Diversity and Relationships among U.S. Maize Inbreds Revealed by Restriction Fragment Length Polymorphisms

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Abstract
Restriction fragment length polymorphisms (RFLPs) have been proposed as molecular markers for characterizing the genetic diversity in maize (Zea mays L.). The objectives of this study were to evaluate the usefulness of RFLP data for (i) elucidating heterotic patterns among maize inbreds and (ii) assessing genetic similarity among related and unrelated lines. Thirty-two maize inbreds from the U.S. Corn Belt were analyzed for RFLPs with two restriction enzymes and 83 DNA probes distributed over the maize genome. Eighty-two probes detected polymorphisms with at least one enzyme. On average, 4.3 variants were found per probe-enzyme combination across all 32 inbreds. Genetic distances among lines, estimated from RFLP data as Rogers’ distance (RD), revealed considerable diversity among lines from Iowa Stiff Stalk Synthetic (BSSS), Reid Yellow Dent (RYD), and Lancaster Sure Crop (LSC). Lines from different heterotic groups had a slightly greater RD mean than unrelated lines from the same heterotic group, yet differences were small when compared with the wide range of RDs for individual lines combinations within each group. RDs between related lines agreed well with expectations based on coancestry coefficients determined from pedigree data with few exceptions. Principal component analyses of RFLP data resulted in a separate grouping of lines from BSSS/RYD and LSC. Dispersion of lines of miscellaneous origins was generally consistent with expectations based on known breeding behavior and pedigrees. Results from this study suggest that RFLP data can be used for assigning inbreds into heterotic groups and quantifying genetic similarity between related lines, but it seems that a large number of probe-enzyme combinations are required to obtain reliable estimates of genetic distance.

Disciplines
Agricultural Science | Agronomy and Crop Sciences | Genetics and Genomics | Molecular Genetics | Plant Breeding and Genetics

Comments

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A. E. Melchinger, M. M. Messmer, M. Lee,* W. L. Woodman, and K. R. Lamkey

ABSTRACT

Restriction fragment length polymorphisms (RFLPs) have been proposed as molecular markers for characterizing the genetic diversity in maize (Zea mays L.). The objectives of this study were to evaluate the usefulness of RFLP data for (i) elucidating heterotic patterns among maize inbreds and (ii) assessing genetic similarity among related and unrelated lines. Thirty-two maize inbreds from the U.S. Corn Belt were analyzed for RFLPs with two restriction enzymes and 83 DNA probes distributed over the maize genome. Eighty-two probes detected polymorphisms with at least one enzyme. On average, 4.3 variants were found per probe-enzyme combination across all 32 inbreds. Genetic distances among lines, estimated from RFLP data as Rogers’ distance (RD), revealed considerable diversity among lines from Iowa Stiff Stalk Synthetic (BSSS), Reid Yellow Dent (RYD), and Lancaster Sure Crop (LSC). Lines from different heterotic groups had a slightly greater RD mean than unrelated lines from the same heterotic group, yet differences were small when compared with the wide range of RDs for individual lines combinations within each group. RDs between related lines agreed well with expectations based on coancestry coefficients determined from pedigree data with few exceptions. Principal component analyses of RFLP data resulted in a separate grouping of lines from BSSS/RYD and LSC. Dispersion of lines of miscellaneous origins was generally consistent with expectations based on known breeding behavior and pedigrees. Results from this study suggest that RFLP data can be used for assigning inbreds into heterotic groups and quantifying genetic similarity between related lines, but it seems that a large number of probe-enzyme combinations are required to obtain reliable estimates of genetic distance.

Information about germplasm diversity and relationships among elite breeding materials is fundamental in the improvement of agricultural plants (Hallauer and Miranda, 1988). In hybrid breeding of maize, knowledge of genetic relationships among inbreds is useful in planning crosses for hybrid and line development, assigning lines to heterotic groups, and identification of inbreds for plant variety protection. Assessment of genetic similarity (or distance) between lines, populations, or races may be based on analysis of pedigree and heterosis data, morphological traits, or molecular markers such as isozymes, and more recently, RFLPs. The coancestry coefficient (Malecot, 1948) between genotypes has been widely used to estimate levels of genetic diversity as well as genetic relationships between cultivars in autogamous crops such as oat (Avena sativa L.; Rodgers et al., 1983; Souza and Sorrells, 1989), wheat (Triticum aestivum L.; Cox et al., 1985b; Murphy et al., 1986), and soybean (Glycine max (L.) Merr.; Cox et al., 1985a). For allogamous crops, including maize, coancestry coefficients have not been as easily determined because pedigree data of lines are often unobtainable or unreliable, especially when selections were made from broad-based populations. Moreover, estimates of relationship based on the coancestry coefficient might be inaccurate because of inadequate simplifications in the underlying model that assumes equal parental contributions and no selection.

