account of the variation present for the trait between the genotypes. The results of the present study were in agreement with the results of, Bhumarannavar (2009) [2], Parajuli (2014) [9], Katba *et al*. (2014) [5], and Sunil and Mohan (2015) [14].

The broad-sense heritability estimated were ranged from 98.92 percent for leaf width to 74.4 percent for leaf length. The leaf width recorded the highest broad-sense heritability of 98.92 followed by the number of leaves per plant (98.29%), plant height (98.11%), yield per hectare (97.02%), internode length (96.78%) and leaf length with (74.4%). The high amount of broad-sense heritability for these traits indicates the least influence of the environment on these characters.

The High estimation of genetic advance over mean (GAM) was observed for the traits *viz.* yield per hectare (132.28), internode length (123.73%), number of leaves per plant (92.39), leaf width (42.62), plant height (39.5) and leaf length (22.41). High estimates of genetic advance over mean reveals

the preponderance of additive gene action in the expression of these traits in tobacco. As a result, phenotypic performance-based selection for these characteristics in segregating generations would probably be more successful. These results were in accordance with earlier studies like Bhumarannavar (2009) [2], Parajuli (2014) [9] and Sunil and Mohan (2015) [14].

The phenotypic correlation is the relationship between the characteristics that can be observed directly. The ability to understand the phenotypic association between yield contributing characteristics aids in the development of a crop improvement programme. The correlations among the 6 traits using 246 genotypes of tobacco evaluated in the present study are shown in Figure 2. The yield per hectare showed a positive and significant correlation with plant height (r_p =0.566), number of leaves per plant (r_p =0.193), internode length (r_p =0.467), leaf length (r_p =0.420), and leaf width (r_p =0.495). In breeding programs, the association of traits can be used to predict the effectiveness of an indirect selection of a trait with the primary goal of improving another trait. If traits are difficult to measure or expensive to quantify, or if they have low heritability, their covariance with traits that have a higher heritability can be explored. As these traits are strongly associated with yield (Figure 1), selecting these traits may be effective in indirectly improving yield. These results are comparable to previous reports of Ramachandra *et al*. (2014), Parajuli (2014) [9], Katba *et al*. (2014) [5], Bhumarannavar (2009) [2], and Patel and Makwana (2002) [10]. The plant height trait showed a positive and significant association with leaf width (r_p =0.628), leaf length (r_p =0.574), Internode length (0.647), and the number of leaves per plant (0.409). This suggests that improving plant height will indirectly help in improving all the other yield traits. The Internode length was significantly correlated with leaf length (r_p =0.562) and leaf width (r_p =0.582). The internode length trait directly influences the leaf length and leaf yield and leaf length showed a strong positive association with leaf width (r_p =0.874), by considering these results, improvement in these traits will be helpful in leaf yield improvement. The number of leaves per plant showed a negative nonsignificant correlation with the leaf width (r_p = -0.071), Leaf length (r_p =-0.099), and a non-significant positive association with Internode length (r_p = 0.006) These findings were analogous to the results of Patel and Kingaonkar (2005) [11], Lalithadevi *et al*. (2002) [6], Pandey *et al*. (1983) [8] and Patel *et al*. (1976) [12].

