

Smith Hazel Selection Index for the Improvement of Maize Inbred Lines under Water Stress Conditions

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ABSTRACT

Drought is one of the major abiotic stress affecting maize production. In order to detect drought tolerant maize inbred lines, an experiment with hundred homozygous inbred lines was conducted during Kharief 2013 and 2014 in factorial randomized block design with two replications, under different moisture management condition. Results showed diversity among the lines in response to moisture management conditions. Assessing lines as per the selection indices lead to identification of few lines viz., KDM-361A, CM-129, KDM-372, KDM-331, KDM-1051, KDM-402, KDM-463, KDM-717, KDM-912A, KDM-932A, KDM-343A, KDM-961, KDM-918A, KDM-1156 and KDM-1236 as drought tolerant ones. Highest genetic advance was observed for maturity traits, plant height, leaf relative water content and chlorophyll content before flowering, germination per cent, primary root length and fresh root weight therefore, they should be used for selecting elite lines for drought related traits.

Key words: Maize, Drought, Selection Index.

INTRODUCTION

Maize grows over a wider geographical and environmental range than any other cereals at an latitude varying from the equator to slightly north and south of latitude 50⁰, from sea level to over 3000 m elevation, under heavy rainfall and semi-arid conditions, cool and very hot climates¹. The diversified usages of maize grain make the crop very special for different stakeholders. It directly contributes almost 10 per cent to the Indian food basket and 5 per cent to the world dietary energy supply. Textile, foundry, corn starch, corn syrup, corn oil dextrose, corn flakes, gluten, grain cake,

lactic acid and acetone are among main products of maize. As the livestock and poultry industries are expanding and getting advanced demand, consumption of maize has increased. Maize is consumed in both fresh and processed forms. The expected demand of maize will increase up to 784 million tons in 2020 and developing countries are the expected consumers of this increased demand^{1,29}. In India not only production and consumption of maize have been rising consistently, the consumption pattern has also changed over the years¹⁹.

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Maize grain yield is limited by various factors and is a problem of immediate practical implication and among various abiotic stresses, inadequate water availability at critical stages of crop growth and development is the major limiting factor for its production and productivity^{3,5,6,7,9,20,24}.

Smith³⁰ proposed a selection model for making selection of several characters simultaneously using discriminant function of Fisher¹⁵. Application of discriminant function as a basis for making selection on several characters simultaneously is aimed at discriminating the desirable genotypes from undesirable genotypes on the basis of their phenotypic performance. Later on, Hazel¹⁷ developed a simultaneous selection model following path analysis approach.

MATERIAL AND METHODS

The experimental materials for the present study comprised 100 homozygous maize inbred lines. The lines were evaluated in factorial RBD with two replications over two years. Each inbred line was planted in two rows experimental plot of 1 meter length with inter and intra row spacing of 60 x 20 cm with recommended package of practices. The materials were evaluated against four moisture management regimes viz;

- **Well Watered (WW):** Irrigated at knee height stage, flowering and grain filling stages.
- **Intermediate Stress (IS):** Irrigated at knee height stage and flowering stage.
- **Mild Stress (MS):** Irrigated at knee height stage
- **Stress (S):** Rainfed.

The meteorological data, including minimum and maximum temperatures, relative humidity (RH) and rainfall were collected throughout the experimental period for both the years¹¹. Observations were recorded on various morphological, maturity, physiological, yield, quality and seedling related traits viz; days to 50 per cent tasseling, days to 50 per cent silking, anthesis-silking interval, days to maturity, plant height (cm), ear height (cm), leaf relative water content (%), canopy

temperature before flowering (°C), canopy temperature before maturity (°C), stomatal count (mm⁻²), chlorophyll content before flowering (SPAD units), chlorophyll content before maturity (SPAD units), ears plant⁻¹, kernels row⁻¹, 100 grain weight (g), grain yield plot⁻¹ (g), protein content (%) and seedling traits viz., seedling germination (%), number of seminal roots, number of crown roots, primary root length (cm), fresh root weight (g) and dry root weight (g). All these characters were used for the construction of selection index in individual and pooled analysis over years by the methodology of Smith³⁰ and Hazel¹⁷. Selection index was constructed by assigning weights to different traits on the basis of the weighing coefficient (β_i) values and genetic advancement for all the traits.

