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# VARIABILITY FOR ROOT MORPHOLOGICAL TRAITS IN TOBACCO (*Nicotiana tabacum* L.)

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**An attempt has been made to study the variability for root morphological traits in18 FCV tobacco germplasm accessions using multi variate analysis during Rabi 2020-21. Significant differences were observed among germplasm accessions for root morphological traits. High heritability coupled with high genetic advance as per cent of mean for root weight, shoot weight, shoot length, root diameter, number of leaves and leaf length suggested the additive gene control and effectiveness for selection. Root length correlated significant positively with all the traits studied except leaf length and ratio of root to shoot length ratio, whereas shoot length correlated significantly negatively with ratio of root to shoot length ratio. Hierarchical clustering analysis categorized 18 germplasm accessions into two major clusters representing high shoot weight and root diameter in cluster 1 and higher shoot length and high ratio of root to shoot weight ratio in cluster 2.Promising trait specific germplasm identified are GT 7 and MRS 3 for root biomass, shoot length and shoot weight.**

## INTRODUCTION

Tobacco (*Nicotiana tabacum* L.) is a major cash crop grown in India. India is the second largest producer of tobacco followed by China. The diverse geographical features of India allowed to grow variety of tobaccos consists of FCV and non FCV tobaccos viz., bidi, hookah, chewing, cigar wrapper, cheroot, burley, Oriental, HDBRG, Lanka, Pikka and Natu) in *Kharif* and rabi seasons.FCV tobacco occupies premier position in export share. Tobacco is grown in an area of 0.42 million hectares and production of 772 million kg tobacco with average productivity of 1815 kg/ha in India (FAOSTAT, 2022). In India,Andhra Pradesh state, FCV tobacco grown in area of 85,756 hawith a production of 181 million kg leaf (Tobacco Board, 2022).India exported FCV tobacco to more than 115 countries and 15047 tonnes of worth US$ 52 million during 2021-22.

In southern light soils of Andhra Pradesh, tobacco is mainly grown under residual soil moisture conditions. Frequent droughts and water logging conditions are common abiotic stressing affecting the tobacco crop. Tobacco varieties require robust root systems for absorption and efficient use of water. The role of root systems in water and nutrient translocation from the soil profiles and its involvement with water as well as nutrient utilization efficiency is well understood in different crops (Comaset al., 2013; White, 2019). The study of root structure in tobacco has paramount importance to keep the pace of varietal improvement to address climate change particularly water stress. There is need to assess the functional root and shoot traits conferring the drought tolerance.

It is important to assess the genetic variability and selection of desirable donor sources for different root morphological traits. In this regard, estimation of various genetic parameters like range, phenotypic coefficient of variation, genotypic coefficient of variation, broad-sense heritability, and genetic advance as a percent mean are helpful in assessing the variability in the germplasm accessions. Association analysis is also helpful for understanding the amount of relationship between root morphological traits and trait combinations in formulating selection criteria for genetic enhancement. Genetic diversity needed for further

**Key words:** variability,Flue cured Virginia tobacco, root length, shoot length, root biomass.

tobacco variety development is maintained in *Nicotiana* germplasm collections and hence, an attempt has been made to assess the genetic variability and classifying the 18 Flue cured Virginia germplasm accessions based on root morphological characteristics, which will be useful for identifying the diverse parents for hybridization and further genetic improvement of FCV tobacco.

## MATERIALS AND METHODS

**Experimental location:** The material for present study consists of eighteen FCV germplasm accessions maintained at ICAR CTRI Research Station, Kandukur. An experiment was laid out in the Augmented Block Design at the Experimental plots of ICAR CTRI Research Station, Kandukur, India during Rabi 2020-21. CTRI Research Station, Kandukur is situated between 15.2165 N latitude and 79.9042 E longitude at an elevation of 23 meters above mean sea level. The soil type of the experimental block of CTRI Research station was red soil with pH in the range of 7.9 to 8.23. The annual rainfall of the location was 1027 mm, which distributed from April to March during 2021-22. The temperature ranges between 20 c to 37 c and relative humidity varies between 62 to 94 per cent.

**Observations:** The observations on root weight, shoot weight, root length, shoot length,root diameter, shoot diameter, number of leaves, leaf length and leaf width were recorded on nine random plants from each accession.

