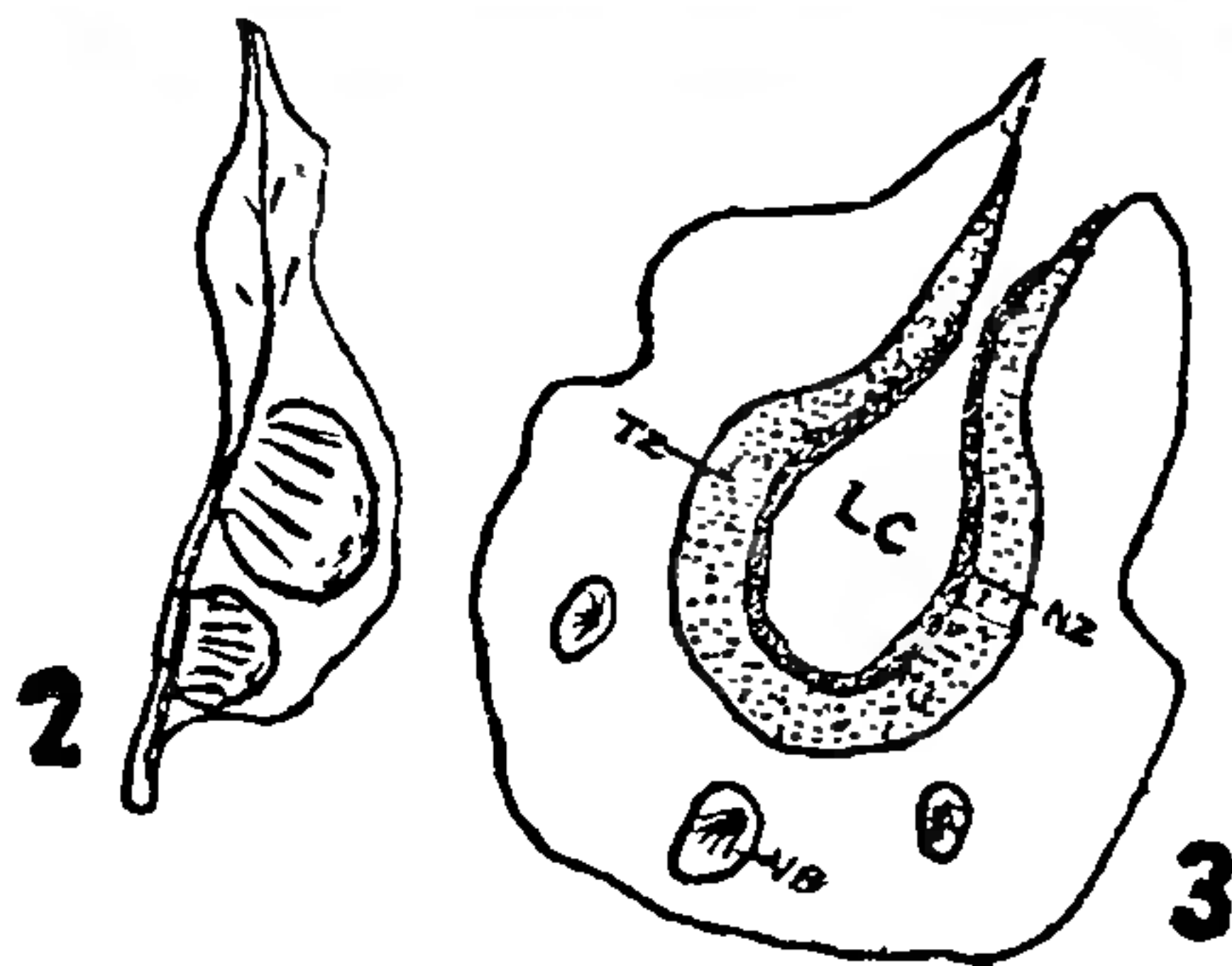


been known as roll galls³ and pit galls⁴. Histology of mature galls of *Symplocos* presents a cecidogenetic picture⁵ involving the inhibition of development and normal differentiation, phenomenon of hypertrophy and adaptive phenomena of the development of nutritive zone and vascular irrigation.



FIGS. 1-3. Fig. 1. Galls of *Symplocos spicata* by *Trioza* sp; Fig. 2. One leaf showing the agglomeration of galls along the midrib regions ($\times 2$); Fig. 3. Transverse section of the gall ($\times 12$). (TZ, Tanniferous zone; LC, Larval chamber; NZ, Nutritive zone; VB, Vascular bundle.)

Further work on the developmental anatomy of the galls is in progress.

Grateful thanks are due to Professor T. N. Ananthakrishnan (Loyola College, Madras) for guidance and encouragement. A. R. thanks the U.G.C. for the grant of Teacher Assistance.

