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**EVALUATION OF THE POTENTIAL OF RFLPs FOR THE STUDY OF
DISTINCTNESS, UNIFORMITY AND STABILITY IN SUNFLOWER**

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Evaluation of the potential of RFLPs for the study of distinctness, uniformity and stability in sunflower

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Introduction

The GEVES (Groupe d'Etude et de Contrôle des Variétés et des Semences) is interested and implicated in the development of DNA profiling techniques for potential use in DUS testing of plant varieties, from several years. One of the research programs conducted by GEVES was the evaluation of the potentials of RFLP markers for distinctness and uniformity testing in sunflower.

Sunflower is a very important oil-seed production crop in France. Every year, there are more than one hundred of new hybrids applied for registration on the French list and new lines studied for plant breeder's rights. With this increasing number of new varieties and inbred lines, often selected from the similar genetic resources, distinction by the usual morphophysiological characters is reduced. Recently, RFLPs were reported to be promising molecular markers for the assessment of genetic variability among sunflower inbred lines (Berry et al., 1994; Gentzbittel et al., 1994; Zhang et al., 1995). Here we present our results on the interline variability (Distinctness) and intraline variability (Uniformity and Stability) obtained from RFLP analysis in sunflower.

Materials and methods

The study of interline variability was carried out on a set of 46 inbred lines of sunflower (public and protected lines), which represent the whole morphophysiological variability observed among the sunflower inbred lines maintained in the French reference collection in GEVES for DUS testing. Among these lines, several pairs are very close or not differentiated by morphological characters. For reason of simplicity and confidentiality, the lines were coded from number 1 to 46; lines 1 to 25 are maintainer (M) lines and lines 26 to 46 are restorer (R) lines. The leaves used for DNA isolation were collected from 5 plants per inbred line and bulked for each line.

To evaluate the variability within lines, 4 inbred lines were chosen for their importance in hybrid variety breeding : HA89, RHA266, CX and PAC2. For each line, 10 to 15 plants were analyzed by RFLPs. The leaves were harvested separately for each plant of the same line.

The methods used for DNA isolation and for RFLP analysis in this study were previously described (Gentzbittel et al., 1994). RFLP profiles observed in autoradiographs were scored visually. The presence or absence of a band in a gel lane was coded by 1 or 0 respectively.

Relationships among the sunflower inbred lines were studied by the estimation of Nei's similarity index F (Nei and Li, 1979) as well as Nei's distance d , expressed as the mean number of nucleotide substitutions per nucleotide site using the computer program developed by Gentsbittel and Nicolas (1990). A UPGMA dendrogram (Sneath and Sokal, 1973) was also constructed, based on the RFLP distances.

All the clones used as probes in our studies were prescreened and have detected polymorphism among sunflower inbred lines (Gentsbittel et al. 1994). The criteria of the choice of these clones were (1) genome coverage, (2) hybridization quality and (3) polymorphic content.

Results

1. Interline variability detected by RFLPs

Genetic variation among the 46 inbred lines of sunflower was assessed with 42 cDNA clones, combined with *Hind*III or *Eco*RI. The 42 probe-enzyme combinations produced a total of 203 fragments and 246 profiles across the 46 inbred lines of sunflower, corresponding an average of 4.8 fragments and 5.8 profiles per probe-enzyme combination. The number of RFLP profiles produced by each probe-enzyme combination ranged from 2 to 17; 62% of probe-enzyme combinations generated 2 to 5 profiles. The average gene diversity (H) (Nei, 1987) was 0.63 (S.E. = 0.83).

Nei and Li's similarity index F as well as the genetic distance d , calculated for the 1035 possible pairwise comparisons between the 46 sunflower inbred lines, are presented in Table 1. The F values ranged from 0.43 (for lines 4 and 31) to 0.98 (for lines 1 and 2), with an average of 0.63. Out of the 1035 possible pairwise combinations, 19 pairs of lines (1.84 %) had a F value more than 0.80; 7 pairs of lines (0.68 %) had a F value more than 0.90. The estimates of the distance d varied from 0.01 to 0.50 (Table 1).

Based on the RFLP distances estimated, an UPGMA dendrogram showing the relationships between the 46 inbred lines of sunflower was constructed (Fig. 1). Two main groups can be observed on the dendrogram: on the top a group of the R lines and on the bottom a group of M lines and there are several subgroups among each principal group. However, four R lines, 26, 38, 40 and 42 have been classed among the M lines. Likewise, two M lines, 5 and 13, have been classed among the R lines. The line 7 has been located out side the two main clusters. On the dendrogram, one can observe a triplet (lines 1, 2 and 18) and four pairs (lines 3 and 4, lines 29 and 34, lines 37 and 39, and lines 28 and 31) of lines which were very close and had a genetic distance less than 0.05 between them (Table 1). At morphophysiological level, lines 1, 2 and 18 can not be distinct; likewise for lines 29 and 34. Line 3 differentiated from line 4 only by one character - leaves denture. Lines 37 and 39 shared a common parent; likewise for the pair of lines 28 and 31. However, the two pairs of lines are declared distinct by morphophysiological characters.

