

Short Communication

Genetic and geographical divergence in horse gram germplasm from Andhra Pradesh, India

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Abstract

Nine characters contributing to seed yield were measured on 20 accessions of horse gram (*Macrotyloma uniflorum* (Lam.) Verd), and subjected to genetic divergence analysis using Mahalanobis statistic and mapping using DIVA-GIS. The accessions were collected from two eco-geographical regions of Andhra Pradesh (India) – North Coastal and Rayalaseema. Based on D^2 values the genotypes were grouped into five clusters. Genetic diversity was not related to eco-geographical distribution. The greatest inter-cluster distance separated clusters II and V, followed by clusters IV, and V, III and IV. Entries in clusters V and II appear suitable as parents for horse gram improvement. The Rayalaseema region is the source of useful variation for days to flowering, maturity and yield.

Keywords: cluster analysis; genetic diversity; Geographic Information System; horse gram

Introduction

Horse gram (*Macrotyloma uniflorum* (Lam.) Verd.) is an arid food legume known to grow well in diverse environmental conditions (poor soils, low rainfall, soil pH from 5 to 7.5, 1800 masl altitude; Duke, 1981). The species is widely grown as a pulse, fodder crop, green manure crop and medicinal crop. In the Indian state of Andhra Pradesh, horse gram is grown in all eco-geographical regions, including Telangana, Rayalaseema and the Coastal region. Significant variability was observed within the germplasm grown in these areas. Seed colour ranges from black to chocolate brown, and protein content from 20 to 25%. The identification and development of high-yielding varieties are key for the full exploitation

of this dryland crop. Hence, an attempt was made to study the genetic diversity and geographical distribution within the germplasm collected from Andhra Pradesh.

Experimental

A set of 20 accessions, based on field performance in previous years, along with two controls (varieties Palem-1 and Palem-2 released by the state agricultural university) were evaluated to study the extent of diversity, identify diverse accessions for breeding programmes and identify geographical areas for future germplasm collection efforts. Each accession was planted in three 3 m rows, with an inter-row spacing of 60 cm and an inter-plant spacing of 10 cm. Recommended cultural practices were followed to grow the crop (Anonymous, 1992). The accessions were grown during the *post-rainy* (*rabi*) season of 2005–2006. The experimental design was a randomized complete block

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Table 1. Cluster composition and cluster means based on D^2 values in horse gram

Cluster (intra-cluster distance D^2 value)	No. of genotypes	Genotypes (source)	Plant height (cm)	Primary branches (no.)	Days to flowering (no.)	Days to maturity (no.)	Pods/plant (no.)	Pod length (cm)	Seeds/pod (no.)	100 seed weight (g)	Seed yield/plant (g)
I (7.41)	7	IC470166, IC426490, IC261297, IC426477, IC261301, IC426479 and Palem-1	96.20	4.18	75.09	105.19	74.91	4.26	5.51	3.61	9.36
II (4.65)	2	IC470171, IC470226	65.95	3.73	75.33	101.16	108.9	4.25	5.4	3.9	13.77
III (5.48)	5	IC470169, IC470264, IC426490, IC470256, IC470265	117.7	4.40	70.87	100.33	94.84	4.36	5.41	4.18	12.58
IV (4.06)	3	IC470213, IC470249 and IC426540	114.74	4.53	72.11	99.66	80.53	4.45	5.33	3.61	14.70
V (6.94)	5	IC470188, IC426520, IC261302, IC426569 and Palem-2	122.56	4.46	81.33	107.93	39.89	4.28	5.23	4.02	4.55
LSD (5%)			30.135	0.451	4.105	4.111	33.244	0.377	0.437	0.372	5.072
LSD (1%)			40.290	0.603	5.489	5.497	44.446	0.504	0.584	0.497	6.781