Morphological data traditionally have been used in plant variety protection and registration for description of identity and distinctness of cultivars and grown under the guidelines of the Union de Protection Obention Végétale (UPOV, 1980); however, morphological characters often do not reliably portray genetic relationships because of environmental interactions and the largely unknown genetic control of these traits (Smith and Smith, 1989a). In addition, classification of maize breeding materials into heterotic groups based on endosperm types (e.g., flint vs. dent) has been recognized as inadequate, because some endosperm types differ only by one gene (Coe et al., 1988).

Biochemical data obtained by separating proteins by using electrophoresis or reversed-phase high-performance liquid chromatography provide superior descriptors of the genotype because they are not significantly affected by environment and their genetic bases are generally well understood (see Stuber et al., 1988; Smith and Smith, 1987). Allozymes have been used extensively in maize to characterize genetic variation among elite inbred lines (Stuber and Goodman, 1983; Smith et al., 1985a,b), commercial hybrids (Smith, 1984, 1988), open-pollinated and exotic populations (Kahler et al., 1986; Smith, 1986), and germplasm collections (Goodman and Stuber, 1983; Doebley et al., 1983). Isozyme data for 21 loci from 72 historically important U.S. maize inbreds revealed considerable genetic diversity, especially among lines from Reid Yellow Dent and Iowa Stiff Stalk Synthetic (Smith et al., 1985a). However, associations among lines obtained from principal component analysis of isozyme data generally were incongruent with their heterotic groups. Combined use of isozyme and chromatographic data allowed unique characterization of 95% of 62 widely used U.S. maize inbreds, and only lines closely related by pedigree through backcrossing had indistinguishable profiles (Smith et al., 1987). Multivariate and cluster analysis of isozyme and chromatographic data were able to reveal subgroups.

Abbreviations: BSSS, Iowa Stiff Stalk Synthetic; cM, centimorgan; kb, kilobase (1000 base pairs); LSC, Lancaster Sure Crop; RD, Rogers’ distance, and GRD, SRD, general and specific Rogers’ distance, and MRD, modified Rogers’ distance; RFLP, restriction fragment length polymorphism; RYD, Reid Yellow Dent.

Restriction fragment length polymorphisms (RFLPs) are genetic markers derived from differences in restriction enzyme digestion patterns of DNA. These markers can be used to determine genetic diversity within and between different biological species, and to measure the level of genetic similarity among members of related species, such as maize. RFLPs are used to study the genetic variability of inbreds adapted to the U.S. Corn Belt, and to compare estimates of genetic similarities among related maize lines.

Materials and Methods

Maize Inbred Lines Examined

Thirty-two public maize lines of current or historic importance in the U.S. Corn Belt were analyzed (Table 1). Nine lines were from the Yellow Dent heterotic group, 11 lines had miscellaneous origins, and 12 lines were from Reid heterotic groups. The genetic background and year of release of the lines are listed in Table 1. The lines were all highly inbred and maintained by self-pollination from seed of individual inbred lines to heterotic groups.

Laboratory

Molecular Genetic Laboratory, Upton, NY, T. Helentjaris (Native Plants, Inc., Johnston, IA).

The DNA probes were chosen on the basis of their single-copy hybridization patterns and to provide a fairly uniform coverage of the genome with at least six probes per chromosome (Table 2). The average map distance between adjacent markers was ~30 cM. The RFLP profiles for inbreds were recorded for each probe-enzyme combination by assigning a number to each unique band on the two autoradiographs tracing back the genome due to (i) the small number of marker loci and (ii) the potential to overcome limitations associated with morphological traits and biochemical markers (Tankersley, 1983). The major advantage provided by RFLPs is the relatively large number of polymorphic loci for each marker enzyme.

Laboratory

Columbia, MO, and D. Grant (Pioneer Hi-Bred International, Inc., Johnston, IA) supplied maize clones provided by B. Burr (Brookhaven National Laboratory).