**Statistical analysis:** Analysis of variance (ANOVA) for Augmented Randomized Block design was calculated using R studio 3.03. Genotypic and phenotypic coefficients of variation were estimated as per the method suggested by Burton and De Vane (1953), heritability and genetic advance were estimated according to Johnson (1955) and Robinson et al. (1949). Pearson's correlation coefficients were calculated for each pair of traits to determine relationships among leaf yield and quality traits. A cluster analysis was done on mean values of eleven traits using hierarchical clustering method using R version 3.0.3.

## RESULTS AND DISCUSSION

### Variability and genetic parameters

Analysis of variance showed significant differences among germplasm accessions for all the traits studied (Table 1). A wide range was observed in root morphological traits (Figure 1). Root weight ranged from 22.5 g to 43.6 g with a mean value of 30.05g, shoot weight from 31.7 g to 147 g with a mean value of 63.38g, root length from 23.5 to 41cm with a mean of 33.57cm and shoot length ranged from 41.7 to166.7 cm with a mean value of 109 cm. Root diameter ranged from 5.7 cm to 12 cm with an average of 7.11 cm, shoot diameter ranged from 5 cm to 7.3 cm with an average of 8.5 cm,number of lateral branches ranged from 4.8 to 11.8 with an average of 5.11 andlength of lateral branches ranged from 3.6cm to10.3cm with an average of 5.1cm.

Knowdledge on the variability in the available germplasm is the preliminary step in any crop improvement programme. The phenotypic and

**Table 1: ANOVA for root and shoot morphological traits**

| PARTICULARS | df | RWT | SWT | RSWR | RL | SL | RSLR | RD | SD | NLB | LL | NL |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Treatment (ignoring Blocks) | 17 | 54.7** | 1272** | 0.04** | 32.12** | 1104** | 0.011** | 2.17** | 0.513** | 4.733** | 4.355** | 26.724* |
| Treatment: Checks | 2 | 189.8** | 308** | 0.013* | 17.26** | 317** | 0.008** | 1.74** | 0.114** | 0.867** | 0.553* | 76.2** |
| Treatment: Test | 14 | 39.3** | 1417** | 0.046** | 30.67** | 966** | 0.011** | 2.33** | 0.486* | 5.575** | 4.781** | 20.603** |
| Treatment: Test vs. Check | 1 | 0.70 | 1166** | 0.007* | 82.00** | 4603** | 0.014** | 0.705** | 1.68* | 0.675* | 5.985** | 13.467* |
| Block (eliminating Treatments) | 4 | 0.93 | 0.5 | 0.005 | 2.167 | 1.567 | 0.003 | 0.152 | 0.358 | 0.628 | 0.038 | 1.9 |
| Residuals | 8 | 0.88 | 2.55 | 0.002 | 2.017 | 1.617 | 0.001 | 0.047 | 0.46 | 0.403 | 0.464 | 2.45 |
| Mean | | 30.0 | 63.3 | 0.542 | 33.57 | 109.28 | 0.33 | 7.11 | 6.09 | 8.58 | 5.11 | 28.48 |
| CV (%) | | 3.13 | 2.69 | 7.96 | 4.09 | 1.082 | 9.24 | 3.01 | 11.42 | 7.48 | 14.15 | 5.41 |