Conclusion

Based on the evaluation of 242 genotypes, it can be concluded that a sufficient amount of genetic variability for various yield and yield attributing traits were generated using a wide range of tobacco genotypes, indicating that there is a huge scope of improvement for these genotypes for all of these traits studied through selection and hybridization in future. Furthermore, all traits under investigation had moderate to high GCV, high broad-sense heritability, and high genetic advance as percent of the mean, indicating predominantly additive gene action. As a result, these yield and yield attributing characteristics have plenty of scope for improvement through selection. Further positive and significant correlation of plant height, number of leaves per plant, leaf length, leaf width, and internode length with yield and high variability for these traits proved their importance in selection for improvement of yield in tobacco.
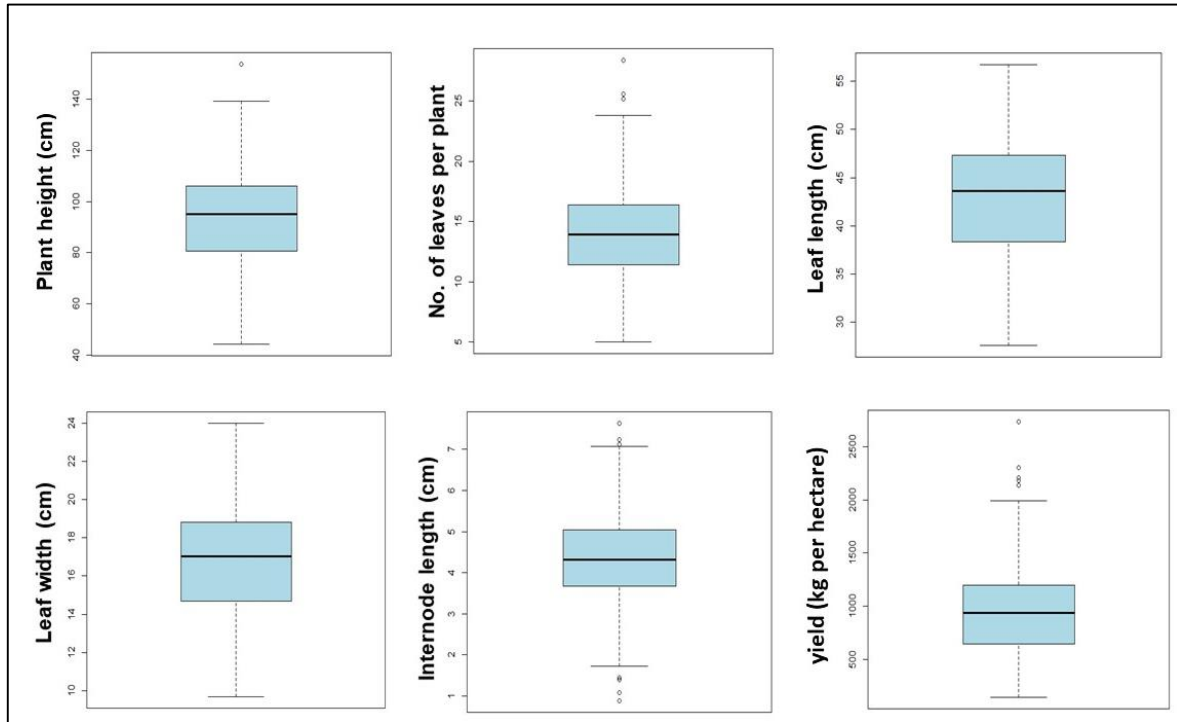
Fig 1: Boxplot analysis of variability for yield and yield attributing traits using 242 genotypes of tobacco.
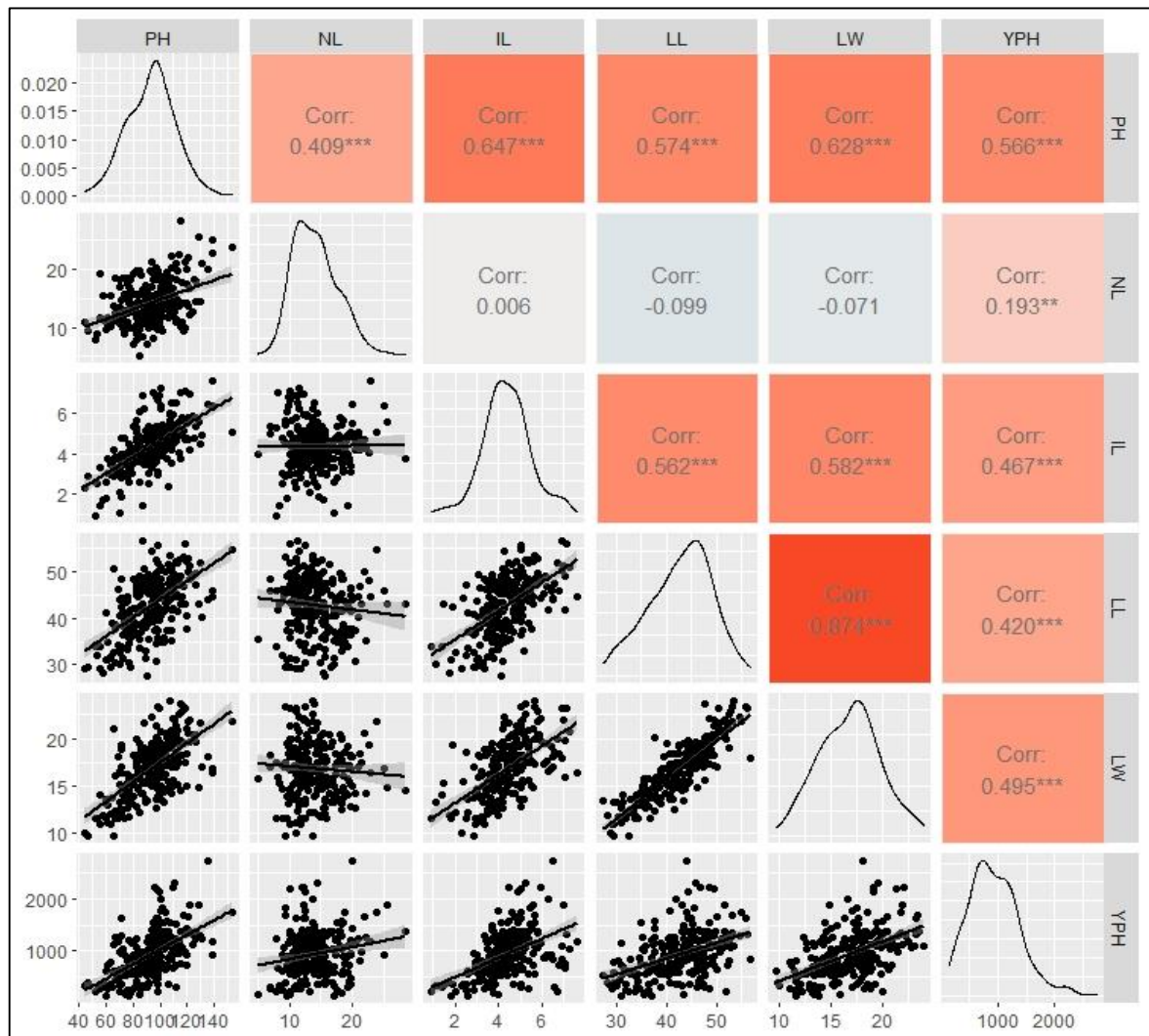
Fig 2: The coefficient of phenotypic correlation among yield-attributing traits in tobacco genotypes included Plant height (PH), number of leaves per plant (NL), internode length (IL), leaf length (LL), leaf width (LW), and yield per ha (YPH). The density plots of each trait's adjusted means (diagonal), scatterplots (below diagonal), and values of phenotypic correlation (above diagonal) between traits are displayed. ** Significant at the 1% global level ($p < 0.01$). *** Significant at the 0.1% global level ($p < 0.001$).