RESULTS

Maturity, morphological, physiological, yield, quality and seedling traits were used for the construction of selection index in individual and pooled analysis over years by the methodology of Smith³⁰ and Hazel¹⁷. Selection index was constructed by assigning weights to different traits on the basis of the weighing coefficient (β_i) values and genetic advancement for all the traits. Perusal of Table-1 revealed that β_i values for 100 lines were highest for maturity traits associated with low genetic advancement values. Days to 50% tasseling exhibited β_i values of -131.05 (Y1), -15208.99 (Y2) and -149.14 (pooled analysis) associated with genetic advancement of -3.59 (Y1), -3.50 (Y2) and -3.63 (pooled analysis). For days to 50% silking β_i values of 134.34, 15211.37 and 150.24 were recorded in Y1, Y2 and pooled analysis associated with genetic advancement values of -4.23 (Y1), -4.41 (Y2) and -4.27 (pooled analysis), respectively. Anthesis-silking interval exhibited highest β_i values of -136.13 in Y1, -15213.76 in Y2 and -151.81 in pooled analyses associated with lowest genetic advancement of -0.63 in Y1 and pooled analysis and -0.64 in Y2. Days to maturity exhibited β_i value of 0.58 (Y1), 0.31(Y2) and 0.23 (pooled analysis) with genetic advancement ranging from -4.53 in Y2

to -4.60 in pooled analysis. Morphological trait viz; plant height exhibited a β i value of 1.52 in Y1, -1923.28 in Y2 and 1.30 in pooled analysis with genetic advancement value of 7.02 in Y1 and Y2 and 7.05 in pooled analysis. Another morphological trait ear height exhibited a β i value of 3850.03 in Y2 followed by 0.21 in pooled analysis and 0.05 in Y1 with corresponding genetic advancement value of 3.64 in Y1 followed by 3.58 in pooled analysis and 3.51 in Y2.

Physiological trait leaf relative water content exhibited β i value of 0.64 in Y1, followed by 0.61 in pooled analysis and 0.52 in Y2 with associated genetic advancement of 7.60 in Y1 followed by 7.58 in pooled analysis and 7.23 in Y2. Canopy temperature before flowering exhibited β i values of 6.25 in Y1, -1.17 in Y2 and -0.28 in pooled analysis with genetic advancement of -1.07 in Y1, -0.92 in Y2 and -0.99 in pooled analysis. Similarly, for canopy temperature before maturity β i value of -7.31 in Y1, 5.05 in Y2 and 1.54 in pooled analysis was observed with genetic advancement of -1.05 in Y1, -0.94 in Y2 and -0.99 in pooled analysis. Stomatal count exhibited β i values in pooled analysis (0.97) followed by Y2 (0.91) and Y1 (0.90) with a corresponding genetic advancement in Y2 (-4.02) followed by pooled analysis (-3.62) and Y1 (-3.61). Chlorophyll content before flowering recorded β i value of 14.98 in Y2 followed by 12.99 in Y1, and 8.63 in pooled analysis associated with genetic advancement of 5.02 in Y1 and pooled analysis and 5.03 in Y2. Similarly, chlorophyll content before maturity exhibited β i value of -33.10 in Y2 followed by -29.46 in Y1 and -19.09 in pooled analysis associated with a genetic advancement of 2.38 in Y1 and pooled analysis and 2.36 in Y2.

Among yield related traits high β i value was recorded for ears plant⁻¹ in Y1 (75.49), Y2 (44.34) and pooled analysis (35.61) associated with low genetic advancement of 0.23 in Y1, Y2 and pooled analysis followed by 100 grain weight in Y2 (16.06), Y1 (8.89), pooled analysis (7.11) associated with genetic advancement of 2.16 in Y1, 2.10 in Y2 and 2.14 in pooled analysis.