A total of 83 genomic DNA clones (Table 2) were used as DNA probes from collections of mapped lines or populations selected directly from Iowa Stiff Stalkers. The DNA probes were labeled by random-primer synthesis and hybridized to genomic DNA from different inbreds. A set of molecular-weight markers was loaded, which was composed of lambda fragments of 2.3, 4.3, 6.7, 9.4, 13.3, and 23.1 kb obtained from single digests of lambda with HindIII, EcoRI, and BglII. The 32 lines were analyzed for their respective RFLP banding patterns of lines on autoradiographs using a set of molecular-weight markers loaded on two different gels; lambda markers and two combinations of EcoRI-HindIII, EcoRI-BglII, and HindIII-BglII. Significance of genetic relatedness among elite lines was determined using RFLP analysis.

Results

Equal quantities of leaf tissue harvested from 10 seedlings per line were lyophilized and bulked. The techniques for plant genomic DNA isolation, separate digests of DNA, and hybridization to lines from the open-pollinated population are hitherto available concerning the genetic diversity for RFLPs in maize. Results from a study by Lee et al. (1989) and for strain identification was first proposed by Burr et al. (1983). The major advantage provided by RFLPs is the potential to overcome limitations associated with morphological traits and biochemical markers (Tankersley, 1983). The major advantage provided by RFLPs is the relatively large number of polymorphic loci for each marker enzyme.
of the number of loci for which two lines differ to the total
number of variants for a given probe. Multilocus Rogers'
formula, which each allele contributes to the discrimination among
lines, was used in this study, the RD is equal to the ratio
indicating no diversity between a pair of inbreds, whereas a
number (83) of loci examined. Hence, a RD value of 0.0
on the correlation matrix of RFLP variant frequencies,
which led to a substantially better discrimination among
inbreds. Calculations of principal components were based
on the covariance matrix of RFLP variant frequencies, to
which each population had been synthesized by crossing 16 unrelated
ancestral lines, are homozygous and homogeneous;
(ii) lines without known common parentage are un-
related to each other (f = 0); and (iii) a line derived from
a recurrent selection program with BSSS, were
formed according to the rules described in Falconer (1981),
by using the following assumptions: (i) All lines, including
descendants of a line, and (ii) selection is absent through all
generations of inbreeding.

The coancestry coefficient, f (Malecot, 1948), was used to quantify the de-
gree of relatedness of inbred lines used in this study. The
coefficient, f, is the probability that two homologous genes drawn at ran-
case that Inbred i was derived
if the RFLP genotype of Line j as well as that of parental
of a complete set of progenitor lines is known. For example,
erotic groups and can be applied without knowledge of the
heterozygosity level of RFLP variants within different het-
[1] allows adjustment for possible differences in the average
distance between unrelated homozygous
where f~j is the coancestry coefficient of i and j, and RD is

\[
 l_{ij} = (1 - f_{ij}) \cdot RD
\]

\[
 l_{ij} = (RD_k + RD_{lj})/2 \quad [2]
\]

\[
 l_{ij} = l_{Oik} - RD_{jk}/2 \quad [3]
\]

Equations Ill to [3] were derived under the following as-
from the hybridization of Inbreds j and k with known RFLP
Applying this equation to the case that Inbred i was derived
A better estimate can be obtained if the RFLP genotype
of any direct progenitors of i and j.

A comparison of the two methods using the same data
of Burr et al. (1988), Helentjaris (1987),
National, to the discrimination among
References:
Burr et al. (1988), Helentjaris (1987),
(1986, personal communication), respectively.
BSSS and RYD × LSC both had a narrower range (0.48-0.74) and a slightly higher mean (0.60). The RDs for line combinations of the type RYD × LSC type line combinations had a similar range (averaging 0.54 and 0.57, respectively). The RDs for combinations of type BSSS × BSSS and LSC × LSC varieties are found between two inbreds. RDs for line variation in the degree of polymorphism among the chromosomes (Table 2); Chromosome 2 was about twice as polymorphic as Chromosome 3.

The maximum number of RFLP variants detected by the 83 DNA probes employed, considering in all inbreds, revealed polymorphisms among the 32 inbreds with at least one of the two restriction enzymes assayed. Altogether, 357 RFLP variants were observed among the 83 DNA probes in 32 maize inbreds from the U.S. Corn Belt. All but one of the 83 DNA probes used in this study with restriction enzyme was considered.

