

A Translocation Tester Set in Pearl Millet

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Summary. Sixteen translocation stocks developed in pearl millet, *Pennisetum typhoides* (Burm.) S.&H. ($2n = 14$) were inter-crossed and the meiotic configurations of F_1 's analysed. A translocation tester set comprising five translocation stocks, each involving two non-homologous chromosomes has been developed.

Key words: *Pennisetum typhoides* – Translocation – Meiotic configurations – Tester set

Introduction

Chromosomal interchanges commonly referred to as “translocations” are important in constructing chromosome maps and offer the possibilities for breaking gene blocks in the chromosomal regions where chances of recombination are rare. They form an important tool for creating directed genetic variation by producing duplications of the defined chromosome segments. In addition, translocation heterozygotes form an important source of aneuploids (Minocha et al. 1979). Burnham (1962) has described various methods for the identification of chromosomes involved in translocations including linkage of semi-sterility with genetic markers, analysis of pachytene configurations, somatic chromosome analysis and study of the meiotic configurations of the F_1 's of trisomic-translocation and inter-translocation crosses. Amongst these methods, the study of meiotic MI configurations in F_1 's of inter-translocation crosses is relatively easy and particularly useful for those species where pachytene analysis is difficult. A tester set is useful in identifying the chromosomes involved in any unknown translocation stock with a minimum number of crosses. A series of translocation stocks with different interchange points and chromosome combinations can be developed and used to delimit the breakpoints more precisely. The procedure given by Burnham et al. (1954) was followed

in developing the translocation tester set. A translocation tester set should have the following characteristics; i) it should comprise of a minimum number of translocation stocks which can identify the chromosomes involved in any unknown interchange; ii) it must identify all the possible chromosome combinations of the haploid complement which can be involved in the interchanges. In a species with $n = 7$ there are $n^2 - n/2$ or 21 possible combinations ($n =$ number of chromosomes in the haploid complement); iii) the translocations should involve only two non-homologous chromosomes; and iv) translocation homozygotes are not accompanied with undesirable position effect on vigour and fertility. This communication describes a translocation tester set developed in pearl millet, *Pennisetum typhoides* (Burm.) S.&H. ($2n = 14$), from the study of meiotic configurations of the F_1 's of inter-translocation crosses. The tester set reported here meets all the requirements proposed above.

Materials and Methods

The material consisted of sixteen translocation stocks (RT-1, -2, -3, -7, -8, -9, -14, -15, -16, -17, -19, -20, -23, -24, -26, and RT-27), each involving two pairs of non-homologous chromosomes in the interchange. These interchanges have been induced through gamma-irradiation in BIL-4, an inbred line of pearl millet. Amongst these, RT-1, -2, -3, -7, -9, -23, -24 and -27 are homozygous for the interchanges (Minocha et al. 1980). The chromosomes involved in the different translocations were identified by examining the diakinesis/metaphase-I configurations in the F_1 's produced by inter-crossing the translocation stocks. If the PMC's in the F_1 of the inter-translocation cross showed two quadrivalents, the chromosomes involved in the two interchanges were different. The presence of a hexavalent in the F_1 indicated that one of the chromosomes involved in the two translocation stocks was common. The occurrence of seven bivalents in the F_1 of two homozygous translocations showed that the chromosomes and chromosome arms involved in the interchange of the two stocks were same. However, the formation of a quadrivalent in such crosses indicated the breakpoints in different arms of the same two chromosomes.

Results and Discussion

The chromosome configurations at diakinesis/meta-phase-I were studied in the F_1 's of the crosses involving sixteen interchanges (RT-1, -2, -3, -7, -8, -9, -14, -15, -16, -17, -19, -20, -23, -24, -26 and RT-27). Out of 120 possible combinations, meiotic configurations were analysed in 87 cross combinations (Table 1). On the basis of meiotic configurations, the parental interchanges were classified into three groups i) involving different chromosomes in the interchange, ii) interchanges with one of the translocated chromosome common and iii) interchanges with both chromosomes common, having breaks in the same or opposite arms of the chromosomes. The formation of seven bivalents in the F_1 of the two (homozygous) interchanges RT-1 \times RT-2 showed the interchanged chromosomes in these stocks to be common. The meiotic configuration of $\theta 4$ observed between the cross of the (homozygous) translocations RT-7 and RT-24 showed that the chromosomes involved in these interchanges are common but have breakpoints in different arms.

On the basis of chromosome configurations in 44 cross combinations, a tester set of 5 translocation stocks has been developed. However, the information on the remaining 43 combinations (marked as "a" in Table 1) is insufficient to draw any conclusion about the chromosome involved in the interchanges because some of the parental interchanges were heterozygous for the interchange. Meiotic configurations of $I_{IV} + 5_{II}$ and 7_{II} were observed in different plants obtained from the F_1 's where both the parental interchanges were heterozygous for the interchange. When one of the translocation stock was homozygous only a ring or chain of four chromosomes was observed in the limited number of plants analysed.

