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Karyotype Analysis of Nainaiqingcai Mustard

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Abstract. Brassica juncea cv. Nainaiqingcai belongs to the mustard vegetables of the cruciferous family. It usually takes the leaves and petioles as the edible parts, and pickled pickle or fresh vegetable as the main way of eating, and occupies an important position in the local agricultural product market. In this research, seven chromosome parameters: chromosome length, relative length index, relative length, arm ratio, centromere index, and type of centromere type were measured. The experiment results showed that the maximum chromosome length was measured 3.60 μm and max arm ratio was determined 1.46, relative length ranged between 3.68% to 7.68%. There are including long (L), medium long (M2), medium short (M1) and short (S) chromosomes four types of relative length. In addition, the maximum centromeric index was measured in 45.66%, centromere type were metacentric (m) chromosomes and submetacentric chromosomes (sm) and the karyotype formula was 2n=36=30m+6sm. Karyotype asymmetry index was 59.631%. The karyotype characteristics was type 2B according to Stebbins's classification criteria. According to the above information, we can drawn a conclusion that 'Nainaiqingcai' is a relatively primitive mustard variety. In this research, the karyotypic characteristics of Nainaiqingcai mustard were revealed from the point of view of cytogenetics.

Key words: Brassica Juncea, Nainaiqingcai, Chromosome, Karyotype.

INTRODUCTION

Brassica juncea is an annual herb of cruciferae brassica annual herbaceous plant, which originated from spontaneous hybridization of the ancestors of B. rapa (AA, n=10) and B.nigra (BB, n=8)[1]. The variety 'Nainaiqingcai' belongs to the mustard vegetables of the cruciferous family. It usually takes the leaves and petioles as the edible parts. People usually pickle it to eat kimchi, but also eat it as fresh vegetable directly. Nainaiqingcai mustard is one of the local winter-spring vegetables in Bijie City, Guizhou Province, which has a large amount of consumption at the local. It is loved by local consumers and plays an important role in the adjustment of agricultural structure and the market of agricultural products in Bijie City. Karyotype analysis is a basic method to study chromosomes, it is a basic work in cytogenetics research. In this experiment, the karyotype analysis was carried out on the typical mustard variety 'Nainaiqingcai' to reveal its chromosome composition, and to provide the basis for determining the genetic composition of Nainaiqingcai mustard.

MATERIALS AND METHODS

Plant Materials

The representative Brassica juncea cv. Nainaiqingcai from Bijie City was used as experimental material.

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Chromosome Preparation

The seeds were soaked for 2 h, then cultured in dark in petri dishes with moist filter paper at 25 °C incubator to the root length of 1-1.5 cm and cut root tips of about 1 cm. Pretreated in 0.002 mol·L-1 8-hydroxyquinoline at 4 °C for 4h, and fixed in Carnoy's solution (acetic acid: absolute ethanol, 1:3, v/v) at 4 °C for 24 h, subsequently, the root tips were macerated in 1 mol·L-1 hydrochloric acid at 60 °C for 8 min, stained with Carbol Fuchsin, and observed under microscope[2].

Karyotype Analysis

Chromosome counts were performed on 30 well-spread metaphase chromosomes from five different root tips. Karyotype analysis referred to the standard of Li et al.[3]. Following parameters were calculated: chromosome relative length, arm ratio, type of chromosomes, index of chromosomes relative length and centromere index. karyotypic formula referred to the standard of Levan et al.[4], and the asymmetry coefficient of karyotypes was calculated by the method of Arano[5], the karyotypes were calculated according to Stebbins's standard[6].

RESULTS

Chromosome Number of Nainaiqingcai Mustard

Metaphase chromosomes and karyotype of Nainaiqingcai mustard root tips were shown in Fig. 1, detailed karyotype parameters of chromosome were listed in Table 1. The chromosome number of 'Nainaiqingcai' was 2n=36.

