



## Research Article

# Heritability and genetic variability studies in the germplasm accessions of flue cured Virginia tobacco (*Nicotiana tabacum* L.)

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## Abstract

The present study was undertaken to ascertain the existence of genetic variability and estimate genetic parameters of yield-related characters in 250 flue-cured Virginia (FCV) tobacco germplasm accessions. Analysis of variance revealed the significance of variability among the accessions for all the studied characters viz., plant height, number of leaves, internodal length, mean leaf area per plant, green leaf yield per plant, and cured leaf per plant. phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the studied traits even though the difference between them is narrow indicating a lesser role of environment in influencing the expression of these traits. Broad sense heritability and genetic advance as percent of mean (GAM) were in the high range for plant height, inter-nodal length, number of leaves per plant, average leaf area, green leaf yield, and cured leaf indicating that selection based on phenotype will be quite effective for these traits. A high magnitude of broad-sense heritability coupled with moderate to high GCV and high GAM was noticed for all the studied characters indicating that additive gene action is involved in the expression of these traits. Thus, the presence of fixable additive gene action makes it possible to use the available variability in further tobacco improvement programs through simple selection.

**Keywords** coefficient of variation, genetic advance, germplasm, heritability, tobacco

## Introduction

Tobacco is a native plant of tropical America, which is known to consist of more than 70 species. *Nicotiana tabacum* L is the chief commercial species, cultivated widely for leaf in about 4.2 million hectares distributed in over more than a hundred countries. The top producers of tobacco are China (36%), India (8.3%), Brazil (7%), and the United States of America (4.6%)[17]. Tobacco is also an excellent source of phytochemicals viz., nicotine, solanesol, seed oil, edible proteins (green leaf), and organic chemicals such as malic acid and citric acid having pharmaceutical, agricultural and industrial uses.

Tobacco is a major cash crop of India. In Karnataka, it is cultivated as rain-fed (*Kharif*) crop on light soils in about 81.364 million hectares producing 106.07 mkg [11]. However, the net returns realized by the farmers are low owing to monsoon vagaries in the changed global climatic scenario and ever-increasing input and labor cost. The best option to increase net returns is by increasing the yield through genetic improvement as there is

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**Table 1. Analysis of variance for 250 germplasm accession for yield and yield related traits**

Source	Df	Plant height	No. of leaves <sup>1</sup> plant	Inter-nodal length (cm)	Average leaf area (cm <sup>2</sup> )	Green Leaf Yield <sup>1</sup> Plant (g)	Cured Leaf Yield <sup>1</sup> Plant (g)
Block (Ignoring Treatments)	9	302.13 **	15.51 **	2.33 **	53824.67 **	153710.97 **	2677.19 **
Treatment (Eliminating Blocks)	251	207.58 **	8.31 **	1.5 **	31698.44 **	57738.63 **	1157.58 **
Treatment: Check	1	4898.45 **	31.25 **	5 **	634665.32 **	224932.05 **	10053.13 **
Treatment: Test and Test vs. Check	250	188.81 **	8.22 **	1.48 **	29286.57 **	57069.86 **	1122 **
Residuals	9	29.34	1.14	0.02	1903.49	4673.49	89.04

little scope for expansion of cultivated areas because of national and international regulations. Genetic improvement in FCV tobacco is hindered due to either limited variability or the fullest utilization of variability existing in the gene pool due to various reasons. Variability for selection is reported to be relatively limited in FCV tobacco [2, 5, 6]. Further, extensive and repetitive use of superior genotypes with common ancestors has reduced the genetic base of the released varieties [12], and therefore, it is essential to broaden the genetic base by creating the essential variation for genetic improvement of yield. The knowledge of existing genetic variability, estimation of genetic parameters for economic yield and its components is of great significance, and hence, the present study was undertaken to ascertain the existing genetic variability, estimate genetic parameters for yield-related characters in 250 germplasm accessions at ICAR- CTRI, Research station, Hunsur, Karnataka, India.

### Methodology

The experimental material for the present investigation comprised of 250 germplasm accessions of FCV tobacco (*Nicotiana tabacum* L.) collected and maintained at ICAR-CTRI research station, Hunsur, Karnataka. The experiment was conducted in augmented block design with ten blocks at ICAR-CTRI research Station, Hunsur, Karnataka. Each block consisted of 25 germplasm accessions and two checks *viz.*, Kanchan and FCH222. Each accession consisted of ten plants each with 100cm and 55cm as inter and intra-row spacing, respectively. All the agronomic package of practices were followed and a healthy crop was raised. Observations were recorded on plant height, number of leaves per plant, internodal length, length, and width of 5<sup>th</sup>, 7<sup>th</sup>, and 9<sup>th</sup> leaves on five randomly selected plants. The average leaf area per plant was calculated using the average length and breadth of the 5<sup>th</sup>, 7<sup>th</sup>, and 9<sup>th</sup> leaf as suggested by Suggs et al [14]. The observations on the total green leaf and cured leaf yields were recorded by harvesting the entire row and average yield per plant computed. Statistical analysis of the data for phenotypic and genotypic coefficients of variation, heritability, and the genetic advance was done by using R software. The phenotypic and genotypic coefficients of variation (PCV and GCV) were estimated according to the method suggested by Burton and deVane [1], while the heritability (broad sense) was computed based on the methods given by Lush [8]. Genetic advance as percentage of mean (GAM) were estimated according to the formula given by Johnson et al., [7].

