

Molecular analysis of the extent of asymmetry in two asymmetric somatic hybrids of tomato

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Summary. Two somatic hybrid plants generated from a single fusion event between Lycopersicon esculentum and irradiated L. pennellii protoplasts have been analyzed at the molecular level. Over 30 loci have been analyzed using isozymes and RFLPs. All loci tested on chromosomes 2-10 were heterozygous, while those loci on chromosome 12 were homozygous L. pennellii in both somatic hybrids. In one of the somatic hybrids, 2850, loci on chromosome 1 were also homozygous L. pennellii. The other somatic hybrid, 28F5, was heterozygous at all chromosome 1 loci tested, but exhibited altered stoichiometry of parental bands as compared to the sexual hybrid. Loci on chromosome 2 from both somatic hybrids have altered stoichiometry, with L. pennellii alleles being four times more abundant than expected. Both somatic hybrids contain the L. esculentum chloroplast genome, while only L. pennellii polymorphisms have been detected in the mitochondrial genome.

Key words: *Lycopersicon esculentum* – Asymmetric somatic hybrids – Protoplast fusion – Restriction fragment length polymorphism

Introduction

Fusing somatic cell protoplasts from different species produces novel genotypes which often cannot be produced via sexual hybridization. In fusions of protoplasts from phylogenetically distant species, chromosome elimination is often observed and, frequently, regeneration of plants from such fusions is dependent on partial elimination of chromosomes from one species (Harms 1983 a, b). Fragmentation of DNA by ionizing radiation may also result in chromosome elimination as well as in deletions and exchanges; radiation increases the frequency of ring chromosomes, bridges and acentric fragments (Evans 1974). Evidence of these events comes from cytological observation of metaphase and anaphase plates of irradiated cells. A practical application of directed chromosome elimination has been the use of radiation to generate asymmetric somatic hybrids (Gupta et al. 1984; Bates et al. 1987; Imamura et al. 1987; Sidorov et al. 1987; Yamashita et al. 1989) and cybrids (for review, Galun and Aviv 1983).

Cytological analysis of asymmetric somatic hybrids has determined the chromosome number and, in a few cases where fusion parents have distinct chromosome morphology, the specific chromosome contribution from each parent may be determined. In fusions of *Arabidopsis thaliana* with *Brassica campestris* (Gleba and Hoffmann 1978), *Atropa belladonna* with *Nicotiana chinensis* (Gleba et al. 1982) and *A. belladonna* with *N. plumbaginifolia* (Gleba et al. 1988), cytological observation detected possible exchanges between the two species' chromosomes. These authors were unable to confirm exchanges in any of these fusions or to identify the chromosomes from each species involved in the possible exchanges.

In the genera *Lycopersicon* and *Solanum*, chromosome morphologies are not distinct enough in somatic cells for cytological analysis of somatic hybrids. However, a nearly saturated linkage map of *L. esculentum* has been produced, which maps more than 300 RFLP markers on all 12 chromosomes (Bernatzky and Tanksley 1986; Tanksley et al. 1988). Utilizing this map, Young and Tanksley (1989) have developed the concept of graphical genotypes. They used 70 mapped RFLP markers to determine the genotypes of 200 BC₁ plants from a *L. esculentum* × *L. chmielewskii* cross and represented them in graphical form. They also looked at F_2 plants from a *L. esculentum* × *L. pennellii* cross. Moore and Sink (1988) utilized four RFLP markers known to be located on chromosome 2 to analyze this chromosome in somatic hybrids of *L. esculentum* fused with *Solanum lycopersicoides*.

We have been attempting to create asymmetric somatic hybrids in tomato, using gamma-rays to induce chromosome elimination and fragmentation (O'Connell and Hanson 1985, 1987; O'Connell et al. 1986). In this paper we describe the use of mapped isozyme and RFLP markers for the molecular characterization of two asymmetric somatic hybrids generated from the fusion of *L. esculentum* cv UC82B with 3-krad-irradiated *L. pennellii* protoplasts. The regeneration and initial characterization of plants from this fusion were previously described (O'Connell and Hanson 1987).