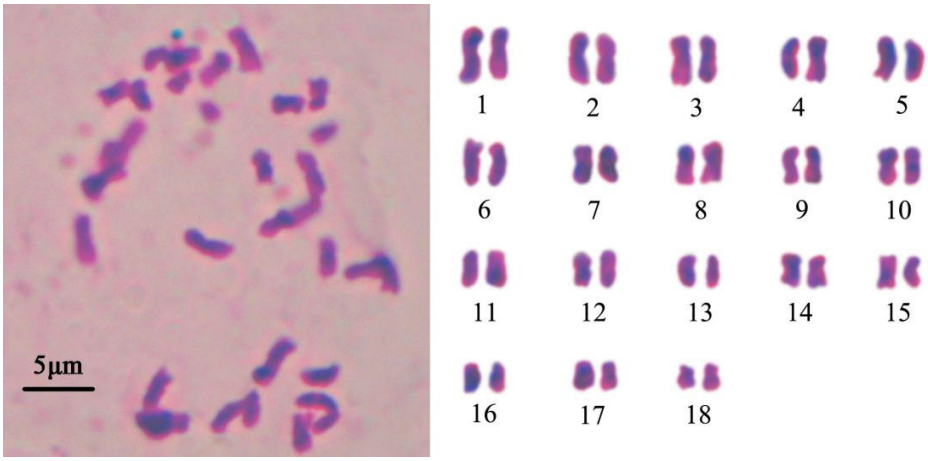

FIG 1. Metaphase chromosomes and karyotype of Nainaiqingcai mustard root tips

Note: The number 1-18 represent chromosome No.

Karyotype Analysis

Chromosome relative length ranged from 3.68% to 7.68%, and chromosome length ratio (longest chromosome / shortest chromosome) was 2.90. The chromosome types included long chromosomes (L), medium long chromosomes2 (M2), medium short chromosomes1 (M1) and short chromosome (S), the constitution of the relative length was 4L+14M2+16M1+2S. The centromeric index ranged from 25.63% to 45.66%, and arm ratio ranked from 1.16 to 2.90. There were only three pairs (the sixth, eleventh and thirteenth chromosome) of submetacentric chromosomes (sm), while the remaining fifteen pairs are all metacentric chromosomes (m). The karyotype formula was 2n=2x=36=30m+6sm. Karyotype asymmetry index was 59.631%, and karyotype characteristics fell into type 2B

according to Stebbins's classification criteria. The chromosome idiogram of Nainaiqingcai mustard were shown in Fig. 2.

TABLE 1. Karyotype parameters of chromosome of Nainaiqingcai mustard

Chromosome No.	Relative length / %			Index of relative length	Type of relative length	Arm ratio	Centromere index / %	Centromere type
	Short arm	Long arm	Total length					
1	3.12	4.56	7.68	1.38	L	1.46	40.65	m
2	3.35	4.04	7.39	1.33	L	1.20	45.37	m
3	2.63	4.29	6.92	1.25	M2	1.63	38.05	m
4	2.85	3.39	6.24	1.12	M2	1.19	45.66	m
5	2.50	3.72	6.22	1.12	M2	1.49	40.17	m
6	1.96	4.21	6.17	1.11	M2	2.15	31.77	sm
7	2.25	3.47	5.72	1.03	M2	1.54	39.40	m
8	2.34	3.35	5.69	1.02	M2	1.43	41.08	m
9	2.40	3.20	5.60	1.01	M2	1.34	42.80	m
10	2.22	3.11	5.33	0.96	M1	1.40	41.72	m
11	1.81	3.40	5.21	0.94	M1	1.88	34.66	sm
12	2.39	2.78	5.16	0.93	M1	1.16	46.20	m
13	1.89	2.94	4.83	0.87	M1	1.56	39.07	m
14	2.14	2.66	4.80	0.86	M1	1.25	44.54	m
15	2.06	2.63	4.69	0.84	M1	1.28	43.86	m
16	1.12	3.24	4.35	0.78	M1	2.90	25.63	sm
17	1.86	2.46	4.31	0.78	M1	1.32	43.05	m
18	1.50	2.19	3.68	0.66	S	1.46	40.64	m

