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Deepak Kaushik
Department of Genetics and
Plant Breeding, CCS Haryana
Agricultural University, Hisar-
Haryana, India

Yogesh Jindal
Department of Genetics and
Plant Breeding, CCS Haryana
Agricultural University, Hisar-
Haryana, India

Amit
Department of Genetics and
Plant Breeding, CCS Haryana
Agricultural University, Hisar-
Haryana, India

Sachin
Department of Genetics and
Plant Breeding, CCS Haryana
Agricultural University, Hisar-
Haryana, India

Tejinder Singh
Department of Vegetable
Science, CCS Haryana
Agricultural University, Hisar-
Haryana, India

Corresponding Author:
Yogesh Jindal
Department of Genetics and
Plant Breeding, CCS Haryana
Agricultural University, Hisar-
Haryana, India

Dissection of yield and component traits based on selection indices in various sorghum (*Sorghum bicolor* L. Moench) genotypes

Deepak Kaushik, Yogesh Jindal, Amit, Sachin and Tejinder Singh

Abstract

Selection indices are constructed using different weights viz. equal weight, genotypic correlation, phenotypic correlation and path coefficient (direct effects) with all possible combination of traits in forage sorghum based on fifteen biometrical characters viz. time of panicle emergence (days), height upto flag leaf (cm), total plant height (cm), stem diameter (mm), third leaf length from top (cm), third leaf breadth from top (cm), panicle length without peduncle (cm), dry matter (%), hundred seed weight (g), green fodder yield (q/ha), dry fodder yield (q/ha), HCN content on fresh weight basis ($\mu\text{g/g}$), protein (%), crude protein yield (q/ha), tannin content on dry weight basis (mg/g) along with their genetic gain and percent relative efficiency relative to green fodder yield. The data were collected from a set of forty nine genotypes of sorghum grown in randomized complete block design with three replications. The best selection indices include the traits namely; dry fodder yield, height upto flag leaf, total plant height, dry matter, dry fodder yield, HCN content on fresh weight basis. The suggested sorghum genotypes on the basis of overall selection indices were GP-236, IS 40921 and GP-298.

Keywords: Sorghum, selection indices, biometrical characters, weights etc.

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is the world's fifth most important crop. Among the cereal fodder crops, sorghum is ranked first because due to its capacity to thrive in poor soil, quick growth pattern, increased yield, flavour, and nutritional value. India's average sorghum feed output is low because a large portion of the country is planted to outdated, native cultivars (Kour and Pradhan, 2016) [4]. As a result of urbanisation, industrialization, and farmers' traditional inclinations, there is little opportunity to expand the area under cultivation of fodder crops. Utilizing agricultural productivity through improved yielding varieties and effective agronomic management is the only optional way to satisfy the need for fodder. Yield is a complex quantitative characteristic that is affected by environmental changes. As a result, direct selection for yield will be unreliable and fruitless. As a result, selection criteria based on yield components might be useful in selecting appropriate plant species. Knowledge of the interrelationships between yield components and the appropriate weightage that should be given to different yield components to achieve maximum gain is thus critical.

Selection is one of the most crucial factors in improving metric features in both animal and plant breeding. It is the best strategy for altering the genetic makeup of a population since it is crucial when genes act additively. Here, selection refers to breeding the highest-quality individuals, whatever that may be. Practically speaking, selection is applied to multiple characters at once rather than just one. This is commonly known as "multi trait selection," and it can be carried out using a number of different selection procedures. The Hazel (1943) [2] selection index approach relies on the simultaneous selection of all component features with their proportionate weights tied to their phenotypic value in order to maximise the correlation between the compounded phenotypic score and the corresponding compounded genetic score. Then, the previous score would discriminate those people with the highest genetic scores in the best way feasible. According to their economic significance, heredity, and genetic and phenotypic linkage, the respective weights are determined. In order to attain greater genetic gain, superior genotypes are chosen for subsequent breeding programmes using the selection index technique. However, the selection index methodology can still be employed if the goal is to improve a certain quality by adjusting the economic weights of the characters. If the variation in this characteristic attributable to one or more auxiliary traits, particularly at the

environmental level, is limited, the rate of genetic progress in a quantitative character can be improved. In this situation, selection can be based on an index that measures the phenotypic value of the trait's divergence from the expected value predicted using a partial regression equation of the auxiliary traits. In this study, selection indices are built using various weights. The genotypes are chosen based on the ranks acquired using various weight methods in the selection index, and the details of the analysis are detailed in the result and discussion section.

