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Metroglyph analysis of maize (*Zea mays* L.) inbreds for preliminary classification and group constellation

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When a large number of accessions are available it is often useful to represent them on two dimensional graph and form preliminary groups which are subsequently subjected to more detailed stratification for specific breeding purposes. In the present investigation inbreds were grouped in to clusters using metroglyph analysis. Index scores were assigned to each glyph to arrive at conclusions about the agronomic potential of the inbreds. The group constellation deviated from the one derived through D^2 analysis. However, pictorial representation of inbreds as brought about by metroglyph analysis can be used as a measure of relative genetic distance among the inbreds.

Key words: D^2 statistic, genetic divergence, group constellation, metroglyph analysis.

INTRODUCTION

The diversified use of maize has led to an increase in demand for greater maize production. In the production of high yielding hybrids it is, however, important that inbreds be diverse and it is well known that more genetically distinct combinations induce higher specific combining ability and result in more yielding hybrids (Hallauer, 1972; Betran et al., 2003). Moreover, quantitative measurement of genetic divergence among individuals have enabled plant breeders to understand the racial affinities and evolutionary pattern in various species of cultivated plants and in making decisions for the selection of best parental combination in hybridization programme (Blackith and Reymont, 1971; Springer and Stupar, 2007; Kage et al., 2013).

Recycling, which provides scope for the enhancement of inbred productivity, has been adopted in 1990's (Mukherjee and Ahuja, 1994) and subsequently, at the Indian Agricultural Research Institute, several inbreds

were developed from diverse populations which could be utilized in hybrid breeding. These inbred lines had lost their geographical and genetical identity of the population from which they were derived. The new set of inbreds need to be classified into preliminary groups which will be subsequently subjected to more detailed stratification for specific breeding purposes. Metroglyph analysis initially given by Anderson (1957) was mainly for establishing relationship among races and biotypes of crop plants. Metroglyph analysis has been used to access the genetic variability not only in maize but also in several crop species across the genus. Maize accessions have been grouped with metroglyph scatter (Saikia et al., 1996; Khumkar and Singh, 2002; Showemimo and Yeye, 2005). Preliminary grouping of genotypes were done through metroglyph analysis in a variety of crop species; Dewan et al. (1992) studied diversity of Indian mustard; Chandra et al. (1997) classified turmeric genotypes; genetic

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variability of two *Hordeum* species were analysed by Laiju et al. (2002); Ghafoor and Ahmad (2005) studied diversity in black gram; Bhargava et al. (2009) used this method for accessing the variability in *Chenopodium*; Khan et al. (2007) studied morphological variation of 7 cotton cultivars; Rashid et al. (2007) grouped basmati rice mutants; Jha et al. (2011) studied variability pattern in chickpea; Kang et al. (2013) used it for grouping sugarcane cultivars. Metroglyph has been of considerable importance with respect to maize which had wide variation of geographic, genetic as well as morphology since maize races had been known to have evolved under several environmental conditions like tropical, temperate, subtropical, high altitude, low altitude etc. It has also been observed that stable diagnostic characters of maize are especially suitable for metroglyph analysis which truly brings about the racial affinities as well as divergence (Mukherjee et al., 1971).

In the present investigation it was, therefore, decided to use this analysis using two highly stable diagnostic characters namely, length of branching space and number of primary branches of the tassel as the ordinates against important yield components, as rays on the glyphs. This thinking was also prompted by the fact that these inbred lines under study had lost their ethnic origin during their handling under population improvement procedures under rigorous selection programme for the agronomic traits. Since no selection was applied for these two tassel traits, it would be worthwhile to study whether these traits would classify the inbreds under similar broad groups as expected of their original population structure since the grouping of inbreds and therein scatters in the graph will mainly be based on these two tassel characters. However, in order to arrive at conclusions about the agronomic or yield potential of the inbreds vis-a-vis, index score analysis was carried out which provide for precise information on the above aspects. It may be pointed out that the objective of metroglyph analysis of derived inbred lines was not to trace their relationship with their parental population since such affinities are well known and moreover they do not contribute in any way to the practical usage of these materials for improvement of productivity.

