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RESEARCH ARTICLE

Identification of New Sources for Good Quality High Biomass Yield and other Promising Traits in Mini Core Collection of Forage Sorghum

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Mini core collection of forage sorghum was evaluated for genetic diversity analysis in randomized block design. Observations were taken for total of thirty traits including quantitative and quality traits. Eleven principal components were extracted on the basis of PCA. First to eleventh principal components explained 16.42, 7.70, 6.98, 6.98, 6.83, 6.69, 5.74, 5.10, 4.87, 4.74, 4.31% of the total variance, respectively. The first eleven principal components had eigen values more than one and explained 75.77 % of the total variability of the original data units. On the basis of principal component analysis genotypes IS 651 and IS 23890 were found to be better for green fodder, dry fodder, DDM and mineral content; IS 28614, G 46 and SSG 59-3 recorded better performance and implied their superiority for fodder yield and resistance against stem borer, shoot fly and grey leaf spot; ICSV 700 was found better for fodder yield and IVDMD and low HCN and lignin content. Use of these genotypes is suggested in breeding programme as different sources/parents for further improvement of forage sorghum for green and dry fodder yield, IVDMD, mineral content and disease resistance.

Key Words: Fodder and yield, Forage sorghum, Mini core, PCA

Introduction

Sorghum is a major staple food crop in semi-arid tropics and among most food insecure people across the world. It could be due to crop's xerophilic characteristics, adaptation potential, quick growing habit, good ratoonability, palatability, digestibility and wide range of potential uses as green fodder, dry roughage, hay and silage. It is recognized worldwide as a "4F" crop especially under moderate inputs and water deficit environments.

In India, sorghum accounts for 1% of the total agricultural GDP. The present acreage under multicut fodder sorghum is one lakh hectares. Now increasing demand for livestock suggests that the fodder sorghum area will be 27.0 million hectares by 2050 (Vision IIMR, 2050). Landraces and wild relatives are rich sources of resistance to diseases, insect pests and other stresses such as high temperature, and drought etc. They are also rich sources of traits to improve food and fodder quality, animal feed and industrial products. To prevent the extinction of landraces and wild relatives, collection and conservation of sorghum germplasm has been accelerated in the past four decades. Since then, it has become an integral component of crop improvement programs (Rosenow and Dahlberg, 2000).

A core collection of 2247 accessions of sorghum was developed in 2001 to enable researchers to have access to a smaller set of germplasm. However, this core collection was found to be too large. To overcome this, mini core (10% accessions of the core or 1% of the entire collection) was developed and is being maintained at ICRISAT, Patancheru, India (Grenier *et al.*, 2001).

Most rapid method to step up livestock production is to enhance nutritive value of the forage sorghum by improving IVDMD (Pedersen *et al.,* 1982). When IVDMD is increased, winter hardiness is decreased, prussic acid glycosides may be increased and maturity is extended (Hoveland and Monson, 1980). A comprehensive analysis for importance of the mineral content in forage animal nutrition reveals that most tropical forages have low mineral contents than the temperate species. Screening of forage sorghum germplasm has shown existence of significant genetic variation for toxic constituents like, hydrocyanic acid and tannin, which reduce the quality of forage sorghum. Structural carbohydrates like NDF, ADF, cellulose and

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lignin are resistant to digestive enzyme and are found in cell wall portion of plant.

A major loss of quality and yield of forage sorghum crop is caused by insect pests like stem borer **(***Chilo partellus***)** (Hiremath *et al.,* 1988). It being an internal borer, its frass and fecal matter remain inside the stem lowering the quality of juice. Keeping in view these facts, a study was undertaken to characterize and assess the genetic diversity in sorghum accessions for morphological variability, quality and biotic resistance.