Material and Methods

A total of forty nine sorghum germplasm lines were assessed, including numerous released varieties, landraces, and advance lines. In the year 2018-19, the research was conducted at the Research Farm Area, Forage Section, Department of Genetics

& Plant Breeding, CCS Haryana Agricultural University, Hisar. The genotypes were grown in a randomised block pattern with heterogeneity controlled in one direction. There were three replications, and each genotype in each replication was grown as two rows, resulting in a total of ten rows in a plot. The plant-to-plant distance was 10 cm, and the row-to-row was 30 cm, with the row length at 3m. The data was recorded on five randomly selected plants in each genotype for 15 morphological and biochemical traits namely; green fodder yield (I₁), time of panicle emergence (I₂), height upto flag leaf (I₃), total plant height (I₄), stem diameter (I₅), third leaf length from top (I₆), third leaf breadth from top (I₇), panicle length without peduncle (I₈), dry matter (I₉), 100- seed weight (I₁₀), dry fodder yield (I₁₁), HCN content on fresh weight basis (I₁₂), protein (%) (I₁₃), crude protein yield (I₁₄), tannin content on dry weight basis (I₁₅).

Table 1: Selection indices and their percent relative efficiency in sorghum genotypes

TRAITS	Equal Weight		TRAITS	Genotypic Cor.		Phenotypic Cor.		Traits	Path coefficient	
	GA	PRE		GA	PRE	GA	PRE		GA	PRE
I ₁	205.53	100.00	I ₁	205.53	100.00	205.53	100.00	I ₁	205.53	100.00
I ₂	7.82	3.80	I ₂	0.79	0.38	0.81	0.40	I ₂	0.73	0.36
I ₃	40.64	19.77	I ₃	19.26	9.37	24.02	11.69	I ₃	0.71	0.35
I ₄	41.64	20.26	I ₄	20.20	9.83	25.74	12.52	I ₄	1.06	0.52
I ₅	2.06	1.00	I ₅	0.08	0.04	0.09	0.05	I ₅	0.28	0.13
I ₆	8.85	4.30	I ₆	0.35	0.17	0.39	0.19	I ₆	2.87	1.40
I ₇	1.74	0.85	I ₇	0.18	0.09	0.26	0.13	I ₇	0.22	0.11
I ₈	9.54	4.64	I ₈	0.76	0.37	0.86	0.42	I ₈	0.02	0.01
I ₉	18.55	9.03	I ₉	4.32	2.10	5.77	2.81	I ₉	23.01	11.20
I ₁₀	1.21	0.59	I ₁₀	0.22	0.11	0.23	0.11	I ₁₀	0.14	0.07
I ₁₁	88.75	43.18	I ₁₁	70.91	34.50	72.78	35.41	I ₁₁	167.04	81.27
I ₁₂	37.77	18.38	I ₁₂	11.94	5.81	12.84	6.25	I ₁₂	0.12	0.06
I ₁₃	1.11	0.54	I ₁₃	0.15	0.07	0.20	0.10	I ₁₃	0.05	0.02
I ₁₄	8.52	4.14	I ₁₄	6.69	3.26	6.90	3.36	I ₁₄	1.68	0.82
I ₁₅	0.84	0.41	I ₁₅	0.01	0.01	0.01	0.01	I ₁₅	0.07	0.03
I _{1,11}	284.41	138.37	I _{1,11}	268.10	130.44	269.79	131.26	I _{1,11}	357.71	174.04
I _{1,4,11}	317.37	154.41	I _{1,4,11}	283.86	138.11	289.98	141.09	I _{1,6,11}	358.38	174.37
I _{1,3,4,11}	349.97	170.28	I _{1,3,4,11}	298.65	145.31	308.68	150.18	I _{1,3,6,11}	358.89	174.61
I _{1,3,4,12,11}	359.32	174.82	I _{1,3,4,11,14}	304.63	148.21	314.81	153.17	I _{1,2,3,6,11}	359.01	174.67
I _{1,3,4,9,11,12}	367.02	178.57	I _{1,3,4,11,12,14}	309.08	150.38	319.62	155.51	I _{1,2,3,5,6,11}	359.09	174.71
I _{1,3,4,8,9,11,12}	368.67	179.37	I _{1,3,4,9,11,12,14}	311.24	151.43	322.46	156.89	I _{1,2,3,5,6,11,12}	359.19	174.76
I _{1,3,4,6,8,9,11,12}	370.06	180.05	I _{1,3,4,8,9,11,12,14}	311.39	151.50	322.65	156.98	I _{1,2,3,5,6,7,11,12}	359.24	174.78
I _{1,3,4,6,8,9,11,12,14}	370.63	180.32	I _{1,3,4,5,8,9,11,12,14}	311.52	151.57	322.78	157.04	I _{1,2,3,5,6,7,8,11,12}	359.29	174.81
I _{1,2,3,4,6,8,9,11,12,14}	371.22	180.61	I _{1,3,4,5,7,8,9,11,12,14}	311.73	151.67	323.03	157.17	I _{1,2,3,5,6,7,8,11,12,15}	359.31	174.82
I _{1,2,3,4,5,6,8,9,11,12,14}	371.40	180.70	I _{1,3,4,5,6,7,8,9,11,12,14}	311.85	151.73	323.16	157.23	I _{1,2,3,5,6,7,8,11,12,13,15}	359.32	174.82
I _{1,2,3,4,5,6,7,8,9,11,12,14}	371.49	180.74	I _{1,2,3,4,5,6,7,8,9,11,12,14}	311.96	151.78	323.27	157.28	I _{1,2,3,4,5,6,7,8,10,11,12,13,15}	359.30	174.81
I _{1,2,3,4,5,6,7,8,9,10,11,12,14}	371.32	180.66	I _{1,2,3,4,5,6,7,8,9,10,11,12,14}	312.00	151.80	323.31	157.30	I _{1,2,3,4,5,6,7,8,10,11,12,13,15}	358.52	174.43
I _{1,2,3,4,5,6,7,8,9,10,11,12,13,14}	370.61	180.32	I _{1,2,3,4,5,6,7,8,9,10,11,12,13,14}	312.04	151.82	323.36	157.33	I _{1,2,3,4,5,6,7,8,10,11,12,13,14,15}	356.97	173.68
I _{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15}	370.91	180.62	I _{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15}	312.06	151.83	323.39	157.34	I _{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15}	343.90	167.32

