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V. M. Samoylov · S. Izhar · K. C. Sink

Donor chromosome elimination and organelle composition of asymmetric somatic hybrid plants between an interspecific tomato hybrid and eggplant

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Abstract Morphology, the extent of elimination of donor chromosomes and the organelle composition of highly asymmetric somatic hybrid plants between a interspecific tomato hybrid *Lycopersicon esculentum* × *L. pennellii* (EP) as donor and a *Solanum melongena*, eggplant (E), recipient, were studied. Morphologically, the somatic hybrids most resemble eggplant but, due to polyploidy, growth is slower relative to both fusion parents. The somatic hybrids produce flowers that are characterized by abnormal styles, stigmas and by anthers which do not produce pollen. Limited amounts of donor EP genomic DNA were found in the three somatic hybrid plants (H18-1, H18-2 and H18-3), by dot-blot hybridization with probe pTHG2, equivalent to 6.23, 5.41, and 5.95% EP, respectively. These percentages translated to the presence of 3.59, 2.90 and 3.19 average-size EP chromosomes in plants H18-1, -2 and -3, respectively. RFLP determination of *L. esculentum*- and *L. pennellii*-specific chromosomes revealed that only fragments of eight to ten out of the 24 EP chromosomes (EP has 12 *L. esculentum* and 12 *L. pennellii* chromosomes) are present in the asymmetric somatic hybrid plants. Loci of *L. esculentum* and *L. pennellii* were evenly represented in plants H18-1, -2, and -3: four to five from *L. esculentum* and four to five from *L. pennellii*. All somatic hybrid plants retained locus TG22, chromosome 4, from both EP species. Although the regeneration of plants, H18-1, -2 and -3 was from one callus, loci TG31 and TG79 of *L. esculentum* chromosome 2 and *L. pennellii* chromosome 9, respectively, were missing in hybrid plant H18-1. The three somatic hybrid plants all had chloroplast DNA fragments specific for *S. melongena*. The mitochondrial genome (mtDNA) in the asymmetric somatic hybrids showed predominantly the pattern of eggplant; however, some eggplant-specific polymorphic bands were not present in the three plants.

Key words Eggplant · Tomato · Asymmetric somatic hybrids · Dot-blot hybridization · RFLP

Introduction

Asymmetric somatic hybridization is a means of increasing genetic variability not only by overcoming sexual incompatibility between species, but also by combining the nuclear, chloroplast and mitochondria genomes in new patterns.

Elimination of donor chromosomes, in order to create asymmetric somatic hybrids, is commonly achieved by irradiation treatment of donor protoplasts (Dudits et al. 1980). To-date, asymmetric somatic hybrid plants have been obtained in many combinations of species (Gleba and Shlumukov 1990). A correlation between the dose of irradiation and the degree of elimination of the donor genome in intrageneric combinations has been demonstrated (Melzer and O'Connell 1992; Kovtun et al. 1993; Trick et al. 1994). Conversely, in intergeneric fusion combinations the irradiation dose seems of minor importance in controlling the elimination of donor chromosomes and the ultimate genome composition of regenerated hybrid plants (Gleba et al. 1988; Wolters et al. 1991; Spangenberg et al. 1994). Even though the parental chromosomes may be maintained for a long time in intergeneric somatic hybrid calli and plants, ones containing only one or a few donor chromosomes (Dudits et al. 1987; Hinnisdaels et al. 1991; Babiychuk et al. 1992) have seldom been reported.

In contrast to the array of recombinations that occur between the two nuclear genomes, the heteroplasmic state of somatic hybrid cells and plants almost always quickly sort-out leading to uniparental transmission of the chloroplast DNAs (cpDNA). By contrast, the mitochondrial ge-

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V. M. Samoylov · K. C. Sink (✉)
Department of Horticulture, Michigan State University, East Lansing, MI 48824-1325, USA

S. Izhar
Institute of Field and Garden Crops, Volcani Center, Agricultural Research Organization, Bet-Dagan 50250, Israel

nomes (mtDNA) often undergo rearrangement and novel types of mtDNA in somatic hybrids are frequently observed (Belliard et al. 1978; Rothenberg et al. 1985). However, it is not clear whether transmission of cpDNA and mtDNA types in intergeneric somatic hybrids is correlated with the nuclear composition of intergeneric somatic hybrids (Wolters et al. 1993) or is dependent on other factors (Wolters et al. 1995).