Material and Method

A field experiment was conducted in Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. It is situated in semi-arid sub-tropical region at 29º10ºN latitude and 75º46ºE longitude with-at elevation of 215.52 m above mean sea level. Hisar has semi-arid and sub-tropical climate with hot dry summer and severe cold winter. Average annual rainfall is about 492.7 mm was received in 33 rainy days, out of which 230.7 mm is received in three months, from July to September due to southwest monsoon. The soil of the experimental field was sandy loam in texture, slightly alkaline in reaction (pH 8.0). Sixty one sorghum genotypes were used in the present study. The experiment was laid out in randomized block design in three replications of two rows of 4m each with inter-row distance of 60 cm intra-row plant distance of 15 cm.

All the recommended agronomical practices for sorghum were followed to raise a good crop during the season. Data for all the traits was recorded from five plants in every replication.

Observations were recorded for various morphological traits like plant height, leaf length, leaves per plant, tillers per plant, leaf breadth, stem girth, green fodder yield and dry fodder yield and for three foliar diseases viz., grey leaf spot **(***Crecospora sorghi***),** zonate leaf spot **(***Gloeocercospora sorghi***)** and sooty stripe **(***Ramulispora sorghi***)** at 35 and 55 days after sowing. Scoring for foliar diseases was done using visual standards adopting the following scale:

1= no symptoms;

3= few scattered lesions/spots;

5= typical lesion developed on leaves covering up to 25% leaf area; 7= coalescing spots covering about 26-40% leaf area, and 9= symptoms severe covering more than 40% of leaf area

And the disease intensity was computed using the formula,

$$\text{Disease intensity} = \frac{\text{Sum of all numerical ratings}}{\text{Total number of leaves observed} \times \text{highest rating}} \times 100$$

All the genotypes were also evaluated for insects attack and observation were recorded for shoot fly **(***Atherigona soccata***)** and stem borer **(***Chilo partellus***)** attack as prescribed by Mathur (1991). For shoot fly data were collected at 14 and 28 days after germination and per cent dead hearts were calculated using the following formula:

$$\%\ \text{Dead heart} = \frac{\text{Number of dead heart/ plot}}{\text{Number of plants/plot}} \times 100$$

For quality estimation, samples of green fodder consisting of stalks after removal of heads were collected from the field and 500 g. was dried to constant weight at 60 ºC for dry matter determination. Then dried was passed through a small chopper, mixed thoroughly and sampled for dry matter determination and laboratory analyses. Neutral deteraent fibre (NDF) (%), acid detergent fibre (ADF) (%), Cellulose (%), Lignin (%) by (Goering and Van Soest (1970); Total phenol (mg/g DM) by Swain and Hillis (1959); Tannin (mg/g DM) by Bruns (1971); Mineral content : Zn, Fe, Cu, Mn, Na, K (µg/g DM) by Atomic Absorption Spectrophotometer; HCN content (mg/100g DM) by Gilchrist *et al.,* 1967; Crude Protein (%) by Micro-Kjeldhal's method; IVDMD (%) by Tilley and Terry (1971); Total soluble sugar (%) by Dubois *et al.,* (1956); DDM (Digestible dry matter) (q/ha) by IVDMD (%) X DFY/100 and º Brix by Refractometer were estimated as per the standard procedure.

The data were statistically analyzed for principal component analysis (PCA) and first two principal components were plotted against each other to find out the patterns of variability among genotypes and characters using statistical software packages of SAS 9.2 software.

Results and Discussion

The estimation of descriptive statistics of thirty traits indicated the existence of diversity among the genotypes. Among all the traits investigated, number of tillers, number of leaves, stem girth, green fodder yield, dry

fodder yield, total phenol, DDM, Fe, Mn, Zn, Cu, Na, Brix, HCN content, shoot fly, stem borer, sooty stripe, zonate leaf spot, grey leaf spot, tannin, lignin recorded higher variation in mean, range, variance and standard deviation.

Principal Component Analysis

The principal component analysis of sixty one genotypes based on correlation matrix yielded the eigen roots and vectors. These values and associated cumulative percentage of variation explained by eigen root have been presented in Table 1. Principal components with eigen values greater than one were selected for interpretation (Kaiser 1958 and Jeffers 1967). The first principal component explained 16.42 % of the total variation. The second to eleventh principal components explained 7.70, 6.98, 6.98, 6.83, 6.69, 5.74, 5.10, 4.87, 4.74, 4.31% of the total variance, respectively. The first eleven principal components had eigen values more than one and altogether explained 75.77 % of the total variability of the original data units.