Kernels row⁻¹ exhibited β i value of 10.21 in Y2, 8.31 in Y1 and 6.32 in pooled analysis associated with genetic advancement values of 1.83 in Y1, Y2 and pooled analysis. Grain yield plot⁻¹ exhibited lowest values of β i in Y1 (0.39), pooled analysis (0.53) followed by Y2 (0.82) associated with highest genetic advancement value of 63.61 in Y1, 64.08 in Y2 and 63.54 in pooled analysis. For protein content β i values were lowest in pooled analysis (0.02) followed by Y2 (0.85) and Y1 (1.45) with associated genetic advancement value of 0.65 in Y1 and Y2 and 0.64 in pooled analysis. Perusal of Table-2 revealed that for seedling trait lowest β i values was recorded for germination percentage in Y1 (0.70), Y2 (0.68) and pooled analysis (0.70) associated with highest genetic advancement value of 8.31 in Y1, 7.39 in Y2 and 7.85 in pooled analysis. Number of seminal roots exhibited β i value of 1.60 (Y1), 1.78 (Y2) and 1.60 (pooled analysis) with genetic advancement value of 0.50 in Y1, 0.60 in Y2 and 0.55 in pooled analysis. Number of crown roots exhibited β i value of 2.86 (Y1), 0.95 (Y2) and 1.64 (pooled analysis) with lowest genetic advancement of 0.53 in Y1, 0.48 in Y2 and 0.50 in pooled analysis. For primary root length a β i value of 1.11 in Y1, 1.18 in Y2 and 1.16 in pooled analysis with genetic advancement value of 3.07 in Y1, 3.14 in Y2 and 3.12 in pooled analysis was recorded. Fresh root weight recorded β i values of 3.36 in Y1, 3.14 in Y2 and 3.65 in pooled analysis and were associated with genetic advancement of 2.08 (Y1), 2.03 (Y2) and 2.05 (pooled analysis), whereas for dry root weight β i values of -4.37 (Y1), -2.90 (Y2) and -4.59 (pooled analysis) associated with genetic advancement of 0.83 (Y1), 0.82 (Y2 and pooled analysis) was recorded. Among 100 inbred lines KDM-361A, CM-129, KDM-372, KDM-331, KDM-1051, KDM-402, KDM-463, KDM-717, KDM-912A, KDM-932A, KDM-343A, KDM-961, KDM-918A, KDM-1156 and KDM-1236 occupied first fifteen ranks for maturity, morphological, physiological, yield, quality and seedling traits in Y1, Y2 and pooled over years analysis (Table-3 and Table -4).

Table 1: Simultaneous selection indices for inbred lines of maize (*Zea mays* L.) for morphological, maturity, physiological, grain yield and yield component and quality traits

Traits	Economic weight	β_i value			Genetic advancement		
		Year 1	Year 2	Pooled	Year 1	Year 2	Pooled
Days to 50% tasseling	1	-131.05	-15208.99	-149.14	-3.59	-3.50	-3.63
Days to 50% silking	1	134.34	15211.37	150.24	-4.23	-4.41	-4.27
Anthesis-silking Interval	0.8	-136.13	-15213.76	-151.81	-0.63	-0.64	-0.63
Days to Maturity	1	0.58	0.31	0.23	-4.57	-4.53	-4.60
Plant height (cm)	1	1.52	-1923.28	1.30	7.02	7.02	7.05
Ear height (cm)	1	0.05	3850.03	0.21	3.64	3.51	3.58
Leaf relative water content (%)	1.2	0.64	0.52	0.61	7.60	7.23	7.58
Canopy temperature before flowering (°C)	1	6.25	-1.17	-0.28	-1.07	-0.92	-0.99
Canopy temperature before maturity (°C)	1	-7.31	5.05	1.54	-1.05	-0.94	-0.99
Stomatal count (mm ⁻²)	1	0.90	0.91	0.97	-3.61	-4.02	-3.62
Chlorophyll content before flowering (SPAD units)	1.2	12.99	14.98	8.63	5.02	5.03	5.02
Chlorophyll content before maturity (SPAD units)	1	-29.46	-33.10	-19.09	2.38	2.36	2.38
Ears plant ⁻¹	1.2	75.49	44.34	35.61	0.23	0.23	0.23
Kernels row ⁻¹	1	8.31	10.21	6.32	2.16	2.10	2.14
100 Grain weight (g)	1	8.89	16.06	7.11	1.83	1.83	1.83
Protein content (%)	1	1.45	0.85	0.02	0.65	0.65	0.64

Table 2: Simultaneous selection indices for inbred lines of maize (*Zea mays* L.) for seedling and root traits

Traits	Economic weight	β_i value			Genetic advancement		
		Year 1	Year 2	Pooled over years	Year 1	Year 2	Pooled over years
Germination (%)	1	0.72	0.68	0.70	8.31	7.39	7.85
Number of seminal roots	1	1.60	1.78	1.60	0.50	0.60	0.55
Number of crown roots	1	2.86	0.95	1.64	0.53	0.48	0.50
Primary root length (cm)	1	1.11	1.18	1.16	3.07	3.14	3.12
Fresh root weight (g)	1	3.36	3.14	3.65	2.08	2.03	2.05
Dry root weight (g)	1	-4.37	-2.90	-4.59	0.83	0.82	0.82

Table 3: Significant differences among maize inbred lines for the superior selection index for morphological, maturity, physiological, grain yield and yield component and quality traits

