

JOINT EVENT

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**Genetic diversity analysis of lentil (*Lens culinaris* Medikus *culinaris*) accessions having high concentration of iron (Fe) and zinc (Zn) using by simple sequence repeat (SSR) markers****Rajendra Darai<sup>1</sup>, Ashutosh Sarker<sup>2</sup>, Krishna Hari Dhakal<sup>3</sup>, Madhav Prasad Pandey<sup>3</sup>, Surya Kant Ghimire<sup>3</sup>, Shiv Kumar<sup>4</sup>, Tara B Ghimire<sup>5</sup>, Jitendra Maharjan<sup>5</sup> and Laxman Aryal<sup>1</sup>**<sup>1</sup>Nepal Agricultural Research Council, Nepal<sup>2</sup>ICARDA, India<sup>3</sup>Agriculture and Forestry University, Nepal<sup>4</sup>International Center for Agricultural Research in the Dry Areas, Morocco<sup>5</sup>Seed Science Research and Technology Division- NARI, Nepal

Nepalese lentils are comparatively rich in iron (Fe) and zinc (Zn) in South Asian countries, making lentil a potential crop of whole food solution to aid in the global battle against the micronutrient malnutrition. Knowledge of genetics underlying the uptake of grain Fe and Zn from soils is required to increase their stable concentrations in lentils. Therefore, in present study, 25 accessions of lentil were characterized using 40 simple sequence repeat (SSR) markers in order to characterize genetic variation available among genotypes having high Fe and Zn concentrations. Out of the 40 SSR markers, 23 markers were found polymorphic while 12 markers were monomorphic and 5 markers were null. These 23 polymorphic markers produced a total of 584 alleles, of which total number of polymorphic alleles were 52 and average alleles per locus was 11.49. The allele number for each SSR locus varied between two to four with an average of 2.97 alleles per marker. Markers PLC 16, SSR 124, SSR 156, SSR 113, SSR 28 and SSR 107 showed higher level of polymorphism indicating the power and higher resolution of those marker systems in detecting molecular diversity. The polymorphic information content (PIC) values for the SSRs loci ranged from 0.14 to 0.57. The pair wise genetic similarity among 25 lentil accessions varied from 0.16 to 0.83. The dendrogram constructed based on genetic similarities among 25 lentil accessions identified five major clusters. Maximum seven accessions were grouped in cluster II followed by six in cluster III while cluster IV contained lowest number of accessions i.e. three accessions indicating their higher genetic similarity. Our result showed that significant genetic variability at molecular level on the basis of SSR markers that can be used towards the development of lentil cultivars having high concentration of Fe and Zn.

rajendra5042@yahoo.co.uk