MATERIALS AND METHODS

The basic material consisted of 32 advance generation maize inbred lines derived from different populations. Each of these populations were synthesized from not less than 30 genetically and geographically diverse germplasm and random mated for at least 3 generations. The experiment was laid in a randomized block design with three replications. A four-row plot of 5-meter length represented each entry. Five plants were tagged randomly from each row and subsequently all observations were recorded on them. Metroglyph analysis was done as per Anderson (1957). Two variables, length of branching space and number of primary branches which explained maximum variation, were plotted on the X and Y axes, respectively. The individual dots of the resulting scatter diagram were replaced by precise but semi-pictorial glyphs,

on each of which the variation of six traits viz. 100-kernel weight, rows per ear, ear length, ear diameter, kernel per row and ear weight were recorded. Each of the character is diagramed by a ray; the ray for any quality had same position on the glyph. For each quality a long ray indicates the individual was high for that quality, a short ray that it had a medium value; no ray at that position indicates that the individual in question had a low value. Index scores were constructed by assigning values of 3 for each long ray, a value of 2 for each short ray and a value of 1 for no ray. Scores were assigned to each glyph and arranged in an index. Genetic distance among 32 inbreds was computed through Mahalanobis' (1936) D^2 statistic. Inbreds were grouped in to clusters following Tocher's method as described by Rao (1952). Preliminary grouping of inbreds based on Metroglyph analysis was compared with the group constellation on the basis of genetic distance following D^2 stastic.

RESULTS AND DISCUSSION

The 32 advance generation maize inbred lines derived from four diverse populations were graphically represented as metroglyph (Figure 1) following Anderson (1957). Group I containing the inbred IPA21-10 was placed farthest from the group XIII with FSA17-2. IPA21-10 and FSA17-2 had contrasting mean values for both the axes. Groups VI and VIII, containing two inbreds each, VII, with three inbreds, and IX, comprising of nine inbreds, were placed closely on the scattered plot. The inbreds of these groups had medium values for both axes. Group IV, containing three inbreds, and Group V, with five inbreds, were lying closer. Inbreds of group IV and V had medium length of branching space whereas number of primary branches ranged from low to medium. Two inbreds of group III had low mean length of branching space and medium number of primary branches. Inbreds clustered in group II had low to medium mean length of branching space and less number of primary branches. Group X with two inbreds had medium to high values for both axes. IPA40-85 clustered in group XI had medium mean length of branching space and high number of primary branches whereas group XII had high mean length of branching space and moderate number of primary branches. Index score classified 32 inbreds into different categories based on yield attributing traits. Index score varied from 9 to 18 (Table 2).

Considering the scatter of groups shown by the glyphs of inbred lines (Figure 1 and Table 1), it was observed that at least six groups were found to represent approximately a single broad cluster comprising group numbers IV, V, VI, VII, VIII and IX. The constituents of the groups in this complex represented somewhat low to medium expression of length of branching space and number of primary branches. A perusal of their original population (data not presented) indicated that these inbreds represented various intermediate values of diagnostic features which in all probability have been maintained even after reshuffling of genes during the population improvement cycles. This however, does not

