

Original Research Article

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## Genetic Analysis and Trait Association in F<sub>2</sub> Interspecific Population in Tomato (*Solanum lycopersicum* L.) using Third and Fourth Degree Statistics

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### ABSTRACT

#### Keywords

Population distribution, Skewness, Kurtosis, Gene action, *Solanum lycopersicum* L., *Solanum habrochaites* L.

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The present investigation was assessed using 235 different F<sub>2</sub> individuals, their parents and F<sub>1</sub> for characters like plant height, moisture, phenol and chlorophyll. These characters are most important for identification of disease effect and characterization for resistance in plants or genotype. Here, in the present study F<sub>2</sub> population was developed from the cross between AT-3 (*Solanum lycopersicum* L.) and IIHR-2101 (*Solanum habrochaites* L.). Then characters which are mentioned above were studied. Regarding the population distribution analysis, only chlorophyll was showed normal distribution in this population while other characters did not show normal distribution in the population. In this cross combination, phenol content was governed by complementary gene action with presence of minor genes, while moisture and plant height were governed by duplicate gene action with dominant property. Above characters interaction was determined through skewness and Kurtosis analysis.

### Introduction

Tomato (*Solanum lycopersicum* Mill., 2n=2x=24) is an important and most widely grown vegetable crop of both tropics and sub tropics of the world (Kalloo, 1988). Tomato ranks third after potato and onion in India but ranks second after potato in the world. India ranks second in the area (0.88 M ha) and second in production (1.88 MMT) in the world (Anonymous, 2015).

However, Tomato production is hampered due to some abiotic and biotic stresses (Vidavski *et al.*, 2008). The current progress is exemplified by detection of gemini virus resistance in related species of tomato and transfer of TLCV tolerance from this source into cultivated one. It is the most devastating viral disease attacking tomato worldwide. Whitefly (*Bemisia tabaci*) is the vector of TLCV, transmitting the virus in a circulative

persistent manner. The disease may cause up to 75% or more reduction in fruit yield and due to its devastating nature, it has become a national problem (Sastry and Singh, 1973; Saikia and Muniyappa, 1989). Mean and genetic variability is the basic requirement for crop improvement as this provides wider scope for selection (Vishnuvardhan *et al.*, 2012). Mean serves as a basis for eliminating undesirable crosses (Shoba *et al.*, 2012). An insight into the nature and degree of distribution present in population is of utmost importance as it forms the basis for selection in any crop improvement programme (Prabhuet *al.*, 2015). The present study was aimed at studying the genetics of different traits, association with disease resistance and its component traits using first, third and fourth degree statistics in segregating generations of tomato.

## **Materials and Methods**

### **Development of F<sub>2</sub> population**

Two genotypes namely IIHR-2101 and AT-3 reported and found earlier as highly resistant and highly susceptible, respectively for three consecutive years, were selected as parents. The cross was made during Rabi 2014-15 to obtain F<sub>1</sub>. The F<sub>1</sub> hybrid seeds were sown in the field and subsequently F<sub>2</sub> seeds were harvested from the respective plants during the year 2015-16.

### **Morpho-physiological characters**

The observations on morpho-physiological characters were taken from five plants each of AT-3, IIHR-2101 and F<sub>1</sub>, whereas 235 F<sub>2</sub> plants were observed individually for plant height, fruit yield per plant, number of fruits per plant, number of primary branches per plant, total chlorophyll content, Phenol content and moisture content and data were recorded using standard procedures (Singh *et al.*, 2015).

## **Statistical analysis**

Frequency distribution of the segregating generation was tested for normality by the Kolmogorov-Smirnov Z-statistics, Cramer-Von Mises and Anderson-Darlington test using SAS system. Mean, Variance and Standard deviation were calculated using Excel Programme.

Skewness, third degree statistics and kurtosis, fourth degree statistics were estimated to understand the nature of distribution of different traits. For the normal distribution skewness is equal to zero in the absence of gene interaction. It is greater and smaller than zero in the presence of average complementary and duplicate interactions, respectively.

Also, gene interactions can be detected by studying the fourth-degree statistics, kurtosis. Which is always negative or mean zero in the absence of gene interaction and is positive only in the presence of gene interaction.

