

# Evidence of Tetrasomic Inheritance in *Beta corolliflora*

**S. M. Reamon-Büttner and G. Wricke**

*Institute of Applied Genetics*

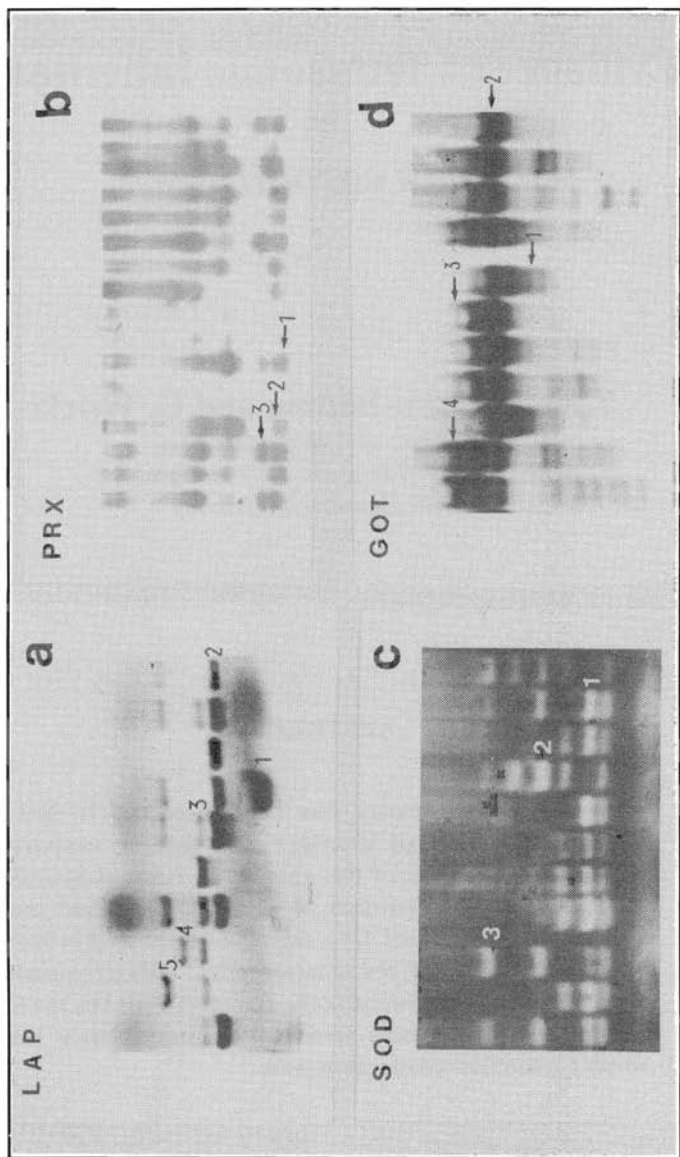
*University of Hannover, Herrenhäuser Str. 2*

*30419 Hannover, Germany*

## ABSTRACT

Tetrasomic inheritance has been detected in *Beta corolliflora* by use of isozymes; this finding supports autotetraploid origin of this species. In triploid hybrids consisting of two genomes of *B. corolliflora* and one genome of *B. vulgaris* (CCV), segregation at *Lap-1* in both species could be analyzed separately. Not only tetrasomic segregation has been found in the gametes formed by the *B. corolliflora* plant which served as the male parent but double reduction products as well.

**Additional Key Words:** wild beet, Corollinae, isozymes, auto-tetraploidy, double reduction



**Figure 1.** The alleles observed at *Lap-1*, *Sod-3* and *Got-3* in *B. corolliflora*.

The wild beet *Beta corolliflora* Zoss. ex Buttler is one of the three species in section Corollinae. The other species are *B. lomatogona* F. et M. and *B. macrorrhiza* Stev. *B. corolliflora* is a tetraploid ( $2n=4x=36$ ) and presumably an autotetraploid (Zossimovich, 1939). It is sexual but with exceptionally rare traces of apomictic tendencies (Jassem and Jassem, 1970). *B. corolliflora* has also been reported to be resistant to curly top virus (Beta Virus 1), mosaic virus (Beta Virus 2) and *Polymyxa betae* (Van Geyt et al., 1990).