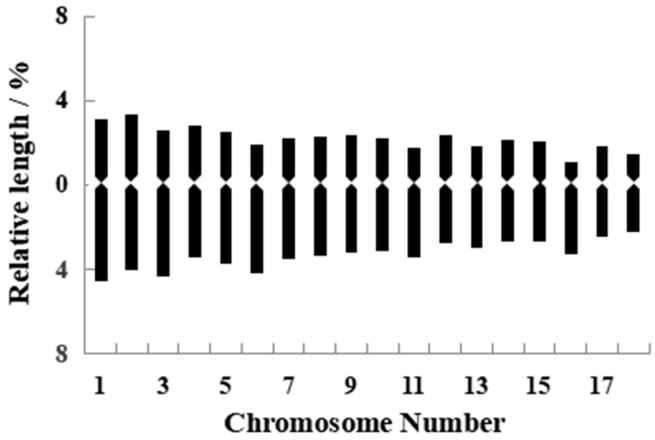

FIG 2. Chromosome idiogram of Nainaiqingcai mustard

SUMMARY

The results of karyotype analysis of Nainaiqingcai mustard were significantly different from those of mustard in other studies. For example, in this experiment, the number of chromosomes with satellites also varies, in this experiment, Nainaiqingcai mustard has no satellites, but some studies have shown two pairs or one pair of satellites or none in other varieties [7]. The karyotype formula of 'Nainaiqingcai' was 2n=2x=36=30m+6sm, chromosome types in this study were m-type and sm-type,no and st-type chromosomes were observed, but Tong et al. observed that its karyotype formula was 2n=2x=18m+12sm+6st or 2n=2x=14m+18sm+4st[8,9]. In terms of chromosome karyotype asymmetry index, the results of this experiment was more similar to Brassica juncea var. Cmssicauels (58.0%), and was far from the result of Brassica juncea var. Cress mustard (55.8%) and Brassica juncea var. Rugosa (66.33%). The basic evolutionary trend of plant karyotypes is from symmetry to asymmetry. Thus, primitive plants have symmetrical

karyotypes. And the more asymmetric the plant karyotype is, the higher its degree of evolution [6]. Therefore, 'Nainaiqingcai' should be a relatively primitive mustard variety in all mustard varieties.

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REFERENCES

1. Wang J.L., He Y., and Zhang Y.Q., et al. A study on origin, evolution and spread of Brassica in china. Zhongguo Nongxue Tongbao. Vol. 22 (2006) No. 8, p. 489-494
2. Wang X.R., Tang H.R., Duan J., et al. A comparative study on karyotypes of 28 taxa in Rubus sect. Idaeobatus and sect. Malachobatus (Rosaceae) from China. Journal of Systematics and Evolution, Vol. 46 (2008) No.4, p. 505-515.
3. Li M.X., and Chen R.Y. A suggestion on the standardization of karyotype analysis in plants. Journal of Wuhan Botanical Research. Vol. 3 (1985) No. 4, p. 297-302.
4. Levan A., Fradga K., and Sandberg A.A. Nomenclature for centromeric position on chromosomes. Hereditas. Vol. 52 (1964) No. 2, p. 201-220.
5. Arano H. The karyotypes and the speciations in subfamily Carduoideae (Compositae) of Japan. Japanese Journal of Botany. Vol. 19 (1965) No. 3, p. 31-67.
6. Stebbins G.L. Chromosomal evolution in higher plants. Edward Arnold Ltd. Press, London, 1971, p. 87-123.
7. Du W., Chen Q.X., and Mo H., et al. Study on somatic chromosome karyotypes of Xinjiang wild rape, B.Campestris, B.Nigra, and B.Juncea. Journal of August 1st Agri. College. Vol. 16 (1993) No. 4, p. 26-31.
8. Tong N.K. Observation on karyotype and chromosome behavior of different varieties of mustard. Journal of Southwest Agricultural University.Vol. 13 (1991) No. 3, p. 321-324
9. Fang P., Chen F.B., and Yao Q.L., et al. karyotype analysis on three types of leaf mustard (Brassica juncea). Journal of changjiang vegetables. Vol. 12 (2014), p. 13-17.