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Characterization and assessment of genetic diversity in local and improved accessions of grass pea (*Lathyrus sativus* L.) for green forage yield traits

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Abstract

Forty-four Grass pea germplasm accessions were classified for agro-morphological characters according to the descriptor of Lathyrus germplasm characterization ofInternational Plant Genetic Resources Institute, Rome, Italy. Genotypes were classified at different growth stages. A total of 43 qualitative characters were studied for morphological characterization. Monomorphic results were obtained for the characters *viz*., plant type,stem wax coating, anthocyanine pigmentation on the leaf, prominence of leaf vein, pigment present on leaves, leaf petiole colour, top leaves petiole end, leaf scale type, flower bud shape, number of pods per peduncle, pod shape, pod curvature, seed shape, seed coat pattern andcotyledon colour.The genotypes were grouped into 6 clusters based on D^2 statistics for 15 metric characters of 44 diverse genotypes. Cluster I was the largest with 32 genotypes, followed by cluster III, five genotypes, cluster IV, four genotypes, and the remaining clusters, each one genotype.The inter-cluster D^2 values revealed a maximum divergence between cluster I and VI (349.82), followed by cluster V and VI (255.68); cluster III and VI (230.07); cluster III and IV (223.64) and cluster IV and VI (200.01). It was observed that L/S ratio was the most significant contributor (30.97%) to genetic divergence, followed by leaflet width (18.08%) and length of primary branch (11.42%). In contrast,the number of seeds per pod and daysto first flowering contributed the least to divergence.

Keywords: D^2 statistic, Divergence, Forage yield, Germplasm, Morphological characterization