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MICROSATELLITE FINGERPRINTING TO DIFFERENTIATE *BRASSICA* VARIETIES

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Microsatellite fingerprinting to differentiate *Brassica* varieties.

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Abstract

Varieties of *Brassica napus* L. *partim* (42 varieties), *Brassica rapa* L. var. *silvestris* (Lam.) Briggs (15 varieties), and *Brassica napus* L. *partim* synthetics (3 varieties) were screened by amplification using a set of eight microsatellite primers. The allele pattern of each of the 60 varieties, using all of the primers, was encoded as a binary matrix. These data were used to produce a distance matrix, and these distances were used in the production of a dendrogram showing the interrelationships of the varieties. Of the varieties screened, eleven varieties could not be differentiated using this method (two groups of four, and one group of three). In addition, the information from two sets of primers was dispensable without degrading the resolving power of the method. Information regarding contrasting results by individual and population sampling is also discussed.

Introduction

The use of DNA-based marker systems, in the estimation of relationships between plant varieties, is of especial interest in terms of development of methods for use in assigning plant breeders rights for new varieties. This group of techniques has the potential to contribute to measurement of Distinctness, Uniformity and Stability (DUS). The most examined area, in terms of published work, is in the use of molecular methods to assess D (e.g. Lee *et al.*, 1996; Law *et al.*, 1996).

We present in this paper an examination of the use of simple sequence repeats (SSR) in the application of a molecular fingerprinting method to *Brassica* spp. SSR, also known as microsatellites, are short regions of DNA consisting of tandemly repeated nucleotide units of between one and five bases. The variation in the number of repeats found in microsatellite regions provide the polymorphisms which have been used to differentiate many eukaryotic species (Weber and May, 1989) and these differences are inherited in a Mendelian fashion. We have used an existing method for SSR typing of *Brassica* spp. (Kresovich *et al.*, 1995; Szewc-McFadden *et al.*, 1996) to examine 60 varieties of Swede rape, Turnip rape and hybrid rape. The method used allowed resolution of the majority of varieties based on allele patterns.

Materials and Methods

Brassica Collection

The sixty varieties of *Brassica* used in this study are shown in Table 1. For convenience, the numbering used in Table 1 is used throughout the paper to refer to the seed stocks.

DNA isolation

Seed DNA was extracted using the method of Chee *et al.* (1995) using 0.1g seed material for each sample from 2 g macerated seed. For some samples, single seeds were extracted to compare to the bulk seed DNA.

PCR Amplification

The primers-pairs used were Bn6A1, Bn9A, Bn12A, Bn26A, Bn38A, Bn59A1, Bn72A and Bn92A1 which had been designed for use in *Brassica* spp. (Kresovich *et al.*, 1995; Szewc-McFadden *et al.*, 1996). The conditions used for amplification were as described by Szewc-

McFadden *et al.* (1996). PCR amplifications were performed on a MJ Research PTC-200 thermal cycler.

Post-PCR Analysis

PCR reactions were examined after electrophoresis on a PROTEAN II xi apparatus (Bio-Rad), through 8 % polyacrylamide gels (160 mm X 160 mm X 1 mm). After electrophoresis, the gels were silver stained (Wray *et al.*, 1981) and dried between cellophane sheets.

Data Analysis

Allele patterns were scored as a binary table. Genetic distances were calculated by means of the program RESTDIST, part of the PHYLIP package, version 3.6 (Felsenstein, 1989). This program uses a modification of the distance method of Nei and Li (1979). Dendrograms were constructed using the NEIGHBOR program from PHYLIP.

Results & Discussion

Data collection

Each of the sixty *Brassica* seed lots was amplified with the eight primer-pairs, and the allele patterns were examined after gel electrophoresis and staining. The number of allele locations scored for each of the primer-pairs was as follows;

- Bn6A1 – 5 alleles
- Bn9A – 6 alleles
- Bn12A – 10 alleles
- Bn26A – 21 alleles
- Bn38A – 7 alleles
- Bn59A1 – 7 alleles
- Bn72A – 4 alleles
- Bn92A1 – 9 alleles

This added up to a total of 69 data points per sample, or 4140 data points in the final matrix (Appendix I).

Data Analysis

The genetic distances were estimated using the RESTDIST program, using a site length of 20 nucleotides (i.e. primer size). A matrix of genetic distances was then produced. This data set (Appendix II) was the basis for further calculations. The dendrogram produce from the full genetic distance matrix (Figure 1) shows that there are three unresolved clusters of *Brassica*. The first cluster was of *B. rapa* varieties (numbers 11, 12, 14 and 22), the second was *B. napus* (numbers 40, 47, 51 and 52) and the third was *B. napus* (numbers 58, 59 and 60). Eleven varieties could not be discriminated using the SSR method presented.

The informational content of each subset of data from individual primer-pairs was examined by its removal, in turn, from the set of data points, followed by dendrogram construction as before. The consequences of removal of data sets are shown in Table 2. The removal of data points can be extended to primer-pairs Bn6A2 and Bn72A with no degradation of variety resolution, or major change in tree topology (data not shown). However this must be regarded as exceptional; the general trend is that increasing the number of primer-pairs in the examination of the samples will increase the resolving power of the technique.

