Supporting Information

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SI Text

Construction and Genotyping of Cytolines. The construction of the 56 cytolines is illustrated in Fig. 1. The genetic composition of the plants throughout the cytoline construction is illustrated in Fig. S1. Three recurrent backcrosses with the nuclear donor parent were realized on 54 from the 56 possible F1s of the diallele cross. F1 seeds from reciprocal crosses between Bur-0 and Ita-0 did not germinate whatever the conditions tested. To obtain the two concerned cytolines, we started backcrosses with the nuclear donor on bridge genotypes. Specifically, a plant from the cross Bur-0 × [Jea × Ita-0] F1 was backcrossed with Ita-0 for the Bur-0^{cy}Ita-0^{nuc} combination; a plant from the cross [Ita-0 × Jea] F1 × Bur-0 was back-crossed with Bur-0 for the Ita-0^{cy}Bur-0^{nuc} combination. Consequently, the genotyping of these cytolines was designed to discriminate Bur-0, Ita-0 and Jea alleles.

For each combination, 29 plants from the third backcross were genotyped with a set of 384 SNP markers (55), among which 134 on average were informative, according to the considered combination. To keep the distance between two genotyped positions below 3 Mb, and the distance between the last and first genotyped positions and the telomeres below 1 Mb, microsatellites were used in those intervals too large between informative SNPs. Among the 56 cytonuclear combinations, 42 cytolines were obtained at this stage. For the 14 remaining combinations, 24 or 48 plants from the selfing descent of plants chosen on their genotype were grown and genotyped at the position(s) were the mother plant was heterozygous to select the corresponding cytoline among the progenies fixed with the nuclear donor allele. The rule was sometimes relaxed in the centromeric regions where polymorphic markers were difficult to find and meiotic recombination is known to be rare. The number of markers used for each cytoline is available in Table S1. The complete list of the markers, with their positions in the genome, are available on the Versailles *Arabidopsis* Stock Center website (publiclines.versailles.inra.fr/).

The cytoplasm of cytolines was verified by sequencing intergenic chloroplastic regions as previously described (25).

Seed Production of Cytolines. Seeds of the 56 cytolines and their eight parental accessions were produced in a large growth chamber (56 m^2, light 16 h at 21 °C, dark 8 h at 18 °C). Sixteen plants of each genotype were grown. The plants were placed according to an experimental scheme designed to randomize the environmental heterogeneities in the chamber, known to be mainly due to border effects. One hundred twenty-eight plants were disposed on each of the eight tables in the chamber (Fig. S2). Plants were sown by groups of genotypes sharing the same nucleus. Seeds of the male sterile cytoline 39CV (Sha^{cy}Cvi-0^{nuc}) (47) were produced by hand pollination with pollen of the surrounding Cvi-0 plants. At the end of their life cycle (i.e., when siliques started to dry), plants were placed in a drying chamber and watering was stopped until complete drying of the plant. Plants were individually harvested and their seed production weighted. Bulks were made with equivalent amounts of seeds produced by each plant of a given genotype.

Four cytolines were still unsatisfactory at the start date of the field experiment, namely Blh-1^{cy}Sha^{nuc}, Bur-0^{cy}Ita-0^{nuc}, Ct-1^{cy}Ita-0^{nuc}, and Ct-1^{cy}Jea^{nuc}, and were therefore not included in this study.

Field Experiment and Phenotypic Characterization. An experiment of 2,700 *A. thaliana* plants was set up at the University of Lille 1 (North, France). The field experiment was organized in five blocks, each one being represented by nine arrays of 66 individual bottom-pierced wells (11 lines × 6 columns, Ø4 cm, vol. ~38 cm^3) (TEKU, JP 3050/66) filled with damp standard culture soil (Huminsubstrat N3; Neuhaus). Each block corresponded to an independent randomization of 540 plants with nine replicates per cytoline (n = 52) and nine replicates per parental accession (n = 8). In each block, the remaining 54 wells were left empty.

