

Original Research Article

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Assessment of Genetic variation in F₃ Generation of FCV Tobacco (*Nicotiana tabacum* L.)

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ABSTRACT

The present investigation was carried out at ZAHRS, UAHS, Shivamogga during 2016-2017 *Kharif* season to study the genetic variability, heritability and genetic advance, in F₃ generation of FCV (Flue Cured Virginia) tobacco cross, TB-70 x TB-102. The mean and variance in sixteen quantitative characters in F₃ generation of the cross TB-70 x TB-102 indicated wide variability among the families for all the traits *viz.*, leaf area per plant, internodal length, plant height, chlorophyll content, specific leaf weight, number of leaves, leaf length, leaf breadth, green leaf yield, cured leaf yield, top grade equivalent, reducing sugar content and nicotine content. GCV and PCV values were relatively higher for leaf area per plant. Heritability estimates were high for all the characters investigated except for nicotine content which exhibited moderate heritability. High heritability combined with high genetic advance as percent mean was observed for plant height, chlorophyll content, specific leaf weight, internodal length, number of leaves per plant, leaf breadth, leaf area per plant, green leaf yield, cured leaf yield, top grade equivalent and reducing sugar.

Keywords

Genetic variation,
FCV Tobacco
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Introduction

Tobacco is a non edible commercial crop which enters the world trade as a leaf. It is priced for its aroma, taste and flavor. It is aptly called as the golden leaf of India Tobacco (*Nicotiana tabacum* L.) is a member of the nightshade family, Solanaceae and is one among the 64 species in the genus *Nicotiana* (Goodspeed, 1954) that carries 48 chromosomes in its somatic cells (2n=48). *Nicotiana tabacum* is a natural amphidiploid derived from hybridization between *N. sylvestris* and *N. tomentosiformis* wild progenitor species (Gerstel, 1960 and Gerstel,

1963) and believed to be originated in tropical America (Akehurst, 1981). Among 64 species of *Nicotiana*, only two species are cultivated *viz.*, *Nicotiana tabacum* L. and *Nicotiana rustica* L. Cultivation of *Nicotiana tabacum* L. is practiced throughout the world, but *N. rustica* is restricted to India, Russia and other Asian countries. The Indian tobacco is grouped in to two major categories *i.e.* *Nicotiana tabacum* and *Nicotiana rustica*. *Nicotiana tabacum* occupies 10 per cent of total cultivated area but produces about 90 per cent volume of this crop, *N. rustica* is major share holder in terms of acreage but is poor yielder and contribute only around 10 per cent

of whole. India is the only country where many different types of tobacco, viz., flue-cured Virginia (FCV), chewing, natu, cigar filler, cigar wrapper, cheroot, hookah, bidi and burley are grown under different agro-climatic conditions.

Variability for different traits in the source population is a prerequisite for crop improvement, since all attempts of breeding and selection would be futile unless major portion of variability is heritable (Mruthunjaya and Mahadevappa, 1995). The measurement of genetic variation and mode of inheritance of quantitative and qualitative traits are of prime importance in planning the crop improvement programme efficiently and effectively. Heritability estimates provides an information about the extent to which a particular character can be transmitted to the successive generations. The knowledge of heritability of a trait thus guides a plant breeder to predict the behavior of succeeding generations and helps in making desirable selections (Cheema *et al.*, 2006).

Keeping the foregoing points in view, the present study on variability and character association in F₃ generation of FCV tobacco (*Nicotiana tabacum* L.) was carried out to estimate variability, heritability and genetic advance for leaf yield and its related traits. The present field experiment was carried out at ZAHRS, College of Agriculture, University of Agricultural and Horticultural Sciences, Navale, Shivamogga during *Kharif* season of 2016.

Materials and Methods

The material for the present study comprised of 25 F₃ families of the cross TB-70×TB-102, two parents TB-70 and TB-102 (Plate.01) and three checks viz Kanchan (High yielding, Black shank and Root knot nematode resistance), Thrupti (Drought tolerance) and

Sahyadri (Drought tolerance) varieties of FCV tobacco

The seedlings of 25 F₃ families of the cross TB-70 × TB-102, their parents with three checks viz Kanchan (High yielding, Black shank and Root knot nematode resistance), Thrupti (Drought tolerance) and Sahyadri (Drought tolerance) varieties of FCV tobacco were planted in Randomized complete block design (Sharma, 2008) during *Kharif* 2016 and recorded observation on X₁- Days to 50 per cent flowering, X₂-Days to maturity, X₃-Plant height (cm), X₄-Chlorophyll content, X₅-Specific leaf weight (mg/cm²), X₆- Stem girth (mm), X₇-Internodal length (cm), X₈- Number of leaves per plant, X₉- Leaf length (cm), X₁₀-Leaf breadth (cm) X₁₁- Leaf area (dm²), X₁₂- Green leaf yield (q/ha), X₁₃- Cured leaf yield (q/ha), X₁₄-Top grade equivalent (q /ha), X₁₅- Reducing sugar (%), X₁₆- Nicotine content (%)

Area =Length x Width x 0.6345.

The data collected for each of the characters listed earlier on individual plant and plot basis were subjected to Analysis of variance [Snedecor and Cochran (1937) And Panse and Sukhatme (1978)] Descriptive statistics Sunder Raj *et al.* (1972) and Estimation of variance components Weber and Murthy (1952).

Results and Discussion

The analysis of variance was carried out for all the sixteen quantitative traits considered for the study. The analysis of variance showing mean squares for different characters is presented in Table.1. The results revealed highly significant differences between the families and no much differences were found within the families for all the characters studied.