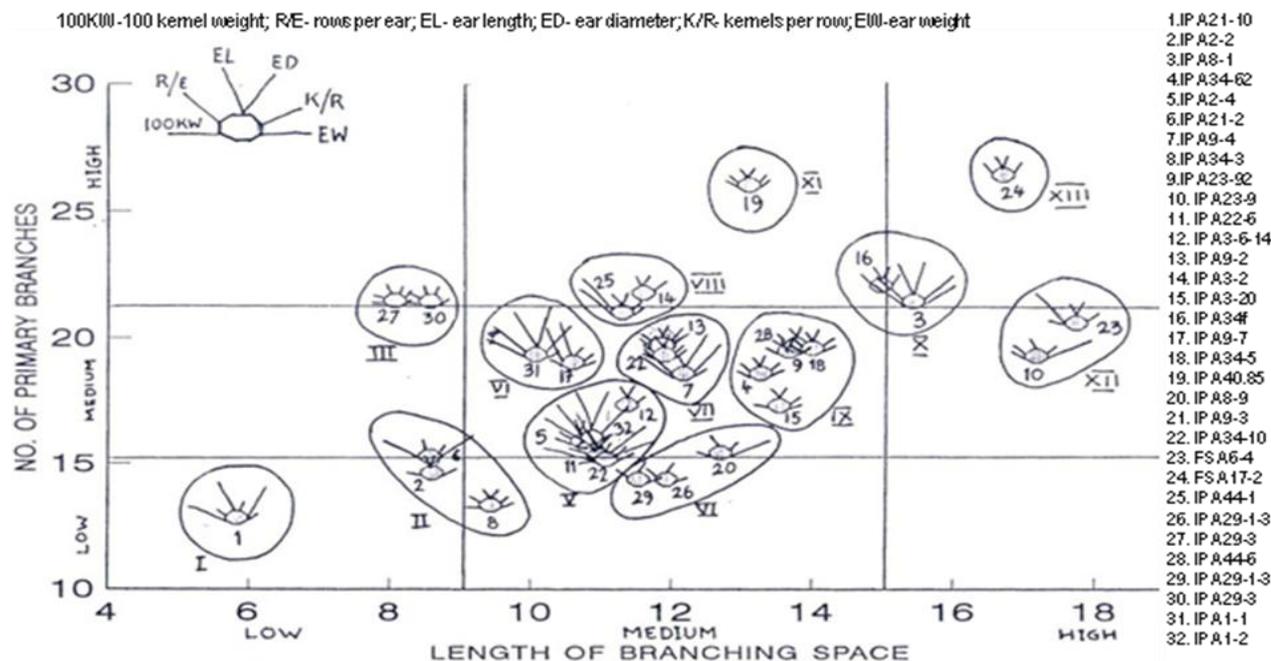


Figure 1. Pictorial representation of 32 inbred lines in the form of metroglyph.

Table 1. Group constellation^a based on D² statistic and metroglyph analysis.

D ² statistic		Group constellation	
		Metroglyph	
I	IPA29-1-3, IPA29-1-5	I	IPA21-10
II	IPA34-62, IPA34-3, IPA22-6, IPA3-6-14, IPA3-20, IPA3-2, IPA8-9, IPA9-3, IPA34-10, IPA29-3	II	IPA2-2, IPA21-2, IPA34-3
III	IPA44-1, IPA44-6	III	IPA29-1-3, IPA29-1-5
IV	IPA9-2, IPA9-7	IV	IPA44-6, IPA44-1, IPA8-9
V	IPA23-92, IPA23-9, IPA34-f, IPA34-5	V	IPA2-4, IPA22-6, IPA3-6-14, IPA9-3, IPA1-2
VI	IPA21-10, IPA21-2,	VI	IPA1-1, IPA9-7
VII	IPA9-4, IPA1-2	VII	IPA9-4, IPA9-2, IPA34-10
VIII	IPA2-2, IPA2-4	VIII	IPA3-2, IPA6-4
IX	IPA8-1	IX	IPA43-62, IPA23-92, IPA34-5, IPA29-3, IPA3-20
X	IPA40-85	X	IPA8-1, IPA 34-f
XI	FSA6-4	XI	IPA40-85
XII	FSA17-2	XII	IPA23-9, FSA6-4
XIII	IPA6-4	XIII	FSA17-2
XIV	IPA1-1		

^aExperiment was laid in a randomized block design with three replications. Genetic distance was computed through D² statistic (Mahalanobis, 1936) and inbreds were grouped in to clusters following Tocher's method (Rao, 1952).

rule out the existence of diversity with respect to the yield components as is evident from the mean values of groups V and VI which indicate higher potential for most of these traits.