### Results and Discussion

Analysis of variance revealed the significance of variability among the accessions for all the studied characters *viz.*, plant height, number of leaves, intermodal length, mean leaf area per plant, green leaf yield per plant, and cured leaf per plant (Table 1). The mean plant height for two hundred and fifty Flue Cured Virginia tobacco germplasm accessions found to be 94 cm, the number of leaves were 17, internodal length was 5.7 cm, and average leaf area per plant was 654 cm<sup>2</sup>, green leaf yield per plant was 598 g, and cured leaf was 51 g (Table 2). Plant height in the studied accessions ranged from 50 cm (Kauka 860 1061ET)-150

**Table 2. Estimates of Mean, Range, Variance components and Genetic parameters for different traits of FCV tobacco germplasm lines.**

Characters	Plant height	No. of leaves <sup>1</sup> plant	Inter-nodal length (cm)	Average leaf area (cm <sup>2</sup> )	Green Leaf Yield <sup>-1</sup> Plant (g)	Cured Leaf Yield <sup>-1</sup> Plant (g)
Genetic parameters						
Mean	93.68	16.76	5.72	654.17	597.64	50.98
Range	Minimum	50	7	213.38	60	5.4
	Maximum	150	28	2439.04	1340	134.4
Phenotypic Variance	200.25	7.57	1.55	36172.49	53515.64	552.87
Genotypic variance	160.46	5.67	1.06	16657.87	49851.54	516.59
Phenotypic Coefficient of Variation (%)	15.10	16.43	21.63	29.05	39.70	46.08
Genotypic Coefficient of Variation (%)	13.52	14.21	17.89	19.72	37.512	44.547
Heritability(h <sup>2</sup> )	80.12	74.83	68.47	46.05	93.15	93.43
Gen. adv. as % of mean	24.93	25.32	30.50	27.56	74.26	88.70
General mean	93.71	16.72	5.75	654.56	597.77	51.02
SE±	4.46	0.98	0.49	98.78	42.80	4.25
CD@5%	12.36	2.07	1.369	273.80	118.64	11.81
CV %	6.7	8.2	12.14	21.34	10.12	11.08

cm (Mammoth-88), number of leaves varied from 7 (Cy-156)-28 (ACR-34-5), while internodal length ranged from 2.7cm (ACR-34-5) -10.14 cm (Cy156), and average leaf area per plant varied from 213.38cm<sup>2</sup> (Golden wilt) -2439.04 cm<sup>2</sup> (Cocker-317). Green leaf yield per plant ranged from 60g (COR-17)-1340g (V-38) while cured leaf per plant ranged from 5.4 g (COR-17)-134.4g (ACR-34-5).

Based on various parameters recorded, different genetic parameters *viz.*, phenotypic variance, genotypic variation, PCV, GCV, heritability (broad sense), and GAM were estimated and presented in Table 2. In general, a considerable amount of variation was observed for all the studied characters. For all the parameters, the phenotypic variance was higher than the genotypic variance. Average leaf area recorded a higher magnitude of phenotypic variance as compared to genotypic variance and cured leaf lower. The estimated phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) was in the high category for cured leaf per plant (42.72 & 46.13), green leaf yield per plant (38.08 & 39.6), average leaf area per plant (26.1 & 26.95) and internodal length (20.73 & 20.85). While PCV and GCV were in the medium category for plant height (13.81 & 14.96) and the number of leaves per plant (15.32 & 16.58). PCV was higher than GCV for all the studied traits even though the difference between them is narrow indicating a lesser role of environment in influencing the expression of these traits. Similar results were reported by Sheraz et al., [14], Chakravarthi et al., [2] and Malleshappa, et al., [9].

Broad sense heritability (h<sup>2</sup>) was higher for cured leaf yield (93.43%) followed by green leaf yield (93.15%) and lower for average leaf area (46.05 %). While, heritability for plant height was 80.12%, internodal length (74.83%), and the number of leaves per plant (68.47%). Broad sense heritability and GAM were in the high range for plant height, inter-nodal length, number of leaves per plant, average leaf area, green leaf yield and cured leaf indicating that selection based on phenotype will be quite effective for these traits. High heritability and GAM for these traits were also reported by Prasanna and Rao [10], Shah et al., [12], Chakravarthi, et al., [2] and Malleshappa, et al., [9]. In the present study, a high magnitude of broad-sense heritability coupled with moderate to high GCV and high GAM was noticed for all the studied characters, which in turn indicates that additive gene action is involved in the expression of these traits. The presence of fixable additive gene action can help in its use in further tobacco improvement through simple selection [4].



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