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Identification of Fe and Zn Responsive Genes in Pearl Millet (*Pennisetum glaucum* L.) through Whole Genome Transcriptome Approach

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Abstract Text:

Micronutrient malnutrition due to iron and zinc deficiencies is a serious public health problem in developing countries. In India alone, about 80% of the pregnant women and 74% of children suffer from iron and zinc deficiency. At present, knowledge of the genes controlling specific steps in the Fe and Zn pathways is still rudimentary hence studying genes of Fe and Zn density has become important. A whole genome RNA-Seq approach was carried out to understand the genes and pathways related to Fe and Zn accumulation in pearl millet. Seedlings of a high Fe and Zn grain density pearl millet inbred ICMB 1505 were exposed to four Fe and Zn stress treatments namely, -Fe -Zn, -Fe +Zn, +Fe -Zn and +Fe +Zn in hydroponics for 12 days (Figure 1). Seedlings were expressed interveinal chlorosis in the leaves due to the non-availability of Fe and Zn compared to control during the stress treatments. At that time, the leaf and root tissues in four treatments were harvested separately. Total RNA was extracted from the treated samples followed by cDNA synthesis. Illumina HiSeq 2500 platform was used to sequence the constructed cDNA libraries. Analysis of differentially expressed genes and

40 genotypes with variable Fe and Zn grain density were selected and tissue samples from different plant parts such as seed, flag leaf, root, stem sheath, panicles at anthesis and panicle at milky-stage were collected. RNA was extracted from the samples to validate the genes associated with Fe and Zn homeostasis. The information will be used for accelerated breeding programmes to improve the Fe and Zn density in pearl millet.

Session Selection:

Maize, Sorghum, Millet, Sugar Cane, and related

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