



Unraveling of Population Genetic Structure of Eggplant Germplasm



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Abstract

Eggplant which is commercially grown for its rich anthocyanin content fruits. Eggplant gene pool is highly flourished with vast diversity for its morphological, biochemical as well as physiological traits. The present study was conducted to understand the population genetics of five different population based on kind of germplasm. The Structure analysis revealed that fourteen genetic sub-clusters (K=14) which spread across all the sampled populations, forming genetically admixture populations and species like *Solanum mammosum*, *Solanum thorium* and *Solanum indicum* were grouped in one sub-cluster and *Solanum macrocarpon* grouped in separate sub-cluster. The obtained result will be helpful for organization of brinjal genotypes and improvise eggplant breeding strategies.

Keywords: Eggplant; SSR-Marker; Population Genetics; Structure

Abbreviations: PIC: Polymorphic Information Content; Nm: Number of Migrants; Ne: Number of Effective Alleles; F: Fixation Index

Introduction

Eggplant is important vegetable belongs to family Solanaceae which is known for its high anthocyanin rich fruits. Eggplant is mainly known as baingan in India, aubergine in UK, brinjal in south-eastern part of Asian continent. Typically, eggplant is an annual crop, with spiny to spineless plant habit and flowers with fused five corolla, five calyx, five stamens. Eggplant flowers are heterostyly in nature, maximum fruits setting can be observed from medium styled flower. In India approximately 12.98 million metric tons was production during 2022. Though, India was second largest producer of eggplant after China, Indian farmers are facing problems in crop management due biotic stress like, fruit and shoot borer, little-leaf disease, and fusarium wilt and whereas abiotic stress like drought [1], Salinity [2], heat, cold and mineral stresses. Eggplant is one of the vast diversified substrata which includes local cultivars, wild species, advanced breeding lines etc., known to have variation in terms of morphology [3], physiology, root and biochemical characters [4] which encounters over biotic and abiotic stress. With this background we conducted and experiment to understand the genetic relationship between eggplant germplasms.

Around fifty-four eggplant germplasms were categorised into four population based on its kind i.e., 1local cultivars (9 genotypes), 2commercial hybrids & released varieties (2+15 genotypes), 3advanced breeding lines (24 genotypes), and 4wild relatives/related species of eggplant (4 species) (Figure 1). The genomic DNA from each germplasm extracted using CTAB method and carried out PCR for 23 SSR markers [5].

The obtained gel profiles were scored and analysed the data using AMOVA, phylogenetic analysis and molecular diversity parameters like number of different alleles (Na), number of effective alleles (Ne), Shannon's Information Index (I), Observed Heterozygosity (Ho), Expected Heterozygosity (He), number of migrants (Nm), Polymorphic Information Content (PIC) value, Fixation Index (F) and F- statistics across populations of eggplant which was previously published in article Faizan et. al. [5]. Simultaneously, the scored marker profiles were subjected to a bayesian model-based clustering algorithm which was applied to multi-locus microsatellite data to infer genetic structure and define the number of clusters (gene pools) in the dataset using the software STRUCTURE V.2.3.4 [6].