Five seeds were sown in each well on 11 March 2013 to mimic the spring seasonal germination cohort observed in natural populations of *A. thaliana* in the North of France. Germination was promoted by stratifying seeds four days at 4 °C in a cold chamber. After the stratification treatment, arrays were preventively treated against dark-winged fungus gnats (Vectobac; 8 mL/L) and placed for 28 d in a frost-free greenhouse that mimics outdoor conditions (no additional light or heating) but protects seeds from rainfall. To reduce microenvironmental variations, arrays were rotated daily in the cold chamber and in the greenhouse. Germination date and germination rate were monitored in the frost-free greenhouse during 13 d after the stratification treatment (see below). Wells were thinned to two seedlings and one seedling 14 and 20 d after the stratification treatment, respectively. Thereafter, and in the main text, the time after sowing is meant counted from the end of the stratification treatment.

Twenty-eight days after sowing, arrays were transported outside to a field located at the University of Lille 1. For each block, the nine arrays were organized according to a grid of three columns and three lines. Soil was tilled to allow arrays to be slightly buried, thereby facilitating root development. Plants were protected from herbivory by vertebrates and slugs as described in ref. 56.

Each plant was scored for a total of 28 phenotypic traits related to germination (n = 5), phenology (n = 4), resource acquisition (n = 3), architecture and seed dispersal (n = 5), fecundity (n = 10), and survival (n = 1) (Dataset S1):

Germination: Germination time (GERM) was measured as the number of days between sowing and the emergence of the first seedling. Using a phenological model integrating both photoperiod length and temperature (56), GERM was scaled in photothermal units (PTUs). Germination percentage was estimated 4, 5, 6, and 13 d after sowing (PGERM4, PGERM5, PGERM6, and PGERM13).

Phenology: Bolting time (BT), flowering interval (INT), and the reproductive period (RP) were scored as the time intervals between germination date and bolting date, between bolting date and flowering date, and between flowering date and date of maturation of the last fruit, respectively. BT, INT, and RP were scaled in PTU. By summing these three phenological traits, we estimated the length of the life cycle (LCYCLE).

Resource acquisition: rosette surface area (AREA expressed in cm^2) and rosette perimeter (PERIM expressed in cm) were measured using a nondestructive approach 28 d after sowing (Fig. S3). At the start of flowering, the maximum diameter of the rosette measured at the nearest millimeter was used as a proxy for plant size (DIAM).

Architecture and seed dispersal: After maturation of the last fruit, the above-ground portion was harvested and stored at room temperature until further phenotyping. Plants were phenotyped for the following architectural and seed dispersal related traits: height from soil to the first fruit on the main stem (H1F), maximum height (HMAX), number of primary branches on the main

stem (NPB), number of basal branches (NBB), and total number of branches (TOTB = NPB + NBB).

Fecundity: Because the number of seeds in a fruit is highly correlated with fruit length (56, 57), total seed production was approximated by total fruit length (FITTOT). Seed production is a good proxy for fecundity in a highly selfing annual species like *A. thaliana* (51). FITTOT was obtained by adding the fruit length produced on the main stem (FITSTEM), the primary branches on the main stem (FITPB), and the basal branches (FITBB). These estimates of fruit length were obtained by counting the number of fertilized fruits produced on each type of branches (FRUITSTEM, FRUITPB, and FRUITBB) and multiplying these counts by an estimate of their corresponding fruit (or silique) length (SILSTEM, SILPB and SILBB), estimated as the average of three representative fruits. We also calculated three ratios corresponding to the percentage of seeds produced by one branch type as a function of the total amount of seed produced: RSTEM = FITSTEM/FITTOT, RPB = FITPB/FITTOT, and RBB = FITBB/FITTOT. We also estimated the rate of fruit abortion (STERILITY) as the number of aborted fruits divided by the total number of fruits.

Survival: All plants that germinated but did not survive were counted as dead (SURVIVAL = 0). Harvested plants were counted as alive (SURVIVAL = 1).

Because all plants carrying a nucleus from Ita-0 were late flowering in this study, they were not able to complete their life cycle before summer heat. Consequently, postflowering traits were not measured on the Ita-0 parental accession, as well as on the cytolines with the Ita-0 nucleus.

Due to the absence of basal branches in most cytolines (Dataset S1), the traits related to basal branches (FITBB, FRUITBB, SILBB, and RBB) were not statistically analyzed in this study.

Data Analysis.