The seven chromosomes were designated by the letters 'a' to 'g'. The nucleolus organizer 'g' was identifiable at diakinesis from its association with the nucleolus. All the seven chromosomes were involved in one set of translocation stocks RT-2, -3, -7, -23. Similarly three sets of translocations i) RT-1, -3, -9, -23, ii) RT-2, -7, -23, -27 and iii) RT-17, -24, -26, -27 involved six of the seven chromosomes of the complement. Even though the above mentioned groups of translocation stocks involved all the seven chromosomes in the interchanges, they do not form a tester set.

For the establishment of a tester set, two translocation stocks were selected which involved any two chromosomes from a set of three chromosomes. RT-2 and RT-8 involved chromosomes a, b, d whereas RT-7 and RT-23 had chromosomes e, f, g involved in the interchange. RT-9 involved chromosomes b-e and these chromosomes were common with the interchanged chromosomes in the four translocation stocks (RT-2, -7, -8 and -23). RT-3 and RT-27 were helpful in the identification of chromosomes involved in all the above five translocation stocks. However, RT-3 and RT-27 are not essential in the translocation tester set as the chromosomes are identifiable from the remaining five translocations. The results of the intercross of these seven translocations are given in Table 2. Thus a translocation tester set comprising RT-2, -7, -8, -9 and -23 has been selected. With the nucleolar organizer chromosome involved in translocation RT-23 in the tester set, a total of five translocations can be used to identify any chromosome involved in an unknown translocation. This set meets all the basic requirements of a tester set given under 'Introduction'.

Using intercross method, translocation tester sets have been developed in barley (Burnham et al. 1954), pea (Lamm and Miravalle 1959), maize (Burnham 1962). Sybenga and

Table 1. Chromosome configurations in the F_1 's of different reciprocal translocation (RT) stocks

RT-1	-2	-3	-7	-8	-9	-14	-15	-16	-17	-19	-20	-23	-24	-26	-27
RT-1	711	2 θ 4	2 θ 4	a	θ 6	a	a	2 θ 4	-	-	2 θ 4	2 θ 4	-	-	θ 6
-2		2 θ 4	2 θ 4	θ 6	θ 6	a	2 θ 4	2 θ 4	-	-	2 θ 4	2 θ 4	-	a	θ 6
-3			2 θ 4	θ 6	2 θ 4	a	-	a	a	-	-	2 θ 4	-	a	θ 6
-7				2 θ 4	θ 6	a	-	a	a	a	-	θ 6	θ 4	a	2 θ 4
-8					θ 6	-	-	-	a	a	2 θ 4	2 θ 4	-	a	θ 6
-9						θ 6	-	a	a	-	-	θ 6	-	a	2 θ 4
-14							-	a	-	a	a	a	a	θ 6	-
-15								a	-	θ 6	-	-	-	-	-
-16									a	a	a	a	a	2 θ 4	-
-17										-	a	a	θ 6	2 θ 4	a
-19											a	a	a	a	a
-20												a	a	a	a
-23														2 θ 4	2 θ 4
-24														θ 6	2 θ 4
-26															2 θ 4

^a Ring of four chromosomes or 7 pairs or both

Table 2. Translocation tester set in pearl millet

	RT-2 (a-b)	RT-3 ^a (c-d)	RT-7 (e-f)	RT-8 (b-d)	RT-9 (b-e)	RT-23 (e-g)	RT-27 ^a (a-d)
RT-2 (a-b)		204	204	06	06	204	06
RT-3 (c-d)			204	06	204	204	06
RT-7 (e-f)				204	06	06	204
RT-8 (b-d)					06	204	06
RT-9 (b-e)						06	204
RT-23 (e-g)							204

^a Five translocations other than RT-3 and RT-27 form a complete translocation tester set (see text)

Wolters (1972) developed a translocation tester set in rye using mitotic chromosome measurements, and analysis of the meiotic F₁ configurations. Tyagi (1975) reported a tester set of five translocation stocks in pearl millet which to our knowledge has not been used for identification of unknown translocations and is not being maintained. Chromosomes involved in a translocation tester set of rye were identified by using Giemsa banding technique (de Vries and Sybenga 1976). Translocation tester sets have also been used to identify the trisomics (Tsuchiya 1961; Sybenga and Wolters 1972).

The translocation tester set developed in pearl millet would enable the identification of large number of translocation stocks with breakpoints at different positions on the chromosomes. Such a series would permit the correlation between linkage groups and chromosomes and in delimiting the loci more precisely to a particular segment of the chromosome. The series of translocation stocks with identified chromosomes could be further used to develop multiple interchange complexes for gametic selection. The possibilities of such stocks are being explored (Brar and Minocha 1982).

Acknowledgement

We thank Prof. J. Sybenga, Department of Genetics, Wageningen for critically going through the manuscript and making valuable suggestions.

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Received September 23, 1981
Accepted December 12, 1981
Communicated by H. F. Linskens

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