Taxation of Genomic Deviation in Tomato and Principal Component Analysis

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*Abstract*— The genetic divergence of Tomato was studied with twenty three selected genotypes using D2 statistics and principal component analysis at Regional Agricultural Research Station, BARI, Akbarpur, Moulvibazar, Bangladesh during 2014 to 2015.The genotypes were grouped into 5 clusters and the maximum number of genotypes were included in cluster I and the minimum number in cluster V.

Keywords— Tomato; genetic diversgence; clustering; D2 analysis; PCA

# Introduction

Tomato (Lycopersicon esculentum Mill., 2n=2x=24) is one of the most important and popular vegetables in the world due to its wider adaptability, higher yield potentiality and suitability for diversified uses in fresh as well as processed food industries [1, 2]. It belongs to the family Solanaceae and its center of origin in Peru Equador region [3,4].and is normally a self-pollinated crop. Tomato is the second most important vegetables after potato [5] and it has great demand as cash crop in the international market [6,7,8]. Tomatoes are rich source of minerals such as Ca, P and Fe and vitamin A, C and antioxidants such as lycopene, glutathione etc. [9-13].Tomatoes are main source of lycopene [14] and the lycopene level in tomato fruit increases 500 times in ripening [15]. High antioxidants of tomato eliminate reactive oxygen species (ROS) and thus lowering the risk of certain chronic diseases such as cancer, strokes etc. in human body [16]. Furthermore, consumption of tomatoes prevent cardiovascular diseases [17, 18] and some other types of cancers, as for example prostate cancer [19, 20].

# Materials and Methods

The experiment was conducted at the vegetables research field and laboratory of the Regional Agricultural Research Station, Bangladesh Agricultural Research Institute, Akbarpur, Moulvibazar, Bangladesh during Rabi season from October 2014 to April 2015. Soil texture was sandy clay (43-85%), silt (<50%) and clay (>20%) and highland soil type with pH 4.5. Twenty three tomato genotypes were used in the present study and the experiment was laid out in randomized complete design (RCBD) with 3 replications. The unit plot size was 4.8 m × 1.0 m and plant spacing was 60 cm × 40cm. Manure and Fertilizers were applied @ 10 ton well decomposed cowdung, 550 kg Urea, 450 kg TSP and 250 kg MP, Gypsum 121kg, Zinc Sulphate 15kg and Boric acid 12 kg per hectare. Half of the quantity of cowdung, half amount of TSP and entire amount of gypsum and boric acid were applied during land preparation. The remaining half of cowdung and TSP was applied during pit preparation before a week of planting. The entire urea and MP were applied in 3 equal installments at 21, 35 and 50 days after transplanting. Irrigation, intercultural operation and pest management were done as and when necessary. Data on plant height (cm), days for 50% flowering, number of flowers per infloresence, number of fruits per cluster, individual fruit weight (g), fruit length (cm) and diameter (cm), pericarp thickness (cm), number of locules per fruit, number of fruits per plant, number of seeds per fruit, % Brix (TSS), yield per plant (kg.) and yield (t/ha) were recorded. Genetic diversity was studied following Malanobsis’s [23] generalized distance (D2) extended by Rao [28]. Clustering of genotypes was done according to Tocher’s Method [28] and principal component analysis was done according to Rao [29]. Mean data for each character were subjected to multivariate principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis and canonical variate analysis (CVA) using GENSTAT 5.5. computer software. Average intra cluster distance was calculated by the formula as suggested by Singh and Chaudhury [30].

# Results and Discussions

On the basis of D2 analysis, twenty-three genotypes of tomato were grouped into five clusters based on D2 values (Table 1). The distribution pattern indicates that the maximum numbers (8) of genotypes was included in cluster I followed by cluster IV and III. The minimum number of genotype (01) was included cluster V. The grouping pattern of the genotypes was found to be random proving that the geographical and genetic diversity were unrelated. Similar grouping pattern in tomatoes were also confirmed by other researchers [31-33].

The characters plant height, fruit diameter and yield per hectare showing positive value in both the vectors contributed maximum towards divergence. So, the divergence in the present materials due to these three traits will offer a good scope for improvement of tomato varieties through selection of parents.

# Conclusion

Crosses involving parents belonging to most diverse genotypes are expected to exhibit maximum heterosis and create wide variability in genetic architecture.

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CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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