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Assessing the Genetic Purity of Tomato (*solanum lycopersicum*) Seedling through SSR Marker

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Abstract: ***Tomatoes (solanum lycopersicum) are widely cultivating vegetable globally, prized for their culinary versatility and nutritional value. The contents of phenolic acids vary among varieties of tomatoes and phenolic acids are known for their antioxidant properties. Tomatoes plants breeding has been performed in Maharashtra state, India by using varieties of hybrid seeds to improve their biologically active phenolic acids contents. In the present investigation, I have selected three hybrid varieties of tomatoes named as T26, T79, Phule Kesari and Phule Jayashri to analyze the genetic purity. Genetic material extraction process applied to tomato leaves was done. The genetic material isolation was done using standard procedure. The genetic material was assessed using Spectophotometry and Gel electrophoresis.***

Keywords: Tomatoes, phenolic acids, hybrid seeds, genetic purity, Maharashtra

1. Introduction

Tomato (*Salanumlycopersicum.* 2n = 2 × = 24), one of the important species of the Solanaceae family that first appeared in the region of Andes Mountains in South America, is one of the most cultivated vegetables in the world. It is known that today, the cultivated tomatoes are developed by using L. hirsutum L. peruvianum and L. pimpinellifolium (Rizwan et al, 2000; Vural et al, 2000). Tomato, which has a 100-year history when it has been taken into culture, has gained a great popularity especially in the last 25 years for food industry. The arrival of tomato varieties to Europe was made by Spanish and Portuguese merchants in the 16th century through seeds (Okumus et al, 2021). The seeds of T79 and T06 are hybrid and Phule Keshari and Phule Jayashri are genotypes used in this study with the help of the Completely Randomized Design. Isolation of genetic material from these seed samples will be carried out and it will be used for the assessment of genetic purity.

One of the most important techniques in this background is the polymerase chain reaction (PCR) by which the traces of DNA can be identified. Morphological characters cannot be used to measure the genotypic differences because these can be changed by the environment. The SSR markers are the important among all the available marker system for variety identification because of the properties of genetic codominance, high reproducibility and multiallelic variation (Dheemanth et al, 2018)

The DNA molecular markers can be used to study the genetic diversity and the variations in the genus Solanum and for selecting the tomato. Simple sequence repeats (SSRs), are also recognized as microsatellites, bear good results in molecular research because of the properties like having high reproducibility. Microsatellites are widely used in the studies of different plant species. Various studies have shown the efficacy of SSR markers for assessing the genetic diversity in the genus Solanum and SSR markers will be used on the DNA isolated in this project. There are many reports signifying the practicality of microsatellite markers for calculating the genetic variability in a wider taxonomic range Estimation of genetic diversity and relationships between germplasm collections are important for facilitating efficient germplasm collection, evaluation and utilization (Jamshed et al, 2016).

Parameters of growth stage:
Percentage of seed germination was calculated by:

Germination Percentage (GP):

$$GP = \frac{\text{Number of Total Germinated Seeds}}{\text{Total Number of Seeds Tested}} \times 100$$

OD was taken on the spectrophotometer with acetone as a control

Sample Hybrid/ Genotype	OD at 260	OD at 280	Ratio of 260/280	Concentration (ng/µl)
T1	0.45	0.29	1.74	74
T2	0.49	0.26	1.84	71.9
T3	0.54	0.36	1.78	86.4
T4	0.65	0.36	1.89	85.5
Mean	**0.53**	**0.31**	**1.81**	**79.45**
C.D.	**0.074**	**0.043**	**0.057**	**6.55**
S.E.	**0.037**	**0.021**	**0.028**	**3.275**

2. Discussion

Plant genomic DNA was isolated by using modified CTAB method from tomato hybrid and genotype. The protocol for DNA extraction using CTAB was modified as per requirement. The modified protocol described in detail earlier in methodology. Isolated DNAs were of good quality and of good concentration. The isolated genomic DNA of tomato were qualified using gel electrophoresis and also qualitativeanalysis. The assessment of genetic purity in crop species is crucial for maintaining the quality and integrity of plant varieties. This DNA was good quality and qualitative. (Agarwal M, and Shrivastava 2008).

The assessment of the purity of the DNA is confirmed by the

A260/280 ratio. For a 'pure' nucleic acid, this value commonly resides in the range of 1.8 to 2.0 (Sambrook et al., 1989). The A260/280 ratios below approximately 1.3 and above 2.3 are indicators of poor quality of the DNA (Seth et al., 2018). Samples with absorbance ratio at A260/280 greater than 2 indicate the presence of carbohydrates and other secondary metabolites (Wilson and Walker, 2010). Higher values of absorbance ratios are evidence of contamination by phenols while lower values indicate the presence of proteins since proteins absorb light at a wavelength of 280 nm (Wilson and Walker, 2010). The presence of RNA in the sample has been also shownto increase the A260/280ratio.

The Genetic material was isolated successfully and the processes of quantative and qualitative analysis was done. The amplification using PCR and diversity assessment is not done and will be carried outfurther.

3. Conclusion

- This varieties DNA was good quality and qualitative.
- The genotypes with distinct DNA profiles may provide useful information for selection of parents to develop new tomato hybrids.
- DNA degradation and RNA contamination was assessed through agarose gel electrophoresis.

Develop more SSR markers specific to tomato to enhance the accuracy of genetic purity assessment.

Implement SSR marker-based quality control measures in seed production to ensure the purity of tomato seeds, thereby reducing the risk of selling impure seeds to farmers.

Utilize SSR markers to select parent plants with desired traits and create new tomato varieties with improved characteristics.

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