



## Genetic variation in auxin induced root traits of tomato (*Solanum lycopersicum* L.) genotypes

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### Abstract

Hybrid tomato if propagated through vegetative method would be of great help to the farmers in reducing the cost of hybrid seeds. Auxin plays crucial role in vegetative propagation by inducing roots in stem cuttings. The objective of the present investigation was to study genetic variation in auxin induced root traits of twenty two tomato genotypes by estimating GCV, PCV, heritability and genetic advance. Stem cuttings of 25-30 days old tomato plants were treated with 500 ppm of IBA solution for 45 seconds to observe length of the longest root, number of lateral roots and fresh root weight. Analysis of variance indicated significant difference among the genotypes in respect of root length, number of lateral roots and fresh root weight. Experimental results revealed that the longest root was recorded in BT 10 (4.17 cm). Number of lateral roots varied from 12.23 to 47.53 with an average of 27.07. Fresh root weight ranged from 18.0 mg to 120.0 mg with an average of 60 mg. The phenotypic coefficient of variation (PCV) for all character was higher than genotypic coefficient of variation (GCV). The estimation of broad sense heritability was the highest for number of lateral roots (87.60). Genetic advance as % of mean was the highest for fresh root weight (87.29). Five genotypes having superior auxin induced rooting pattern were identified based on rooting index value.

**Keywords:** tomato, auxin, root traits, gcv, pcv, heritability and rooting index

### Introduction

Tomato (*Solanum lycopersicum* L.) belongs to family solanaceae is the most important vegetable crop of world. It is the main supplier of many plant nutrients and provides an important nutritional value to the human diet (Willcox *et al.*, 2003) [19]. The demand for the crop is year-round, owing to the versatility of its usage in both fresh and processed food preparation.

Root is an important plant organ that absorbs water, nitrogen or other nutrients more efficiently, resists pathogens, penetrates deeper into the soil. Hurd (1974) [10] hypothesized that in dry environments, genotypes with more extensive root systems would have a yield advantage over those with smaller root systems. In maize, increased root thickness appear to confer tolerance to the corn rootworm (Peters *et al.*, 1982) [15]. Derera *et al.* (1969) [6] reported a correlation between number of nodal roots and grain yield of wheat in an artificially drought stressed environment. A positive correlation between yield and root length in maize hybrid B73\_Mo17 was reported by Mackay and Barber (1986) [14].

Yield improvement in tomato is one of the important breeding objective in which breeders lay emphasis on selection of aerial traits like number of fruits per plant, average fruit weight, fruit length, fruit girth and yield *per se* whereas a little or no emphasis is made for selection of efficient root system to improve yield.

Recently, breeders have considered genetic improvement of root morphological traits to increase crop yield production (de Dorlodot *et al.* 2007) [5]. Breeding for particular root system traits may improve adaptation of crops to specific environmental conditions such as drought. Larger root biomass is favourable for

greater uptake of water and nutrients under drought conditions, thus resulting in greater growth and yield (Ehdaie *et al.*, 2010) [7]. Current methods of studying roots tend to be labour intensive and have, therefore, seldom been exploited in large studies required to determine the potential for breeding for particular traits.

Use of auxins in promoting adventitious root development of stem cuttings has been widely documented. Auxins promote the initiation of lateral roots primordia and enhance transport of carbohydrates to the cutting base needed for root growth (Hartmann *et al.*, 1990) [9]. The purpose of treating cuttings with auxins is to increase the percentage of rooting, root initiation, number and uniformity of rooting (AL-Barazi and Schwabe, 1982) [2]. Indole butyric acid (IBA) of auxin group is a plant bio-regulator and it is the leading plant hormone used to promote the formation of roots and to generate new roots in the cloning of tomato plants through cuttings. Waheed *et al.* (2015) [18] studied the effect of IBA on early root formation of tomato hybrid cuttings. Kachru *et al.* (2017) [12] studied the effect of IBA on root formation in tomato stem cuttings.

Genetic variation in auxin induced rooting pattern is of paramount importance for selection of root traits in improving yield of vegetatively propagated plants. Tomato hybrids if propagated through vegetative method would be of great help to the farmers in reducing the cost of hybrid seeds. Presence of genetic variability in the population is a pre-requisite for improvement in a character. Review of literature regarding genetic variation in root characters of field crops has been investigated to some extent. But the availability of literature

regarding genetic variation in auxin induced root characters of different crops is very meagre. In the present investigation an attempt has been made to study genetic variation in auxin induced root characters of tomato genotypes.

