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## Analysis of Genotypic Diversity in Sesame as Based on Morphological and Agronomic Traits

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### Abstract

Germplasm banks, as pools of the genetic variability are fundamental for the developmental research of crop species. This variability must be characterised by genetic and phenotypic parameters for the identification of duplicates and the organisation of core collection, and as a support in the choice of parents for breeding programs. When genetic variability is narrowed using traditional breeding methods for a long period then induced mutations are one of the most important approaches for broadening the genetic variation to circumvent the bottleneck conditions. Although, sesame is an ancient and advantageous oilseed crop it is still at an early stage of breeding which is reflected by its' poor yield performance. This study aims to analyse genetic diversity of sesame germplasm and mutants from India and Ethiopia. Agro-morphological variation in the sesame germplasm was estimated using 14 morphologic and agronomic descriptors to characterise and identify genetic diversity. A total of 36 sesame landraces were collected from the sesame growing areas throughout India and Ethiopia. The collection was evaluated for seed yield, yield related characters and morphological characters. A large amount of variation was recorded for 14 morphologic and agronomic traits. D2 analysis and cluster analysis indicated no strict or narrow relationship between observed genetic diversity and geographical differentiation. Cluster analysis identified seven main clusters based on agro-morphological characters indicating the diversity which could mainly be attributing to diverse agro-climatic conditions. D2 analysis revealed that the crossing between the genotypes, Utawadia, Humera, and DSS would most likely express a considerable amount of heterosis in F1 generation and also provide a wide spectrum of recombinants in segregating generations. Principle component analysis revealed that the first three vectors explained 70.52 % of total multivariate variation. Canonical correlation studies indicated that the development characters such as capsule number per plant, capsule length, days to flowering, plant height, branches number per plant, and seed yield were the major determinates of the genetic diversity in the collection. Single plant selection was made from these populations based on different agromorphic traits and yield potential. These results have an important implication for sesame germplasm characterisation, improvement, agro-morphological evaluation and conservation.

**Keywords:** Capsule length, genetic diversity, germplasm, multivariate analysis