



Genetic divergence in land race collections of rabi sorghum [*Sorghum bicolor* (L.) Moench.]

A. V. Umakanth, R. Madhusudhana, K. Madhavi Latha, Swarnlata Kaul and B. S. Rana

National Research Center for Sorghum, Rajendranagar, Hyderabad 500 030

(Received: June 2002; Revised: August 2003; Accepted: August 2003)

The grain productivity of rabi sorghum [*Sorghum bicolor* (L.) Moench.] in India is very low (610 kg/ha) as much of the cultivated area is under land races which are very poor yielders. To enhance the productivity levels of rabi sorghum, prior information on the nature and magnitude of genetic diversity present in germplasm collections is a pre-requisite. An attempt in the present investigation was therefore made to study the nature and magnitude of genetic divergence for grain yield and its components and also to identify divergent parents from distantly related clusters for suitable hybridization.

Forty one land races collected from different geographic regions of Maharashtra along with three established lines from the national programme were grown in a randomized block design with three

replications during rabi season of 2001-02 at the National Research Centre for Sorghum, Hyderabad. Five randomly selected plants from each line were utilized for recording observations on days to 50 % flowering, plant height (cm), head weight (g), panicle length (cm), number of primaries per panicle, number of seeds per branch, 100 seed weight (g) and grain yield per plant (g). Genetic diversity was studied using Mahalanobis D^2 statistic and clustering was done following Tocher's method [1].

The genotypes were grouped into 14 clusters (Table 1) indicating the presence of appreciable amount of diversity among the genotypes under study. The maximum number of genotypes (25) were grouped in cluster I, followed by cluster II (6) and cluster VIII (2). Clusters III to VII and clusters IX to XIV were distinct

Table 1. Distribution of 41 rabi sorghum local land races and three checks in different clusters

Cluster No.	No. of strains/cluster	Name of strains	Origin
I	25	PU-12, PU-17, PU-27, PU-24, PU-25, PU-30, PU-15, PU-32, M35-1, PU-2, PU-16, PU-20, PU-29, PU-11, PU-33, PU-23, PU-18, PU-8, PU-24, PU-5, PU-6, PU-1, PU-7, PU-10, CSV 216R	Shalu jowar, Junoni local-3, Bhamla tanda maldandi, Mangalwedha maldandi-2, Mangalwedha maldandi-3, Tandulwadi maldandi-2, Junoni local-1, Sultanpuri local, Mohol, Bikkulinge local, Junoni local-2, Mangud local, Tandulwadi maldandi-1, Eknud local-2, Chugi maldandi-2, Mangalwedha maldandi-1, Udunwadi local, Limb local-1, Mangalwedha maldandi-2, Sherwadi local, Umbergaon local, Pandharpur local, Gomewadi local, Eknud local-1, NRCS/AICSIP
II	6	RSLG-262, RSP-1, RSLG-227, RSLG 383, RSP-3, PU-26	Rahuri Sorghum Local Germplasm (MPKV, Rahuri), Tandulwadi local (Dagdi)
III	1	PU-31	Tandulwadi maldandi-3
IV	1	PU-28	Chugi maldandi-1
V	1	RSLG-241	Rahuri sorghum local germplasm
VI	1	CSV14R	NRCS/AICSIP
VII	1	PU-4	Kusmod local
VIII	2	PU-13, PU-14	Kerewadi local-1, Kerewadi local-2
IX	1	PU-34	Darganhalli maldandi
X	1	PU-21	Kaulee local-1
XI	1	PU-19	Kachrewadi local
XII	1	PU-3	Tandulwadi local
XIII	1	PU-22	Kaulee local-2
XIV	1	PU-9	Limb local-2

from the rest with each one of them having a single genotype indicating their uniqueness from breeding point of view.

PU-22 (XIII) is suggested to obtain superior genotypes from the segregating generations so that low yield constraints in rabi sorghum can be overcome.

Table 2. Average intra (along diagonal) and inter cluster values of D^2 among different clusters in sorghum

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	3.10	4.73	3.83	4.25	4.44	4.32	4.22	5.15	4.06	6.20	5.05	5.39	6.77	5.75
II		2.77	6.34	6.85	4.33	4.42	6.74	7.02	5.47	5.33	4.82	7.09	6.81	6.72
III			0.00	1.98	5.43	4.36	2.75	6.11	5.79	6.44	7.15	5.52	5.93	7.39
IV				0.00	5.67	4.31	3.63	5.77	6.30	7.81	7.78	4.93	6.84	7.74
V					0.00	4.49	5.86	6.32	6.26	5.56	5.39	5.99	6.35	6.45
VI						0.00	5.63	7.32	6.46	6.61	7.23	4.11	6.89	8.68
VII							0.00	6.90	6.11	5.88	7.30	6.82	5.19	6.53
VIII								2.70	4.17	9.32	4.99	7.18	9.51	4.91
IX									0.00	7.77	3.76	6.66	9.08	4.61
X										0.00	6.59	9.55	3.56	7.62
XI											0.00	8.39	8.27	4.08
XII												0.00	10.0	9.54
XIII													0.00	8.28
XIV														0.00

Intercluster distances presented in Table 2 reveal maximum divergence between cluster XII and cluster XIII (10.00) followed by cluster X and cluster XII (9.55), cluster XII and cluster XIV (9.54) and cluster VIII and cluster XIII (9.51). In the present study, genotypes evolved in the same area were grouped into different clusters indicating that genetic diversity was not necessarily parallel to geographic diversity which confirmed the earlier reports [2, 3].

Cluster VIII recorded highest mean grain yield per plant, head weight and number of primaries per panicle. Cluster XII showed high mean for 100 seed weight and panicle length. Clusters II and VI were early compared to other clusters.

Maximum amount of heterosis is generally expected in cross combinations involving the parents belonging to most divergent clusters [4,5]. On the basis of inter cluster distances and per se performances observed in the present study, a hybridization programme involving PU-13, PU-14 (VIII), PU-3 (XII), PU-4 (VII), CSV14R (VI), PU21 (X), PU-28 (IV) and

Acknowledgements

We are grateful to National Agricultural Technology Project (NATP) for providing funds to carry out this research.

References

1. Rao C. R. 1952. Advanced statistical methods in biometrical research. John Wiley and Sons, New York.
2. Kadam D. E., Patil F. B., Bhor T. J. and Harer P. N. 2001. Genetic diversity studies in sweet sorghum. J. Maharashtra Agril. Univ., **26**: 140-143.
3. Gurpreet Singh, Singh H. C., Ram Krishna and Sunil Kumar Singh. 2001. Genetic divergence in *Sorghum bicolor* (L.) Moench. Ann. Agric. Res., **22**: 229-231.
4. Ramanujam S., Tiwari A. S. and Mehra R. B. 1974. Genetic divergence and hybrid performance in mungbean. Theor. Appl. Genet., **45**: 211-214.
5. Singh S. P. and Sharma J. R. 1989. Genetic improvement of pyrethrum. IV. Selective divergence, heterosis and potential hybrid clones. Theor. Appl. Genet., **78**: 841-846.