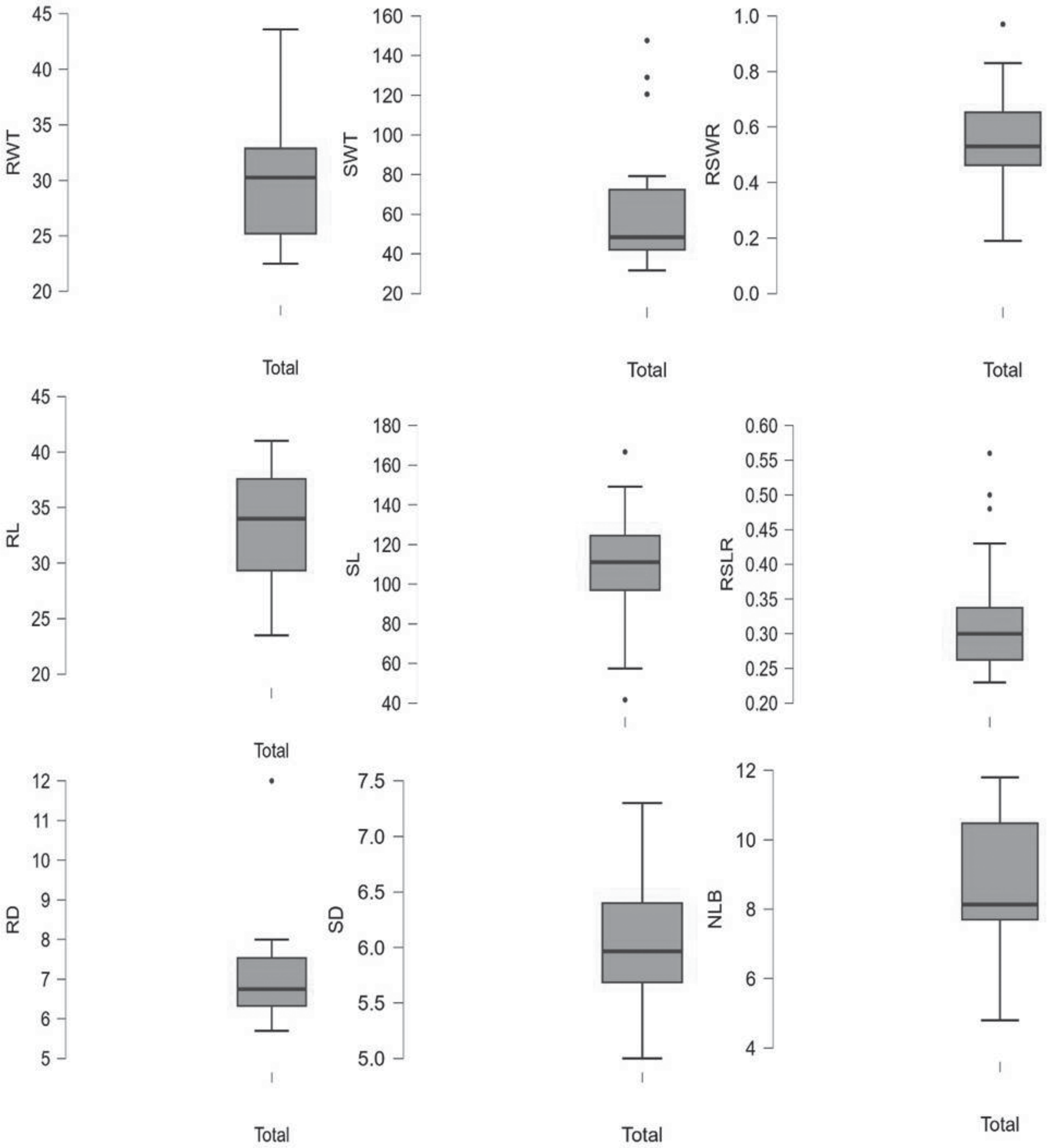

**Figure 1: Boxplot variation for root and shoot morphological traits**

genotypic coefficient of variation and heritability along with genetic advance as percent of mean are presented in Table 2. High genotypic coefficient of variation and phenotypic coefficient of variation mean was observed for root weight, shoot weight, shoot length, root diameter, ratio of root to shoot weight and root length to shoot length ratio. Heritability is an indicator of the transmission of characters from parents to their progeny. Heritability is classified as low (below 30%), medium (30%–60%) and, high above (60%). The estimates of heritability help the plant breeder in the selection of genotypes from a diverse genetic population. Therefore, high heritability helps in effective selection for a particular character. The genetic advance is a useful indicator of the effective and efficient selection progress that can be expected as a result of exercising selection on the base population. Genetic Advance as per cent of mean (GAM) was classified into low (0-10%), moderate (10.1-20%) and high (>20%) (Johnson et al., 1955). High heritability coupled with high genetic advance as per cent of mean was observed for all traits studied except shoot diameter suggesting the additive gene control and effectiveness for selection.

**Correlation and cluster analysis**

Root weight has showed significant positive correlation with root diameter and shoot diameter, whereas shoot weight correlated positive significantly with root diameter and negatively with root to shoot weight ratio (Table 3). Root length correlated significant positively with shoot length, number of lateral branches and number of leaves. Shoot length with number of leaves and negatively correlated with root to shoot length ratio. Root diameter has showed significant positive correlation with shoot diameter, root weight.