Result and Discussions

The variations among sorghum genotypes for different traits were found highly significant. The correlation coefficients between green fodder yield and its component traits among themselves were estimated at genotypic and phenotypic levels but not presented here. Selection indices were constructed taking all 15 morphological-biochemical traits. A number of selection indices were worked out using equal weight (as 1), genotypic correlation coefficients and phenotypic correlation coefficients and path coefficients as weight. Also the expected genetic gain obtained from selection index of green fodder yield with equal weight was considered 100 per cent to work out percent relative efficiency of different indices. All the possible combination of selection indices for various combination of traits are presented in Table 1 and consecutively ranked on the basis of their percent relative efficiency in increasing the green fodder yield. From the Table 1 in case of equal weight, the most

influencing trait is dry fodder yield (I₁₁) which causes an increase of 88.75% in genetic advance. As the traits sequentially added for increasing the percent relative efficiency to get the best combination of trait, we got the 8 traits combination namely; green fodder yield (I₁), height upto flag leaf (I₃), total plant height (I₄), third leaf length from top (I₆), panicle length without peduncle (I₈), dry matter (I₉), dry fodder yield (I₁₁), HCN content on fresh weight basis (I₁₂) after that no subsequent increase in percent relative efficiency (180.05). While in case of genotypic and phenotypic correlation as weight, the most important trait is dry fodder yield (I₁₁) which causes an increase of 88.75% in genetic advance. The sequential addition and removal of traits to find the best combination of traits for increasing green fodder by taking correlations as weight, we found green fodder yield (I₁), height upto flag leaf (I₃), total plant height (I₄), stem diameter (I₅), panicle length without peduncle (I₈), dry matter (I₉), dry fodder yield (I₁₁), HCN content on fresh weight basis