2. Intraline variability of sunflower inbred lines revealed by RFLP

Evaluation of the intraline variation in four inbred lines of sunflower was performed with 30 probes, combined with *Hind*III or *Eco*RI. Ten plants for RHA266, 13 for CX, 14 for PAC2

and 15 for HA89 were studied. Evaluation of the variation within each line was based on the comparison of the fragment profiles revealed by each probe-enzyme combination. Table 2 shows the results from the comparison.

In line HA89, 2 of the 15 plants studied were different from the others by one and 9 probe-enzyme combinations respectively. For line CX, 3 of the 13 plants analyzed were differentiated with the other plants by 6, 1 and 4 probe-enzyme combinations respectively. Within line RHA266, 3 of the 10 plants were distinguished from the others by just one probe-enzyme combination. In line PAC2, no intraline variability has been detected by the 30 probe-enzyme combinations analyzed.

Discussion

The average number of RFLP variants detected by probe-enzyme combination across the 46 lines studies was about 6; this result confirmed the reports made by Berry et al. (1994) and by Gentzbittel et al. (1994) and Zhang et al. (1995); this means that the cultivated sunflower has a relatively high level of RFLP which is comparable with those reported in maize (Messmer et al., 1991, Smith et al; 1991, Livini al et. 1992). This level of polymorphism is three times higher than that revealed by isozymes in sunflower inbred lines (Quillet et al. 1992; Bourgoïn-Grenèche, personal communication). The gene diversity calculated for the 46 inbred lines with this set of selected probes is on average 0.63, which is similar to that obtained on an other set of sunflower inbred lines (Zhang et al., 1995) but superior to the 0.49 reported by Berry et al. (1994).

The RFLP data obtained allowed a separation of M lines from R lines, with a few exceptions. This confirm the previous reports (Berry et al., 1994; Gentzbittel et al., 1994; Zhang et al., 1995) as well as the results obtained from isozymes (Bourgoïn-Grenèche, personal communication), and is in concordance with the difference in morphology between these 2 types of lines in sunflower. Among the 46 lines analyzed, there are the 7 pairs of lines (1-2, 1-18, 2-18, 3-4, 29-34, 37-39 and 28-31) for them no difference (1-2, 1-18, 2-18, 3-4 and 29-34) or just some very small differentiation (37-39 and 28-31) can be observed from each other, based on morphological characters. From RFLP data, these pairs of lines showed the biggest similarity index values (> 0.90). Such a result proved the good precision of RFLPs on the estimation of genetic distance between inbred lines in sunflower.

Intraline variability has been detected by RFLP in three of the four lines analyzed; the degree of this variability varied according to line. This kind of variability has been already revealed by isozyme analysis and observed in the field on other sunflower inbred lines. There appear two explanations for some intraline variability on RFLP in cultivated sunflower. Firstly, the cultivated sunflower is an outbreeding species with forced selfpollination, secondly, RFLP loci have not been taken into consideration in the breeding programs until now. It should be indicated that these four inbreds examined in this study presented a good uniformity of morphological characters in the field. The heterogeneity may have a consequence in the study of distinctness based on DNA profiling because the more the degree of heterogeneity of a line is high, the more the distinctness of that line from the others is easy.

Conclusions

The results of the present study show that the RFLP data are potentially very useful in description and identification of sunflower inbred lines. RFLP has also been proved to be

very powerful tools to determine the relations and to measure the genetic distance between lines. Compared with morphological characters, RFLPs have many advantages as descriptors of lines and varieties : unlimited number, independence of culture conditions, high level of polymorphism. This type of descriptor is especially useful to the cultivated sunflower which is extremely susceptible to the culture conditions ; the phenotype of a same inbred sunflower line may vary with the culture conditions and year. Thus, the whole set of reference varieties and lines has to be grown and observed each year and this is very expensive. The usual morphophysiological characters used for DUS testing in sunflower show more and more limits to describe correctly the numbers of inbred lines and varieties that increase year by year. In the future, the combination of both the classic morphophysiological characters and a genetic distance based on RFLP data in sunflower would improve the accuracy of description of inbred lines and varieties in the DUS testing and strengthen plant breeder's rights. Furthermore, the DNA markers like RFLPs might play an important role in the establishment of essential derivation because of its high number and good precision.