Model. Each trait was modeled separately using the following mixed model (1):

$$Y_{bncij} = \mu + \alpha_b + \beta_n + \gamma_c + (\alpha\beta)_{bn} + (\beta\gamma)_{nc} + L_{i(b)} + C_{j(b)} + E_{bncij},$$

where Y_{bncij} is the phenotype of the cytoline with nucleus n and cytoplasm c, measured on the ith line and jth column of block b. Parameters α_b, $L_{i(b)}$ and $C_{j(b)}$ correspond to the (fixed) effect of block b and the (random) effects of line i and column j within block b, respectively. These three effects account for the environmental variation within the experimental field. Parameters β_n, γ_c and $(\beta\gamma)_{nc}$ correspond to the main fixed effects of nucleus n and cytoplasm c and their interaction, respectively. A block × nucleus interaction parameter $(\alpha\beta)_{bn}$ was also added to account for observed phenotypic differences between nuclei across blocks. E_{bncij} is the error term. Depending on traits, the error variance was chosen to be either homogeneous or nucleus (i.e., heterogeneous) dependent

$$E_{bncij} \hookrightarrow \mathcal{N}(0, \sigma^2), i.i.d.(\text{homogeneous})$$
$$E_{bncij} \hookrightarrow \mathcal{N}(0, \sigma_n^2), indpt(\text{heterogeneous}).$$

For each trait, selection between homogeneous or heterogeneous assumption for the variance of the error term was performed on the basis of the BIC criterion.

As illustrated in Fig. 3, accounting for heterogeneous error variance was relevant for many traits, and significantly improved the accurate identification of parental pairs contributing to cytonuclear interactions. We also considered the inclusion of block × cytoplasm and block × cytoplasm × nucleus interactions in the model. However, adding these extra terms precluded the heterogeneous error variance assumption due to numerical instability [nonconvergence of the restricted maximum likelihood (ReML) procedure, inconsistent estimated effects, and/or degrees of freedom for parental pair contrasts]. Nonetheless, fitting the model with the additional interaction terms and homogeneous error variances for each trait led to results similar to those obtained with the mixed model (1): the same cytoplasm × nucleus interactions were detected across traits, except for the traits INT and FRUITPB (results not shown).

Because variation in rosette surface area and rosette perimeter may indirectly result from variation in germination time, the term GERM was also added as a covariate in the statistical model for the traits AREA and PERIM. All random effects were assumed to be Gaussian and independent, with a mean equal to 0. The line and column variances are σ_l^2 and σ_c^2, respectively.

Inference was performed using ReML estimation, using the PROC MIXED procedure in SAS 9.1 (SAS Institute) for all traits with the exception of SURVIVAL, which was analyzed using the PROC GLIMMIX procedure in SAS 9.3. For all traits and genotypes, LSMs were computed.

Test for interactions in specific pairs of parents. To identify pairs of parents that contribute to the nucleus × cytoplasm interaction, the hypothesis H0 $\{[(\beta\gamma)_{kl} - (\beta\gamma)_{kk}] - [(\beta\gamma)_{lk} - (\beta\gamma)_{ll}]\}$ was tested for all pairs of parents (k,l) and all quantitative traits. A global correction for multiple testing was performed to control FDR (54) at a nominal level of 5%.

Cytoplasmic Diversity in a Local Metapopulation of *A. thaliana*. To evaluate cytoplasmic diversity in the local metapopulation TOU (37, 51), polymorphisms were analyzed (i) in four chloroplast intergenic regions (MatK-trnK, ndhC-trnV, rbcL-accD, ndhF-rpl32) for 24 individuals located in 11 stands (TOU-A1-41, TOU-C-2, TOU-D-5, TOU-E-7, TOU-F-1, TOU-I-2, TOU-P-6, TOU-Q-2, TOU-R-9, TOU-S-1, TOU-T-1, TOU-T-2, TOU-T-3, TOU-T-4, TOU-T-5, TOU-T-6, TOU-T-7, TOU-T-8, TOU-T-9, TOU-T-10, TOU-T-14, TOU-T-15, TOU-T-16, TOU-T-17) and (ii) in two mitochondrial regions (atp8-orf107c, ccmC) for 12 individuals (TOU-A1-41, TOU-C-2, TOU-D-5, TOU-E-7, TOU-F-1, TOU-I-2, TOU-P-6, TOU-Q-2, TOU-R-9, TOU-S-1, TOU-T-1, and TOU-T-8) (Dataset S2). Individuals TOU-T-2 to TOU-T-7, TOU-T-9, TOU-T-10, and TOU-T-14 to TOU-T-17 were assumed to carry the same cytoplasm as their sister plants with the same chlorotype. All chloroplast and mitochondrial polymorphisms were analyzed as described in ref. 25. The pairwise distances between the 11 stands range from 50 m to 1 km.

