

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

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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 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 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 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.