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BASIC CHROMOSOME NUMBER AND THE PROBABLE ORIGIN OF THE GENOMES IN *BRASSICA*

Introduction

THE prevalence of aneuploidy of $n = 8, 9, 10, 11, 12, 17, 18, 19$ and 24 in the different species of the genus *Brassica* made this an interesting material for determining the basic chromosome number. The previous literature on meiotic chromosome pairing in haploid *B. campestris* L. var. *toria*⁷ ($n = 10$) and *B. oleracea*^{1,2} ($n = 9$) suggests that the basic chromosome number in this genus is less than the lowest chromosome number $n = 8$ seen in *B. nigra*. Secondary association at meiosis has been observed by several workers in the different *Brassica* species and the basic chromosome number is deduced basing on the maximum number of groups of secondarily associated bivalents at metaphase-I. The exact number reported by the different workers differed to a great extent. Alam¹ and Catcheside^{2,3} found it to be 7, while Sikka¹⁰ found it to be 5. Röbbelen⁹ identified six morphological groups of chromosomes at pachytene in the three genomes 'a', 'b' and 'c' and considered the basic chromosome number to be six. He identified the duplicate sets of chromosomes at pachytene in the three genomes on the basis of secondary association at pachytene in some interspecific F_1 'aac' hybrids.

Stebbins¹¹ considered that secondary association can be utilised for understanding the ancient polyploid nature of a species or a genus, but it may be considerably modified by segmental interchange, duplication of chromosome segments and phenomena not related to polyploidy and as such is not to be considered as a reliable index of the exact basic chromosome number. Although the evidence from somatic chromosomes can be considered useful to some extent, in *Brassica*,

because of their small size, even the position of the centromere could not be located with any confidence, and as such even when banding techniques were applied recognizable bands may not be observed. In view of these considerations, evidence from somatic chromosomes and secondary association at diakinesis are not considered to be decisive enough to determine the basic chromosome number.

Since the study of chromosomes at pachytene facilitates observations of even minor structural differences of the chromosomes, the evidence obtained from pachytene morphology is considered here. From the investigations made here on the morphology of pachytene chromosomes in four diploid *Brassica* species,¹³ and their pairing in three interspecific F_1 hybrids^{4,5} and two intergeneric F_1 *Raphanobrassica* hybrids an attempt is made to determine the basic chromosome number and to decide the nature of the 'a', 'b' and 'c' genomes of *Brassica*.

Results and Discussion

The pachytene chromosomes in the four diploid *Brassica* species¹³ could be sorted out into six morphological types designated as A, B, C, D, E and F in the three genomes 'a', 'b' and 'c' of *Brassica* belonging to the species *B. campestris* ($n = 10$), *B. nigra* ($n = 8$) and *B. oleracea* ($n = 9$) respectively. The frequency of the types differed in each of the three genomes and some of the types in some genomes were missing in the others. Chromosomes with the same morphology and recognised under the same type such as B, C, E or F paired with each other forming bivalents and occasional trivalents and quadrivalents at pachytene, diakinesis and metaphase, in the three interspecific F_1 'aac' hybrids,⁴ and two intergeneric F_1 *Raphanobrassica* hybrids with 'abr' ($2n = 27$) and 'acr' ($2n = 28$) genomes (in press) proving their genetic homologies. From these findings the basic chromosome number for *Brassica* is considered to be $x = 6$, a conclusion which is in agreement with that of the previous workers^{1-3,6,9}.

Two morphologically distinct nucleolus organising chromosomes were present in each of the three genomes 'a', 'b' and 'c' which did not pair with each other in the F_1 hybrids studied.⁵⁻¹³ A numerical correspondence in the number of nucleolus organising chromosomes has been observed in the pachytene complements of the four diploid *Brassica* species studied. The species *B. juncea* var. *gracilis* ($n = 18$, 'ab') and *B. napus* var. *oleifera* ($n = 19$, 'ac') contained four nucleolus organising chromosomes each, two of which belonged to the 'a' genome while the other two in each of the latter species belonged to the 'b' and 'c' genomes respectively¹³. Based on the

numerical correspondence in the nucleolus organising chromosomes in the diploid species and their synaptic relationships in the interspecific F_1 'aac' hybrids^{4,5} combined with the finding of the presence of six morphological types of chromosomes, the genomes 'a', 'b' and 'c' are considered as segmental allotetraploids probably obtained after doubling in the genome from an F_1 hybrid which might have arisen from two ancestral parents with a basic chromosome number of $x = 6$, and the species *B. carinata* ($2n = 34$), *B. juncea* ($2n = 36$) and *B. napus* ($2n = 38$) are considered as allo-octoploid hybrids.

A comparative study of the pachytene chromosomes of the 'a', 'b' and 'c' genomes shows that some of the types of chromosomes present in the genome 'a' are missing in the 'b' and 'c' genomes and some are present in different numbers in the three genomes. It appears from this that the actual parent that contributed to the 'a' genome differs from that which gave rise to the 'b' and 'c' genomes in terms of some translocations and other structural alterations.

My thanks to Prof. J. Venkateswarlu for guidance throughout the conduct of this work.

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Waltair 530 003 (A.P.), October 17, 1977.

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ACANTHOCORIS SCABRATOR FABR. A NEW PEST OF MANGO

Acanthocoris scabrator. Fabr. (Hemiptera—Coreidae) was observed for the first time as a pest of mango fruits in India. It was seen infesting mango fruits at Trivandrum in September, 1976. Letroy has recorded its occurrence in India¹. Previous records of this