The findings are in agreement with findings of Kang and Lee (1996), Ayana and Bekele (1999); Yadav and Pahuja 2013; Jain *et al.,* 2011; Jain and Patel, 2012 & 2016. Other yield contributing traits were also positively correlated with each other indicated that selection may be done in positive direction based on these traits towards crop improvement program. The PCA grouped the 30 traits in to eleven components which accounted for total (100%) variability among the studied genotypes. According to Chatfield and Collins, (1980) components with an eigenvalue of < 1 should be eliminated so that fewer components are dealt with. Furthermore, Hair *et al.* (1998) suggested that, eigenvalues greater than one are considered significant and component greater than 0.3 were considered to be meaningful.

The first principal factor (PF) showed high loading for plant height, leaf length, dry fodder yield, green fodder yield, DDM and Mn (Table 2). Number of tillers and number leaves per plant were found to have high loading on PF-2. PF-3 enabled high loading for Na, Cu and Fe. PF-4 had high loading for shoot fly dead heart, stem borer and grey leaf spot. The fifth principal factor enabled high positive loading for lignin and HCN and IVDMD and brix had high negative loading. The sign of loading indicates the direction of relationship between the factor and the variables, as correlation study showed IVDMD and brix are negatively correlated with

Table 1. Total variance explained by different principal components in sorghum genotypes

Principal components	Eigen value	Variation explained (%)	Cumulative variation explained (%)
1	4.92	16.42	16.42
2	2.12	7.07	23.48
3	2.09	6.98	30.47
4	2.09	6.98	37.46
5	2.05	6.83	44.29
6	2.01	6.69	50.99
7	1.72	5.74	56.74
8	1.53	5.10	61.85
9	1.46	4.87	66.72
10	1.42	4.74	71.46
11	1.29	4.31	75.77

both lignin and HCN. The sixth principal factor had variables like ADF, cellulose, phenol and Zonate leaf spot incidence whereas, PF-7 showed high loading for stem girth, tannin, crude protein and Zn. The eighth principal factor exhibited high loading for K only. Total soluble sugar showed factor loading on PF-9 while, the tenth principal factor enabled loadings of NDF. The eleventh principal factor had high loading for variable sooty stripe incidence. Genotypes with PF1 score therefore would have high level variability of these quantitative traits. Chozin, 2007, Mujaju and Chakuya, 2008 and Ali *et al.,* (2011) reported important contribution of the PF1 in total variability while studying different traits. The second and third PF explained 2.16 and 1.28 eigenvalues and contributing 24.08% and 14.31% variations, respectively. Overall, the PCA analysis under this study showed that phenotypic markers are useful in genotypes of sorghum and able to identify few key traits that accounted for the largest variability. Ali *et al.,* 2011; Akatwijuka *et al.,* 2016 and Jain & Patel, 2016 too observed similar observations.

Among the principal factors, Factors 1 and 2 can be regarded as fodder yield factors cumulatively, while Factors 3 and 8 can be regarded as mineral factors. The factors 4 and 11 can be regarded as diseases factors. The factors 5, 7 and 9 can be regarded as quality factors. The factors 6 and 10 could be antinutritional factors.

In the present study, principal factor analysis was carried out using principal component method, which does not require assumption of multivariate normal distribution of population in contrast to the other methods like maximum likelihood method (Jaiswal, 2000). Initially the data were analyzed without any rotation but it failed to load all the variables meaning thereby

Table 2. Factor loading of different characters with respect to different principal factor (Varimax rotation)