Table 1: Analysis of variance for yield and yield attributing characters in tobacco genotypes

Source of variation	Df	Plant height (cm)	Inter node length(cm)	Leaf length (cm)	Leaf width (cm)	Number of leaves per plant	Yield per ha (Kg)
Block (ignoring Treatments)	5	2.67 ns	0.06 ns	15.48 ns	0.56 *	0.9 ns	10486 ns
Treatment (ignoring Blocks)	245	338.34 **	7.76 **	39.15 **	12.34 **	43.73 **	202271**
Treatment: Check	3	888.41 **	0.21 ns	61.8 **	1.91 **	19.93 **	63640**
Treatment: Test vs. Check	1	182.96 **	3.97 **	10.06 ns	31.42 **	11.65 **	569934**
Treatment: Test	241	332.14 **	7.87 **	38.99 **	12.39 **	44.16 **	202471**
Residuals	15	6.26	0.25	9.98	0.13	0.75	15992.05
Mean		93.38	4.53	42.76	16.85	14.59	949.84
A Test Treatment and a Control Treatment CD @ 5%		6.44	1.3	8.13	0.94	2.24	148.28
CV (%)		2.67	11.2	7.4	2.18	5.93	13.3

Table 2: Genetic parameters concerning yield and yield attributing traits in tobacco genotypes

Trait	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	GAM (%)
		Max	Min				
Plant height (cm)	93.38	152.49	44.44	19.33	19.52	98.11	39.5
Internode length (cm)	4.53	7.64	0.9	60.97	61.97	96.78	123.73
Leaf length (cm)	42.76	54.83	27.06	12.59	14.6	74.4	22.41
Leaf width (cm)	16.85	24.00	9.82	20.77	20.89	98.92	42.62
Number of leaves per plant	14.59	28.4	5.19	45.17	45.56	98.29	92.39
Yield per ha (Kg)	949.84	2736.00	144.00	47.5	48.22	90.02	132.28

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