

論文の内容の要旨

生産環境生物学専攻

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論文題目 **Studies on the salinity stress responses of pearl millet (*Pennisetum glaucum* L.)**

(トウジンビエの塩ストレス応答に関する研究)

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) plays important role in food security in arid and semi-arid areas of India and Africa. It is well known for its abiotic stress tolerance capacity including drought, salinity and high temperature. However, it lags behind the other cereals in terms of research and development. To study and research the salinity stress tolerance potential of pearl millet we used different biotechnological approaches. The aim of study was to understand the molecular and biochemical responses of pearl millet to salinity stress.

Our transcriptome (RNA sequencing) analysis able to find out salinity stress responsive genes and pathways of pearl millet. A comparative transcriptome analysis between the salinity tolerant (ICMB 01222) and salinity susceptible (ICMB 081) lines was conducted under control and salinity conditions. Physiological studies revealed that the tolerant line ICMB 01222 had higher growth rate and ability to accumulate higher amount of sugar in leaves under salinity stress. A total of 11,627 differentially expressed genes (DEGs) were identified in both lines. Unigenes involved in ubiquitin-mediated proteolysis and phenylpropanoid biosynthesis pathways were upregulated in the tolerant line. Unigenes encoding SBPs

(SQUAMOSA promoter binding proteins), which are plant-specific transcription factors, were differentially expressed only in the tolerant line. Functional unigenes and pathways that are identified can provide useful clues for improving salinity stress tolerance in pearl millet.

We also performed the small RNA sequencing to find out the salinity stress responsive small RNAs, especially MicroRNAs (miRNAs). In total, 81 miRNAs were identified as a salinity stress responsive miRNA (30 miRNAs as an up-regulated miRNAs and 51 miRNAs as a down-regulated miRNAs). Interestingly, significantly upregulated pearl millet miRNAs belong to miR159 family, which was previously reported to be involved in various abiotic stress responses. In total, 448 mRNAs genes of pearl millet were identified as target genes. Among these target genes 122 mRNAs were identified as a transcription factor (25 % of total target gene). Pathway analyses showed that differentially expressed miRNAs and their target genes might regulates Auxin responsive pathway. This suggests that miRNAs play an important role in salinity stress tolerance in pearl millet. This result could be used to improve salinity stress tolerance in upland crops.

In our transcriptome analysis we discovered many salinity stress responsive gene. We performed the functional characterization of one of the salinity stress responsive gene called, PgNAC21 (NAC transcription factor 21). Gene expression analysis revealed that *PgNAC21* expression is induced by salinity stress and abscisic acid (ABA) treatment. Relative to control plants, *Arabidopsis* plants overexpressing *PgNAC21* exhibited better seed germination, heavier fresh weight and greater root length under salinity stress. Overexpression of *PgNAC21* in *Arabidopsis* plants also enhanced the expression of stress-responsive genes. Our data demonstrate that *PgNAC21* functions as a stress-responsive NAC TF and can be utilized in transgenic approaches for developing salinity stress tolerance in crop plants. Our all studies generate useful information to understand the molecular mechanism of salinity stress tolerance

in pearl millet. This information can be used by breeders to breed new salinity stress tolerant crop plants by transgenic approaches.