Characters/PF	PF-1	PF-2	PF-3	PF-4	PF-5	PF-6	PF-7	PF-8	PF-9	PF-10	PF-11
Dry fodder yield (q/ha)	0.9571	0.071	0.005	-0.038	-0.025	0.018	-0.004	-0.089	0.047	-0.036	0.091
Green fodder yield(q/ha)	0.947*	0.1	0.068	-0.025	-0.011	-0.031	-0.16	-0.072	0.025	0.003	0.053
Plant height (cm.)	0.924*	-0.064	0.122	0.014	-0.016	-0.088	-0.068	-0.135	-0.005	0.079	0.009
DDM (q/ha)	0.901*	-0.007	0.03	-0.011	-0.308	0.014	0.018	0.075	0.019	-0.106	-0.063
Leaf length (cm.)	0.640*	-0.02	0.293	-0.076	0.052	-0.079	0.069	0.012	0.299	0.116	0.207
Mn (µg/g DM)	0.456*	-0.254	0.139	0.139	-0.041	-0.095	-0.423	0.276	-0.161	0.073	-0.299
No. of tiller/plant	-0.010	0.927*	-0.133	0.080	0.012	0.028	-0.07	0.048	0.068	-0.005	0.048
No. of leaves/plant	0.097	0.898*	0.029	-0.165	0.210	-0.050	0.096	-0.017	-0.015	-0.011	-0.095
Na (µg/g DM)	0.007	0.014	0.779*	0.032	-0.162	0.004	-0.094	-0.044	0.252	0.154	0.012
Cu (µg/g DM)	0.180	0.001	0.726*	0.263	-0.008	0.024	-0.071	-0.119	-0.222	0.045	-0.266
Fe (µg/g DM)	0.300	-0.285	0.638*	-0.061	-0.117	0.043	-0.06	0.157	-0.134	-0.3	-0.02
Shoot fly dead heart	-0.171	-0.065	0.171	0.827*	-0.006	-0.007	-0.015	-0.002	-0.118	0.027	0.014
Stem borer dead heart	0.276	-0.085	-0.074	0.805*	-0.033	-0.1	-0.098	0.094	0.034	0.001	-0.081
Grey leaf spot	-0.214	0.127	0.06	0.647*	-0.016	0.332	0.211	0.08	0.105	-0.152	-0.087
Lignin (%)	0.137	0.035	-0.149	-0.162	0.702*	0.058	0.214	0.072	-0.085	-0.112	-0.321
IVDMD%	0.184	-0.129	0.007	0.015	-0.619*	0.019	0.016	0.316	0.007	-0.135	-0.24
Brixº	0.284	-0.117	0.404	-0.07	-0.582*	-0.04	0.064	0.045	-0.19	-0.047	0.088
HCN(mg/kg)	-0.123	0.153	-0.01	0.065	0.567*	0.05	0.239	0.324	-0.233	-0.01	0.33
ADF (%)	-0.078	-0.011	-0.019	-0.019	-0.008	0.827*	0.038	-0.105	0.006	0.1	-0.163
Cellulose (%)	-0.016	-0.122	-0.015	0.11	0.171	0.688*	-0.016	0.413	0.129	0.22	0.065
Total phenol (mg/g DM)	-0.141	-0.129	-0.12	0.118	0.327	0.540*	-0.228	0.081	0.405	-0.124	-0.024
Zonate leaf spot	-0.224	0.055	0.082	0.264	0.226	0.499*	-0.066	-0.167	-0.100	-0.327	0.346
Stem girth (mm.)	0.034	-0.130	-0.167	-0.057	0.036	0.130	0.763*	-0.014	0.161	0.035	0.044
Tannin (mg/g DM)	-0.365	0.172	0.065	0.164	0.125	-0.061	0.574*	0.209	-0.137	-0.203	0.043
Zn (µg/g DM)	-0.049	0.168	0.164	0.102	0.243	-0.247	0.419*	-0.364	-0.199	0.38	-0.048
Crude protein (%)	-0.091	0.291	-0.265	-0.018	0.243	-0.040	0.478*	-0.179	0.372	-0.289	0.068
K (%)	-0.176	0.051	-0.02	0.095	-0.038	-0.036	0.006	0.843*	0.040	0.061	0.033
Total soluble sugar %	0.200	0.064	0.028	-0.033	-0.096	0.015	0.109	0.066	0.807*	-0.101	0.017
NDF (%)	0.019	-0.028	0.030	-0.060	0.017	0.235	-0.072	0.075	-0.126	0.864*	-0.001
Sooty stripe	0.322	-0.075	-0.187	-0.156	-0.018	-0.113	0.108	0.07	0.042	-0.013	0.780*

that it could not provide much information regarding the idea of correlation between the variables and the principal factors.

