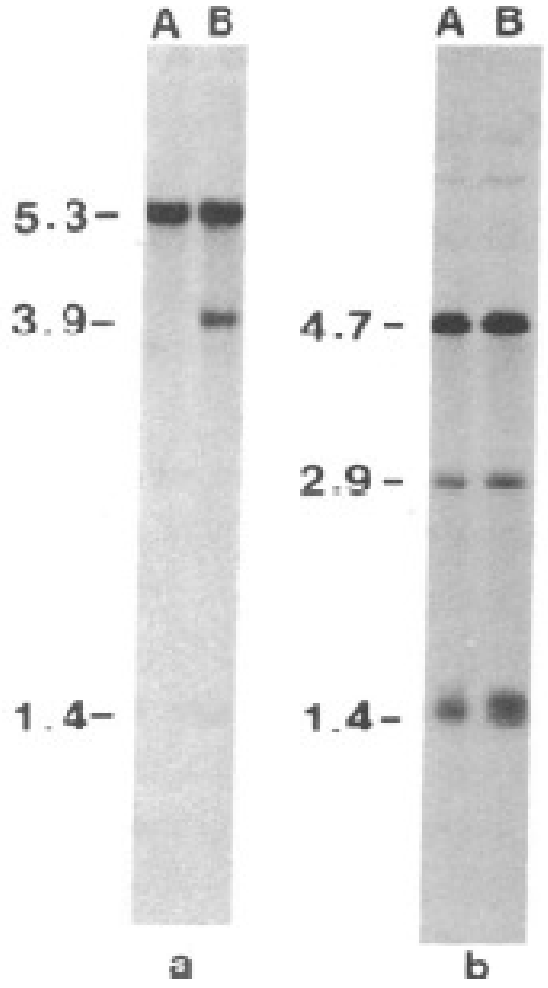


FIG. 1. Ribosomal DNA variation found in two families of asexual *Taraxacum*. Lane A, nonparental rDNA genotype. Lane B, parental rDNA genotype. (*a*) An *Eco*RI digest shows the loss of a restriction site in the nonparental genotype that produces 3.9- and 1.4-kb fragments in the parental genotype. (*b*) Double digestions with *Dra* I and *Bst*EII show that the nonparental genotype has small changes in fragment length (<50 base pairs) compared to the ≈1.4-kb fragments of the parental genotype. These fragments were visualized by hybridization with pTEE5.

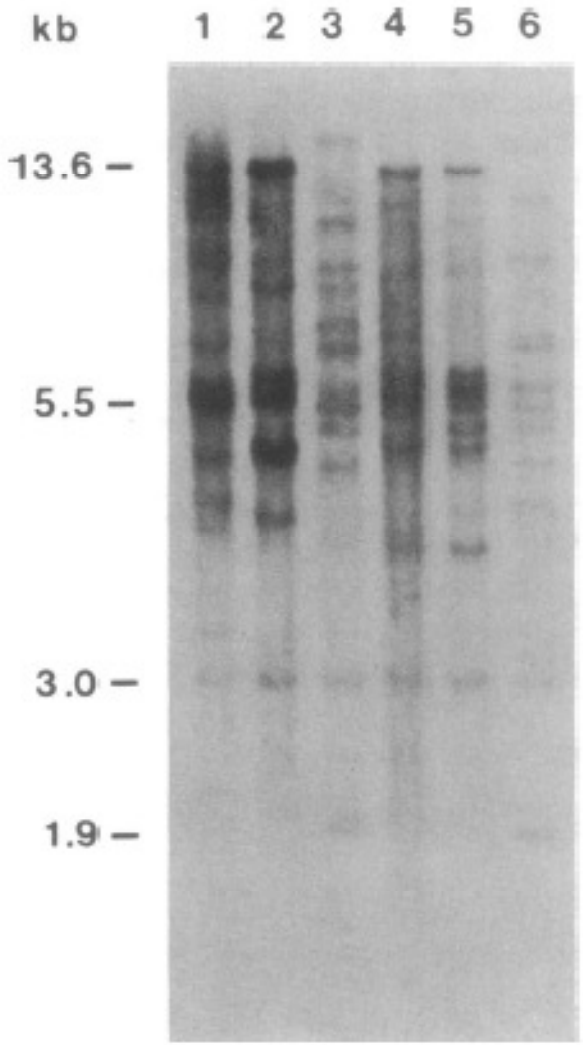


FIG. 5. Restriction fragment length variation among six individuals digested with *Eco*RI and hybridized with the *Pst* I inserts of pZML793 (*Adh1*). Lanes 1 and 2, *T. officinale* collected from Nevada and Kentucky, respectively, shown for comparison. Lanes: 3, offspring of P1; 4, offspring of the single P2 variant offspring; 5, P2 variant offspring; 6, sibling of the P2 variant offspring, which represents an individual with parental rDNA. Although the individuals in lanes 3 and 5 have the same nonparental rDNA genotype, their *Adh1* genotypes differ.