This analysis grouped TOU-A1-41, TOU-C-2, TOU-F-1, TOU-R-9, TOU-T-8, TOU-T-9, TOU-T-10, TOU-T-14, TOU-T-15, TOU-T-16, and TOU-T-17 in the previously described Z cytotype, whereas TOU-D-5 and TOU-S-1 were grouped in the previously described AA cytotype. These two cytotypes are very close to both the cytotype of the parental accession Jea and the cytotype Y, where fell TOU-P-6 (25). TOU-Q-2, TOU-T-1, TOU-T-2, TOU-T-3, TOU-T-4, TOU-T-5, TOU-T-6, TOU-T-7, and TOU-T-8 were grouped in the previously described BA cytotype. TOU-E-7 and TOU-I-2 correspond to cytoplasmic haplotypes that have not been described in a set of 95 worldwide accessions.

A cytoplasmic phylogenetic network of the TOU cytotypes was constructed using the same strategy as in (25) (Fig. S5).

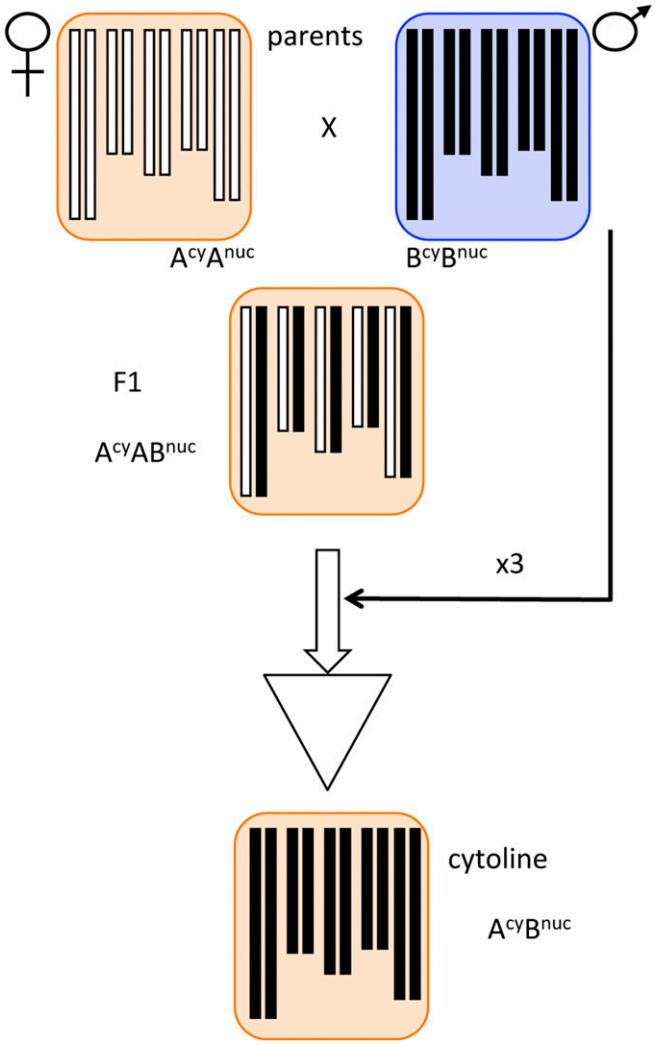

Fig. S1. Genetic composition of the plants throughout the cytoline construction. The 10 bars represent the five chromosome pairs of *A. thaliana*, with colors illustrating allelic origin (white: accession A, black: accession B). The background color of the rectangle stands for the origin of cytoplasm (orange: accession A, blue: accession B). After at least three backcrosses and genotyping, symbolized by the inversed triangle, the cytoline obtained possess the nuclear genome of parent B in the cytoplasmic background of parent A.

