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SHORT COMMUNICATION

Assay of Genetic Architecture for Identification of Waterlogging Tolerant Pigeonpea Germplasm

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Abstract The experiment was conducted to identify the waterlogging stress tolerant genotypes in pigeonpea. Waterlogging treatment was given to the plants at vegetative stage after treatment the survival rate was assessed. Out of 128 germplasm pool, 38 survived and the survival rate was estimated along with Mahalanobis D^2 cluster analysis. The range of survival percentage for both pot and field were found between 26.6 and 73.3 with the standard deviation of 14.82 for pot screening and 14.29 for field screening. The pot survival percentage mean for all 38 accessions were found higher than field survival which clearly indicates that environment poses an effect on the performance of the genotypes. The Mahalanobis cluster analysis revealed five clusters. Out of five clusters, two were found comparatively tolerant than the others. The tolerant germplasm can also be used as donor parents in hybridization programs for development of water logging-tolerant genotypes. The identified tolerant germplasms may be utilized to incorporate waterlogging tolerance in the short-duration pigeonpea pool.

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Pigeonpea is an important pulse crop of India. It belongs to family Fabaceae, with a genome size of around 833.1 Mbp having eleven linkage groups [1]. In India, pigeonpea is grown on 5.06 million hectare area with the production of 3.20 million tons. Asia alone contributes about 89% in global area and 87% in global production with productivity around 649 kg/ha [2]. Pigeonpea is considered relatively low in productivity which is attributed to various factors which include narrow genetic base for harvest index, resistance to water logging abiotic stress, poor crop management and changing climatic conditions. In India, water logging during the rainy season caused by torrential rainfall is an important production constraint. Nearly 8.5 million ha of arable land is prone to water logging of which pigeonpea cultivation accounts for 1.1 million ha of the total area under pigeonpea. High soil moisture percentage is a leading cause of productivity loss amounting to 25–30% of annual production [3]. Since pigeonpea is primarily grown in deep vertisols, where annual rainfall varies between 600 and 1500 mm, water logging becomes a serious threat to pulse productivity [3]. Singh and coworker [4] reported that pigeonpea is more water sensitive during the germination whereas vegetative stage is more sensitive to waterlogging stress incomparison to mature plants. In water logging condition, oxygen levels in the soil declines and carbon dioxide concentration increases, which adversely affect the development of plant roots [5]. Water logging blocks the respiration of roots, resulting in a severe decline in energy status of root cells affecting important metabolic processes of plants [6]. The root microflora is

also affected by water logging, which ultimately leads to the nutrient imbalance in the soil [7–9] and plant health. Waterlogged soil hampers the gaseous diffusion rates by 100 times than the normal [10]. Other adverse effects of water logging on plant developments are yellowing and senescence of leaves, a decrease in leaf area, dry matter, and membrane stability index of roots and leaves [11, 12]. Water logging stress produced the greatest reductions in nodule nitrogenase activity in pigeonpea [13]. Water logging alters the biochemistry of usual ATP production by switching from an oxidative to substrate-level phosphorylation, favors glycolysis and fermentation, yielding only 2 molecules of ATP rather than 38 ATP per glucose molecule [6]. Since water logging is an important abiotic stress, which causes the loss in yield productivity in pigeonpea, it is imperative to identify a viable solution for this problem. Hence, the development of tolerant genotypes is the most efficient and economical way to minimize losses. The present study was aimed at providing an insight into the genetic structure for waterlogging tolerance in pigeonpea.

All the 128 pigeonpea germplasms were planted as per Randomized complete block design (RCBD). Water logging treatment was given to plants at vegetative stage (25 days after sowing). Before application of water stress treatment, the number of plants in each row were counted. The stress treatment was imposed by submerging all rows of the field with water in such a way that the soil surface of row remained at least 20 mm under water for 6 days. Seventh day post treatment the survived plants in each row were enumerated and the rate of survival was estimated with reference to the number of plants before treatment. Plant survival counts were based on final plant stand at maturity. The germplasms exhibiting tolerance upon treatment were also planted in the pot. These germplasms were analyzed for Mahalanobis D^2 analysis [14] for obtaining the cluster of germplasm with different survival percentages. The dendrogram and the cluster diagram were also prepared for both pot screening and field screening.