There were at least three groups namely, I, XI and XIII which comprise one inbred line each. Group I containing

the solitary inbred IPA 21-10 gave the highest expression of ear weight and also ear length while it represented comparatively high values for other components also even though it qualified as the most distinct from all others in having lowest expression of two diagnostic feature of the tassel on the contrary group XIII containing

Table 2. Index score^a of 32 inbreds based on six yield components

Index score	Inbreds
9	IPA3-6-14, IPA3-2, IPA44-1, IPA44-6
10	IPA2-2, IPA34-f, IPA34-5, FSA17-2,
11	IPA23-92, IPA9-2, IPA3-20, IPA40-85, IPA8-9, IPA29-3, IPA29-1-5,
12	IPA34-62, IPA21-2, IPA34-3, IPA23-9, IPA9-3, IPA34-10, FSA6-4, IPA29-1-3
13	IPA2-4
14	IPA9-7, IPA6-4
15	IPA21-10
16	IPA9-4, IPA22-6
17	IPA1-1, IPA1-2
18	IPA8-1

^aIndex scores were constructed by assigning values of 3 for each long ray, a value of 2 for each short ray and a value of 1 for no ray. Scores were assigned to each glyph and arranged in an index.

the inbred FSA 17-2 representing the other extreme for tassel traits (highest values) was found to be the poorest with respect to the yield components. Apart from these two groups the other groups found scattered at different levels of expression of number of primary branches and length of branching space, contained inbred lines possessing generally intermediate values of yield components. The only exception could be noticed in case of IPA 8-1 which fell under group X but possessed maximum values of all the yield components. These results support our contention that groupings made on the basis of metroglyphs of diagnostic features contribute towards preliminary identification of diversity grouping of breeding entries which have undergone random mating for several generations and also for their worth in the breeding programme. Several workers had suggested metroglyph analysis for preliminary classification of genotypes (Chandra, 1977; Kotaiah et al., 1986; Mishra and Rao, 1990; Satyan et al., 1991; Showemimo and Yeye, 2005; Khan et al., 2007; Punitha et al., 2010; Jha et al., 2011; Kang et al., 2013). Though Saikia (1996) observed overlapping index scores, nevertheless, considerable reliance can be laid on the index score assigned to the various inbred lines to judge their potential (Satyan et al., 1991). It could be seen (Table 2) that the highest index score of 18 was given to the inbred line IPA 8-1 which qualified as the most promising for all the yield components followed by the two sister lines IPA1-1 and IPA1-2 (index score of 17). The minimum index score of 9 was exhibited by two sets of sister lines namely, IPA 3-6-14, IPA 3-2; IPA 44-1 and IPA 44-6. Incidentally these four inbred lines occupy the same broad cluster based on tassel traits. This brings us to an important conclusion that index score analysis may help identify the most promising inbred lines but it does not reflect the diversity pattern which can however be assessed only from groupings based on metroglyph. For instance group I which is widely divergent from groups namely, X, XI, XII and XIII had constituents exhibiting

wide range of expression of yield components including even the highest expression in group X for ear weight, group I for number of kernels per row and also comparatively high expression of other traits as well. Thus, in order to maximise heterosis and maintain *per se* parental performance in a single cross hybrid it will be advisable to select parents from such groups instead of selecting only on the basis of index score or on the *per se* performance. It could be observed that metroglyph analysis and grouping of inbreds, primarily based on two highly variable diagnostic traits, had similarities as well as dissimilarities with the clustering of inbreds based on Mahalanobis' D^2 statistic (Table 1). Differences were noticed with respect to the number of inbreds included in a group. However, pictorial representation of inbreds (Figure 1) as brought about by the scattered plot of metroglyph analysis can be used as a measure of relative genetic distance among the inbreds. Metroglyph analysis was found to be useful for preliminary classification of germplasm and its divergence study (Khumkar and Singh, 2002; Jha et al., 2011; Kang et al., 2013). Coupled with index score, metroglyph could be of great use in preliminary screening and classification of genotypes when large number of accessions is available. The group constellation deviated from the one derived through D^2 analysis. However, pictorial representation of inbreds as brought about by metroglyph analysis can be used as a measure of relative genetic distance among the inbreds.

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