Frequency distribution for each trait was considered significantly deviates from zero at the 0.05 probability level if that value was greater than twice of its standard error. Skewness and kurtosis and its standard error was calculated using SAS software system.

## **Results and Discussion**

### **Development of F<sub>2</sub> population**

The two parents used in the study were AT-3 (developed at AAU, Anand) and IIHR-2101 (procured from IIHR, Bangalore) maintained at Anand Agricultural University, Anand. IIHR-2101 a wild species of the tomato (*Solanum habrochaites*) was selected for its high resistance to tomato leaf curl disease (Lieu, 2000). But as the fruits of *Solanum habrochaites* are not up to commercial

standards, it is not recommended for commercial cultivation. Plant growth habit of IIHR-2101 being indeterminate is not suitable for field cultivation on commercial scale. The other parent AT-3 belonging to *Solanum lycopersicum*, a cultivated species, although produces fruits of good quality with determinate plant growth habit is suitable for field cultivation but it is highly susceptible to tomato leaf curl disease. From F<sub>2</sub> seeds, 235 plants were successfully grown along with parents and F<sub>1</sub> during *kharif*-2016-17. The phenotypic data from these plants were used for further analysis.

**Phenotyping of F<sub>2</sub> population**

The mean, range and variance of F<sub>2</sub> population of AT-3 × IIHR-2101 is given in table 1. To test the goodness of fit for various characters of F<sub>2</sub> segregating population, there were three tests carried out like Kormogorov-siminrnov Z-statistics, Cramer-Von Mises and Anderson Darling tests. Their results are presented in table 2.

Here, three population fitting tests were carried out for all four characters using SAS software among them all characters were found significant to its p value except chlorophyll. In this experiment, according to population distribution fitting test, this population is normally distributed for chlorophyll content and other are not. Here in

this experiment phenol, moisture and plant height were not segregate normally they are associated with any gene action. To find out that gene action we were used the third and fourth degree statistics.

**Skewness and Kurtosis analysis**

Quantitative characters show discrete variation in the population. They are also known as the matrix characters. Their distribution study gives the idea and nature of gene action and number of genes controlling the traits using skewness and kurtosis, respectively. In the present study, skewness and kurtosis were calculated for phenol, chlorophyll, moisture and plant height. Skewness for phenol content was 0.9064 and kurtosis was 0.6143, for chlorophyll skewness was observe as -0.1153 and kurtosis was 0.04577, skewness for moisture was recorded as -4.665 and kurtosis was -0.1205 as per figure 1. In the present study, TLCV resistance indicating traits like phenol, chlorophyll, moisture and height were considered for testing their distribution in the F<sub>2</sub> segregating population. Phenol showed platykurtic with positive skewed distribution in population. Chlorophyll and moisture content showed platykurtic with negative skewness and leptokurtic with negative skewness distribution respectively, in the population. Plant height showed platykurtic with negatively skewed distribution.

**Table.1** Mean, range and variance of F<sub>2</sub> population of AT-3 × IIHR-2101

Trait	AT-3 Mean	IIHR-2101 Mean	F <sub>2</sub> of AT-3 × IIHR-2101			
			Mean	Range	SD	Variance
PH	116.6	175.43	241.98	44-501	101.71	10345.58
NPB	5.5	6	3.99	1-10	1.51	2.29
CHL	5.88	9.97	8.83	0.15-15	3.44	11.83
PHE	0.56	1.08	1.14	0.30-2.56	0.51	0.26
MOI	41.49	81.44	79.56	26.11-86.62	5.32	28.33