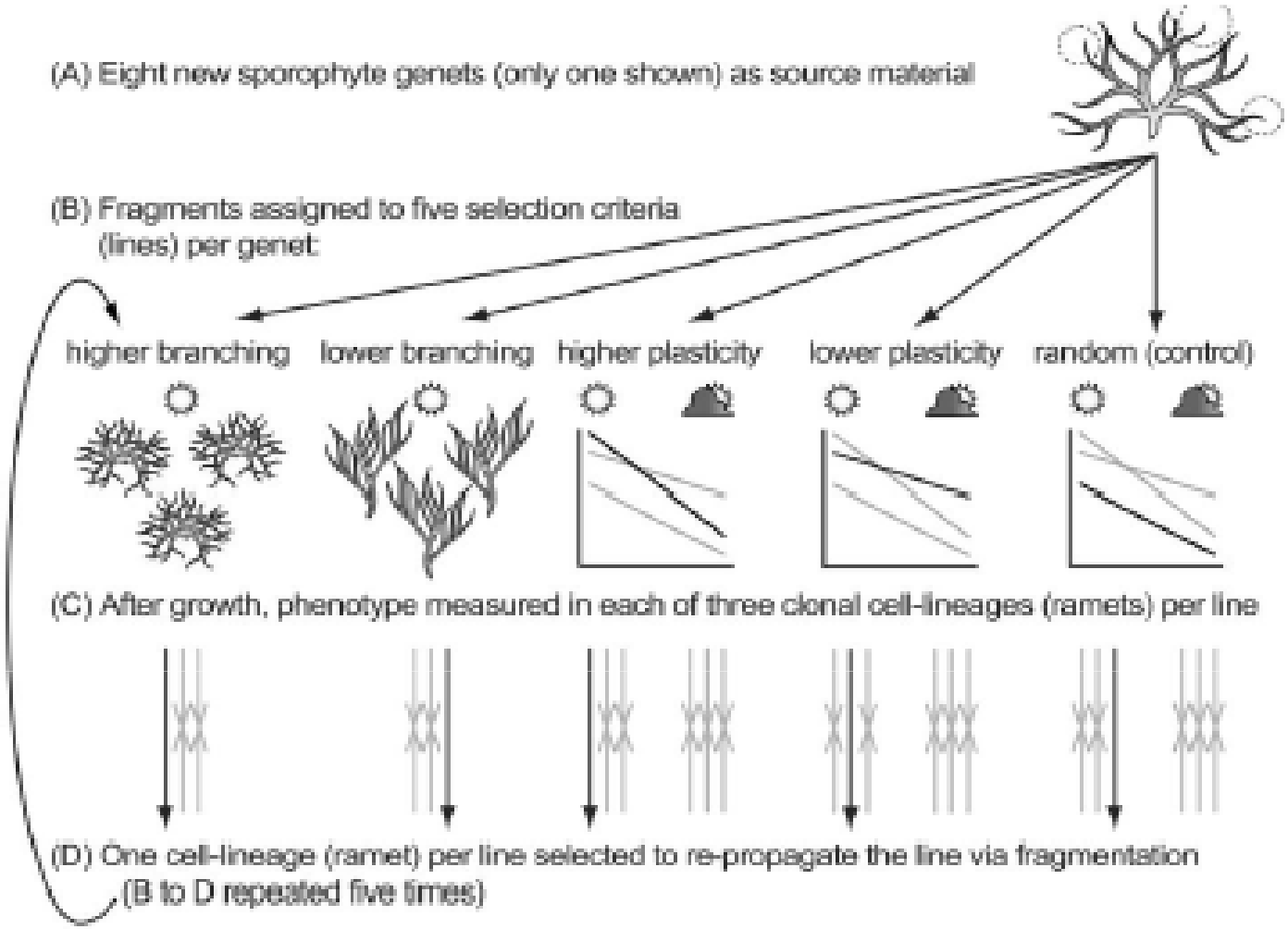
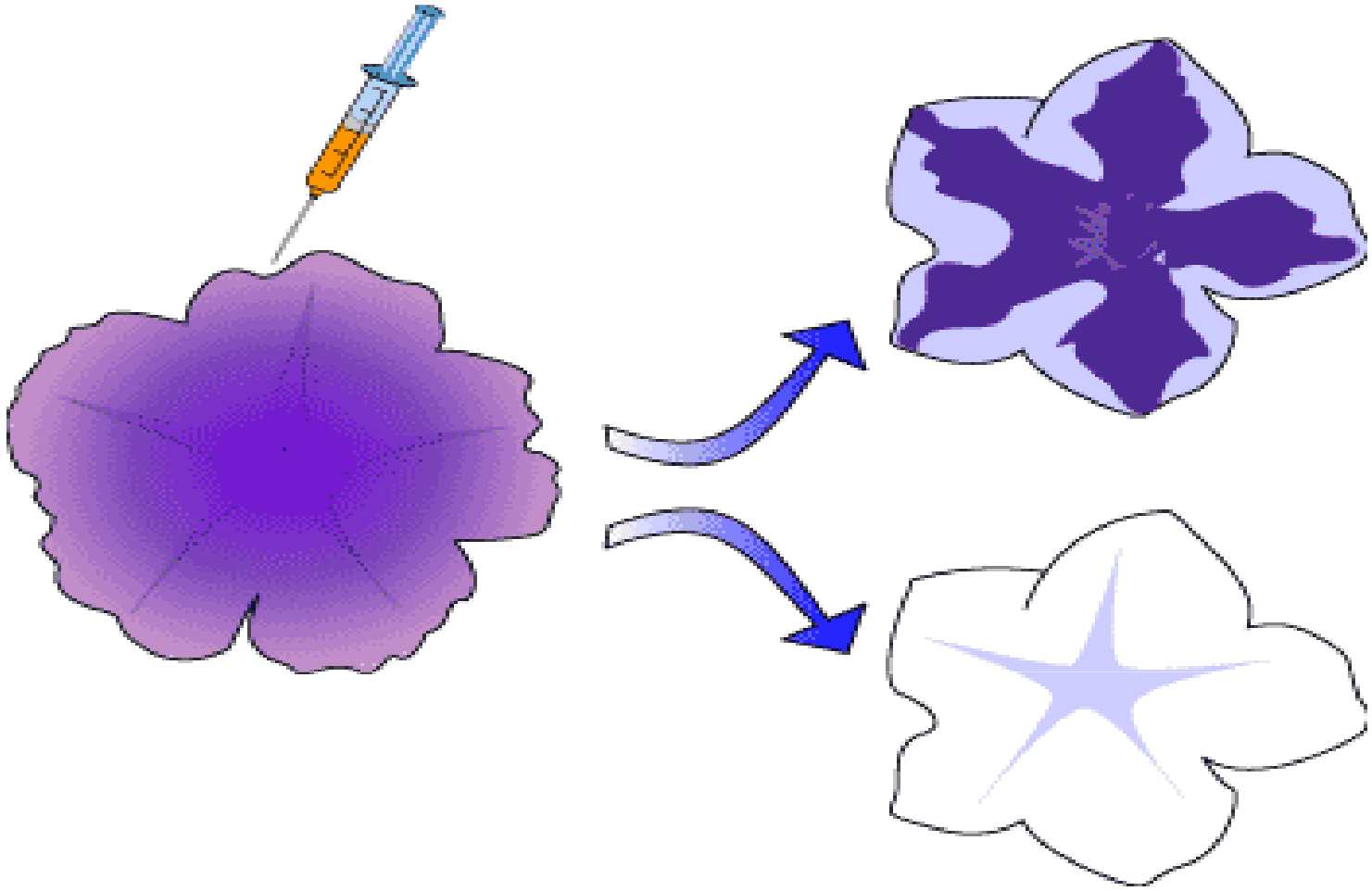