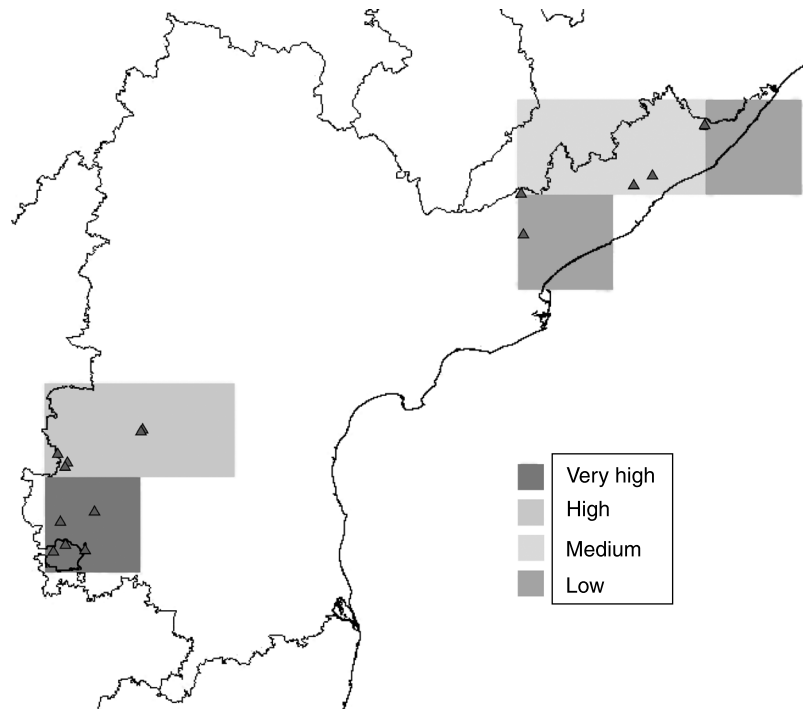


Fig. 1. Distribution and grid map showing the diversity index of horse gram accessions for seed yield per plant in Andhra Pradesh (India).

design with three replications. Nine morphological, phenological and reproductive characters (Table 1) were measured from five randomly selected plants at maturity. Mean trait values were used to derive Mahalanobis (1936) D^2 statistics using the Windostat statistical package. The D^2 values were treated as generalized distances to cluster the populations following Tocher's optimization method, as described by Rao (1952). Latitude and longitude at the collection site were recorded using a handheld global positioning system (Garmin, GPS 12). The quantitative and GPS data were used for mapping the accessions based on their traits using DIVA-GIS software v5.2.

Discussion

On the basis of the D^2 analysis, the 20 accessions were grouped into five clusters (Table 1). Cluster I was the largest group, containing seven entries, followed by clusters III and V with five entries each, and IV and II with, respectively, three and two entries. The range of intra- and inter-cluster distances was 4.06–7.41 (Table 1) and 8.9–22.2, respectively. The greatest inter-cluster distance separated clusters II and V, followed closely by clusters IV and V, and III and IV, indicating that these clusters were genetically the most outlying. The geographical origins of the entries along with a grid map generated using DIVA-GIS for seed yield per plant are provided in Fig. 1. Entries sharing a similar geographical origin grouped into

different clusters, indicating that geographical distribution and genetic divergence are not related. Thus, collection should be based on agromorphological characterization and standard sampling procedures (Brown and Marshall, 1995). The clustering of the entries suggested that the exchange of genetic stocks, genetic drift, spontaneous variation and natural and artificial selections applied for developing varieties suited to local needs may all have played an important role in generating genetic diversity (Arunachalam and Ram, 1967; Dhobal and Rana, 1994). Entries in cluster IV were the best performing in terms of yield and the number of primary branches. Those in cluster III had high seed weight, seed number per pod and earlier days to flowering, while those in cluster II tended to have more pods per plant and a shorter plant height. Crop improvement is most likely to be achieved if parental combinations involve entries belonging to different outlying groups (clusters II and V, II and IV and III and IV).

The DIVA-GIS grid map revealed that entries from the Rayalaseema region were the most diverse for seed yield per plant (Fig. 1), days to flowering and to maturity.

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