The genus *Lycopersicon* is a well documented resource of valuable agronomic traits. Recently, we reported on the production and analysis of asymmetric somatic hybrid calli between *Lycopersicon esculentum* × *L. pennellii* (+) *Solanum melongena* and suggested a hypothesis to explain the elimination of the donor genome in such intergeneric fusions (Samoylov and Sink 1996). In the present paper, the morphology, degree of donor chromosome elimination and organelle composition of the three highly asymmetric somatic hybrid plants that were regenerated is presented. The phenomenon of frequent polyploidization of the recipient genome in asymmetric somatic fusion experiments (Gleba et al. 1988; Wijbrandi et al. 1990a; McCabe et al. 1993; Puite and Schaart 1993) in regard to our hypothesis is also discussed.

Materials and methods

Plant materials

Seeds of *S. melongena* L. (line 410, 2n=2x=24) were used. Kanamycin-resistant (KmR^+) plant A54 of the sexual hybrid *L. esculentum* Mill. × *L. pennellii* L. (2n=2x=24), herein EP, was provided by Dr. R. Jorgensen, DNAP, Oakland, California. EP has a T-DNA insert mapped to *L. esculentum* chromosome 12 (Chyi et al. 1986). Seeds of *L. esculentum* (cv VF36, 2n=2x=24) and *L. pennellii* (cv LA716, 2n=2x=24) were provided by Dr. C.M. Rick, Tomato Genetics Resource Center, University of California. Three intergeneric asymmetric somatic hybrid plants, H18-1, H18-2 and H18-3, were obtained by PEG/DMSO fusion of gamma-irradiated mesophyll protoplasts of a KmR^+ interspecific hybrid EP with mesophyll protoplasts of the eggplant, *Solanum melongena* (Samoylov and Sink 1996).

DNA extraction

DNA was isolated from plants growing in a greenhouse and the concentrations were measured spectrophotometrically (Doyle and Doyle 1990).

Dot-blot and Southern analysis

For dot-blot analysis serial dilutions (0–275 ng/dot) of genomic DNA from plants of *L. esculentum* × *L. pennellii* (EP) and *S. melongena*, along with 275 ng (in triplicate) of DNA from each hybrid plant, were placed on Hybond-N (Amersham) nylon membrane according to the directions of the Schleicher and Schuell Minifold Apparatus (Keene, USA).

For Southern analysis of genomic and mtDNA, approximately 5 µg of total DNA was digested with 40 U of restriction enzyme (*Dra*I, *Eco*RI, *Eco*RV, *Hin*dIII) for 16 h. For Southern hybridization of cpDNA, 300 ng of genomic DNA was digested with 3 U of the restriction enzyme *Hin*dIII for 16 h.

Fragments were separated by electrophoresis for 16 h on 0.9% agarose gels in TAE buffer. DNA was transferred to Hybond-N^+ (Amersham) nylon membranes and Southern hybridizations were performed as described by Sambrook et al. (1989).

Probes

The relative amount of EP nuclear DNA in the somatic hybrid plants was quantified with a tomato species-specific repetitive DNA probe, pTHG2 (Zabel et al. 1985), provided by Dr. P. Zabel, Wageningen Agricultural University, The Netherlands.

