

Genomics Approach for Excavation of NAS Genes from Nutri Rich Minor Millet Crops: Transforming Perspective from Orphan Plants to Future Food Crops

Authors : Mahima Dubey, Girish Chandel

Abstract : Minor millets are highly nutritious and climate resilient cereal crops. These features make them ideal candidates to excavate the physiology of the underlying mechanism. In an attempt to understand the basis of mineral nutrition in minor millets, a set of five Barnyard millet genotypes were analyzed for grain Fe and Zn content under contrasting Fe-Zn supply to identify genotypes proficient in tolerating mineral deficiency. This resulted in the identification of Melghat-1 genotype to be nutritionally superior with better ability to withstand deficiency. Expression analysis of several Nicotianamine synthase (NAS) genes showed that HvNAS1 and OsNAS2 genes were prominent in positively mediating mineral deficiency response in Barnyard millet. Further, strategic efforts were employed for fast-track identification of more effective orthologous NAS genes from Barnyard millet. This resulted in the identification of two genes namely EfNAS1 (orthologous to HvNAS1 of barley) and EfNAS2 (orthologous to OsNAS2 gene of rice). Sequencing and thorough characterization of these sequences revealed the presence of intact NAS domain and signature tyrosine and di-leucine motifs in their predicted proteins and thus established their candidature as functional NAS genes in Barnyard millet. Moreover, EfNAS1 showed structural superiority over previously known NAS genes and is anticipated to have role in more efficient metal transport. Findings of the study provide insight into Fe-Zn deficiency response and mineral nutrition in millets. This provides millets with a physiological edge over micronutrient deficient staple cereals such as rice in withstanding Fe-Zn deficiency and subsequently accumulating higher levels of Fe and Zn in millet grains.

Keywords : gene expression, micronutrient, millet, ortholog

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