Tetrasomic inheritance is an important characteristic of autotetraploid species. Through use of isozymes, it has been demonstrated in tetraploid crop species such as potato (Quiros and McHale, 1985) and alfalfa (Quiros, 1982) as well as in naturally occurring tetraploid species in Saxifragaceae (Soltis and Soltis, 1989; Wolf et al., 1989). If *B. corolliflora* is an autotetraploid, then it would also be expected to exhibit tetrasomic inheritance.

## MATERIALS AND METHODS

The *B. corolliflora* seeds were obtained from the Beta Gene Bank, Braunschweig, Germany and the Institute of Plant Breeding and Acclimatization, Bydgoszcz, Poland. About 460 plants from 10 accessions were used for the isozyme analysis.

Hybrids between *B. corolliflora* ( $4x=36$ , BGRC 035314, Transcaucasian) and *B. vulgaris* (CMS,  $2x=18$ ) were also used as material for the detection of tetrasomic segregation in *B. corolliflora*. The hybrids were triploid ( $3x=27$ ) with two chromosome sets from *B. corolliflora* and one from *B. vulgaris* or a genome composition of CCV. They had intermediate morphology between the two species.

Four enzyme systems, namely leucine aminopeptidase (LAP), peroxidase (PRX), superoxide dismutase (SOD), and glutamate oxaloacetate (GOT) were used. The electrophoretic conditions and staining procedures were described elsewhere (Reamon-Ramos and Wricke, 1992). To determine the genotypes in *B. corolliflora*, it was assumed that each individual possessed four genes at each locus. It was also assumed that banding intensity reflected allelic dosage.

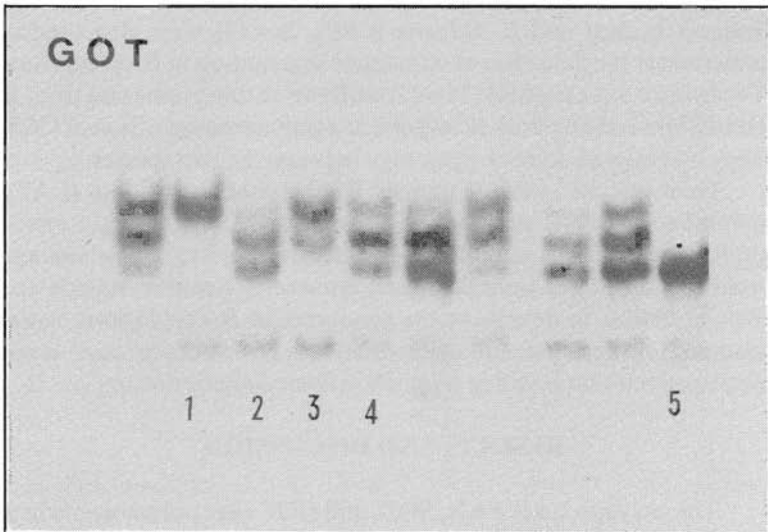
## RESULTS AND DISCUSSION

The enzymes LAP, PRX, SOD, and GOT were polymorphic in at least one locus in the different *B. corolliflora* accessions. *Lap-1* is a monomer and a total of five alleles were found (Figure 1a). *Prx-1*, which is also a monomer, was observed at the most cathodal zone.

Three alleles have been identified (Figure 1b). *Sod-3* and *Got-3*, the slowest migrating zones in these enzymes, exhibited three (Figure 1c) and four alleles (Figure 1d), respectively. Both are dimeric enzymes.

The presence of balanced (symmetric) and unbalanced (asymmetric) heterozygotes was evident particularly at *Sod-3* and *Got-3*. For example, at *Got-3* of an accession segregating for numbers 2 and 4 alleles, aside from the two types of homozygotes, three types of heterozygotes were observed: 2244 (symmetric), 2224 and 2444 (asymmetric) (Figure 2). The occurrence of three types of heterozygotes is in agreement with the expectation for an autopolyloid species segregating in a locus with two alleles. Unbalanced heterozygotes were not observed in the diploid species *B. lomatogona* which contained similar number of alleles at *Sod-3* and *Got-3*. Further, many plants in the populations investigated were found to contain more than two different kinds of alleles at *Sod-3*, *Got-3* and *Prx-1* which could only be accounted to tetrasomic inheritance.