Materials and methods

Plant material

Seeds of *L. pennellii*, LA 716, collected in Atico, Peru, were generously provided by C. Rick, Tomato Genetics Stock Center, University of California, Davis. Seeds of *L. esculentum* cultivar UC82B were from Petoseed Co. Somatic hybrids MOC 1732850F5 and MOC 17328F5 were isolated from a single regenerating callus generated from a fusion of 3-krad-irradiated *L. pennellii* and *L. esculentum* cultivar UC82B protoplasts, as described previously (O'Connell and Hanson 1987).

DNA isolation and DNA probes

Total DNA was isolated from lyophilized leaf tissue as described by Murray and Thompson (1980), except that DNA was diluted with four vol. of sterile distilled water and precipitated after cesium chloride centrifugation rather than undergoing dialysis. Chloroplast DNA (cpDNA) of L. esculentum was isolated following the protocol of Saltz and Beckman (1981). DNA to be used as probes was either nick-translated (Rigby et al. 1977) or oligolabelled (Feinberg and Vogelstein 1983) with α^{32} P-GTP. The nuclear DNA composition of somatic hybrids was analyzed using gel-purified fragments of mapped tomato cDNA clones (Bernatzky and Tanksley 1986) as probes. cpDNA was analyzed using oligolabelled L. esculentum cpDNA. Clone 2D4, a 2.1-kb L. pennellii mitochondrial Sall fragment which contains no known coding sequence but occurs in multiple copies in the mitochondrial genome (McClean and Hanson 1986), was used to analyze mitochondrial DNA (mtDNA).

Southern and hybridization conditions

Restriction enzyme digests were of $10 \ \mu g$ total DNA for at least 4 h at $37 \ ^{\circ}$ C. Electrophoresis, Southern transfer, hybridization and washes have been previously described (Melzer et al. 1989). Quantitation of autoradiograph images was performed with a laser densitometer.

Isozyme analysis

Approximately 0.5 g (wet weight) of leaf tissue was ground in 0.12 M reduced glutathione, adjusted to pH 7.6, with 1 M Tris. Samples were kept on ice during processing. Samples were absorbed into paper wicks and electrophoresed on starch gels and stained as described in Bernatzky and Tanksley (1986).

Chromosome counts and pollen staining

Root tips were collected from rooting shoots, tips were incubated for 4 h at $18 \,^{\circ}$ C in 2 mM 8-hydroxyquinoline. Tissue was hydrolyzed 20 min in 4 N HCl at room temperature, rinsed with water, stained with acetocarmine and squashed. Viable pollen was determined after staining as described by Alexander (1969).

Results

Selection and morphology

Previously, we had observed that the differences in leaf shape of hybrids between L. esculentum and L. pennellii were indicative of increased ploidy (O'Connell et al. 1986). Most of the regenerants scored as somatic hybrids using isozyme markers had a leaf shape typical of a tetraploid (O'Connell and Hanson 1987). However, one regenerant had a leaf shape typical of a diploid. Somatic hybrids MOC 1732850F5 and MOC 17328F5 (hereafter referred to as 2850 and 28F5, respectively) were selected for detailed molecular analysis based on their morphology. Somatic hybrid 2850 was similar to the sexual F₁ (Fig. 1), having relatively thin leaves, intermediate leaf shape and open growth habit. Flowers had non-exserted stigmas like L. esculentum, but the corolla tube was somewhat enlarged. Overall, the morphology of 2850 suggested it was not tetraploid. Somatic hybrid 28F5, which was a regenerant from the same callus (i.e. same fusion event) as 2850, had characteristic tetraploid morphology with thick, round, wrinkled leaves, dense growth habit and exserted stigmas.

Cytological characterization and fertility

Inspection of root-tip squashes of either parent showed the expected diploid count of 24 chromosomes. Chromosome counts of 2850 revealed 44 ± 2 chromosomes; this was surprising since this individual had the leaf shape typical of a diploid. Counts of 28F5 were not possible

ESC F₁ SH PENN

Fig. 1. Comparison of leaf shape of somatic hybrid 2850 with fusion parents. Genotypes are as indicated

