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Genomic Status of *Brassica tournefortii* Gouan

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Summary. The various 20-chromosome cross-compatible taxa of *Brassica* belonging to the *A* genome can be put, purely on a morphological basis, into three groups — oleiferous, rapiferous and leafy. *B. tournefortii*, another 20-chromosome species of *Brassica*, was crossed with a taxon of each of the above groups with the object of finding its genetic divergence on the basis of meiotic synapsis in the hybrids. All the hybrids were sterile. More bivalents (4 II) were noticed in the hybrid involving the oleiferous taxon than in the rapiferous or leafy ones (2 II). It is inferred, on the basis of genetic equivalence of hybrids dependent upon the pairing relationship in meiotic metaphase, that *B. tournefortii* is of later origin and has been evolved from the oleiferous group. A new genome, *D*, has been assigned to *B. tournefortii* to distinguish it from the other *A* genome taxa of *Brassica* because of the low cross-compatibility, hybrid sterility and very little gene flow between the hybrids.

Introduction

The different cross-compatible 20-chromosome species of *Brassica* belonging to the *A* genome can be broadly classified into three groups purely on a morphological basis-oleiferous, rapiferous and leafy. Another 20-chromosome species of *Brassica*, *Brassica tournefortii* Gouan, occurring wild, has been reported by Olsson (1954) to be cross-incompatible with the leafy and oleiferous groups and, therefore, was assigned a separate species status. In this paper, the genomic homology between *B. tournefortii* and the three groups of 20-chromosome species of *Brassica* is assessed to find whether *B. tournefortii* is sufficiently cytogenetically different to constitute a separate genome of its own.

Material and Methods

Crosses were made between a single representative (*B. campestris* ssp. *oleifera* var. yellow searson, *B. campestris* ssp. *rapifera* and *B. campestris* ssp. *narinosa*) from each of the three groups, oleiferous, rapiferous and leafy, which form the cross-compatible 20-chromosome *A* genome complex and *B. tournefortii* (Fig. 1) in 1965–66. The F_1 hybrids of these crosses were raised and cytomorphologically confirmed. Anthers were fixed in aceto-alcohol (1:3) and squashed in acetocarmine.

Results and Discussion

Cross-compatibility relationship

It is clear from Table 1 that the cross-compatibility between the representatives of the oleiferous, rapiferous and leafy groups of *A* genome and *B. tournefortii* is very low and that more crossed seeds and hybrids were obtained with the oleiferous representative than with the other two.

Meiotic behaviour

All three interspecific hybrids, *B. campestris* ssp. *oleifera* var. yellow sarson × *B. tournefortii.*, *B. campestris* ssp. *rapifera* × *B. tournefortii* and *B. campestris* ssp. *narinosa* × *B. tournefortii*, were completely sterile and had greatly reduced chromosome pairing at meiosis. Their reduction division was generally characterized by the predominance of p.m. c's with 20 unpaired chromosomes. They differed markedly from one another in the number of chromosomes showing meiotic synapsis. Ssp. *narinosa* × *B. tournefortii* and ssp. *rapifera* × *B. tournefortii*

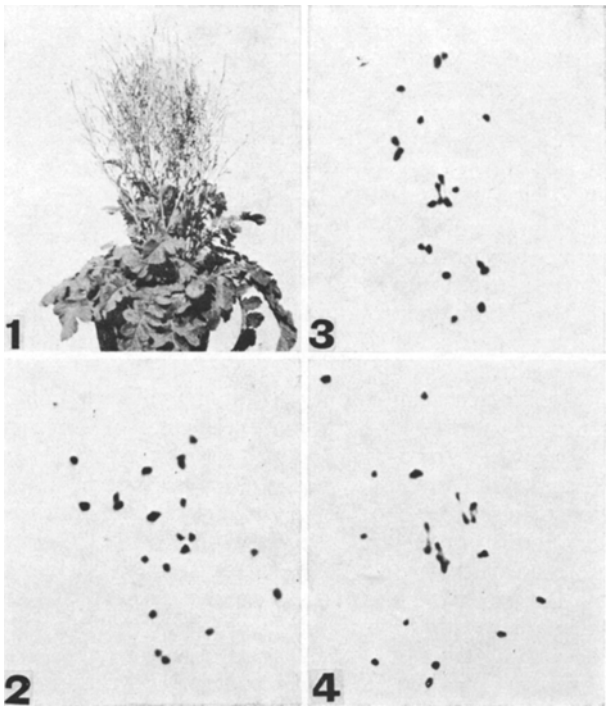

Fig. 1. Plant of *Brassica tournefortii*

Fig. 2. Metaphase I of the hybrid *B. campestris* ssp. *narinosa* × *B. tournefortii* — 20 I