Figure 1: Protocol for cell-lineage selection on growth form and its plasticity within genets of *Asparagopsis armata*. For each of eight new sporophyte genets (*A*), 24 apical fragments were used to start five selection lines (selection for higher branch proliferation, selection for lower branch proliferation, selection for higher plasticity in branch proliferation, selection for lower plasticity in branch proliferation, and a control line of random selection), with three clonal cell lineages in each (*B*). After growth in a focal environment (where a sun symbol denotes abundant light and a cloud + sun symbol denotes shade), the degree of branch proliferation (on the basis of individual ramets) or its plasticity (on the basis of ramets grown in abundant light paired a priori with ramets grown in shade) was measured in each clonal cell lineage (*C*). According to the selection criterion, one ramet per selection-genet combination was selected to propagate that line anew by fragmentation (*arrowed lineages*) and the remaining ramets were discarded (*crossed lineages*; *D*). For each selection-genet combination, steps *B*–*D* were repeated until clonal cell lineages had been selected among five times.



La scoperta che la metilazione del DNA é un importante processo di regolazione permanente e anche trans-generazionale é stata fatta in piante transgeniche per una copia in più di un gene per il colore. In quel caso invece di aumentare il colore é diminuito nelle piante transgeniche in cui le due copie del gene sono state metilate. La metilazione poi é rimasta nelle generazioni successive.