7 8 9 10 11 12 6 5 CD49B Idh-I 6 Pgdh -CD41 * CD 14 CD61 *-CD29A CD32A CD56 CD29D# CD2 -Cab-3 Rhcs-18 CD31A 0.08 Pgm-1 -CD 38A -CD25B CD38B CD 13A CD 6 B CDIS СОЗАВ CD34A 6Pgdh-2 Pem-2 CD25A CD7A CD6A Cab-Adb-1 CD 5 1 CD12 Got -2 Pgi-1 CD35 CD 3 9 CD 28 CD40 CD328 -CD 2 1 A Rbcs-3 -CD5 Est-3 -Aco-1 CD4A -CD62 срэзв -CD19 -Cab-5 6Pgdh S₁ E F P

Fig. 3. Starch gel analysis of Pgi-1 activity. *Lanes E, P, F* and *S1* contain *L. esculentum, L. pennellü*, the sexual hybrid and somatic hybrid 2850, respectively

due to root-rot infection which eventually killed this plant. Pollen viability for 2850 was 4.4%. Somatic hybrid 2850 readily set fruit but not seed. Extensive crossing with *L. esculentum* resulted in a single viable seed. Germinated in vitro, the seedling was grossly abnormal, the shoot exhibited no apical dominance and produced a typical witches-broom morphology.

Isozymes and RFLP analysis

Despite having a morphology associated with a diploid hybrid, somatic hybrid 2850 had close to a tetraploid number of chromosomes, 44. In order to determine if there was a specific chromosome deletion responsible for this unusual phenotype, the genotype of the two somatic hybrids, 2850 and 28F5, was determined using molecular markers. Thirty-one loci on 11 of the 12 tomato chromosomes were analyzed for 2850 (Fig. 2) while 13 loci on 11 chromosomes were analyzed for 28F5.



A cursory evaluation of the molecular markers indicated that both somatic hybrids were heterozygous at loci on chromosomes 2-10. We were unable to test chromosome 11, as we only had one cDNA clone mapped to this chromosome, and we were unable to score its polymorphism. A more detailed analysis of the loci on chromosomes 1 and 12 was performed, since the *L. esculentum* copies of these chromosomes were suspected to be missing on the preliminary screen.

Analysis of chromosome 12

Loci at both ends and the middle of chromosome 12 were tested in the somatic hybrids. Three isozymes which are mapped on chromosome 12, Pgi, Aco and 6-Pgdh, were homozygous for the *L. pennellii* allele in both somatic hybrids (Fig. 3). Two RFLP loci which map to chromosome 12, CD2 (Fig. 4) and CD6A, were homozygous for the *L. pennellii* banding pattern in both somatic hybrids. These analyses indicate that both of the *L. esculentum* homologues of chromosome 12 are missing in the two somatic hybrids.

Analysis of chromosome 1

Three RFLP loci, CD15, CD12 and CD28, were used to characterize the complement of chromosome 1 homologues in the two somatic hybrids. Somatic hybrid 2850 displayed only the *L. pennellii* hybridization pattern, indicating that both of the *L. esculentum* homologues for chromosome 1 were missing. Somatic hybrid 28F5 displayed both the *L. pennellii* hybridization pattern and a weak signal with the *L. esculentum* pattern for CD15 (Fig. 5). These signals were quantitated, and the densitometric analysis indicated that the *L. esculentum* band was five times less abundant in 28F5 than the corresponding band in the F_1 hybrid.

Fig. 4. Autoradiogram of total DNA probed with cDNA clone 3-17 encoding the chromosome 12 gene CD2. All *lanes* contain 10 µg Eco-RV-digested DNA. *Lanes E, P, F, S1* and S2 contain *L. esculentum, L. pennellii*, the sexual hybrid, and somatic hybrids 2850 and 28F5, respectively. Bands of interest are indicated by *arrow heads*

contain the 8.1-kb fragment unique to L. esculentum cpDNA and are missing the 5.8- and 2.2-kb fragments

unique to L. pennellii cpDNA.

A cloned fragment of *L. pennellii* mtDNA, 2D4, which is present in several copies in both parental mitochondrial genomes (McClean and Hanson 1986), was chosen to approximate the nature of the mitochondrial genomes in the somatic hybrids. NruI, SalI, HindIII and EcoRI digests of total DNA were probed with nicktranslated 2D4 (Fig. 8). None of the digests revealed any *L. esculentum*-specific bands. SalI and EcoRI digests showed *L. pennellii*-specific bands, with the SalI digest exhibiting altered stoichiometry in the banding pattern. The NruI and HindIII digests contained unique banding patterns distinct from either parental pattern.