Bulked verses single seed extracts

A subset of the primer-pairs was used to examine the effect on allele patterns found in individual seed compared to the bulked seed for all varieties. A single individual from each seed lot was extracted and analysed by SSR in comparison to the bulked samples used previously. The findings from these experiments, an example of which is shown in Fig. 2, was that Turnip rape showed great deal of heterogeneity, with an average of approximately 50% common alleles when comparing single and bulked samples. The heterogeneity of Swede rape varieties was much lower, as might be expected from their breeding patterns.

Conclusions

The ability of the SSR technique to differentiate between varieties of *Brassica* has been shown, but problems remain. The resolving power needs to be increased to permit differentiation of all varieties, most simply by an increase in the number of primer-pairs used to examine this *Brassica* collection. Automation of the allele sizing techniques (Ziegle *et al.*, 1992) would increase the number of samples which could be examined, but would, counter-intuitively, reduce the resolution of data obtained. In slab gels, samples of interest can be placed in adjacent wells and allele correspondence can be ascertained with a high degree of certainty. However, when the same analysis is performed using automatic methods, a degree of inaccuracy is inevitable. The practice of "binning", grouping together of alleles within a certain size range, is routinely utilised. The relative merits of automation verses older methods will only become apparent when the same techniques are compared on the two systems. However, there are indisputable advantages in the use of polyacrylamide gels, most obviously the relative cost and availability when compared to automatic systems.

The ultimate goal is the use of molecular methods in one, or more, elements of DUS. The survey presented here, using microsatellites, shows the need to conduct trials of methods on large collections of varieties. Problems may not become apparent if the testing is performed using small numbers.

The cut-off between utility as an identification method and a practical method for D testing is one which can only be determined empirically, and is likely to differ for each technique. To permit development of a method for D it may be necessary to decide upon one method to test across a number of groups, each testing a collection of varieties that have been granted PBR. Although microsatellites are a tried and tested identification system, a method with a higher resolving power might be required. Potential candidates include automated versions of AFLP (Vos *et al.*, 1995) and ISTR (Rohde, 1996).

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TABLE 1. BARSSICA VARIETIES USED.

No.	Species	Crop	Type	Variety	Comments
1	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Forage	Interval	-
2	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Forage	Hobson	-
3	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Forage	Hungry gap	-
4	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	BC95-106	-
5	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Mars	-
6	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	SW02769	-
7	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Corona	-
8	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Acrobat	-
9	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Aries	-
10	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Canyon	-
11	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Spring	Skye	-
12	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Spring	SWA3152	-
13	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Spring	Merit	-
14	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Spring	SWB3156	-
15	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Spring	SWA3157	-
16	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Lila	-
17	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Rebel	-
18	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Sprinter	-
19	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Maskot	-
20	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	SWB2777	-
21	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Winter	Triton	-
22	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Winter	Debut	-
23	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Winter	Fimbul	-
24	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Winter	Salut	-
25	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Winter	SW01622	-
26	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Spring	Riina	-
27	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Winter	Debut	-
28	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Spring	Kova	-
29	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Commanche	Treated seed
30	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Apex	Treated seed
31	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Aries	-
32	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Synthetic	Hyola 401	Treated seed
33	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Synthetic	Hyola 38	Treated seed
34	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Synthetic	Synergy	Treated seed
35	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Spring	Agena	Treated seed
36	<i>Brassica rapa</i> L. var. <i>silvestris</i> (Lam.) Briggs	Turnip Rape	Spring	Kulta	-
37	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Maskot	Treated seed
38	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Cobra	Treated seed
39	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Acrobat	Treated seed
40	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Falcon	Treated seed
41	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Solar	-
42	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Express	Treated seed
43	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Starlight	-
44	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Inca	Treated seed
45	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	x	Corsair	Treated seed
46	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	x	Mlch58	-
47	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Contact	-
48	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	x	Mlch56	-
49	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Capitol	-
50	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	Briol	-
51	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Hansen	Treated seed
52	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Gazelle	Treated seed
53	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Columbus	-
54	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Winter	Bristol	-
55	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	CSH P003	-
56	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	x	Pactol	-
57	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	x	Cocktail	Treated seed
58	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	x	Superol	-
59	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	Spring	CSHP001	-
60	<i>Brassica napus</i> L. <i>partim</i>	Swede Rape	x	Concept	-

TABLE 2. EFFECT OF REMOVAL OF PRIMER-PAIR ALLELE DATA FROM THE DATA SET.