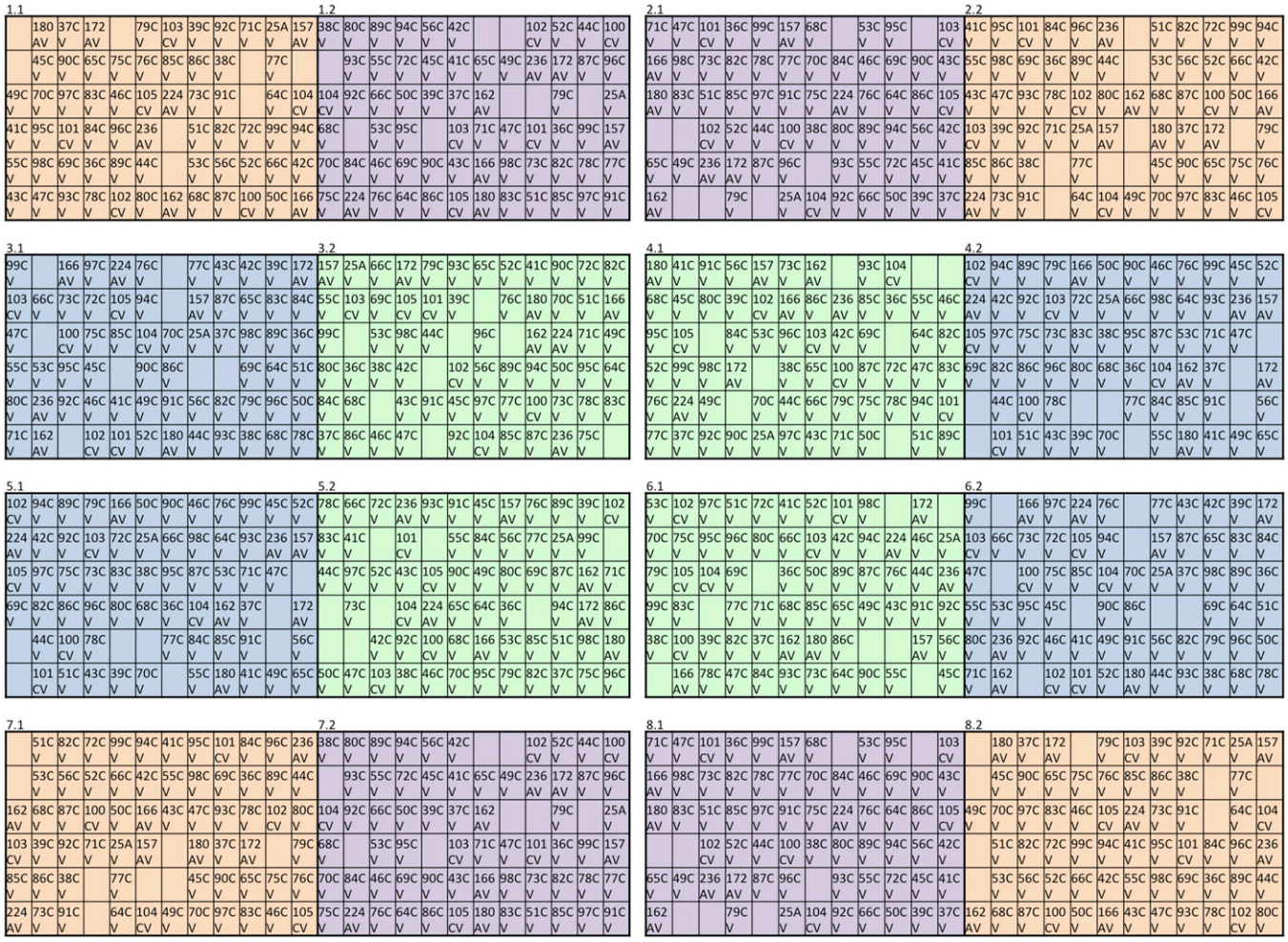

Fig. S2. Experimental design for seed production. Each of the eight tables present in the growth chamber was divided in two parts. One plant per genotype was placed in each half of table. The positions were randomized in each block (colors). Genotypes are designed according to their accession name in the Versailles stock center (AV suffix for parental accessions, CV suffix for cytolines; Table S1). Empty positions were left empty or used to grow seeds from sister plants of some cytolines (not used in this study).