The frequency (%)

<table>
<thead>
<tr>
<th>Inbred</th>
<th>RD</th>
<th>Frequency</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>B44</td>
<td>0.48</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B37</td>
<td>0.67</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B46</td>
<td>0.62</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B52</td>
<td>0.67</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BI4</td>
<td>0.60</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B86</td>
<td>0.50</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B55</td>
<td>0.25</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A619</td>
<td>0.37</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Oh43</td>
<td>0.50</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LSC</td>
<td>0.20</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BSSS</td>
<td>0.50</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RYD</td>
<td>0.20</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The mean Rogers' distance of the respective inbred in combination with lines from the Lancaster Sure Crop heterotic group with greatest (0.65) and smallest (0.56) mean RD heterotic group. Mo17 and B86 were the LSC lines, respectively. The high mean RD of heterotic group. Mo17 and B86 were the LSC lines, respectively. The high mean RD of heterotic group. Mo17 and B86 were the LSC lines, respectively. The high mean RD of heterotic group. Mo17 and B86 were the LSC lines, respectively. The high mean RD of heterotic group. Mo17 and B86 were the LSC lines, respectively. The high mean RD of heterotic group. Mo17 and B86 were the LSC lines, respectively. The high mean RD of heterotic group. Mo17 and B86 were the LSC lines, respectively.
Among the BSSS lines, B37 and B46 had the greatest (0.65) and B38 and B39 had the smallest (0.57) mean RD to the LSC lines. The RYD lines did not differ in their mean RD to LSC lines, except for Wf9, which had a low RD to most LSC lines, especially Mo17 and H99. Standard errors of the RD estimates in Table 4, calculated by the jackknife method (Miller, 1974), were 0.05 in all instances.

When RD values were partitioned into general (GRD) and specific (SRD) Rogers’ distances according to the factorial model proposed by Melchinger et al. (1990), GRD accounted for 62 and 45% of the variation among RDs in the BSSS × LSC and RYD × LSC line combinations, respectively. This indicates that the RD of a specific combination of lines differed in many instances considerably from the value expected on the basis of the mean RD of the respective lines in combination with all lines from the other heterotic group. A noteworthy example is B73 X Mo17, which had the smallest RD of all BSSS lines with Mo 17, although this cross is known for its outstanding hybrid performance and heterotic response (Lee et al., 1989; W.A. Russell, 1989, personal communication).
Table 5. Mean, minimum, and maximum Rogers' distances (RD) calculated from restriction fragment length polymorphism data of 83 DNA probes for inbreds of miscellaneous origins in combination with nine inbreds derived from the Iowa Stiff Stalk Synthetic (BSSS) population and eight inbreds from the Lancaster Sure Crop (LSC) heterotic group.

<table>
<thead>
<tr>
<th>Inbred</th>
<th>BSSS inbreds</th>
<th>LSC inbreds</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>Min.</td>
<td>Max.</td>
</tr>
<tr>
<td>M14</td>
<td>0.57</td>
<td>0.53</td>
</tr>
<tr>
<td>B50</td>
<td>0.57</td>
<td>0.51</td>
</tr>
<tr>
<td>B52</td>
<td>0.59</td>
<td>0.53</td>
</tr>
<tr>
<td>B54</td>
<td>0.62</td>
<td>0.59</td>
</tr>
<tr>
<td>B57</td>
<td>0.63</td>
<td>0.54</td>
</tr>
<tr>
<td>B75</td>
<td>0.59</td>
<td>0.49</td>
</tr>
<tr>
<td>B77</td>
<td>0.60</td>
<td>0.54</td>
</tr>
<tr>
<td>B79</td>
<td>0.58</td>
<td>0.48</td>
</tr>
<tr>
<td>R177</td>
<td>0.65</td>
<td>0.59</td>
</tr>
<tr>
<td>De811</td>
<td>0.62</td>
<td>0.53</td>
</tr>
</tbody>
</table>

Disregarding line B86, which was derived from B52 (Table 1). Disregarding line B14, the predominant parent of De811 (Table 1).