Out of 128 germplasms, 38 survived under waterlogging stress treatment up to maturity. These 38 Pigeonpea germplasms exhibited a significant variation among the genotypes. The range of survival percentage for both pot and field were found to be between 26.6 and 73.3 with the standard deviation of 14.82 for pot screening and 14.29 for field screening. The pot survival percentage mean for all 38 accessions was found higher than that for field, which clearly indicates that environment poses an effect on the performance of the genotypes (Fig. 1). The Mahalanobis D^2 analysis confirmed five different clusters among all genotypes (Fig. 2). The cluster mean as shown in Table 1 indicated that the cluster II have the lowest cluster mean, containing five genotypes and showed meager survival rate, while cluster IV showing highest survival percentage with cluster mean at 69.97. The cluster I was the biggest cluster (18 genotypes) with cluster means around 36.09. The other cluster with cluster mean for survival rates are shown in Fig. 2. The Mahalanobis cluster analysis showed that percentage variation within the cluster was 15.75%, while 84.25% variation was present between clusters. The inter-cluster distances varied from 62.91 (between cluster II and cluster IV) to 15.42 (between cluster I and cluster II). The highest inter-cluster distance was found between cluster II and cluster IV (62.91) (Fig. 3). The inter-cluster proximity was maximum between clusters I and II indicating lesser diversity. Cluster II showed maximum genetic distance with cluster IV, followed by cluster V, hence clusters II and IV exhibited wider genetic diversity among them. On the basis of D distance, the genotype of cluster II and IV has shown a cluster mean difference of 44.33 which means the cluster IV genotype have 44.33% higher survival than the cluster II. The genotypes comprising of cluster IV can directly be used in the breeding program for development of waterlogging tolerant varieties. Tolerant germplasm can also be used as donor parents in hybridization program for developing tolerant genotypes. This is especially needed to incorporate water logging tolerance in the short-duration pigeon pea pool. It will eventually lead to the reduction in overall losses caused by water logging in pigeonpea. The use of tolerant genotypes is the best and efficient way to manage waterlogging stress in pigeonpea. According to Khare et al. [15], the initial stage of seedling establishment is the most critical factor for pigeonpea under water logging stress. Present study confirmed the performance of various susceptible germplasm as sensitive [16] and germplasms viz., ICP-14092, ICP-14085, ICP-10948 etc., as tolerant [17, 18]. The genotypic differences for water logging tolerance at seedling level were screened for pigeonpeas in various studies [16, 17, 19–21]. Sultana and colleagues [18] reported that hybrids exhibited greater survival rates as compared to germplasms, elite inbred lines or varieties. The studies suggested that maturity duration of varieties are correlated with water logging stress. Genotypes with higher days to maturity can sustain longer in waterlogged soil than short duration pigeonpea. Thus there is an urgent need to incorporate water logging tolerance into the early maturing pigeon peas. It will eventually lead to the reduction in overall losses caused by waterlogging in pigeon pea. The genotypes in cluster IV and cluster II are highly diverse and the possible F1 crosses from the above-selected genotypes can be used as transgressive segregants in later generations and be useful for this orphan crop to help against water stress to boost our Indian pulse production under climate resilient agriculture.