The mitochondrial genomes in 2850 and 28F5 are not identical, since the hybridization patterns in the SalI and HindIII digests are different between these two individuals.

Analysis of chromosome 2

Visual inspection of the isozyme gels and of the autoradiograms indicated that for most of the markers scored as heterozygous, the two parental alleles were present in equivalent amounts. This was not true for the loci mapped to chromosome 2. The loci, CD35, CD37, Cab-1, Rbcs-1 and Rbcs-3, all showed a stronger *L. pennellii* signal. The abundance of each parental banding pattern was quantitated, and the densitometric tracing indicated that the *L. pennellii* signal was four times more abundant than the corresponding band in the F₁ hybrid. Data for CD37 are shown in Fig. 6.

Both somatic hybrids 2850 and 28F5 contain only

L. esculentum cpDNA, as detected in Southerns probed

with labelled total cpDNA (Fig. 7). Both 2850 and 28F5

Organelle genomes

brids 2850 and 2855, respectively. Bands of interest are indicated by arrow heads

Fig. 5. Autoradiogram of total DNA probed with cDNA clone 3-82 encoding the chromosome 1 gene CD15. All *lanes* contain 10 μ g EcoRV-digested DNA. *Lanes* are described in Fig.4. Bands of interest are indicated by *arrow heads*







Fig. 6. Autoradiogram of total DNA probed with cDNA clone 3-288 encoding the chromosome 2 gene CD37. All *lanes* contain 10 µg DraI-digested DNA. *Lanes E, P, F* and *S1* contain *L. esculentum, L. pennellii,* the sexual hybrid and somatic hybrid 2850, respectively. Bands of interest are indicated by *arrow heads*



Fig. 7. Identification of chloroplast genomes present in somatic hybrids 2850 and 28F5. All *lanes* contain 4 μ g EcoRI-digested total DNA. Nick-translated tomato chloroplast DNA was used as probe. *Lanes E, P, C, S1* and *S2* contain *L. esculentum, L. pennellii*, tomato cpDNA, and somatic hybrids 2850 and 28F5, respectively. *Arrow heads* indicate bands which differentiate *L. esculentum* and *L. pennellii*



Fig. 8. Identification of mitochondrial genomes present in somatic hybrids 2850 and 28F5. All *lanes* contain 4 μ g total DNA restricted with either NruI, SaII, HindIII or EcoRI. Hybridization was with mitochondrial probe 2D4. *Lanes* as in Fig. 7. *Lane L* contains HindIII-digested lambda DNA

Discussion

The fusion of L. esculentum and L. pennellii protoplasts and regeneration and initial characterization of 21 somatic hybrids were described previously (O'Connell and Hanson 1987). Using isozymes and RFLPs, we present a detailed molecular analysis of two of these regenerants, 2850 and 28F5, which regenerated from a single fusion product. Both somatic hybrids are asymmetric; they do not contain a full complement of chromosomes from each parent used in the fusion. Both 2850 and 28F5 have lost both copies of chromosome 12 of L. esculentum. In addition, 2850 has lost both copies of L. esculentum chromosome 1. The weak intensity of the L. esculentum signal in Southerns probed to look at the CD15 locus may indicate that 28F5 has lost one copy of L. esculentum chromosome 1 or is chimeric with respect to loss of chromosome 1.

Chromosome elimination is well documented in somatic hybrids, particularly in intergeneric and interfamilial fusions (Harms 1983 a, b). One possible explanation for chromosome elimination is cell-cycle asynchrony. In the somatic hybrid parental species, chromosomes may not mix at metaphase, but assemble into blocks or clusters resulting in uneven segregation at mitosis (Kao et al. 1974; Constabel et al. 1977; Gosch and Reinert 1978). Asynchrony results when nuclei from rapidly dividing cells (suspension culture cells) and nuclei from slowly cycling or arrested cells (leaf mesophyll cells) are fused. Fusions of this type often result in intermediate cycling times (Weber et al. 1976; Gleba and Hoffmann 1978) and partial elimination or gross chromosomal alterations in chromosomes of the slower cycling parent (Kao et al. 1974; Constabel et al. 1977; Kao 1977; Chien et al. 1982; Pental et al. 1986). Elimination of chromosomes from callus cultures of somatic hybrids has been observed over several months (Kao 1977; Binding and Nehls 1978; Gleba and Hoffmann 1978; Krumbiegel and Schieder 1981; Chien et al. 1982). The elimination of L. esculentum chromosomes from somatic hybrids 2850 and 28F5 may reflect such an asynchrony of parental nuclei.