The failure of principal factor analysis without rotation to draw sensible conclusions prompted to go for analysis with rotation. Varimax method of orthogonal rotation (Kaise, 1958) was utilized to rotate the factor axes. This is the most commonly used method and can be placed in a meaningful biological context (Titz, 1983). All the 30 variables showed high loadings on different principal factors and none of them was left after rotation of the principal factor axes. Moreover, it clearly grouped the similar type of variables by loading them together on a common principal factor.

The sign of loading indicates the direction of relationship between the factor and the variables, as correlation study showed IVDMD and brix are negatively correlated with both lignin and HCN. Similar results was observed in rapeseed by Valiollah, 2014 in which PF 1 had high positive loadings for days to flowering and days to maturity and high negative loadings for duration of flowering. These results are in conformity with that of Yadav *et al.,* (2003) who found that principal factor analysis identified nine principal components which explained 79 % variability. Loadings of similar type of variables on a common PC permitting to designate them as fodder yield factor, insect-pests attack factor disease incidence factor etc. as per type of variable loaded with. Abe *et al.***,** (2013) analysed 31 sorghum landrace accessions for chemical analysis. The PCA revealed that the first four PCs contributed 71.77 per cent of the variability among sorghum grain landrace accessions.

Using the principal factor scores (PF scores), four different graphs were plotted to represent the position of genotypes on X and Y-axis taking two most important factors at one time and to chalk out the breeding plan for further improvement by identifying superior parents

for hybridization/-crossing programme. The genotypes HJ 541, ICSV 700, COFS 29, IS 28614, SSG 59-3, S 540-2 and G 46 were found high in dry fodder yield, green fodder yield and DDM and stood out towards the positive portion of PF1 axis in the plot, whereas the genotypes which had high Na, Cu and Fe clustered towards the positive side of PF 3 axis (Fig. 1) and such genotypes were IS 651 and IS 23890. The genotypes placed towards the positive end of the PF-1 and PF-3 are supposed to be superior collectively both for high yield and mineral content. On the basis of the present investigation, genotypes IS 651, S 540-1 and HJ 541 have been identified superior for both the characters collectively.

The genotypes HJ 541, ICSV 700, COFS 29, IS 28614, SSG 59-3, S 540-2 and G 46 were found having high dry fodder yield, green fodder yield and DDM stood out towards the positive portion of PF1 axis in the plot, whereas the genotypes which had low stem borer, shoot fly and grey leaf spot incidence clustered towards the negative side of PF4 axis (Fig. 2) and such genotypes were IS 28614, G 46, SSG 59-3, and S 540-2. The genotypes placed towards the positive end of the PF-1 and negative end of PF-4 are supposed to be superior collectively both for high yield and biotic resistance. On the basis of present investigation, genotypes IS 28614, G 46 and SSG 59-3 have been identified superior for both the characters collectively.

The genotypes ICSV 700, COFS 29, IS 28614 and HJ 541 were found having high dry fodder yield, green fodder yield and DDM stood out towards the positive portion of PF1 axis in the plot, whereas the genotypes which had high brix and IVDMD and low lignin and HCN clustered towards the negative side of PF 5 axis (Fig. 3). IVDMD and brix had high negative factor loading so genotype towards negative side are superior and such genotypes were S 473-1, ICSV 700, IS 2205 and S 540-1. The genotypes placed towards the positive end of the PF-1 and negative end of PF-5 are supposed to be superior collectively for high yield, and high brix, IVDMD, low lignin and HCN. On the basis this investigation, genotypes ICSV 700 has been identified superior for these characters collectively.