Primer-pair data removed	Number of unresolved varieties	Number of unresolved clusters
None	11	3
Bn6A2	11	3
Bn9A	13	4
Bn26A	17	6
Bn38A	15	4
Bn59A	12	3
Bn72A	11	3
Bn92A	14	4
Bn6A2 & Bn72A	11	3

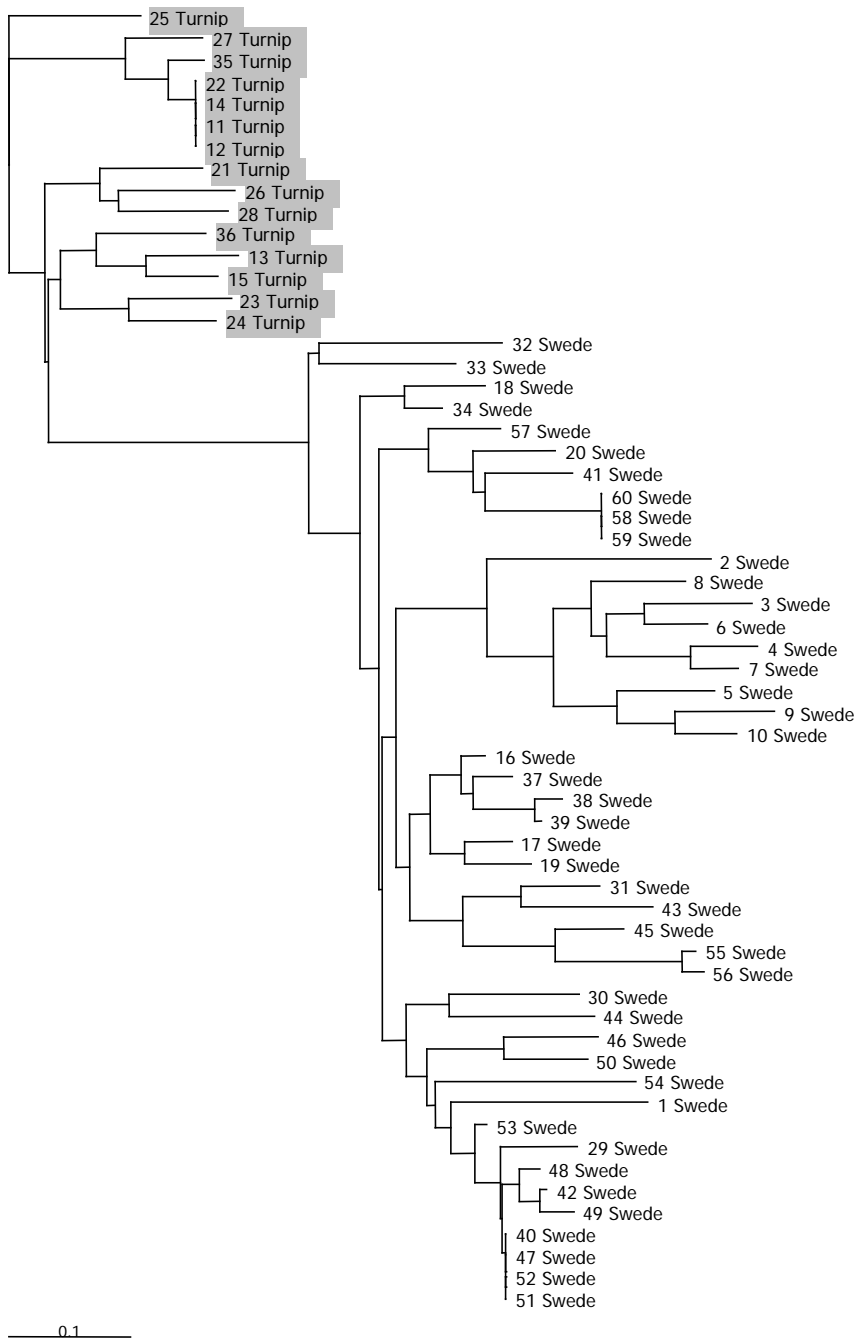


Figure 1. Dendrogram representing the comparison of bulked-seed allele patterns. Note Turnip Rape varieties are shaded to allow easy identification. See Table 1 for the variety numbers.

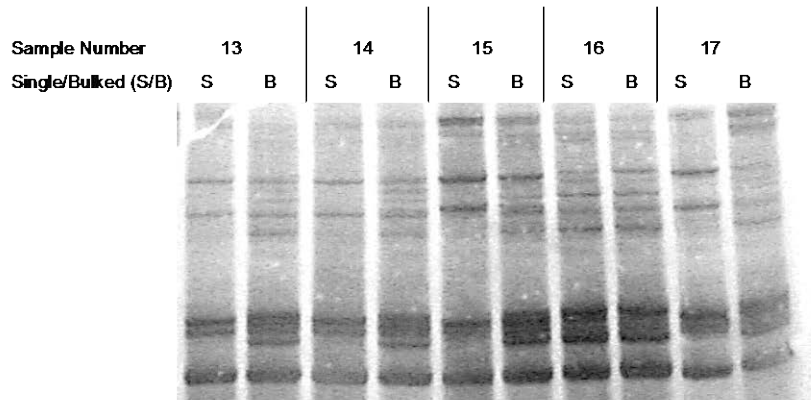


Figure 2. Silver stained polyacrylamide gel, showing allele patterns obtained from single and bulked seed extracts of *B. rapa* varieties, using primer-pair Bn38A1. Note the greater number of alleles in the bulked seed extracts.