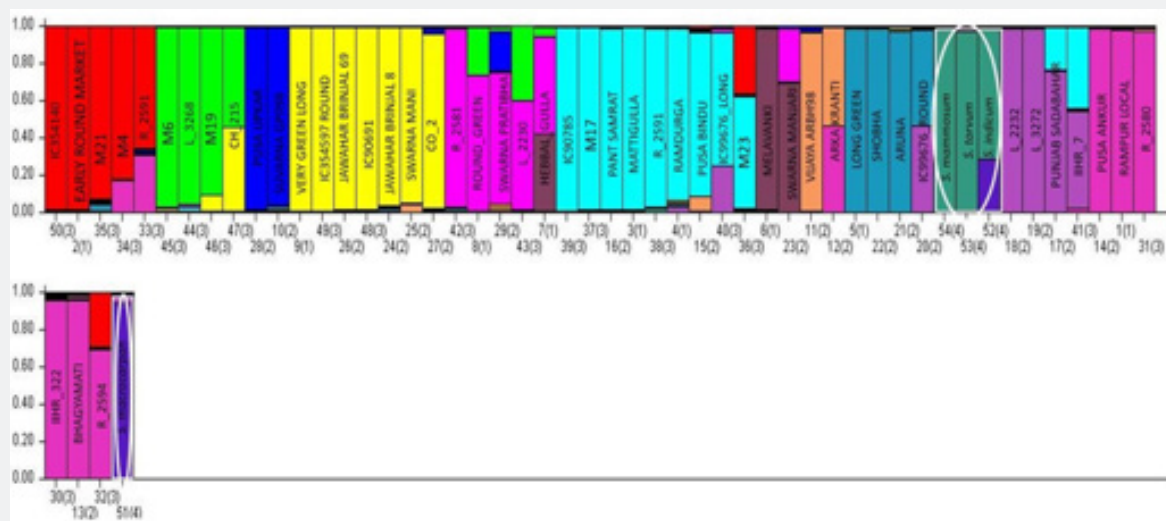


Figure 1: Population structure observed for four populations of total fifty-four eggplant germplasm. *The white circled accessions were K=11 and K=14.

Population genetic structure estimated the number of genetically distinct populations (K) besides diversity parameters. In the analysis to arrive at optimal K value for 54 genotypes of eggplant, an ad hoc statistical analysis was approached. Based on second order rate change of the likelihood function with respect to K (ΔK), Structure Harvester [7] was used to estimate K using $\ln P(D)$ values (Table 1). The ΔK value of Evan no’s algorithm predicted K=14 (Figure 2) by differentiating the individuals in

sub-populations. This analysis indicated the presence of fourteen genetically heterogenous clusters in admixture form for eggplant four sub-populations. Analysis of present experiment revealed that, all the five sub-populations POP1 (Local cultivars), POP2 (Hybrids & Released varieties), POP3 (Advanced breeding lines) and POP4 (Wild/related species of eggplant) formed an admixture of major cluster as revealed by the Structure analysis.

Table 1: Structure stimulation summary exhibiting $\ln P(D)$ values at length of burning period 10000.

Parameter name	Run name	K-Value	$\ln P(D)$	Car [$\ln P(D)$]
Binjal_Burn_X	Binjal_Burn_X_run_1	1	-3084.7	20.5
Binjal_Burn_X	Binjal_Burn_X_run_2	2	-2807.8	103
Binjal_Burn_X	Binjal_Burn_X_run_3	3	-2404.1	114.3
Binjal_Burn_X	Binjal_Burn_X_run_4	4	-2288.2	198.8
Binjal_Burn_X	Binjal_Burn_X_run_5	5	-2067.5	177.8
Binjal_Burn_X	Binjal_Burn_X_run_6	6	-1986.4	212.8
Binjal_Burn_X	Binjal_Burn_X_run_7	7	-1904.7	243.3
Binjal_Burn_X	Binjal_Burn_X_run_8	8	-1845.7	214.4
Binjal_Burn_X	Binjal_Burn_X_run_9	9	-1762.4	351.4
Binjal_Burn_X	Binjal_Burn_X_run_10	10	-1620.6	180.9
Binjal_Burn_X	Binjal_Burn_X_run_11	11	-1752.1	525.6
Binjal_Burn_X	Binjal_Burn_X_run_12	12	-1589.6	218.6
Binjal_Burn_X	Binjal_Burn_X_run_13	13	-1675	526.3
Binjal_Burn_X	Binjal_Burn_X_run_14	14	-1610.9	395.5
Binjal_Burn_X	Binjal_Burn_X_run_15	15	-1642.2	507.5