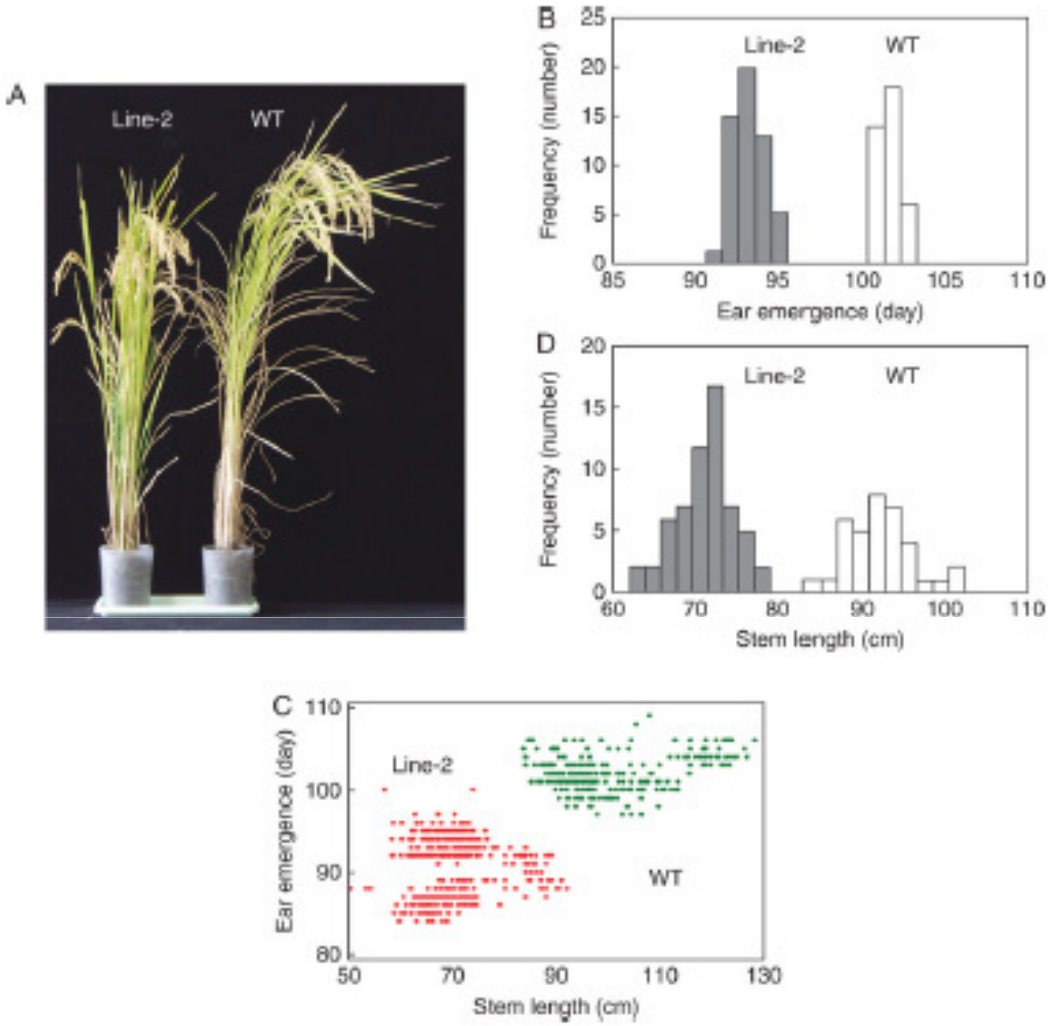


FIG. 1. Phenotypic properties. (A) Features of mature rice plants (*Oryza sativa* ssp. *japonica*, 'Yamadanishiki'). The wild-type (WT, right) and F_7 progeny of Line-2, (Line-2, left) were cultivated under standard field conditions, and photographed at maturity. (B) Distribution of the stem length and heading days. Fifty to 130 plants each of the wild type and Line-2 were measured every year. As the representative, values for 54 F_8 Line-2 plants (Line-2) and 36 wild-type plants (WT), both harvested in 2005, are depicted for heading days (ear emergence, upper panel) and stem length (lower panel) based on the stem–leaf plot obtained from the tests for normality with 95% confidence. The mean for the ear emergence was 101·8 ± 0·70 d for the wild type and 93·1 ± 0·98 d for Line-2. The mean for the stem length of the wild type and the Line-2 plants was 95·2 ± 4·14 and 71·4 ± 3·6 cm, respectively. (C) Relationship between the stem length and the ear emergence (heading days). The mean value for each item (ear emergence and stem length) in each year (1998–2005) was statistically calculated as described above and plotted. The Line-2 (red) samples were F_2 (1998) to F_8 (2005) (the total number was 429), and wild-type plants (green) from the corresponding years (the total number was 1017) were also measured. The horizontal and vertical axes indicate stem length and ear emergence, respectively. Note that each spot does not necessarily represent an individual plant due to many overlaps.

Two lines, one treated with azacytidine, the other control

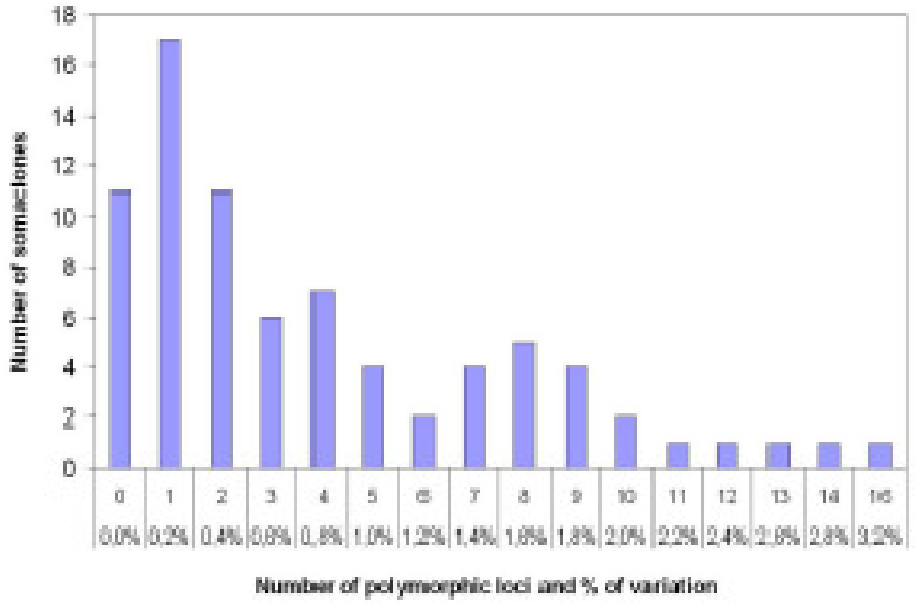


Figure 1
Distribution of polymorphic AFLP (*EcoRI/MspI*) loci in *V. vinifera* somaclones. Numbers of somaclones depending on the numbers of polymorphic AFLP loci are presented. Percentages of variation (number of polymorphic loci/total number of detected loci) are given.