The following 31 tomato genomic clones were used to analyze the composition of *L. esculentum*- and *L. pennellii*-specific chromosomes in asymmetric somatic hybrid plants: chromosome 1, TG24, TG83 and TG53; chromosome 2, TG31 and TG48; chromosome 3, TG130, TG152 and TG94; chromosome 4, TG123, TG95 and TG22; chromosome 5, TG96, TG23 and TG69; chromosome 6, TG118, TG73 and TG115; chromosome 7, TG20 and TG128; chromosome 8, TG45 and TG16; chromosome 9, TG18, TG79 and TG35; chromosome 10, TG43 and TG63; chromosome 11, TG47 and TG30; chromosome 12, TG68, TG111 and TG28 (Tanksley et al. 1992). The TG clones were provided by Dr. S. Tanksley, Cornell University. The mapped positions of the clones used in the analyses are shown in Fig. 3.

The 21.9-kb tomato chloroplast *Pst*I fragment (P-2) was used for cpDNA analysis (Phillips 1985). The mtDNA was probed using pZmE1, a 2.4-kb *Eco*RI fragment encoding corn cytochrome c oxidase subunit II (Fox and Leaver 1981), provided by Dr. B.B. Sears, MSU.

Probes were labeled with ^{32}P using the Random Primer DNA Kit (Gibco, BRL). Hybridizations were visualized and quantified by using the Molecular Dynamics PhosphorImager (Sunnyvale, USA) with a Zeos computer system running Molecular Dynamics ImageQuant (v. 33) software. Filters were exposed to Kodak X-OMAT film for documentation.

Results

Regeneration and morphology

A total of 208 KmR^+ calli were selected following PEG/DMSO fusion from all γ-irradiation levels (100, 250, 500, 750 and 1000 Gy; 123, 9, 6, 53 and 17 calli, respectively) on donor protoplasts of EP (+) eggplant. The 30 selected calli were confirmed as hybrids by PCR amplification of the *Npt*II gene, RAPD patterns and Southern hybridizations (Samoylov and Sink 1996). Only callus H18, selected from the 100-Gy irradiation after 12 months in culture, regenerated a few multiple shoots among which three, H18-1, H18-2 and H18-3, taken from independent sites, were removed, rooted and transferred to the greenhouse. Somatic hybrid calli selected from all other irradiated donor-recipient combinations have not regenerated shoots after 2 years.

Morphologically, the hybrid plants resemble eggplant but growth is slower relative to the fusion parents. Leaf shape and morphology of the hybrid plants closely resemble that of eggplant (Fig. 1A). After 8-months growth in a greenhouse the three somatic hybrids flowered. Eggplant has dark purple flowers composed of five fused petals with five anthers per flower. Flowers of EP have five yellow separate petals and five anthers. The somatic hybrids produce dark purple flowers, but each is usually composed of six separate petals and six anthers (Fig. 1B). Most hybrid

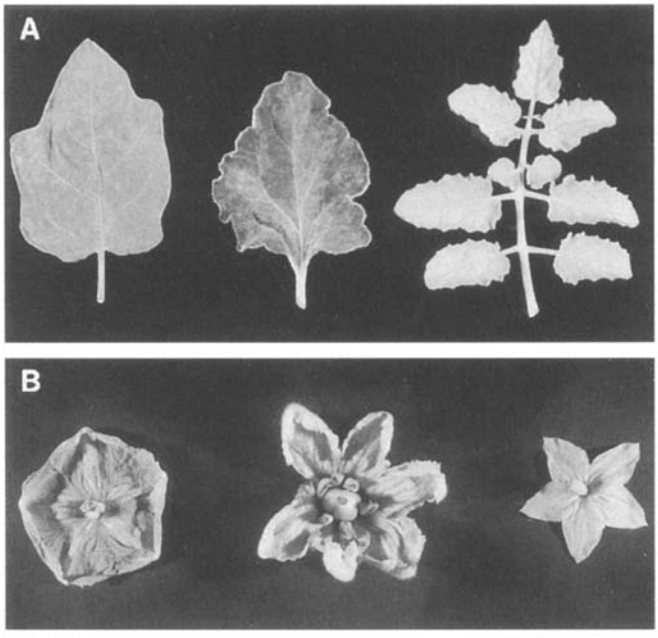

Fig. 1 Leaves (**A**) and flowers (**B**) of *S. melongena* (left), somatic hybrid H18-1 (center) and *L. esculentum* × *L. pennellii* (EP)