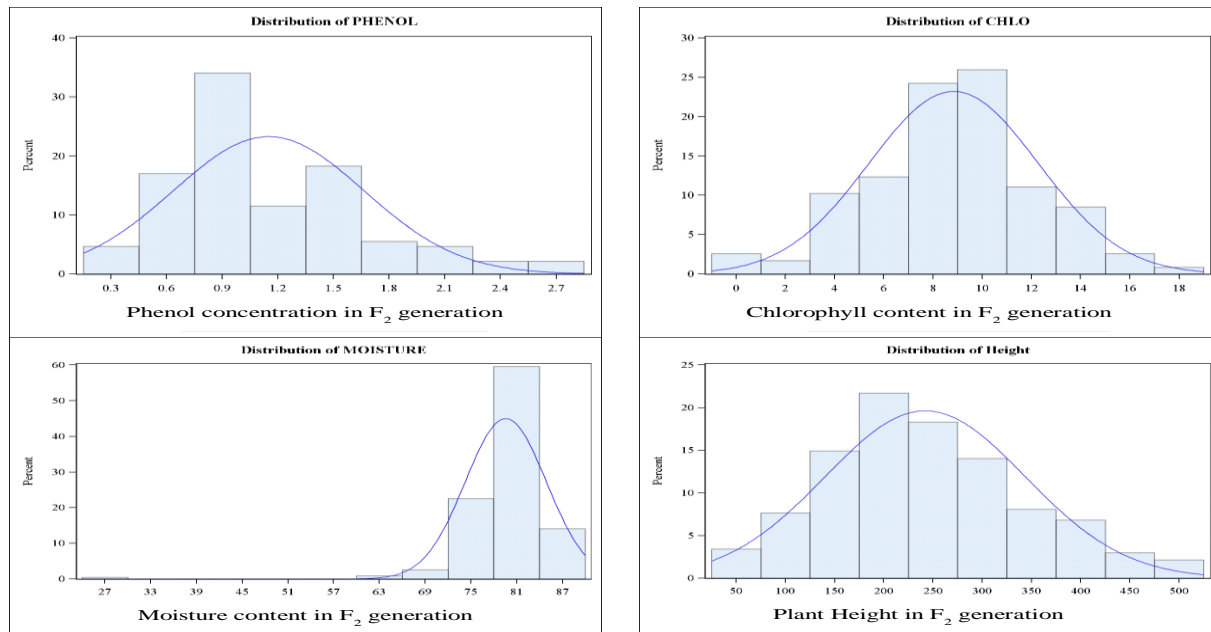
PH: Plant height, NPB: No. of primary branches, CHL: Chlorophyll content (mg/g), PHE: Phenol content (g/100g), MOI: Moisture (%)

**Table.2** Kormogorov-siminrnov Z-statistics, Cramer-Von Mises and Anderson Darling tests and their statistical values

Characters	KS		CM		AD	
	Statistics	p value	Statistics	p value	Statistics	p value
Plant height	0.08*	0.010	0.241*	0.005	1.380*	0.005
Chlorophyll	0.048 <sup>ns</sup>	0.150	0.649 <sup>ns</sup>	0.250	0.396 <sup>ns</sup>	0.250
Phenol	0.140*	0.010	0.682*	0.005	3.999*	0.005
Moisture	0.12*	0.010	1.040*	0.005	6.88*	0.005

KS: Kolmogorov-Simirnov Z-statics, CM: Cramer-Von Mises, AD: Anderson-Darling, \*: significant, ns: non-significant

**Fig.1** Distribution pattern of various characters in F<sub>2</sub> segregating generation of tomato.



On the basis of above results, phenol content was considered to be governed by complimentary gene interaction with presence of large number of minor genes with increasing effect. Chlorophyll content was governed by duplicate gene interaction with more number of minor genes. Moisture was governed by duplicate gene interaction with increasing gene effect with dominant property. These results were found in accordance with Banu and Jagadeesh (2014). They found that the plant height and test weight showed platykurtic with right skewed distribution indicating the

presence of more number of minor genes. According to them, selection was rapid under mild selection from existing variability found among the F<sub>2</sub> population of Rice.

In conclusion distribution study of matric characters in segregating generation gave the idea and nature of gene action and number of genes controlling the traits using skewness and kurtosis, respectively. Skewness for phenol content was 0.90 and kurtosis was 0.61, for chlorophyll skewness was observe -0.11 and kurtosis was 0.045, skewness for moisture was

recorded -4.66 and kurtosis was -0.12 in the present study. TLCV resistance indicating traits like phenol, chlorophyll, moisture and plant height were considered for testing their distribution in the F<sub>2</sub> segregating population. Phenol showed platykurtic with positively skewed distribution in population. Chlorophyll and moisture showed platykurtic and negatively skewed and leptokurtic negatively skewed distribution in the population. Plant height showed platykurtic with negatively skewed distribution. According to skewness and kurtosis, phenol content was found to be governed by complimentary gene interaction with presence of large number of minor genes with increasing effect. Moisture was governed by duplicate gene interaction with increasing gene effect with dominant property.

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