Year-1			Year-2			Pooled over years		
Rank	Line	Scores	Rank	Line	Scores	Rank	Line	Scores
1	KDM-361A	1863.51	1	KDM-361A	7224.31	1	KDM-361A	1428.44
2	CM-129	1861.93	2	CM-129	7221.71	2	CM-129	1427.72
3	KDM-372	1855.07	3	KDM-372	7219.42	3	KDM-372	1422.89
4	KDM-331	1852.69	4	KDM-331	7205.21	4	KDM-331	1417.61
5	KDM-1051	1821.23	5	KDM-1051	7167.97	5	KDM-1051	1394.19
6	KDM-402	1809.57	6	KDM-402	7150.36	6	KDM-402	1381.33
7	KDM-463	1806.54	7	KDM-912A	7136.10	7	KDM-463	1374.29
8	KDM-912A	1802.15	8	KDM-717	7135.10	8	KDM-717	1372.97
9	KDM-717	1800.42	9	KDM-463	7131.89	9	KDM-912A	1371.73
10	KDM-343A	1788.68	10	KDM-932A	7100.57	10	KDM-932A	1351.56
11	KDM-932A	1787.99	11	KDM-961	7097.23	11	KDM-343A	1348.53
12	KDM-961	1779.66	12	KDM-343A	7095.40	12	KDM-961	1346.42
13	KDM-918A	1767.11	13	KDM-918A	7064.19	13	KDM-918A	1332.40
14	KDM-1156	1756.17	14	KDM-1156	7046.40	14	KDM-1156	1322.36
15	KDM-1236	1736.41	15	KDM-1236	7030.12	15	KDM-1236	1304.18

Table 4: Significant differences among maize inbred lines means for the superior selection index for seedling and root traits

Year-1			Year-2			Pooled over years		
Rank	Line	Scores	Rank	Line	Scores	Rank	Line	Scores
1	KDM-361A	123.78	1	KDM-361A	123.66	1	KDM-361A	125.20
2	CM-129	120.38	2	CM-129	119.01	2	CM-129	120.95
3	KDM-343	119.49	3	KDM-372	118.47	3	KDM-343	119.68
4	KDM-402	118.19	4	KDM 343A	118.15	4	KDM-372	119.56
5	KDM-717	117.83	5	KDM-717	117.94	5	KDM-717	119.32
6	KDM-372	117.29	6	KDM 402	116.55	6	KDM 402	118.80
7	KDM-1236	116.68	7	KDM-932A	116.21	7	KDM-932A	117.74
8	KDM-932A	116.43	8	KDM-1156	114.82	8	KDM-1156	116.54
9	KDM-912A	116.06	9	KDM-463	114.77	9	KDM-463	116.33
10	KDM-1156	115.82	10	KDM-912A	112.75	10	KDM-912A	115.19
11	KDM-1051	115.60	11	KDM-1236	112.08	11	KDM-1236	115.17
12	KDM-331	115.42	12	KDM-331	112.08	12	KDM-1051	114.54
13	KDM-463	114.98	13	KDM-1051	111.87	13	KDM-331	114.49
14	KDM-918A	114.65	14	KDM 961	111.69	14	KDM-918A	113.88
15	KDM-961	114.28	15	KDM-918A	111.44	15	KDM-961	113.72

DISCUSSION AND CONCLUSIONS

Plant breeders are generally interested in simultaneously improving several traits, or improving one trait without affecting the performance of others. One way of selecting for more than one trait at a time in a breeding program is through selection index. It is a procedure that provides a single criterion for selection among genotypes by including combinations of several traits. The objective of a selection index is to find a linear combination of phenotypic values that maximizes the expected gain in aggregate genotype. Smith³⁰ proposed a general method for handling more than one trait at a time in a plant breeding program. He developed a selection index based on a linear combination of phenotypic values weighted in such a way that expected gain in aggregate genotypic value would be maximized. The weights are calculated using information on 1) the economic value of each trait, and 2) the phenotypic and genotypic variances of each trait and the respective covariances among traits. The same index was also proposed by Hazel, but using estimated values for phenotypic and genotypic parameters. He presented the genetic basis for the construction of selection indices and outlined methods for estimating the required variances and covariances. They made use of the idea by Fisher¹⁵, who had suggested the concept of discrimination function and said that since genetic values cannot be determined, but it is possible to approximate its values using a linear function of observable phenotypic values. This index is now known as the Smith-Hazel index. Taking advantage of selection indices was first proposed by Smith in order to improve the plants. Hazel¹⁷ extended the index procedure for the selection of individuals in animal populations. This method labeled as Smith-Hazel index³⁵ was afterwards developed by Baker¹⁰ and widely used in different breeding programs. The most desirable approach to improve characteristics such as grain yield is simultaneous selection based on related traits^{13,21}.