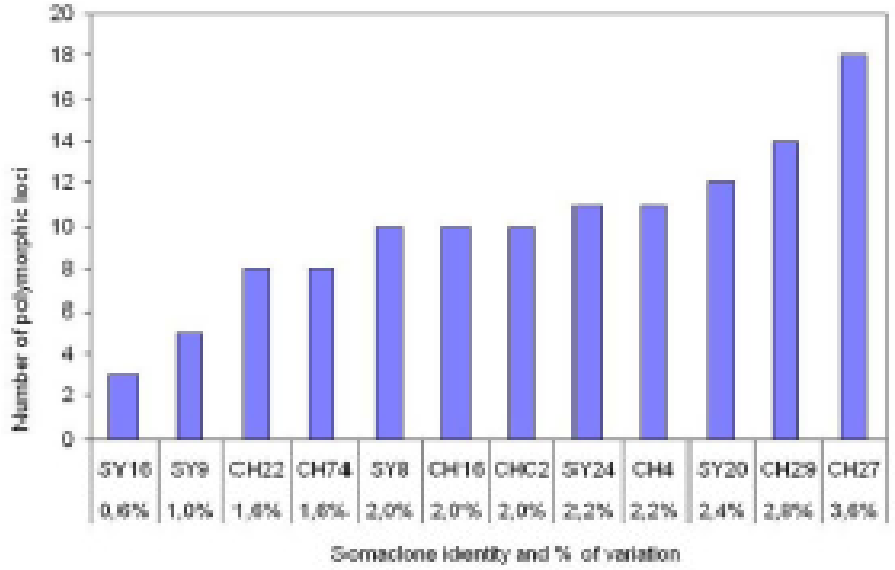


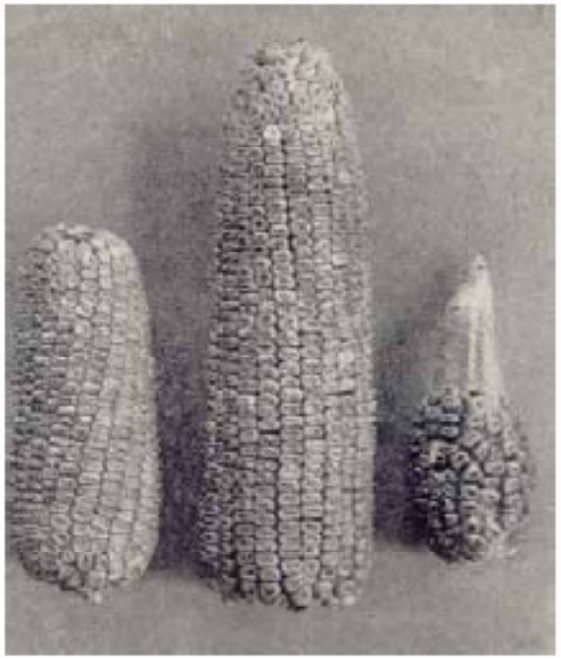
Figure 2
Distribution of polymorphic MSAP (*EcoRI/MspI* and *EcoRI/HpaII*) loci in 12 *V. vinifera* somaclones. Numbers of polymorphic MSAP loci in 12 selected 'Syrah' (SY) and 'Chardonnay' (CH) somaclones. Percentages of variation (number of polymorphic loci/total number of detected loci) are given.

Table 3: Polymorphic MSAP bands present in somaclones irrespective of cultivar origin.

Primers	Locus (size in bp)	Syrah	Chardonnay	Total
E32HM35	373	2	2	4
E33HM46	343	2	5	7
	352	2	4	6
E42HM84	303	3	5	8
	488	1	3	4
	490	2	2	4
E45HM34	212	3	7	10
	242	3	2	5
E46HM84	333	1	3	4
	358	3	7	10
	384	2	4	6

The magic of heterosis

The Hebrew University of Jerusalem



הקרן הלאומית למדע

eusol

Uri Krieger[1], Zachary B Lippman[2] & Dani Zamir[1]

Intercrossing different varieties of plants frequently produces hybrid offspring with superior vigor and increased yields, in a poorly understood phenomenon known as heterosis[1,2]. One classical unproven model for heterosis is overdominance, which posits in its simplest form that improved vigor can result from a single heterozygous gene[3–8]. Here we report that heterozygosity for tomato loss-of-function alleles of *SINGLE FLOWER TRUSS* (*SFT*), which is the genetic originator of the flowering hormone florigen, increases yield by up to 60%. Yield overdominance from *SFT* heterozygosity is robust, occurring in distinct genetic backgrounds and environments. We show that several traits integrate pleiotropically to drive heterosis in a multiplicative manner[9], and these effects derive from a suppression of growth termination mediated by *SELF PRUNING* (*SP*), an antagonist of *SFT*. Our findings provide the first example of a single overdominant gene for yield and suggest that single heterozygous mutations may improve productivity in other agricultural organisms.