The knowledge of diversity and genetic relatedness among genotypes helps to identify donor parental lines for hybridization programs. Various researchers viz., Sarala and Rao 2008; Malleshappa et al 2020, Sarala et al 2020; Nanda et al (2021) and Gangadhara et al (2021) studied variability and diversity of Flue Cured Virginia tobacco germplasm accessions for leaf yield and its component traits. In the present study 18 germplasm accessions including three checks were classified into major cluster (I and II)using Euclidean distance (Figure 2). The distribution of genotypes originating from different geographical regions grouped into different clusters shows no parallelism between genetic diversity and geographical distribution. Hence, cluster patterns suggest that geographical variation need not necessarily be related to genetic diversity.

Cluster I, consist of three accessions, which are characterized by highest shoot weight and root diameter, whereas cluster II has 15 accessions with highest shoot length and leaf length. Cluster I

**Table 2: Genetic parameters for root and shoot morphological traits**

| PARTICULARS | RWT | SWT | RSWR | RL | SL | RSLR | RD | SD | NLB | LL | NL |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Minimum | 22.50 | 31.70 | 0.19 | 23.50 | 41.70 | 0.23 | 5.70 | 5.00 | 4.80 | 3.60 | 21.30 |
| Maximum | 43.60 | 147.60 | 0.97 | 41.00 | 166.7 | 0.56 | 12.0 | 7.30 | 11.8 | 10.30 | 34.50 |
| Mean | 30.056 | 63.389 | 0.542 | 33.578 | 109.289 | 0.33 | 7.118 | 6.094 | 8.583 | 5.111 | 28.48 |
| ó$^2$p | 39.352 | 1417.365 | 0.046 | 30.679 | 965.925 | 0.011 | 2.337 | 0.486 | 5.575 | 4.781 | 20.60 |
| ó$^2$g | 38.469 | 1414.815 | 0.045 | 28.663 | 964.309 | 0.01 | 2.289 | 0.027 | 5.172 | 4.317 | 18.15 |
| GCV | 20.636 | 59.339 | 38.932 | 15.944 | 28.414 | 30.051 | 21.257 | 2.673 | 26.495 | 40.651 | 14.95 |
| PCV | 20.872 | 59.392 | 39.709 | 16.496 | 28.438 | 31.324 | 21.476 | 11.443 | 27.509 | 42.781 | 15.93 |
| $h^2_{(bs)}$ | 97.755 | 99.82 | 96.122 | 93.427 | 99.833 | 92.035 | 97.974 | 5.458 | 92.766 | 90.288 | 88.10 |
| GA | 12.651 | 77.528 | 0.427 | 10.676 | 64.009 | 0.196 | 3.09 | 0.079 | 4.519 | 4.073 | 8.25 |
| GAM | 42.092 | 122.305 | 78.743 | 31.794 | 58.569 | 59.474 | 43.408 | 1.289 | 52.646 | 79.686 | 28.96 |

**ó $_g$** - Genotypic variance **GCV** - Genotypic coefficient of variance **$h^2_{(bs)}$** - Heritability (Broad sense)
**ó $_p$** - Phenotypic variance **PCV** - Phenotypic coefficient of variance **GAM** - Genetic advance as percentage of Mean

**Table 3: Phenotypic correlation coefficients of root and shoot morphological traits**

| PARTICULARS | RWT | SWT | RSWR | RL | SL | RSLR | RD | SD | NLB | LL | NL |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **RWT** | 1 | | | | | | | | | | |
| **SWT** | 0.46 | 1 | | | | | | | | | |
| **RSWR** | -0.105 | -.807** | 1 | | | | | | | | |
| **RL** | 0.432 | 0.038 | -0.135 | 1 | | | | | | | |
| **SL** | 0.286 | -0.459 | 0.293 | .565* | 1 | | | | | | |
| **RSLR** | -0.044 | .738** | -.624** | -0.122 | -.843** | 1 | | | | | |
| **RD** | 0.569* | .611** | -0.346 | 0.389 | -0.128 | 0.427 | 1 | | | | |
| **SD** | 0.529* | 0.452 | -0.065 | 0.306 | -0.126 | 0.313 | .540* | 1 | | | |
| **NLB** | 0.292 | -0.052 | 0.049 | 0.551* | 0.393 | -0.155 | -0.042 | 0.267 | 1 | | |
| **LL** | 0.133 | -0.104 | 0.482* | -0.462 | -0.179 | -0.094 | -0.149 | 0.246 | -0.297 | 1 | |
| **NL** | 0.556* | 0.139 | -0.123 | .515* | .472* | -0.207 | 0.433 | 0.292 | 0.355 | -0.172 | 1 |

