



Article

Transcriptome Analysis of Tolerant and Susceptible Maize Genotypes Reveals Novel Insights about the Molecular Mechanisms Underlying Drought Responses in Leaves

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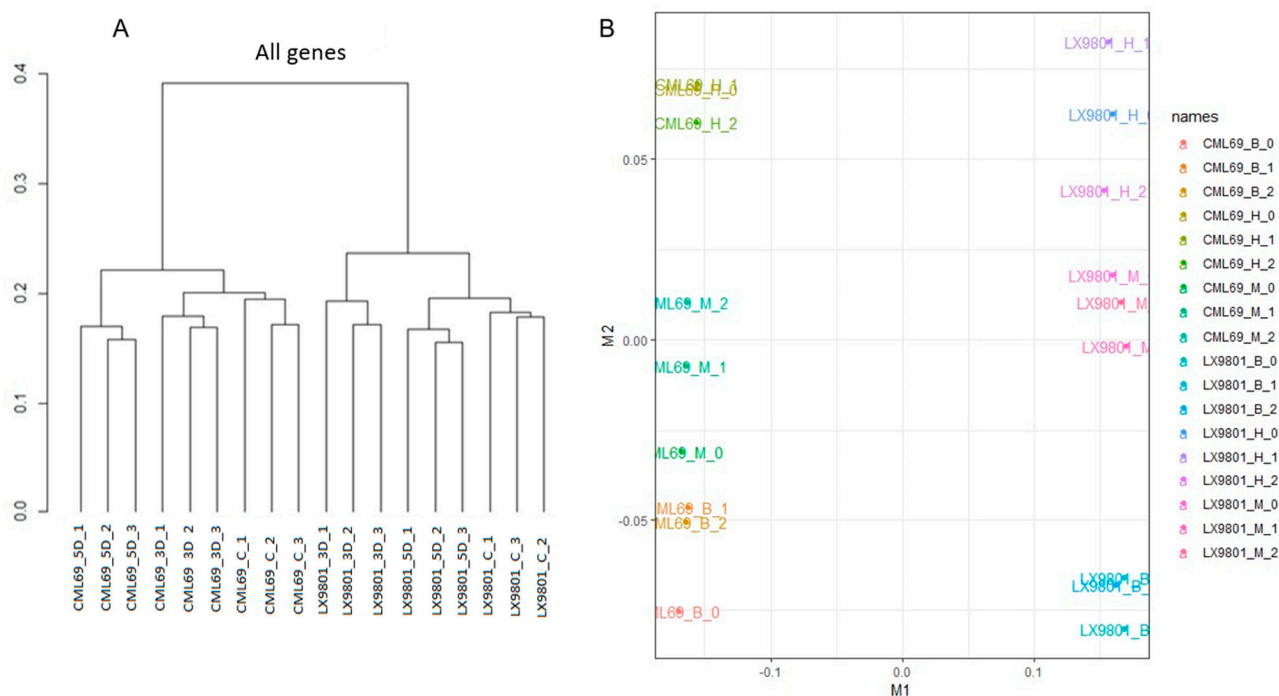


Figure S1. Correlation of the expression values of the biological replicates of both samples. **(A)** Dendrogram depicting correlation among replicates of the same sample on global expression profiles at C, 3D, and 5D drought stress. **(B)** Multidimensional scaling (MDS) plot analysis of the sample gene expression profiles. Each genotype was categorically grouped according to the similarity of individual replicates. B represents control (C), M represents three days (3D), while H represents five days (5D) drought treatment. 0, 1, 2 illustrates individual biological replications of the samples.