The inbreds from BSSS, RYD, and LSC are given in Table 5. B57, R177, and De811 had a high mean RD to both heterotic groups, indicating that these lines and their respective parental populations represent germplasm sources unrelated to the BSSS and LSC lines. B52, B54, and B75 seemed to be more closely related to LSC germplasm than to BSSS germplasm. With the exception of B75, however, differences in the mean RD to each heterotic group were small compared with the wide range of RDs within each group, which overlapped in all instances. All other lines, including B77 and B79, showed similar mean RDs of medium size to both heterotic groups in harmony with the results reported by Lee et al. (1989).

Genetic Distances among Related Inbreds

Among the 32 maize inbreds analyzed in this study, 12 pairs of lines were related by pedigree with an estimated coancestry coefficient ranging from 0.125 to 0.75 (Table 3). In most instances, RDs determined from the RFLP genotype of the lines were in close agreement with RD estimates calculated from Eq. (1) or (3). Significant deviations between RD and RD (greater than twice the estimated standard error of the RD estimator obtained by the jackknife method) were found for line combinations B73 × B84, B38 × B46, and Oh43 × A619. For B73 × B84, the discrepancy was very likely attributable to an underestimation of . Both lines originated from advanced cycles of a recurrent selection program, but selection, which is known to cause a further reduction in the actual effective population size (Harris et al., 1984), was ignored in calculating for lack of suitable treatment.

Rank correlations of RD with RD and 1 - f were almost identical (rs=0.71 and 0.74, respectively) and significantly (P < 0.01) greater than zero.

Principal Component Analyses of RFLP Data

Figure 3 presents the results from principal component analysis of RFLP data for all 32 inbreds. The PC1, PC2, and PC3 scores for each inbred are plotted on the graph.
et al., 1990; Lee et al., 1990) and is approximately consistent with the amount of genetic variation detected per probe-enzyme combination was 4.3 in our study. The average number of RFLP variants detected per probe was 100, which is similar to previous findings. Our results showed that there were 10,000 RFLPs revealed in the genetic diversity for RFLPs in a larger set of lines.

In addition, our results provided information about the genetic diversity for RFLPs in a larger set of lines, which was used as a paradigm for examining potential applications of RFLP analyses in hybrid maize breeding. The slightly greater mean RD for the BSSS × LSC (0.54) and BSSS × LSC (0.52) than the BSSS × BSSS (0.50) and LSC × LSC (0.50) line combinations of type BSSS × BSSS and LSC × LSC was moderate (<8%), especially for (i) assessment of genetic similarity of related and (ii) assignment of inbreds of unrelated lines.

The LSC lines were more widely spread, with the spread of the BSSS and LSC lines were B57, B77, B79, and R177 (Fig. 3B). B77 and B79 were widely spaced from each other and occupied positions approximately intermediate to the BSSS and LSC lines. B77 was closer to MolT, and B79 closer to the Oh43 BSSS lines, this result was not unexpected, because the LSC lines are known to represent a genetically broad population, on the basis of their breeding history (Sprague, 1946), estimates of genetic variation for agronomic traits (Hallauer et al., 1983), and estimates of genetic similarity at the molecular level. Regarding the LSC lines, this result was not unexpected, because LSC is known to represent a genetically broad population, on the basis of its breeding history (Sprague, 1946), estimates of genetic variation for agronomic traits (Hallauer et al., 1983), and estimates of genetic similarity at the molecular level.

The lower mean RD of the BSSS × BSSS (0.50) compared with the 20 to 30% increase in heterosis for grain yield generally observed in single crosses of unrelated lines. However, the relative increase in heterosis for yield for crosses among unrelated lines was twice the amount observed in comparable isozyme studies (Stuber and Goodman, 1983; Smith et al., 1983). Two randomly selected inbreds derived from BSSS, RYD, and LSC were evaluated for polymorphisms with a set of restriction enzymes. The average number of RFLP variants detected per probe was 100, which is similar to previous findings. Our results showed that there were 10,000 RFLPs revealed in the genetic diversity for RFLPs in a larger set of lines, which was used as a paradigm for examining potential applications of RFLP analyses in hybrid maize breeding.

The group of inbreds from BSSS, RYD, and LSC was largely consistent with their known phylogenetic relationships. Lines from BSSS and LSC formed two clearly separated groups. BSSS-derived lines were more widely spread, with genetic relationships. Lines from BSSS and LSC were more widely spread, with genetic relationships. Lines from BSSS and LSC were more widely spread, with genetic relationships.
Assignment of Inbred Lines to Heterotic Groups

Although heterotic groups are of great concern to maize breeders, the currently dominating heterotic combinations have received greatest use in the U.S. Corn Belt, lines containing reliable estimates of similarity. The efficiency of hybrid breeding programs.