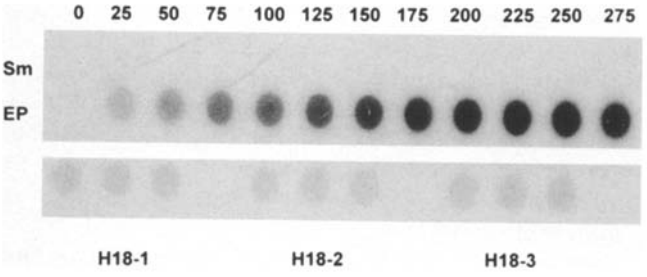

Fig. 2 Dot-blot hybridization of genomic DNAs with tomato species-specific probe pTHG2: *Sm=S. melongena*, *EP=L. esculentum* × *L. pennellii* and somatic hybrid plants H18-1 to H18-3 in triplicate. 0: 275 ng of Sm or EP genomic DNA

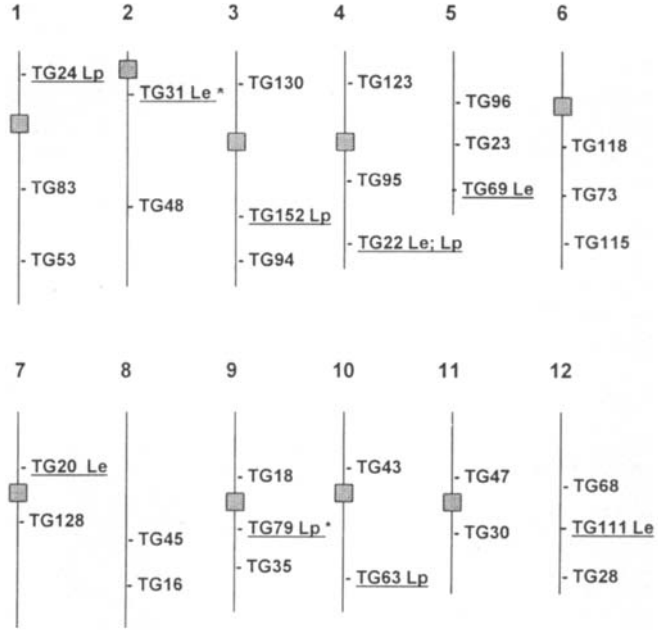

Fig. 3 Tomato map indicating approximate location of selected RFLP markers used for determination of *L. esculentum* (Le) – and *L. pennellii* (Lp) – specific chromosomes in asymmetric somatic hybrid plants H18-1, H18-2, H18-3. The *shaded areas* indicate putative centromere location. *Underlined markers* are present. * not present in plant H18-1

flowers produce an abnormal style and stigma and are characterised by anthers without pollen.

Elimination of donor nuclear DNA

The amount of EP DNA in hybrid plants was determined by dot-blot analysis. The species-specific 452-bp repeat pTHG2 is randomly located in all chromosomes of *L. esculentum* (Zabel et al. 1985); thus, the value of hybridization of pTHG2 to *L. esculentum* DNA was used as the standard at 100%. The hybridization signal of the pTHG2 probe to *S. melongena* DNA was negligible. The value of hybridization of probe pTHG2 to *L. pennellii* and EP DNAs relative to *L. esculentum* DNA was found to be 100% (Samoylov and Sink 1996). Thereafter, the percent of EP repeats in somatic hybrid plants was determined by a comparison of the degree of hybridization of pTHG2 to DNA from the hybrid plants with that hybridizing to EP (Fig. 2). The calibration plot showed linearity of hybridization of pTHG2 in a concentration series of DNA from EP (data not shown). The percent of EP DNA in plants H18-1, -2 and -3 was 6.23, 5.41 and 5.95%, respectively. Consequently, the amount of EP DNA in hybrid plants H18-1, -2 and -3 was calculated according to Samoylov and Sink (1996) and found to be equivalent to 3.59, 2.90 and 3.19 average-size EP chromosomes, respectively.