Fig. 3. Metaphase I of the hybrid *B. campestris* ssp. *rapifera* × *B. tournefortii* — 2 II + 16 I

Fig. 4. Metaphase I of the hybrid *B. campestris* ssp. *oleifera* var. yellow sarson × *B. tournefortii* — 4 II + 12 I

Table 1. *Showing the results of crosses between different 20-chromosome A genome species of Brassica and B. tournefortii*

Cross	No. of flowers pollinated	No. of seeds obtained	No. of seeds sown	No. of matromorphic plants	No. of hybrid plants	Hybrid percentage
B. campestris ssp. *oleifera* var. yellow sarson × *B. tournefortii*	2143	248	248	222	31	12.5
B. campestris ssp. *narinosa* × *B. tournefortii*	2191	132	132	121	11	8.3
B. campestris ssp. *rapifera* × *B. tournefortii*	2407	292	292	271	23	7.8

Table 2. *Showing chromosome association at metaphase I in the hybrids of A genome species of Brassica and B. tournefortii*

Cross	Configuration	No. of cells	Percentage
B. campestris ssp. *oleifera* var. yellow sarson × *B. tournefortii*	4 II + 12 I	9	7.5
	3 II + 14 I	11	9.1
	2 II + 16 I	13	10.8
	1 II + 18 I	24	20.0
	20 I	63	52.6
B. campestris ssp. *narinosa* × *B. tournefortii*	2 II + 16 I	4	3.3
	1 II + 18 I	17	14.1
	20 I	99	82.5
B. campestris ssp. *rapifera* × *B. tournefortii*	2 II + 16 I	14	11.6
	1 II + 18 I	20	16.6
	20 I	86	71.7

showed less meiotic chromosome pairing, whereas ssp. *oleifera* var. yellow sarson × *B. tournefortii* had the maximum number of such chromosome associations (Table 2, Figs. 2—4). The univalents in these hybrids as usual were found to divide at metaphase I. They usually lagged while the bivalents disjoined and moved to the opposite poles. Subsequent stages of division were marked by a high degree of irregularity which led to the complete breakdown of the meiotic process and the formation of non-viable empty pollen grains. None of the hybrids produced any seeds.

Much of the confusion in the nomenclature of the cross-compatible 20-chromosome species of *Brassica* has been removed by Olsson (1954) by lumping the various taxa into one species, *B. campestris*. These taxa were earlier considered by various authors to be taxonomically separate species. The other 20-chromosome wild species, *B. tournefortii*, was considered by Olsson to be a separate species because it was morphologically distinct and cross-incompatible with the various taxa of the leafy and oleiferous groups of *B. campestris*. He did not obtain any hybrid seed by crossing the above taxa with the wild species. Also, the rapiferous group was not included in his crossing programme with the wild species.

In the present investigation, a representative taxon of all the three groups, oleiferous, rapiferous and leafy, from among the compatible 20-chromosome *A* genome species has been included in the crosses with the wild species *B. tournefourtii* to determine the crossability relationship. Also, their F_1 hybrids were obtained and the genomic relationship studied on the basis of their meiotic pairing.

It may be concluded, purely on the basis of low cross-compatibility, hybrid sterility and very little gene flow between *B. tournefortii* and the *A* genome species, that the genome of *B. tournefortii* has developed a strong genetical barrier in its genetic system, is quite different from that of *A*, and can be designated as *D* genome (Narain and Prakash, 1968).

Judging by the crossability relationships among the various taxa of *A* genome with *B. tournefortii*, *B. tournefortii* is more closely related to the oleiferous than to the rapiferous and leafy subspecies. The relationship is even extended to the meiotic synapsis of their F_1 hybrids. More bivalents were found (4 II) in the oleiferous × *B. tournefortii* hybrid than in the rapiferous or leafy hybrids. Further evidence supporting this, although beyond the scope of the present investigation, has been found in the meiotic behaviour of their F_1 hybrids with *Brassica nigra* (Narain and Prakash, 1970) which represents phylogenetically the lowest number in the species. This throws light on the assumption that *B. tournefortii* is of later origin and might have arisen from the oleiferous group.

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