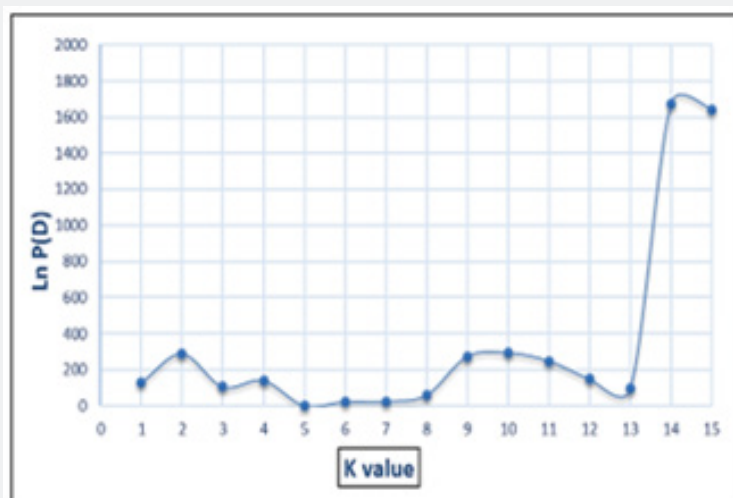


Figure 2: Estimation of population using Ln P(D) derived ΔK for K=1 to K=20.

Population genetic structure analysis of eggplant accessions/ individuals shows the different genetic variability that make up the population and divides the population into genetically distinct clusters [7]. The population genetic structure elucidated in the present study indicates fourteen (K=14) genetically distinct populations for 54 accessions of eggplant. The admixture or heterogenous cluster pattern may be due to high genetic flow or genetic drift. The genotypes under different populations were categorised as pure or admixture and for categorisation purpose accessions with more than 0.80 score were considered as pure and less than 0.80 as admixture [8]. This type of genetically admixture populations were previously reported by Hurtado et al. [7] and Ge et al. [9] during the assessment of 52 and 92 accessions of eggplant, respectively. From study we can clear estimate that

ΔK reached at its high peak at K=14 as a result whole population was divided into fourteen subcluster out of which *Solanum mammosum*, *Solanum torvum* and *Solanum indicum* were grouped in one sub-cluster (K=11) and *Solanum macrocarpon* grouped in separate sub-cluster (K=14). Further, which validated through the genetic distance observed from Structure analysis shown high genetic distance compared to another sub-cluster (Figure 3). The population structure analysis resulted into fourteen subgroups and generally followed a previously published PCA and phylogenetic classification scheme [2]. The information presented in this report may be of great utility for the germplasm management and breeding of eggplant and the obtained data can be utilized to get clear picture about Hardy-Weinberg law.

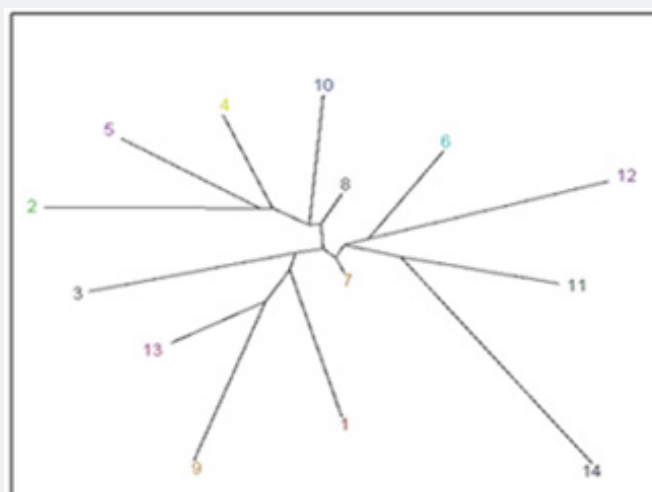


Figure 3: Population genetic distance observed for eggplant germplasm.

Conclusion

Our study resulted that the fifty-four eggplant germplasm which comprises of local cultivars, commercial hybrids & released varieties, advanced breeding lines, and wild relatives/ related species of eggplant were sub-clustered into fourteen (K=14) genetically heterogenous clusters in admixture form for eggplant four sub-populations. In which *Solanum mammosum*, *Solanum torvum* and *Solanum indicum* were grouped in one sub-cluster (K=11) and *Solanum macrocarpon* grouped in separate sub-cluster (K=14). The population genetic distance showed the sub-cluster K=14 is having maximum distance compared to other sub-clusters. The revealed data can be utilised for germplasm management and breeding of eggplant.

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