## Materials and Methods

### Experimental Materials

Twenty two tomato genotypes namely BT 1, BT 10, BT-17, BT-101, BT-106, BT-136, BT-317, BT 12-2, BT 112-1, BT 428-3, BT 442-2, BT 506-1, BT 12-3-2, BT 17-2-5, BT 19-1-1-1, BT 22-4-1, BT 306-1-2, BT 429-2-2, BT 433-2-3, Arka Vikas, Pusa Ruby & Arka Rakshak (hybrid) were taken for this investigation. Tomato seeds were collected from AICRP on Vegetable Crops, OUAT, Bhubaneswar and sown in the nursery bed as well as in poly pots during the year 2018-19 at AICRP on Vegetable Crops.

### Experimental design and procedure

The laboratory experiments were conducted at Department of Plant Breeding and Genetics, OUAT, Bhubaneswar following complete randomised design with two replications. Epicotyl portion of 25-30 days old seedlings was excised at a distance of 10 cm from the cotyledon and cuttings of ten seedlings were treated with 20 ml of 500 ppm aqueous IBA solution for 45 seconds, then washed thoroughly with tap water and kept in beakers filled with distilled water to study variation in rooting pattern of the genotypes.

### Data collection

Five cuttings were examined randomly for root induction on 10<sup>th</sup> day of treatment for each experiment. The experiments were repeated four times at an interval of 20-25 days. Data were recorded on length of the longest root, number of lateral roots produced per cutting and fresh root weight. The mean data were subjected to different statistical analysis.

### Data analysis

#### Analysis of variance

The data collected for each quantitative trait were subjected to analysis of variance (ANOVA) using procedures of SAS version 9.3, after testing the ANOVA assumptions. Before pooling the data across environments, test of heterogeneity for error of variance was done. The difference between treatment means was compared using CD value at 1% probability level.

#### Estimates of variance components

The phenotypic and genotypic variances and coefficients of variation were estimated from ANOVA according to the method suggested by Singh and Chaudhary (1985), heritability in broad sense (H) by Burton and De Vane (1953)<sup>[4]</sup> and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (1955)<sup>[11]</sup>.

#### Estimation of rooting index (RI)

Rooting behaviour of each genotype was expressed in terms of rooting index and it was calculated as follows. The mean (M) and standard error of mean (SE) were used to suitably code the data as 0, 1 and 2 to classify a character into three groups (low, medium and high). For a character, genotypes having lower value than  $M - SE$  were scored as 0; higher than  $M + SE$  as 2 and between  $M - SE$  &  $M + SE$  were scored as 1. The scored value

of all the characters was added to get rooting index that ranged from 0 to 6. Higher RI value indicates superior rooting pattern and lower RI value indicates inferior rooting pattern.

## Results

Analysis of variance indicated significant variation in root length (RL), number of lateral roots (NLR) and fresh root weight (FRW) in IBA treated stem cuttings of different tomato genotypes.

### Variation in root length (RL)

Variation in root length of stem cuttings of different tomato genotypes is presented in Table 1. Root length of the genotypes varied from 1.21 cm to 4.17 cm with an average of 2.24 cm. BT 10 recorded significantly the longest root (4.17 cm) and BT 306-1-2 recorded the shortest Root (1.21 cm). Arka Vikas and Pusa Ruby were at par with each other in respect of their root length. Eight genotypes showed above average (> 2.24 cm) root length and rest of the genotypes had below average root length.

**Table 1:** Mean value of tomato genotypes in respect of auxin induced root traits (Av. of 4 expt.)

Genotype	RL (cm)	NLR	FRW(mg)
V1. BT 1	2.09	21.13	39.0
V2. BT 10	4.17	35.89	120.0
V3. BT-17	1.63	13.61	18.0
V4. BT-101	2.05	33.61	89.0
V5. BT-106	2.34	24.53	52.0
V6. BT-136	2.84	33.20	93.0
V7. BT-317	2.19	47.53	114.0
V8. BT 12-2	2.89	35.84	98.0
V9. BT 112-1	3.20	35.41	73.0
V10. BT 428-3	2.54	34.48	75.0
V11. BT 442-2	2.19	18.06	55.0
V12. BT 506-1	3.11	44.00	119.0
V13. BT12-3-2	1.52	21.10	22.0
V14. BT 17-2-5	1.31	19.05	28.0
V15. BT 19-1-1-1	1.92	20.08	39.0
V16. BT 22-4-1	1.92	28.41	67.0
V17. BT 306-1-2	1.21	18.38	18.0
V18. BT 429-2-2	1.94	12.23	20.0
V19. BT 433-2-3	1.84	15.90	25.0
V20. Arka Vikas	1.68	27.13	74.0
V21. Pusa Ruby	1.98	25.50	94.0
V22. Arka Rakshak (hybrid)	2.69	30.58	72.0
Mean	2.24	27.07	64.0
CD (1 %)	0.57	8.21	7.0

### Variation in number of lateral roots (NLR)

Number of lateral roots is presented in Table 1. Significant difference was observed among the genotypes in respect of number of roots produced. Number of lateral roots varied from 12.23 to 47.53. BT 317 (V7) recorded significantly the highest number of lateral roots (47.53) and it was statistically at par with BT 506-1 (44.0). BT 429-2-2 produced the lowest number of roots.