Each of the 31 RFLP probes was hybridized to DNA from *L. esculentum*, *L. pennellii*, EP, *S. melongena* and plants H18-1, -2 and -3. To determine useful polymorphisms, DNAs from the parental genotypes were digested with the restriction enzymes *Dra*I, *Eco*RI, *Eco*RV or *Hin*dIII. With these four enzymes polymorphisms were observed between genotypes with all probes tested except for TG95 and TG96. Only polymorphic bands between *L. esculentum* and *L. pennellii* which were also present in EP were used to score the presence or absence of the corresponding chromosomes in the asymmetric somatic hybrid plants. Although polymorphisms between *L. esculentum* and *L. pennellii* were not found with probes TG95 and TG96, only one of the parents had a unique band, so they were scored as not present due to the absence of the corresponding band in the somatic hybrid plants. RFLP analysis revealed that the somatic hybrid plants EP (+) E possessed only 8–10 fragments out of 12 *L. esculentum*- and 12 *L. pennellii*-specific chromosomes (Fig. 3). Loci of both species of EP were evenly represented: four to five from *L. esculentum* and four to five from *L. pennellii*. All so-

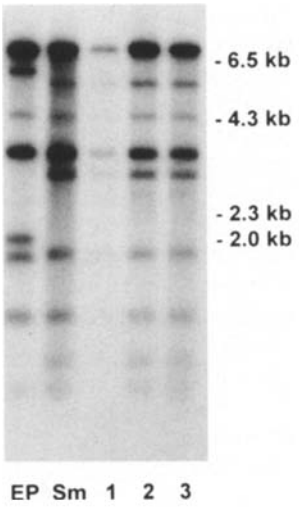

Fig. 4 Southern hybridization of cpDNA from *L. esculentum* × *L. pennellii* (*EP*), *S. melongena* (*Sm*) and somatic hybrid plants H18-1 (*1*), H18-2 (*2*) and H18-3 (*3*). Total genomic DNA was digested with *Eco*RI and hybridized with the 21.9-kb tomato chloroplast *Pst*I fragment (P-2)

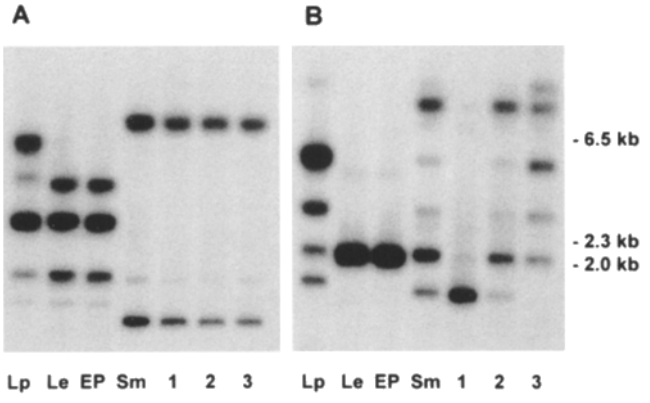

Fig. 5 Southern hybridization of mtDNA from *L. esculentum* (Le), *L. pennellii* (*Lp*), *L. esculentum* × *L. pennellii* (*EP*), *S. melongena* (*Sm*) and somatic hybrid plants H18-1 (*1*), H18-2 (*2*) and H18-3 (*3*). Total DNA was digested with *Hin*dIII (**A**) and *Eco*RI (**B**) and hybridized with the pZmE1 probe

matic hybrid plants retained locus TG22, chromosome 4, from both species of EP. Loci TG31 and TG79 of *L. esculentum* chromosome 2 and *L. pennellii* chromosome 9, respectively, were missing in hybrid plant H18-1.