Table.1 Analysis of Variance (MSS) for sixteen quantitative characters in F3 \rightarrow generation of FCV tobacco of the cross TB-70 x TB-102

Source of variation	DF	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆
Replication	1	7.35	9.6	20.26	3.48	0.0074	1.17	0.0544	0.2706	0.313	0.21	8.52	2.16	0.06	0.0025	1.454	0.0202
Genotypes	29	233.16**	254.19**	795.19**	17.876**	5.167**	8.85**	0.8675**	17.29**	40.26**	29.02**	3005.05**	346.62**	6.30**	2.12**	9.74**	0.0099**
Error	29	11.83	12.22	79.95	0.985	0.6298	1.68	0.0499	1.15	6.44	2.19	175.22	45.30	0.53	0.18	0.908	0.0029

Table.2 Descriptive statistical parameters for sixteen quantitative characters in F3 families derived from the cross TB-70 x TB-102

Sl. no.	Characters	Mean±SEm	Range		Skewness	Kurtosis
			Min	Max		
1	X ₁	119.62±2.39	92.50	127.00	-1.60	1.24
2	X ₂	152.27±2.43	125.50	161.5	-1.41	0.95
3	X ₃	168.64±6.21	122.52	190.46	-1.11	0.59
4	X ₄	15.48±0.69	12.19	25.99	2.59	7.07
5	X ₅	8.84±0.55	5.44	12.02	0.26	0.71
6	X ₆	24.29±0.90	19.80	26.55	-0.71	0.56
7	X ₇	3.28±0.15	2.40	4.23	-0.04	1.50
8	X ₈	15.97±0.74	10.77	19.70	-0.35	1.58
9	X ₉	47.95±1.76	39.48	55.82	-0.44	1.04
10	X ₁₀	25.86±1.02	17.99	31.65	-0.33	0.84
11	X ₁₁	128.51±9.21	70.25	190.46	0.15	1.35
12	X ₁₂	78.49±4.67	49.37	96.56	-0.32	0.74
13	X ₁₃	9.27±0.51	6.16	12.05	-0.22	1.19
14	X ₁₄	5.67±0.29	3.69	7.23	-0.27	1.18
15	X ₁₅	12.71±0.66	10.18	18.33	-1.16	0.25
16	X ₁₆	1.05±0.03	0.97	1.23	1.26	1.31

Table.3 Variability parameter for sixteen quantitative characters in F₃ families derived from the cross TB-70 x TB-102

Sl. no.	Characters	PCV (%)	GCV(%)	h ² (%)	GAM (%)
1	X ₁	9.25	8.76	90.34	17.22
2	X ₂	7.58	7.22	90.83	14.18
3	X ₃	12.19	10.98	81.08	20.36
4	X ₄	19.84	18.77	89.55	36.59
5	X ₅	19.25	17.03	78.27	31.05
6	X ₆	9.45	7.79	68.06	13.24
7	X ₇	20.68	19.52	89.11	37.96
8	X ₈	19.02	17.79	87.51	34.28
9	X ₉	10.08	8.58	72.42	15.03
10	X ₁₀	15.27	14.16	85.97	27.05
11	X ₁₁	31.03	29.27	88.98	56.87
12	X ₁₂	17.84	15.64	76.88	28.25
13	X ₁₃	19.93	18.32	84.45	34.67
14	X ₁₄	18.93	17.36	84.12	32.81
15	X ₁₅	18.16	16.54	82.94	31.02
16	X ₁₆	7.69	5.64	53.80	8.52

The descriptive statistical parameters *viz.*, mean, range, skewness and kurtosis with respect to all the sixteen quantitative characters in F₃ families of the cross TB-70 × TB-102 of FCV tobacco are tabulated in Table. 2. The results with regard to variability parameters *viz.*, phenotypic co-efficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h²) and genetic advance as per cent of mean (GAM) in respect of cured leaf yield and its attributing characters in F₃ families of the cross TB-70 × TB-102 of FCV tobacco are tabulated in (Table.3) are briefly outlined below.

Different parameters such as mean, range, genotypic and phenotypic coefficients of variance and correlation as well as path analysis of important characters towards cured leaf yield have been worked out for each family. As per mean performance in the

families of F₃ generation showed high cured leaf yield, green leaf yield, top grade equivalent.

The findings of present investigation lead to the conclusion that isolation of genotypes with higher cured leaf yield along with good quality attributes is possible amongst the genotypes studied. The characters *viz.*, leaf area per plant internodal length, plant height, chlorophyll content, specific leaf weight, number of leaves, leaf length, leaf breadth, green leaf yield, cured leaf yield. Top grade equivalent, and reducing sugar content displayed sufficient variability. Hence, these characters could be improved by selection. The character nicotine content showed low variability and hence there would be little scope of improvement of this character through selection. The differences between PCV and GCV for the characters *viz.* leaf area per plant internodal length, plant height,

chlorophyll content, specific leaf weight, number of leaves, leaf length, leaf breadth, green leaf yield, cured leaf yield, Top grade equivalent, and reducing sugar content was narrow indicating lesser influence of environment on these characters. Therefore, phenotypic values are reliable in selecting the genotypes for these characters.

Heritability estimates were high for all the characters investigated except for nicotine content which exhibited moderate heritability. High heritability combined with high genetic advance as per cent mean was observed for plant height, chlorophyll content, specific leaf weight, internodal length, number of leaves per plant, leaf breadth, leaf area per plant green leaf yield, cured leaf yield, top grade equivalent and reducing sugar. It indicates that most likely the heritability is due to additive gene effects and selection may be effective for these traits.

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