### Variation in fresh root weight (FRW)

Fresh root weight ranged from 18.0 to 120.0 mg with an average of 64.0 mg (Table1). The maximum fresh root weight was observed in BT 10 (120.0 mg) and it was statistically at par with

BT 506-1 (119.0 mg) and BT-317 (114.0 mg). BT-17 and BT 306-1-2 recorded the minimum fresh root weight (18.0 mg).

**Estimates of genetic parameters**

Presence of genetic variability in the base population is a pre-requisite for selection of superior genotypes over the existing genotypes. The analysis of variance for different characters (Table 2) indicated the existence of highly significant differences for the root characters under study at 1% level of significance suggesting that the genotype are genetically divergent from each other and there is ample scope for selection of characters from these diverse sources for root length, number of roots per cuttings and fresh root weight.

In this study, the phenotypic coefficient of variation (PCV) was relatively greater than genotypic coefficient of variation (GCV) for all traits indicating the influence of environment in expression of different root characters. The highest GCV (51.15) and PCV (61.69) was observed in case of fresh root weight indicating more variability is present in the population for this character (Table 2).

The highest heritability was observed for number of lateral roots (87.60) and the lowest for fresh root weight (68.75).

The highest genetic advance as % of mean was recorded in fresh root weight (87.29). For root length PCV was low, heritability was moderate and genetic advance as % of mean was low as compared to number of lateral roots and fresh root weight. In case of fresh root weight, low heritability (68.75) was accompanied with high genetic advance (as % of mean) and this revealed that the character is governed by additive gene effects. The low heritability is being exhibited due to high environmental effects.

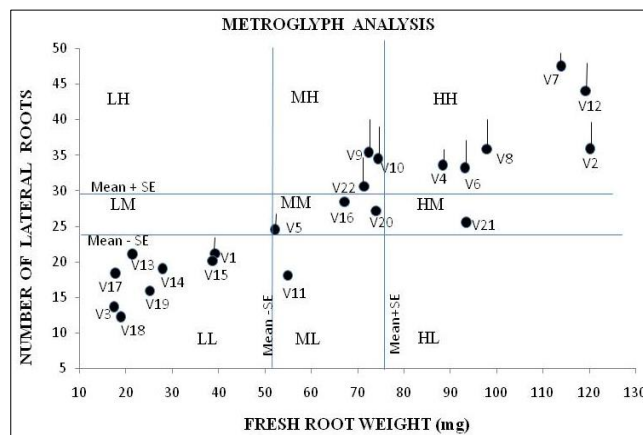
**Table 2:** Estimates of genetic parameters for different auxin induced root traits

Genetic Parameters	Root length (cm)	Number of lateral roots	Fresh root weight (mg)
Mean sum of square	1.948**	367.36**	4746.36**
Mean	2.24	27.07	64.00
Range	1.21 – 4.17	12.23 – 47.53	17.50 – 120.25
$\sigma^2_g$	0.447	88.70	1065.50
$\sigma^2_p$	0.608	101.25	1549.78
GCV	29.84	34.88	51.15
PCV	34.81	37.17	61.69
Heritability %	73.51	87.60	68.75
GA as % of mean	52.67	67.04	87.29

**Metroglyph analysis for classification**

Metroglyph analysis of Anderson (1957) [3] was followed with slight modification for classification of tomato genotypes. For plotting of the glyph (a small circle that represents the position of a genotype on the graph) fresh root weight and number of lateral roots were taken on X- axis and Y- axis respectively (Fig.1). Variation for each character was divided into three groups i.e. low (value below Mean – S.E.), medium (value between Mean – S.E. and Mean + S.E.) and high (value above Mean + S.E.). Variation for root length was depicted by length of bar on the glyph. Low value for root length was represented by no bar on glyph, medium value for root length by short bar and high value for root length was presented by long bar. Genotypes were found to be distributed in six groups like LL, ML, MM, HM, MM & HH out of nine groups. Eight genotypes present in LL group have lower

fresh root weight and lower number of lateral roots. ML (medium value for fresh root weight and lower value for number of lateral roots) and HM group (higher value for fresh root and medium value for number of lateral roots) each contained one genotype. MM (medium value for both fresh root weight and number of lateral roots) and MH (medium value for fresh root weight and higher value for number of lateral roots) group each contained three number of genotypes, but all the genotypes present in MH group had higher value for root length (long bar on glyph). In MM group only one genotype (V5) had medium value for root length (represented by short bar) and other two had lower value for root length (represented by no bar). The most desirable HH group (higher value for fresh root weight and number of lateral roots) included six numbers of genotypes of which four (V2, V6, V8 & V12) had higher value for root length and two (V4 & V7) had medium value for root length (Fig. 1).