Determination of organelles

Hybridization of the P-2 probe with blots containing *Eco*RI-digested total DNA revealed that all three hybrids contain only cpDNA fragments specific for *S. melongena* (Fig. 4). The mtDNA genome in the asymmetric somatic hybrids was predominantly from eggplant; however, some eggplant-specific polymorphic bands were not present in plants H18-1, -2, -3 (Fig. 5).

Discussion

Morphological and molecular analyses of the nuclear and organelle genomes of intergeneric asymmetric hybrid plants of *L. esculentum* × *L. pennellii* (+) *S. melongena* were carried out. Morphologically, the somatic hybrids most resemble eggplant, but growth is slower due to polyploidy. The plants produce flowers that are characterized by abnormal styles and stigmas and by anthers which do not produce pollen.

It has been shown that dot-blot analysis using species-specific repetitive DNA probes can be used quantitatively to determine the relative amount of donor DNA remaining in asymmetric hybrids (Imamura et al. 1987; Piastuch and Bates 1990; Kovtun et al. 1993). Correlation between flow cytometry and dot-blot data permitted an estimation of the genome composition of selected EP (+) E calli (Samoylov and Sink 1996). Subsequently, a combination of these techniques was used to monitor the ploidy level and the amount of donor DNA in the three regenerated hybrid plants. The plants grown in a greenhouse maintained a ploidy level close to 4n (data not shown); but according to dot-blot analysis the relative amount of donor EP DNA in somatic hybrid plants H18-1, -2 decreased from 4.77 and 5.14 (Samoylov and Sink 1996) to 3.59 and 2.90 average-size EP chromosomes, respectively, over a period of 6 months. These results correlate with those obtained by Derks et al. (1992) that the nuclear DNA content can vary, even among individual shoots from the same hybrid callus. These authors suggested that during callus growth the nuclear DNA content per cell can change leading to a non-homogeneous DNA distribution in a particular callus. Decrease of the donor DNA by 23–34% in somatic hybrid calli within 6 months of culture has also been observed by Trick et al. (1994).

It has been shown that RFLP analysis is an effective means of characterizing qualitatively the genome composition of asymmetric somatic hybrids (Wijbrandi et al. 1990a). Although RFLP allows determination of the specific composition of donor and recipient chromosomes in asymmetric somatic hybrid plants (Melzer and O'Connell 1992), the presence of an RFLP marker does not necessarily imply the presence of a particular intact chromosome (Puite and Schaart 1993). Moreover, study of tomato+potato fusion hybrids by genomic in situ hybridization revealed that when tomato chromosomes are present in duplicate they are difficult to detect by RFLP (Jacobsen et al. 1995). To study the nuclear composition of somatic hybrid plants H18-1, -2, -3 and to determine which of the specific chromosomes of *L. esculentum* and *L. pennellii* were eliminated/retained we selected 2–3 RFLP markers located on opposite arms of each tomato chromosome. Such an analysis revealed that no intact chromosomes of *L. esculentum* or *L. pennellii* were present in the hybrid plants. Although the regeneration of plants, H18-1, -2 and -3 was from one callus, loci TG31 and TG79 of *L. esculentum* chromosome 2 and *L. pennellii* chromosome 9, respectively, were missing in hybrid plant H18-1.

Comparison of the dot-blot and RFLP data permitted an estimate of the average size of EP fragments retained in somatic hybrid plants. According to the dot-blot analysis, the amounts of EP DNA retained in somatic hybrid plants H18-1, -2, -3 were equivalent to 3.59, 2.90 and 3.19 average-size EP chromosomes, respectively. The above amounts of EP DNA are represented by eight (H18-1) to ten (H18-2 and -3) fragments of *L. esculentum*- and *L. pennellii*-specific chromosomes in somatic hybrid plants. Thus, the average size of chromosome fragments retained in plants H18-1, -2 and -3 is equivalent to 0.449, 0.290 and 0.319 average-size EP chromosome, respectively. Moreover, the established map position of the *Npt*II selectable marker gene, in the T-DNA insert located on chromosome 12 of *L. esculentum* (Chyi et al. 1986), combined with a saturated molecular map of tomato (Tanksley et al. 1992), allowed an approximate determination by RFLP of the tagged chromosome-fragment size in EP. TG markers 68 and 28, distal and proximal to the *Npt*II locus, respectively, were not present in plants H18-1, -2 or -3. Thus, the size of the tagged fragment, retained in the three asymmetric somatic hybrid plants, does not exceed 53.0 cM.