(I₁₂), crude protein yield (I₁₄) was the best traits' combination to increase the percent relative efficiency (151.5, 157.04 for genotypic and phenotypic correlations, respectively). When we took path coefficient as weight, then as in other cases dry fodder yield (I₁₁) causes an increase of 167.04% in genetic advance. The best combination of traits here was green fodder yield (I₁) and dry fodder yield (I₁₁) after that there was no significant increase in percent relative efficiency was observed. On this basis, we could argue that the selection index consisting of dry fodder yield, height upto flag leaf (I₃), total plant height (I₄), dry matter (I₉), dry fodder yield (I₁₁), HCN content on fresh weight basis (I₁₂) was considered more reliable as it was commonly having highest relative efficiency in all methods. The results were in accordance with Biswas *et*

al. (2001) ^[1], Jain and Patel (2012) ^[3], Vemanna *et al.* (2013) ^[5] *etc.*

The index score values were worked out for all four weight methods for all genotypes and the genotypes are ranked based on their index score in Table 2. Genotype IS 40921 ranked first in equal weight method followed by GP-236 as second and GP-298 as third. While GP-236 ranked first followed by IS 40921 as second and GP-298 as third for genotypic correlation, phenotypic correlation and path coefficient taken as weight. The rankings were pretty much same for genotypic correlation, phenotypic correlation and path coefficient taken as weight while there is slight variation if we consider equal weight for selecting genotypes.

Table 2: Ranking of Sorghum genotypes for different weight

Rank	Equal weight	Genotypic Cor.	Phenotypic Cor.	Path Coefficient
1	IS 40921	GP-236	GP-236	GP-236
2	GP-236	IS 40921	IS 40921	IS 40921
3	GP-298	GP-298	GP-298	GP-298
4	HC308	HC308	HC308	HC308
5	PGN 66	HC 260	HC 260	PGN 66
6	IS 2919	PGN 66	PGN 66	HC 260
7	HC 260	IS 2919	IS 2919	IS 5127
8	SPV 2191	IS 5127	SPV 2191	IS 2919
9	IS 651	SPV 2191	IS 5127	IS 1328
10	IS 1328	IS 651	IS 651	SPV 2191
11	IS 1004	IS 1004	IS 1004	IS 1004
12	IS 3244	GP-311	GP-311	IS 651
13	IS 5127	S713	S713	GP-311
14	IS 3299	SOPPON	SOPPON	IS 3299
15	S713	IS 3299	IS 3299	SOPPON
16	SOR 5510	IS 3244	IS 3244	IS 3244
17	GP-311	SOR 6453	SOR 6453	S713
18	IS 585176	IS 1328	IS 1328	SOR 6453
19	SOPPON	IS 585176	IS 585176	GP-318
20	GP-318	PGN 56	PGN 56	IS 585176
21	PGN 56	GP-318	GP-318	GFS 5
22	HJ 513	GFS 5	GFS 5	SOR 5510
23	IS 608	SOR 5510	HJ 513	PGN 56
24	SOR 6453	HJ 513	SOR 5510	SOR 5578
25	Suent	SOR 5578	SOR 5578	IS 608
26	SOR 5578	G-800	G-800	G-800
27	GFS 5	Suent	Suent	Suent
28	HJ 541	IS 608	IS 608	HJ 513
29	G-800	IS 40398	IS 40398	IS 40398
30	SOR 668	HJ 541	HJ 541	HJ 541
31	IS 40398	SH1591	SH1591	SOR 668
32	SH1591	IS 585186	IS 585186	SH1591
33	IS 40717	SOR 668	SOR 668	IS 40717
34	IS 585186	IS 40717	IS 40717	IS 585186
35	SSG 233	HC 171	HC 171	PGN 9
36	PGN 9	SSG 233	SSG 233	HC 171
37	HC 171	SOR 6408	SOR 6408	Dairy green
38	SOR 6408	SOR 5504	SOR 5504	SSG 233
39	GP-237	Dairy green	Dairy green	SOR 5504
40	Dairy green	GP-237	GP-237	GP-237
41	SOR 5504	PGN 9	PGN 9	SOR 6408
42	IS 144849	IS 144849	IS 144849	IS 144849
43	IS 285913	HC136	HC136	IS 285913
44	HC136	IS 285913	IS 285913	IS 285831
45	IS 585159	IS 285831	IS 285831	HC136
46	IS 285831	IS 585159	IS 585159	IS 585159
47	GP-297	SOR 5449	SOR 5449	SOR 5449
48	SOR 5449	IS 3947	IS 3947	IS 3947
49	IS 3947	GP-297	GP-297	GP-297

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