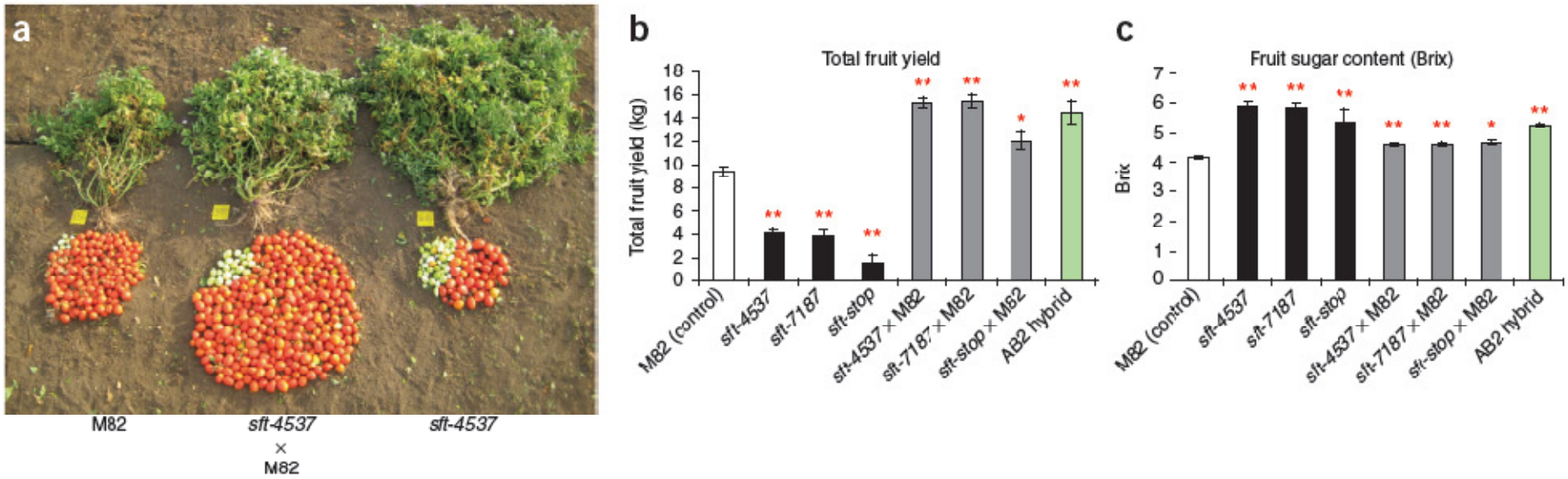


Figure 1 Heterozygosity for loss-of-function mutations in *SFT* drives heterosis in tomato. (**a**) Representative plant and total fruit yield from a high-yielding M82 inbred control plant (left), a low-yielding homozygous loss-of-function mutant allele of *SFT* (*sft-4537*, right; Online Methods) and a highly heterotic *sft-4537*/+ heterozygote (middle). All genotypes are isogenic in the M82 background. (**b**) Statistical comparison of mean values (± s.e.m.) for total fruit yields between three independently derived *sft/sft* homozygous mutants (carrying the *sft-4537* weak allele, *sft-7187* strong allele and *sft-stop* strong allele, respectively; Online Methods), the inbred M82 control and the F_1 *sft*/+ hybrids of the *sft/sft* mutants with M82. Total fruit yields from all three *sft*/+ heterozygotes were heterotic over M82 controls, and *sft-4537*/+ and *sft-7187*/+ heterozygotes achieved the same yields as AB2, which is a leading commercial processing-tomato hybrid. (**c**) Statistical comparison of mean values (± s.e.m.) for fruit sugar content (Brix value) showing an intermediate effect for *sft*/+ heterozygotes relative to M82 controls (low sugar) and *sft/sft* homozygotes (high sugar). Lines marked with asterisks are significantly different from the M82 control according to the 'compare with control' (Dunnett's) method: $*P < 0.05$, $**P < 0.01$. Similar results were obtained using multiple comparison analysis (Tukey-Kramer test; $**P < 0.05$) for total fruit yield, which revealed a significant difference between AB2 and *sft*/+ heterozygotes compared to M82 plants and *sft/sft* homozygotes. For Brix values, all four groups of genotypes were significantly different from each other (Tukey-Kramer test; $**P < 0.05$).