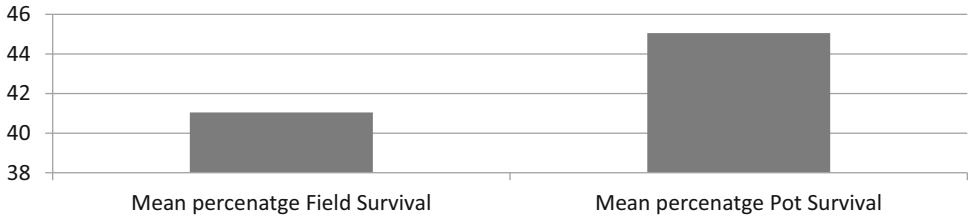

Fig. 1 Survival rates for pot screening and field screening

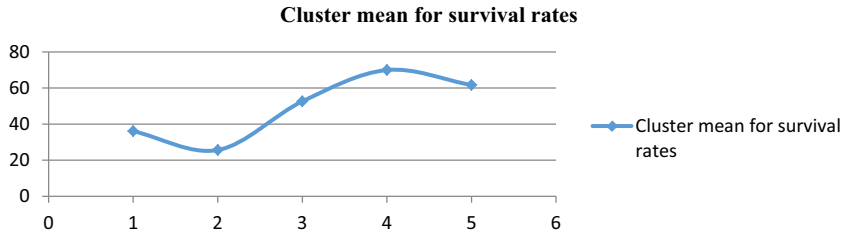

Fig. 2 Survival percentage for different clusters for pigeonpea

Table 1 Cluster analysis of 38 pigeonpeagermplasm for waterlogging stress

Sl. no	Clusters name	Genotypes	Cluster mean
1	Cluster 1	ICP-3046, ICP-3451, ICP-4029, ICP4317, ICP-6929, ICP6992, ICP-8012, ICP-9414, ICP-9655, ICP-9691, ICP-11833, ICP-12142, ICP-12654, ICP-13191, ICP-14471, ICP-14900, ICP-15049 and ICP-15068 (18 Germplasms)	36.09
2	Cluster 2	ICP-8384, ICP-11281, ICP-11543, ICP-11910, ICP-14545 (5 Germplasms)	25.64
3	Cluster 3	ICP-8793, ICP-8840, ICP-9336, ICP-11015, ICP-12105, ICP-12596, ICP-13633, ICP-14801, ICP-16264 (9 Germplasms)	52.60
4	Cluster 4	ICP-10654, ICP-13579, ICP-14638, ICP-14976 (4 Germplasms)	69.97
5	Cluster 5	ICP-12515, ICP-14832 (2 Germplasms)	61.65

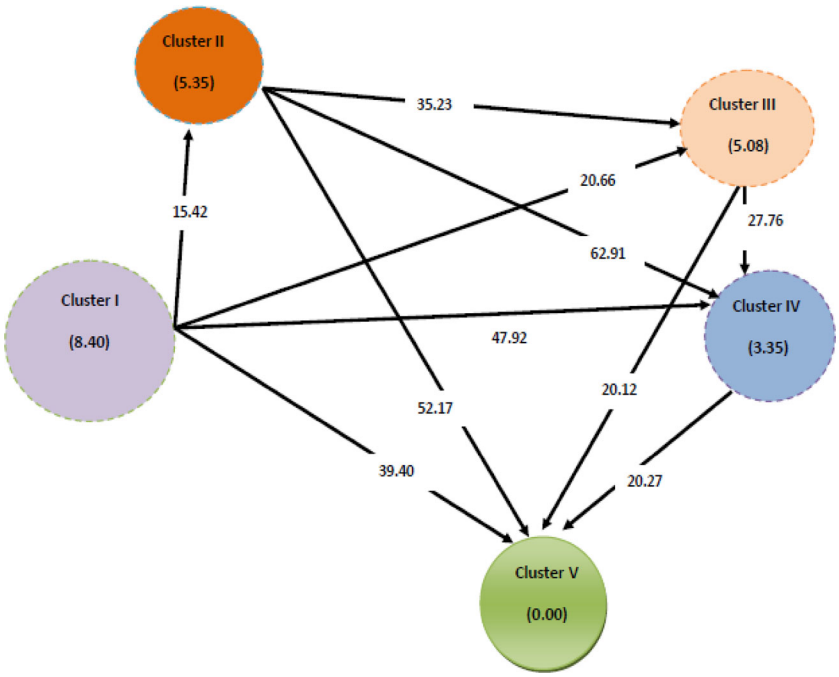

Fig. 3 Cluster diagram of obtained clusters

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Compliance with Ethical Standards

Conflict of interest The authors declare that they have no conflict of interest.

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