Similar results were reported by Bucheyeki (2008) while studying morphological characterization of Tanzanian sorghum [*Sorghum bicolor* (L.) Moench]

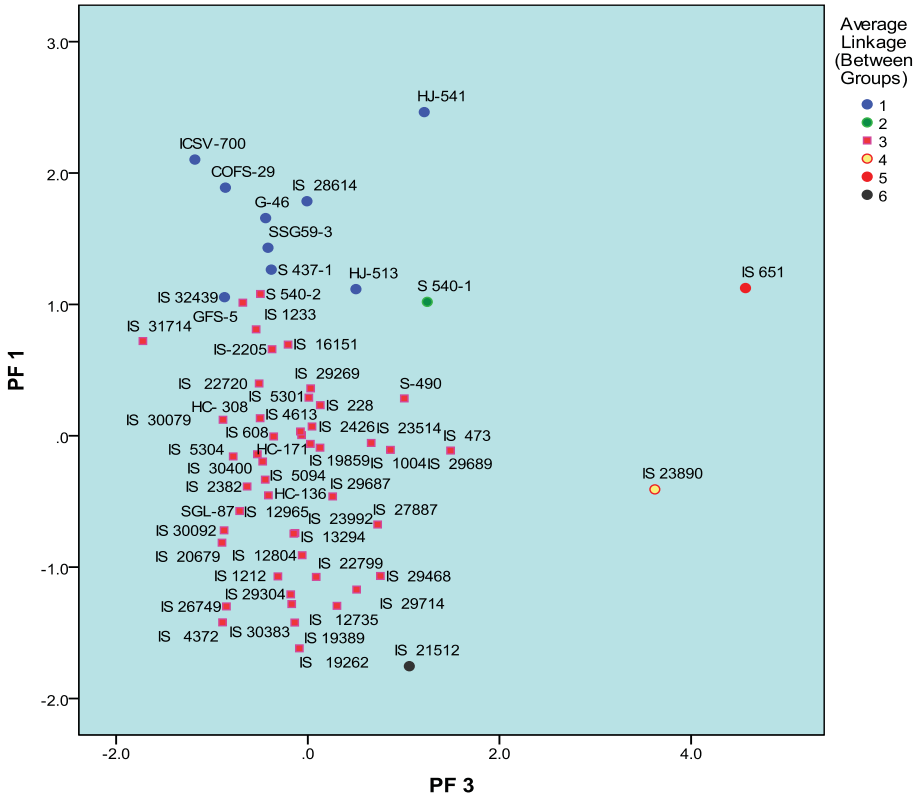

Fig. 1. Distribution of sorghum genotypes based on Principal Factor 1 and 3

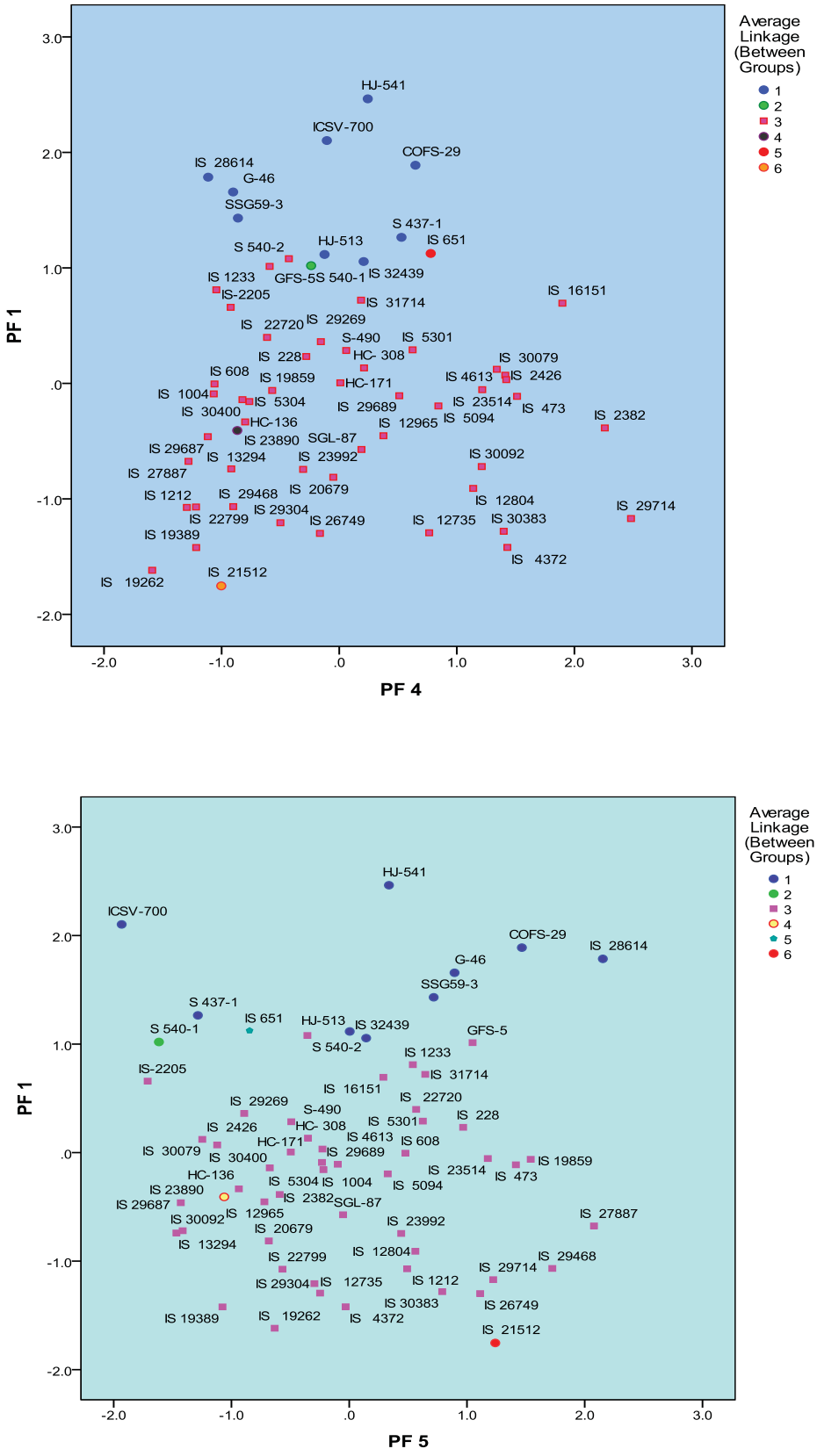

Fig. 3. Distribution of sorghum genotypes based on Principal Factor 1 and 5

landraces. Other researchers too recorded more than 70 % contribution to variability by the first two-to-six principal components (Haussmann *et al.,* 2000). However, Grenier *et al.* (2001) observed 48.8 % of the variance with the two axes of the principal components. Gerrano (2010) reported genetic diversity in sorghum using phenotypic marker in 22 sorghum accessions. The principal component analysis showed that the first five principal components (PC) contributed 87 % of variability among the accession. Leaf number, days to 50 % flowering, number of internodes, plant height and panicle width contributed mainly to PF 1 and leaf width, leaf area, grain yield, leaf sheath length, internodes length and panicle weight to PF 2. Yadav *et al.* (2003) characterized 90 sorghum genotypes on the basis of plant height, leaf length, leaf breadth, stem girth, number of tillers, number of leaves and disease parameters and three, visual fodder quality parameter. Four PC had eigen values greater than one explaining 73.57 % variability. Abe *et al*. (2013) analyzed 31 grain sorghum landrace accession were used for chemical analysis. The PCA revealed that the first four PC contributed 71.77 % of the variability among sorghum landrace accessions.

It is concluded that first eleven principal components had explained 75.77% of the total variability among the sorghum genotypes tested and it indicated the presence of excellent opportunity to bring about improvement through hybridization. Use of these genotypes is suggested in breeding programmes as different sources/parents for further improvement of forage sorghum for green fodder yield, dry fodder yield, IVDMD and mineral content.

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