*Statistical significance at 0.05

| | | | |
|---|---|---|---|
| RWT- Root weight | SWT- Shoot weight | RD-Root diameter | SD- Shoot diameter |
| RL-Root length | SL-Shoot length | NL- Number of leaves | NLB-Number of lateral branches |
| RSWR- Ratio of root to shoot ratio | | RSLR-Ratio of root to shoot length | |

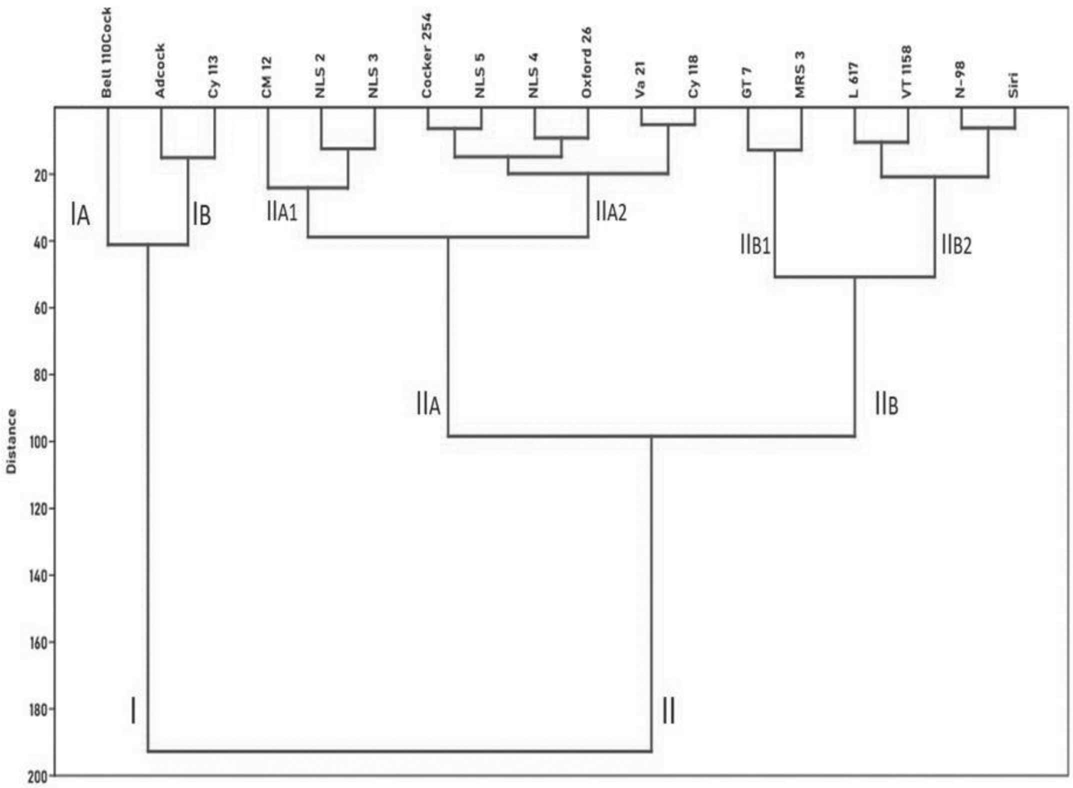

**Figure 2: Euclidean distance based clustering of 18 germplasm accession using root and shoot morphological traits**

divided into two groups, IA with single accession with highest shoot weight and root diameter and IB with two accessions of low root diameter. Cluster II is divided into two groups (IIA and IIB) of 9 and 6 accessions respectively. Mean performance of the clusters with respect to root and shoot traits indicated high cluster mean value for shoot weight, shoot length and number of leaves were recorded in cluster IIB.Trait specific genotypes identified are Bell 110(root length, root diameter and root weight),MRS 3(root weight, shoot diameter and number of root lateral branches) and GT 7 and NLS 2 (root length).Intercrossing of divergent groups could be used to greater opportunity for recombination which can releases hidden variability and breaks linkage. Population derived from such diverse crosses are expected to show wide range of genetic variability and provides scope for isolating transgressive segregants in the advance generation.

## CONCLUSION

Significant differences were observed among the germplasm accessions studied for root and shoot traits. High heritability coupled with high genetic advance as per cent of mean for root and shoot traitssuggested the additive gene control and effectiveness for selection. Promising trait germplasm accessions identified will serve as donors for the development of drought tolerant tobacco varieties.

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