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ABSTRACTS



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conditions by analyzing their genetic molecules. In the study, we focused on understanding the responsive genes of tomatoes under drought conditions. We analyzed RNASeq data from different tomato genotypes, tissue types, and different drought durations. We used a time series scale to identify early and late drought-responsive gene modules and applied a machine learning method to identify the best responsive genes. We found six candidate genes of tomato; Fasciclin-like arabinogalactan protein 2 (FLA2), Amino acid transporter family protein (ASCT), Arginine decarboxylase 1 (ADC1), Protein NRT1/PTR family 7.3 (NPF7.3), BAG family molecular chaperone regulator 5 (BAG5) and Dicer-like 2b (DCL2b) (FLA2, ASCT, ADC1, NPF 7.3, BAG5 and DCL2b) that were responsive to drought. We further constructed their protein-protein interaction network to identify their potential interactors and found them drought responsive drought-responsive proteins. The candidate genes can help to explore the adaptation of tomato plants under drought conditions. The identification of these candidate genes and modules can have far-reaching implications for molecular breeding and genome editing in tomato, providing insights into the molecular mechanisms that underlie drought adaptation. This research underscores the importance of the genetic basis of plant adaptation, particularly in changing climates and growing populations

Keywords: Abiotic stresses, Molecular breeding, Machine learning, Responsive genes, Adapted crops

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Heritability and Diversity Analysis Detect Year-round Jute Genotypes Based on Vegetative and Reproductive Parameters

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Abstract

It is highly challenging to produce jute seed throughout the year in Bangladesh due to the fluctuating climate. Thus, this experiment was carried out to determine the ideal sowing time and choose a genotype of jute for year-round cultivation in order to produce jute vegetables throughout the year. The experiment was conducted at Jute Agriculture Experimental Station (JAES), Bangladesh Jute Research Institute (BJRI), Jagir, Manikganj in two consecutive years from February, 2018 to January, 2019 and February, 2019 to January, 2020. Three indigenous Germplasm (Merha red, Merha green and Birol red) of *Corchorus capsularis* collected from different location from Bangladesh and Accession-3840 of *Corchorus olitorius* collected from Genetic Resources and Seed Division of Bangladesh Jute Research



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Institute were used as treatments and BJRI released variety BJRI deshi pat shak-1 and Bangladesh Institute of Nuclear Agriculture (BINA) released variety BINA pat shak-1 were used as control. The crops were sown at first week of every month from February-November, 2018 and 2019. The experiment was conducted using Randomized Complete Block Design (RCBD) with three replications. The lowest values of different yield contributing parameters; pod/plant, seed/pod, 1000-seed weight, branches/plant and seed yield/m² was found in November of 2018 and 2019. Moreover, the highest leaf yield was found in the month of May in both the years. The longest seed to seed duration was found in Accession-3840 and the lowest was recorded in Merha red, Merha green and Birol red, respectively in both years. The results of the study suggest that these three genotypes may be used as the possible year round jute genotypes in future.