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Table 2. Intraline variability revealed by RFLPs in four sunflower inbred lines

Lines	Nb of plants analysed	Nb. of probe-enzyme combinations assayed	N° of the plant	Nb. of probe-enzyme combinations distinguishing this plant from the others
HA89 (CD)	15	29	p1	1
		29	p2	9
CX	13	30	p5	6
		30	p13	1
		30	p14	4
RHA266	10	30	p3	1
		30	p7	1
		30	p8	1
PAC2	14	30	0	0

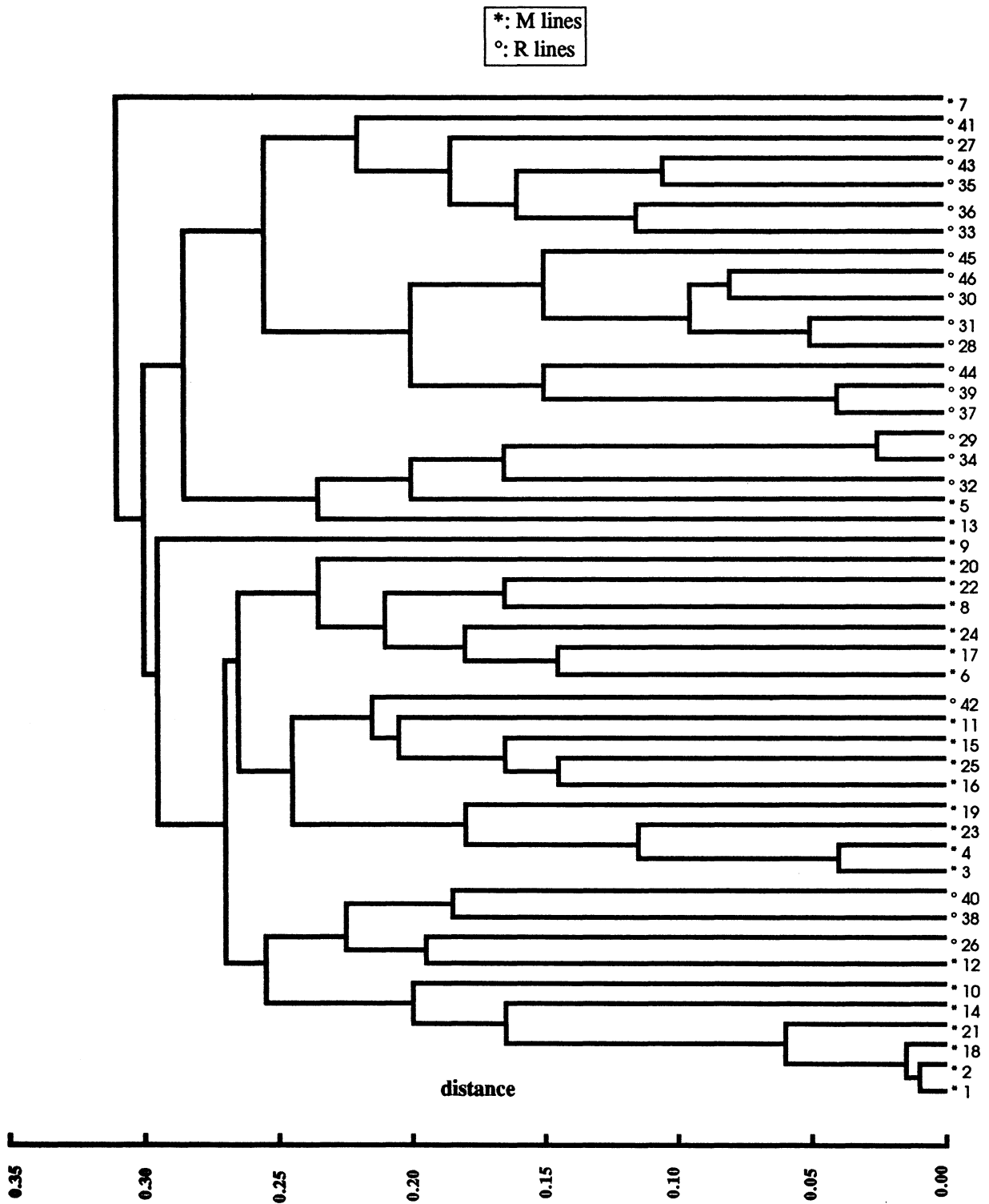


Fig. 1. UPGAM dendrogram generated from Nei's genetic distance estimates (Table 1) for the 46 sunflower inbred lines.

Table 1. Nei and Li's F index (below diagonal) and estimates of nucleotide substitutions per nucleotide site (above diagonal) for pairwise combinations among the 46 inbreds of sunflower

Table with 46 rows and 46 columns. The diagonal elements represent Nei and Li's F index, and the upper triangular elements represent estimates of nucleotide substitutions per nucleotide site. The table is symmetric across the diagonal.