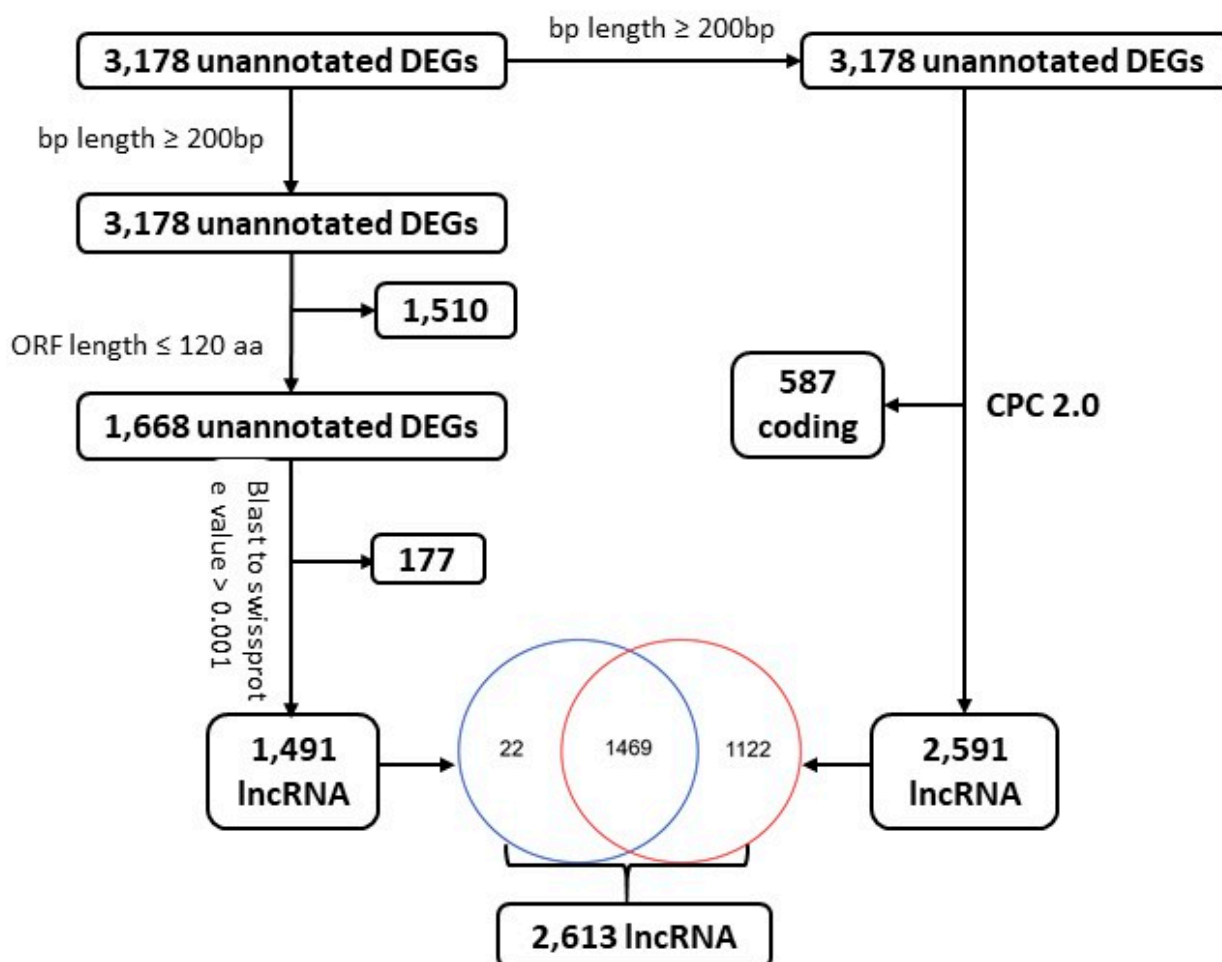


Figure S2. Analysis of 3,178 unannotated drought-responsive DEGs. CPC 2.0 generated 587 coding and 2,591 long non-coding RNAs. The ORF method generated 1,491 long non-coding RNAs. In total, 2,613 out of 3,178 were long non-coding RNAs.

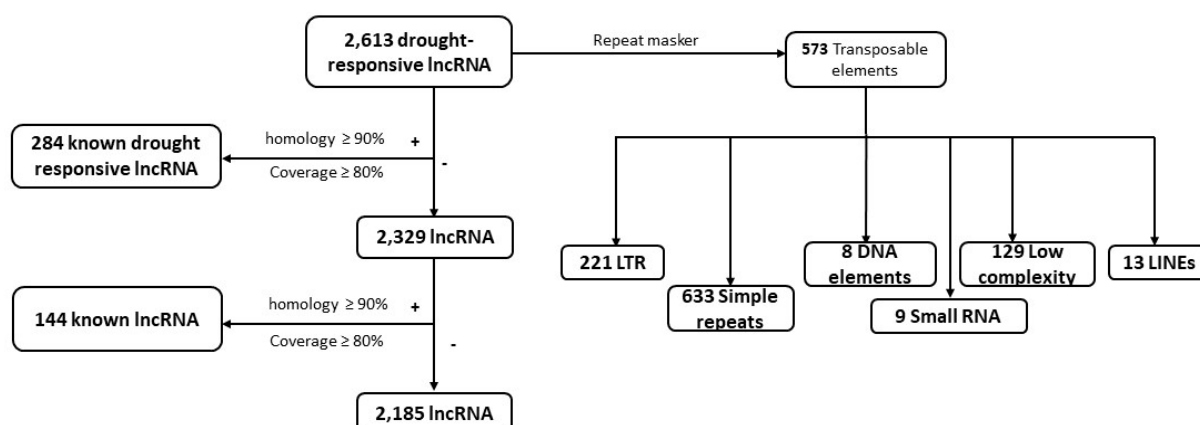


Figure S3. Analysis of 2,613 drought-responsive long non-coding RNAs (lncRNAs). 428 (284+144) are homologous to previously reported lncRNAs. 573 lncRNAs were identified to be Transposable elements (TEs) by RepeatMasker.