The weak signal of L. esculentum locus CD15 in Southerns of 28F5 might suggest 28F5 is chimeric with respect to loss of L. esculentum chromosome 1. Morphologically, 28F5 was uniform and did not exhibit variation in leaf morphology on different shoots. Complete loss of L. esculentum chromosome 1 is associated with certain morphological features, therefore, it is unlikely that 28F5 is chimeric as a result of regeneration from more than one cell with different L. esculentum chromosome 1 compositions. It is possible that L. esculentum chromosome 1 was undergoing elimination in planta.

Asynchrony of nuclei during mitosis is useful in explaining the loss of both copies of *L. esculentum* chromosomes from these somatic hybrids. Complete failure of chromosome 1 or 12 to line up on the metaphase plate would result in at least one daughter cell with no copies of that *L. esculentum* chromosome.

L. pennellii protoplasts used in these fusions were exposed to 3 krad of gamma-radiation. This is not a lethal dose in L. pennellii and we did not expect L. pennellii chromosome loss to occur. It is unlikely that the radiation treatment triggered some specific function in L. pennellii for elimination of foreign chromosomes.

The apparent amplification of L. pennellii chromosome 2 is of interest because the ribosomal RNA genes are located on this chromosome. Variation in ribosomal RNA gene copy number has been observed in tissue culture-derived plants of flax (Walbot and Cullis 1985), triticale (Brettell et al. 1986), potato (Landsmann and Uhrig 1985), Nicotiana svlvestris (De Paepe et al. 1983) and intergeneric tomato somatic hybrids (Moore and Sink 1988). In the intergeneric tomato somatic hybrids, three additional chromosome 2 loci indicated extra copies of this chromosome from the suspension cell protoplast parent S. lycopersicoides (Moore and Sink 1988). It is thought that the "stress" of tissue culture may trigger gene and possibly chromosome amplification. Why ribosomal RNA genes are more sensitive to this stress is unclear.

The karyotypes of the somatic hybrids correlate well with their morphology. Somatic hybrids 2850 and 28F5 differ in their copies of *L. esculentum* chromosome 1. Chromosome 1 contains at least one locus involved in the quantitative trait, leaf ratio (Tanksley et al. 1982). Therefore, the increased leaf thickness and rounder leaf outline in 28F5 compared to 2850 are likely a dosage effect of this chromosome 1 gene. Similarly, one of five QTLs for stigma exsertion was found on chromosome 1 (Tanksley et al. 1982). This QTL caused an effect opposite to the predicted parental effect, i.e. *L. pennellii* alleles at this locus resulted in reduced stigma exsertion. Somatic hybrid 2850 contains only *L. pennellii* chromosome 1 and has a non-exserted stigma.

Both somatic hybrids inherited *L. esculentum* cpDNA and predominantly *L. pennellii* mitochondrial DNA in the region surrounding 2D4 sequences. No evidence of cpDNA recombination was detected and sorting-out of chloroplasts appeared complete.

Inter- and intra-molecular recombination occurs in plant mtDNA (Lonsdale et al 1984; Shirzadegun et al. 1989), and recombination between parental mitochondrial genomes (i.e. inter-genomic recombination) has been demonstrated in somatic hybrids (Rothenberg et al. 1985; Rothenberg and Hanson 1988). Inheritance of one parental mitochondrial genome with no evidence of recombination has been observed as well (Shepard et al. 1983). Novel bands in the NruI and HindIII digests and altered stoichiometry of bands in the SalI digest suggest that the mtDNA may have undergone unusual recombination reactions. We cannot distinguish between inter- or intra-genomic recombination, as we have only analyzed a small percentage of the 300 to 400-kb mitochondrial genome.

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