Two other methods of selection are recognized as appropriate for simultaneous

improvement of more than one trait, these are independent culling and tandem selection. Independent culling requires the specification of levels of merit for each trait, an individual with a phenotypic value below this minimum level for any trait is not selected. With tandem selection, the traits are selected one at a time until they are improved to the desired level. Once a trait reaches that desired level of improvement, selection begins on the next trait and so on until all traits have been improved¹⁶. Selections among diverse germplasm types should, therefore, be met with difficulty by following individual characters because of the differential response of the genotypes towards improvement for the component tolerance traits. This necessitates the use of some balanced selection criteria, which takes into consideration all important tolerant attributes simultaneously, so as to end up with overall greater selection advance³⁶.

Highest β_i value was recorded for anthesis-silking interval followed by days to 50% silking, days to 50% tasseling, ears plant⁻¹, chlorophyll content at maturity, chlorophyll content at flowering, 100 grain weight and kernels row⁻¹, whereas grain yield plot⁻¹ recorded highest genetic advancement followed by leaf relative water content, plant height, chlorophyll content at flowering, days to maturity, days to 50% silking, days to 50% tasseling, stomatal count and ear height. For seedling and root traits highest β_i value was observed for dry root weight followed by fresh root weight whereas germination per cent recorded maximum genetic advancement followed by primary root length, fresh root weight, dry root weight, number of seminal roots and number of crown roots. Traits with high genetic advancement values indicate improvement over the base population. These traits together formed efficient selection indices and these traits could be useful for simultaneous improvement in the lines. It was observed that inclusion of characters one by one in the function gave fluctuating changes in the value of genetic advance and relative efficiencies over yield.

Similar results were found by Robinson *et al*²⁸., when selection index was

first applied for genetic improvement of maize. Selection index involving three characters, viz., plant height, ears plant⁻¹ and yield was found to be 30 per cent more efficient than selection based on yield alone. Later St. Martin *et al*³¹, evaluated the use of selection indices for the improvement of opaque-2 corn for simultaneously improving protein and kernel quality. The most efficient indices were those with four or five traits. They concluded that the successful application of selection indices requires a measure of subjective judgment on the trait of the breeder. Selection indices are the best technique to determine selection criteria that clarify relationships among traits and aim to select many traits simultaneously that mainly affected grain yield. Selection indices composed of many major yield components traits are more efficient than the ones having one trait. Plant height, 1000 grain weight and number of kernels row⁻¹ were used in selection index in maize for their large consideration on grain yield⁸. High relative efficiency was obtained when selection index was composed of ear diameter, number of grains ear⁽⁻¹⁾ and number of ears plant^{(-1),33}. Traits viz., grain number ear⁽⁻¹⁾ and grains row⁽⁻¹⁾ together were used as a selection index for improving maize grain yield by Biktash and Mohammad¹². Selection index depends on scientific approach for increasing efficiency of breeding program; therefore, this study aimed to estimate some genetic parameters (β_i and genetic advance) and constructing several selection indices for 100 maize inbred lines. Also, this Smith Hazel index was used to identify the top ranking elite lines with greater tolerance to drought stress. Asghar and Mehdi⁴ used data on yield and quality traits among S₁ families of *Zea mays* L. *Saccharata* to construct Smith-Hazel selection indices and reported it to be the most efficient selection index in improving the aggregate genotype of yield traits for most of the selection strategies. Ziyomo and Bernardo³⁷ constructed a selection index used to combine information from several traits correlated with drought tolerance in maize. Selection was based on both grain yield under drought and

ASI. Based on the estimates of genetic and phenotypic variances and covariances for these two traits, a Smith-Hazel index would be useful and this index has a predicted relative efficiency of 1.13. Al-Obaidy *et al*², reported that selection indices including grain yield were more important than others and the best selection index was composed of grain yield, ears plant⁻¹ and grain weight which led to the identification of superior genotypes.

Selection index led to the identification of fifteen elite lines viz; KDM-361A, CM-129, KDM-372, KDM-331, KDM-1051, KDM-402, KDM-463, KDM-717, KDM-912A, KDM-932A, KDM-343A, KDM-961, KDM-918A, KDM-1156 and KDM-1236 on the basis of the rankings and scores generated by selection index in both individual years and pooled over years analysis for maturity, morphological, physiological, yield, quality, seedling and root related traits. Similar studies with different objectives were conducted by Brim *et al*¹⁴, Mulamba and Mock²³, Kauffmann and Dudley¹⁸, Nawar *et al*²⁵, Modarressi *et al*²², Asghar and Mehdi⁴, Prasanna *et al*²⁶, Ziyomo and Bernardo³⁷ and Al-Obaidy *et al*², for identification of populations/families/ genotypes/lines.

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