In the hybrids between *B. corolliflora* and *B. vulgaris*, it was possible to observe directly the meiotic products of *B. corolliflora*. At *Lap-1* in the hybrids, the two bands of *B. vulgaris* migrated faster than that of *B. corolliflora*. Thus, the segregations in each species could be

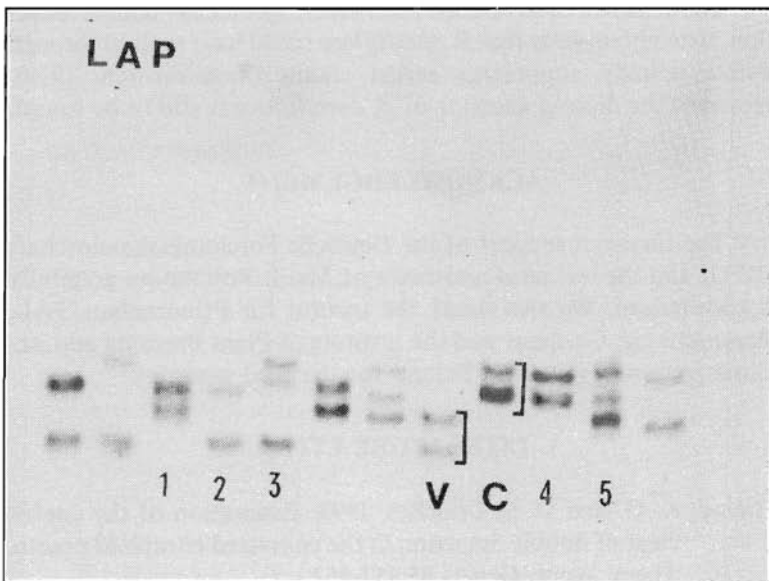


**Figure 2.** The two kinds of homozygotes and the three kinds of heterozygotes at *Got-3* of *B. corolliflora* segregating for two alleles.

scored separately (Figure 3). The putative genotype of the *B. corolliflora* used as pollen donor was *Lap-1-3445* and the segregation found in 24 hybrids is shown in Table 1.

Assuming tetrasomic segregation without crossing-over between the locus and the centromere (chromosome segregation), the genotypes *Lap-1-34*, *35*, *45* and *44* are expected from the gametes of a *B. corolliflora* plant with genotype *Lap-1-3445*. But the additional presence of genotypes *Lap-1-33* and *55* in the gametes of a plant which contained only single doses of these alleles suggests that double reduction must have occurred. In order to have an expected frequency of at least five in every class (Snedecor and Cochran, 1980), the chi-square test was performed putting all homozygous and heterozygous plants each in one class. Under the assumption of random chromatid segregation, the chi-square value was not significant (Table 1).

Double reduction results in two sister chromatids being recovered in a single gamete. A prerequisite to double reduction is multivalent pairing with a cross-over between a locus and its centromere followed by the two pairs of chromatids passing to the same pole in anaphase I (adjacent segregation). Therefore, detection of double reduction in the gametes of an asymmetrical heterozygote is an unequivocal evidence



**Figure 3.** LAP segregation in the hybrids between *B. corolliflora* (C) and *B. vulgaris* (V). Five of the six genotypes found in *B. corolliflora* are shown: (1) 34, (2) 33, (3) 45, (4) 35, and (5) 55.

**Table 1.** Segregation found in the meiotic products of a *B. corolliflora* plant with putative genotype *Lap-1-3445*. Expected values under random chromatid segregation.

Lap-1-	GENOTYPES		NUMBER OF PLANTS	
			Observed	Expected
	33		2	
	44		3	8
	55		3	6.85
	45		6	
	34		6	16
	35		4	17.15
	Total		24	24.00
				$\chi^2 = 0.16$ ns

of quadrivalent formation, followed by crossing-over and tetrasomic segregation as were also found in *Hyla versicolor* (Marsden et al., 1987) and potato (Haynes and Douches, 1993). Cytological study of the *B. corolliflora* male parent revealed two to three quadrivalents per cell which is in support of tetrasomic inheritance.

The detection of tetrasomic inheritance, specifically double reduction, strongly suggests that *B. corolliflora* could have evolved through autotetraploidy, supporting earlier claims (Zossimovitch, 1939). However, the diploid ancestor of *B. corolliflora* is still to be found.

### ACKNOWLEDGEMENT

The financial support of the Deutsche Forschungsgemeinschaft (DFG) and the technical assistance of Ms. I. Robota are gratefully acknowledged. We also thank the Institut für Pflanzenbau, FAL, Braunschweig, Germany and the Institute of Plant Breeding and Acclimatization, Bydgoszcz, Poland for the seed material.

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