In fusion experiments with taxonomically remote species, irradiation treatment of donor protoplasts is now commonly employed to direct chromosome elimination for the creation of asymmetric hybrids. However, a correlation between the level of irradiation and the extent of asymmetry has not been observed in a study of asymmetric hybrids between γ-irradiated (range of 100–1000 Gy) donor *Atropa belladonna* (+) *Nicotiana tabacum* (Gleba et al. 1988). Wolters et al. (1991) found no difference in the elimination of potato DNA from *S. tuberosum* (+) *L. esculentum* asymmetric hybrids when g-irradiation doses of 50 and 500 Gy were compared. Spangenberg et al. (1994) also found that the degree of elimination of donor chromosomes from X-irradiated Italian ryegrass protoplasts was not dose dependent for asymmetric somatic hybrids in the range of 25–250 Gy. A correlation was however found between an increase of irradiation dose and further fragmentation (more smaller and fewer larger fragments) of double-stranded plant DNA (Schoenmakers et al. 1994). Derks et al. (1992) reported the absence of intact donor chromosomes in the genome composition of asymmetric somatic hybrids obtained when 300 Gy was given to the donor. Our results suggest that even a relatively low dose of 100 Gy of γ-irradiation was effective in directing chromosome elimination of the donor and breakage of the donor genome, to the extent that only 8–10 fragments of 0.290–0.449 average-size EP chromosomes were present in somatic hybrid plants. These results support the idea that, in somatic fusion experiments with phylogenetically remote species, irradiation directs the elimination of the donor (Gleba et al. 1988). But the degree of elimination may be affected by other factors; indeed, such factor(s) infrequently allowed the regeneration of fertile somatic hybrid plants, possessing only one donor chromosome (Dudits et al. 1987). Moreover, highly asymmetric plants have even been obtained without any pre-treatment of the donor genome (Babiychuk et al. 1992).

At the same time, in asymmetric somatic fusion experiments, the phenomenon of polyploidization of the recipient genome has been frequently observed (Gleba et al. 1988; Wijbrandi et al. 1990b; McCabe et al. 1993; Schoenmakers et al. 1993) and several explanations have been proposed. For instance, Wijbrandi et al. (1990a) suggested that hybrid cells with a high proportion of donor genome were better balanced (around the tri-, penta- or hepta-ploid level), and therefore more viable, than cells with a low proportion of the donor genome. Puite and Schaart (1993) found that the percentage of the donor DNA in hybrid calli was dependent on the amount of recipient DNA: the level of donor DNA was highest when a large amount of DNA of the recipient genome was present. These authors suggested that polyploidization of the recipient genome may be a necessary mechanism by which the proliferation at high numbers of the irradiated damaged donor chromosomes occurs. In our study (Samoylov and Sink 1996), flow cytometric analysis revealed that the vast majority of somatic hybrid calli that did not regenerate shoots were 5–9n polyploids. A correlation of an increase in the amount of donor EP DNA with the ploidy level of asymmetric somatic hybrid calli/plants also has been observed. The three asymmetric somatic hybrid plants obtained were regenerated after 12 months in culture only from calli with a ploidy level close to 4n and such calli occurred only when the donor EP had received 100 Gy. After 8 months growth in a greenhouse, the three somatic hybrid plants, H18-1, -2 and -3, maintained a near-tetraploid level and even after 11 months still, appear to be polyploid. The phenomenon of polyploidization of the recipient genome in asymmetric fusion experiments is in good agreement with our hypothesis (Samoylov and Sink 1996) that, in fusion experiments with phylogenetically remote species, irradiation of the donor protoplasts in fact directs chromosome elimination; but the degree of elimination may depend on the size of the donor and recipient genomes, e.g. the ratio (donor:recipient) between the DNA content of species involved in fusion. Irradiation treatment of one of the genomes does prevent the normal proliferation of its chromosomes in somatic hybrids; thus, irradiation determines the genome of which species, involved in fusion, should be eliminated. Therefore, the irradiated genome becomes a "donor" and the non-irradiated a "recipient". Proliferation of the irradiated donor genome/chromosomes introduced via somatic hybridization is a perturbation event for the recipient genome, which may hamper normal function. Thus, to restore normal functioning of the recipient genome the elimination of the donor genome should take place in somatic hybrid cells. However, according to our hypothesis, elimination depends on the size of the donor and recipient genomes, e.g. the ratio (donor:recipient) between the DNA content of species involved in fusion. Thus, in fusion experiments between species having similar nuclear DNA contents, the recipient genome does not have a quantitative DNA advantage over the donor genome. Conversely, the elimination of the donor genome has already been determined by irradiation. Consequently, the recipient genome may through synthesis attain a quantitative DNA ad-