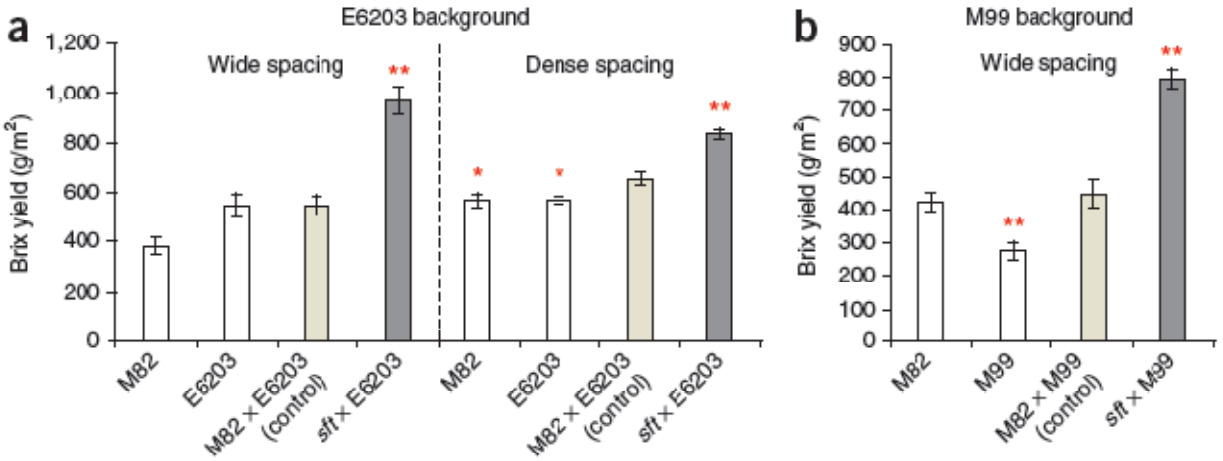


Figure 2 *sft*/+ heterozygosity causes heterosis in distinct genetic backgrounds and growth conditions. In the tomato industry, genotypes with high yield and Brix value (that is, high values of Brix-yield, the multiplied output of Brix and total fruit yield measured in g/m^2) are the most efficient for the production of various tomato concentrates. (**a**) Statistical comparison of Brix-yield between *sft*/+ heterozygotes in the background of a full-genome hybrid between M82 and the processing-tomato line E6203 (dark gray) (Online Methods), the homozygous inbred lines M82 and E6203 (white) and the hybrid (M82 × E6203) control (light gray). Experiments were performed in both wide- and dense-spacing conditions (Online Methods). (**b**) Statistical comparison of Brix-yield between *sft*/+ heterozygotes in the background of the large-fruited fresh market tomato line M99 (dark gray) (Online Methods), the homozygous inbred lines M82 and M99 (white) and the hybrid controls (M82 × M99) (light gray). The mean values (± s.e.m.) for each genotype marked by asterisks reflect a significant difference from the control hybrids according to the 'compare with control' (Dunnett's) method: $*P < 0.05$, $**P < 0.01$. Similar results were obtained using multiple-range means comparison (Tukey-Kramer test; $**P < 0.05$), which revealed a significant difference between *sft*/+ heterozygotes and their corresponding controls.