**Fig 1:** Grouping of tomato genotypes through metroglyph analysis

**Selection of genotypes for superior rooting pattern**

Existence of genetic variability in respect of different root characters encourages selection for improvement of root traits. Tomato genotypes showed variable auxin response in their rooting behaviour. In some genotypes root length was short but number of lateral roots and fresh root weight were high; in some other genotypes root length, number of lateral roots and fresh root weight were low and some exhibited higher value for all three root traits (Table 3). Therefore, the three root parameters were considered together to predict rooting pattern of auxin treated stem cuttings. Rooting response of vegetatively propagated genotypes was expressed in terms of rooting index. Higher rooting index indicates superior rooting pattern and lower index indicates inferior rooting pattern.

Scored value and rooting index of the genotypes is presented in Table 3. Rooting index of the genotypes varied from 0 to 6. The lowest RI value was observed in genotypes BT-17, BT 12-3-2, BT 17-2-5, BT 19-1-1-1, BT 306-1-2, BT 429-2-2 and BT 433-2-3 and their scored value was low (0) for each trait indicating inferior rooting pattern. In genotypes BT-101, BT 112-1, BT 428-3 and Arka Rakshak (hybrid) rooting index was 5.0, hence their rooting pattern was superior. BT-106 had scored value 1 for each trait and rooting index value was 3, therefore its rooting pattern was neither inferior nor superior. In genotypes BT 10, BT -136, BT -317, BT 12-2 and BT 506-1 the scored value for each trait was high (2) and hence rooting index value was 6 indicating

superior rooting pattern. In four genotypes (BT 442-2, BT 22-4-1, ArkaVikas & Pusa Ruby) rooting index value was 2 and in one genotype (BT 1) rooting index value was 1.

**Table 3:** Scored value and auxin induced rooting index of tomato genotypes

	RL	NLR	FRW	Rooting index (RI)
V1. BT 1	1	0	0	1
V2. BT 10	2	2	2	6
V3. BT-17	0	0	0	0
V4. BT-101	1	2	2	5
V5. BT-106	1	1	1	3
V6. BT-136	2	2	2	6
V7. BT-317	1	2	2	5
V8. BT 12-2	2	2	2	6
V9. BT 112-1	2	2	1	5
V10. BT 428-3	2	2	1	5
V11. BT 442-2	1	0	1	2
V12. BT 506-1	2	2	2	6
V13. BT12-3-2	0	0	0	0
V14. BT 17-2-5	0	0	0	0
V15. BT 19-1-1-1	0	0	0	0
V16. BT 22-4-1	0	1	1	2
V17. BT 306-1-2	0	0	0	0
V18. BT 429-2-2	0	0	0	0
V19. BT 433-2-3	0	0	0	0
V20. Arka Vikas	0	1	1	2
V21. Pusa Ruby	0	0	2	2
V22. Arka Rakshak (hybrid)	2	2	1	5

## Discussion

Studies on root traits provide much valuable information to the breeders. Genetic variation in natural root system of different crops was studied by many researchers. Lovelli *et al.* (2012) [13] investigated root length and diameter of hydroponically grown tomato plants. Gil *et al.* (2016) [8] studied the morphology and biomass variations in root system of young tomato plants. Alaguero-Cordovilla *et al.* (2018) [1] studied root system architecture in diverse tomato genotypes at early growth stages. Samejima and Tsunematsu (2016) [16] investigated the genotypic variation in rice varieties screened for deep rooting under field conditions in West Africa. Variability study on auxin induced root traits of tomato was very scanty. Genotypic coefficient of variance provides information on the genetic variability present in base population. Genetic coefficient of variance together with heritability estimates would give the best picture of the amount of advance to be expected from selection (Burton and Devane, 1953) [4]. Thus, the heritable portion of the variation could be more useful with help of heritability estimates. Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotype. Hence, knowledge on heritability coupled with genetic advance is more rewarding. Genetic advance (GA) under selection referred to the improvement of characters in genotypic value for the new population compared with the base population under selection at given selection intensity.

## Conclusion

From this investigation it may be concluded that roots developed from auxin treated stem cuttings of tomato genotypes showed genetic variability in respect of root length, number of lateral roots and fresh root weight. Genotypes BT 10, BT -136, BT 12-2

and BT 506-1 were identified as having superior rooting pattern. Genotypic differences observed in auxin induced root traits may have an importance in breeding programs related to adaptation in drought and salinity prone areas.

## Rooting Response of IBA Treated Stem Cuttings of Some Tomato Genotypes



**Fig 2**

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