vantage and so eliminate the donor. The recipient genome may create this advantage by duplication of the genome and, thus, polyploidization of the recipient genome in asymmetric somatic hybrids occurs. Moreover, if the recipient is not able to eliminate irradiated DNA of the donor, the polyploid level of the asymmetric somatic hybrids remains relatively stable. Thus, polyploidization in many cases may result in the low shoot regeneration frequency of somatic hybrids, especially when genomes of taxonomically remote species are mixed. Conversely, for fusion experiments with species characterized with a higher DNA ratio for the recipient as in the case of *Daucus carota* (donor) and *Nicotiana tabacum* (recipient), we may assume that *N. tabacum* is already approximately 10n relative to *D. carota* [nuclear DNA ratio 9.4:1; DNA contents of *N. tabacum* and *D. carota* are 8.75–9.63 and 0.98 pg, respectively (Arumuganathan and Earle 1991)] and fertile somatic hybrid plants with only one chromosome of the donor were obtained in this instance (Dudits et al. 1987). Hinnisdaels et al. (1991) also reported the production of highly asymmetric fertile somatic hybrids between *N. plumbaginifolia* and *Petunia hybrida* [the DNA contents of *N. plumbaginifolia* and *P. hybrida* are 4.74 and 2.64 pg, respectively (Arumuganathan and Earle 1991)]; however, somatic hybrids containing *Petunia* chromosomes or fragments, maintained a tetraploid *Nicotiana* level. Certainly, our hypothesis has to be further tested by somatic fusion experiments involving species with similar and different size genomes.

The determination of the organelle composition of somatic hybrid plants was based on earlier results from this laboratory (Levi et al. 1988) which demonstrated success in using the P-family probes (Phillips 1985) and the pZmE1 clone (Fox and Leaver 1981) for the detection of cpDNA and mtDNA in somatic hybrids. It has been reported (Wolters et al. 1993) that the transmission of cp- and mt-DNA types in intergeneric somatic hybrids was correlated with the nuclear composition of the hybrids. Our study revealed the transmission of eggplant-type cpDNA and mtDNA in plants H18-1, -2, -3, although some bands of eggplant mtDNA were missing in the banding profiles of somatic hybrids. These results might be expected, because selection of somatic hybrids based on cytoplasmic traits was not a factor in our experiments. Despite the correlation of our results with those obtained by Wolters et al. (1993) they are in contrast with results more recently obtained by Wolters et al. (1995) where no correlation was found between the nuclear genome composition and the transmission of cpDNA and mtDNA of somatic hybrids between *S. tuberosum* and *L. esculentum*.

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