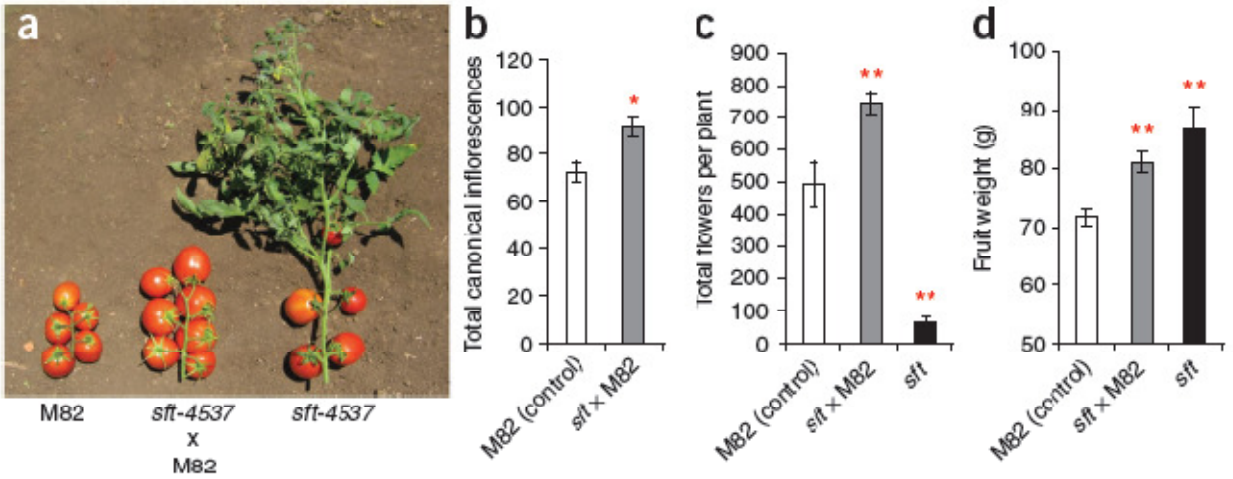
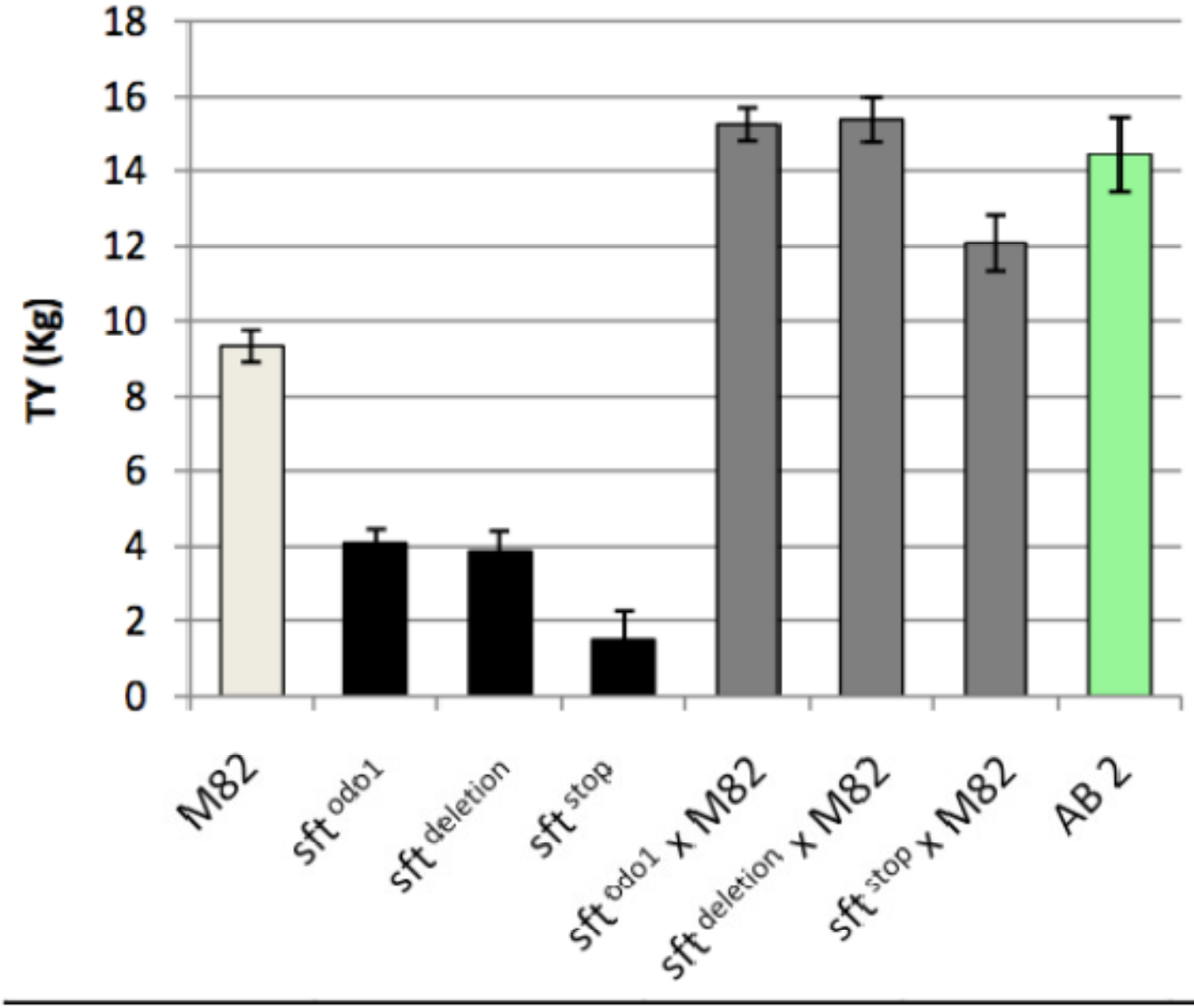


Figure 3 *SFT*-dependent heterosis arises from multiple phenotypic changes on component traits that integrate to improve yield. (**a**) Representative inflorescences from M82 plants (left), *sft*/*sft* homozygous mutants (right) and *sft*/+ heterozygotes (middle). The *sft*/*sft* homozygotes produce only a few inflorescences before reverting to indeterminate vegetative branches that infrequently produce single fertile flowers, which were counted. Because canonical multiflowered inflorescences almost never form, *sft*/*sft* mutant plants have the fewest inflorescences, flowers and fruits of any genotype. (**b**–**d**) Quantification and statistical comparison of three component traits for yield. (**b**) *sft*/+ heterozygotes (dark gray) produce more inflorescences compared to M82 plants. As canonical inflorescences almost never form in *sft*/*sft* homozygous mutants, no data was collected for this genotype. (**c**) *sft*/+ heterozygotes produce the most flowers per plant of all genotypes (are overdominant) and show an additive effect for fruit weight (**d**), with a *d*/[*a*] value of 0.25. Mean values (± s.e.m.) were compared to the M82 isogenic line (white) using the 'compare with control' (Dunnett's) method when three genotypes were present, and a *t*-test analysis was performed when two genotypes were present (total inflorescence). Significant differences compared to M82 plants are represented by asterisks: $*P < 0.05$, $**P < 0.01$.

Single gene heterosis in sft/+ heterozygotes is independent of mutant allele



A flow chart describing the experimental ODO breeding method