Assessment of Genetic Similarity among Related Inbreds

f. The results presented in Table 3, especially the comparison of RD between the RYD and LSC open-pollinated varieties calculated from isozyme data of 13 and 18 loci and BSSS/RYD heterotic pattern, respectively. BSCB#3 and BS10, respectively, belonged to the LSC and B79, this was not unexpected, because several progen-}

nantly non-RYD parents in its pedigree. All other lines of miscellaneous origins were either closely related to RYD and LSC populations, possibly as a result of se-

genetically divergent from each other than the original lines from the other heterotic group. Among the lines of miscellaneous origin, RFLP analyses identified only B57, R177, and De811 as rep-

fined to these heterotic groups based on pedigree in-

Thus, our results concerning the precision of RD and BSSS/RYD heterotic pattern, respectively. The MRD values, therefore, suggests that the BSSS alleles) per locus and consequently should be smaller than those reported here and by Atchley et al. (1988). Cox et al. (1985a,b) described similar analyses for 43 hard red winter wheat cultivars and 115 soybean cultivars, respectively, yet with a considerably smaller number of marker loci. Both the soybean and wheat analyses had smaller levels of as-

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nantly non-RYD parents in its pedigree. All other lines of miscellaneous origins were either closely related to RYD and LSC populations, possibly as a result of se-

genetically divergent from each other than the original lines from the other heterotic group. Among the lines of miscellaneous origin, RFLP analyses identified only B57, R177, and De811 as rep-

fined to these heterotic groups based on pedigree in-
groups. The second property is a function of the genetic variation within each group and of the sampling error associated with individual RD estimates, which depends on the number of probe-enzyme combinations analyzed.

A major result of the present study with respect to these properties was that RDs for line combinations from different heterotic groups (BSSS X LSC, RYD X LSC) had only slightly higher means than those from the same heterotic groups (BSSS X BSSS, LSC X LSC), especially when compared with the wide range of RDs within each group (Fig. 2). From this, two conclusions can be drawn: (i) reliable heterotic grouping of a line of unknown heterotic pattern requires determination of its mean RD to a large number of representative lines from each heterotic group; (ii) the number of probe-enzyme combinations employed in this study seems to represent a lower limit. Considering the low level of genetic differences between the BSSS/RYD and LSC lines and also the sizeable standard error of RD (±0.05 in most cases), one probably has to employ a larger number of markers to reduce the chances of misclassification.

Despite these limitations and the small proportion (18.4%) of the total variation explained by the first three principal components, principal component analysis resulted in a clear separation of the BSSS (and most RYD) lines from the LSC lines (Fig. 3A). Moreover, lines of miscellaneous origins were mostly grouped in agreement with known breeding behavior or pedigree information (Fig. 3B): Mo 17 and Oh43 were found to represent distinct germplasm within the LSC heterotic group, as described by Dudley (1984); B52, B54, B75, 38-11, and Wf9 from RYD were positioned within or adjacent to the spread of the LSC lines, which is in harmony with the assignment of these lines to the LSC heterotic groups based on breeders' experience [A.R. Hallauer, Report of the North Central Corn Breeding Res. Conf. (NCR-2 Meeting, Rosemount, IL; 24-25 Feb. 1987]. Deviating from this source of information, however, our results suggested that B57 and R177 represent germplasm sources diverse from LSC.

In conclusion, our results support the proposal of Lee et al. (1989) that RFLP-based genetic distance estimates are useful for assigning maize inbreds to established heterotic groups and investigating relationships among inbred lines. Principal component analysis of RFLP data provided a fairly accurate portrayal of associations among lines according to their origin from different heterotic groups and pedigree relationships. However, our data suggest that a large number of probe-enzyme combinations is needed to measure the genetic distance between maize inbreds with sufficient precision. Once an RFLP data base for a large number of lines has been established, it could assist the breeder in (i) partitioning breeding materials into well-defined or new heterotic groups, (ii) rapid and systematic integration of new lines of unknown genetic background into these heterotic groups, (iii) quantifying the genetic similarity between related and unrelated inbreds, and (iv) choice of divergent parents for creating new source populations in line development that have good chances of yielding transgressive segregates (Melchinger et al., 1988).

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