ORIGINAL RESEARCH ARTICLE

Exploring genetic diversity of Ashwagandha (*Withania somnifera* L.) in the deccan plateau region

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ABSTRACT

During Rabi 2018-19, at the Medicinal and Aromatic Plant Research Station, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad, the experiment was set up in a Completely Randomized Block Design with various genotypes of Ashwagandha as a treatment and replicated thrice. The genotypes were systematically evaluated by grouping them into different clusters using Mahalanobis D² statistical analysis. The results indicated a highly significant difference among the genotypes, and these genotypes were classified into 11 clusters. They were comprised of 17 genotypes followed by cluster IV and cluster VIII with two genotypes each, whereas clusters II, III, V, VI, IX, X and XI were monotypic or solitary. The intra-cluster distance varied from 0.00 to 4207.69. Maximum Intra cluster distances were observed in Cluster VIII followed by clusters I and IV. The inter-cluster D² values revealed the highest inter-cluster space marked between IX and X, followed by VII and VIII, indicating wider genetic diversity between these groups. Selecting parents from these diverse clusters (IX, X, VII and VIII) for hybridization would help achieve novel recombinants. The maximum mean value for dry leaf weight per plant was recorded in cluster VIII, followed by cluster X. The highest dry root weight per plant was recorded in the genotypes of cluster VIII, followed by cluster IX. The highest alkaloid was noticed in cluster IV, followed by cluster X. Based upon high yielding and high alkaloid genotypes with significant inter and intra-cluster distances, it is advisable to attempt crossing between the genotypes from cluster IV (Poshita, CIM-Pratap), cluster VIII (NMITLI-101, NMITLI-118), cluster IX (CIM-Chetak) and the genotype of cluster X (RAS-65).