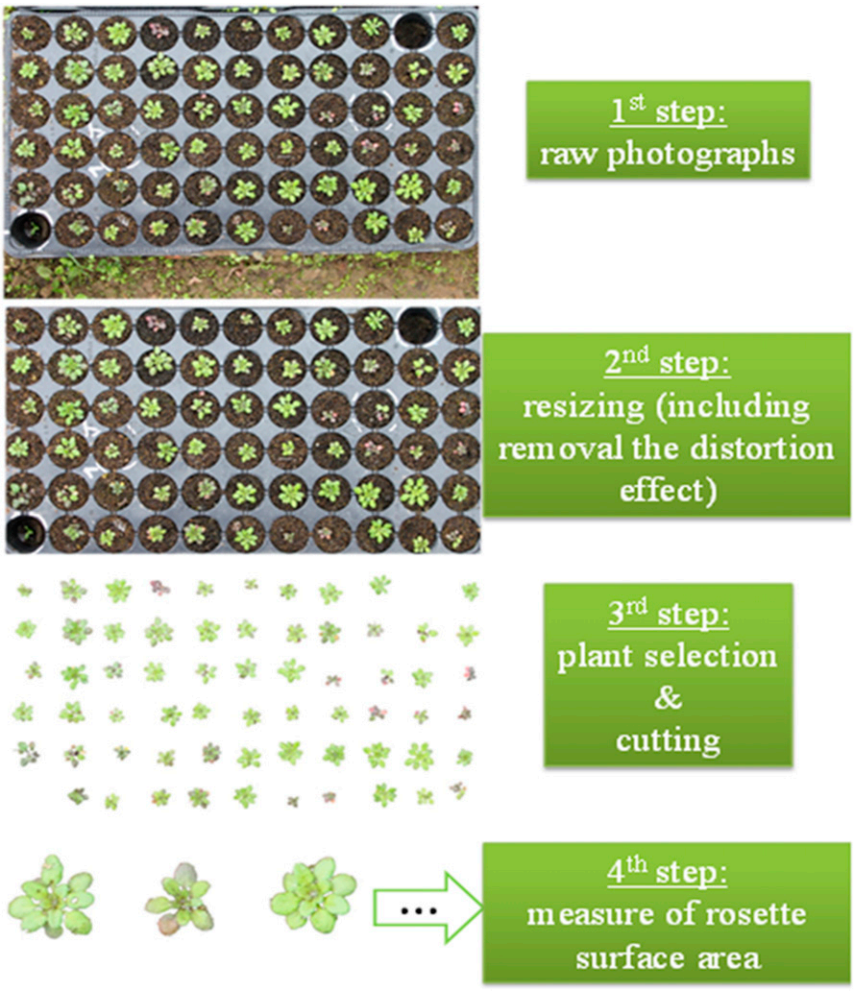

Fig. S3. Measure of rosette surface area (AREA). Rosette surface area (AREA) was measured using a nondestructive approach, by imaging each tray 28 d after sowing, and using a Canon digital camera (model EOS 500D). Each image of an array was submitted to a four-step treatment. In the first step, a photograph of each array was taken in the field. In the second step, the raw photographs were centered, detrapezoided, and resized using the software Adobe Photoshop CS3 Extented (version 10.0) and the software ImageMagick (version 7:6.6.2.6–1ubuntu4.2; Available from www.imagemagick.org/script/index.php). In the third step, plants were then manually selected from background using the software GIMP 2.8 (Available from www.gimp.org/). Background-free images were then cutted using a custom Perl script to obtain an individual background-free image for each plant of the experiment. In the fourth step, rosette surface area and rosette perimeter of each plant were then estimated using the ImageJ software (version 4.01; Universal Imaging). Rosette surface area was automatically estimated for each plant on pretreated photographs using the Area Set Measurement command, which first estimates the number of pixels defined by an object and then converts this number into a metric value of surface (cm^2 in this study). Rosette perimeter was automatically estimated for each plant on pretreated photographs using the Perimeter Set Measurement command, which estimates the length of the outside boundary of the rosette image.

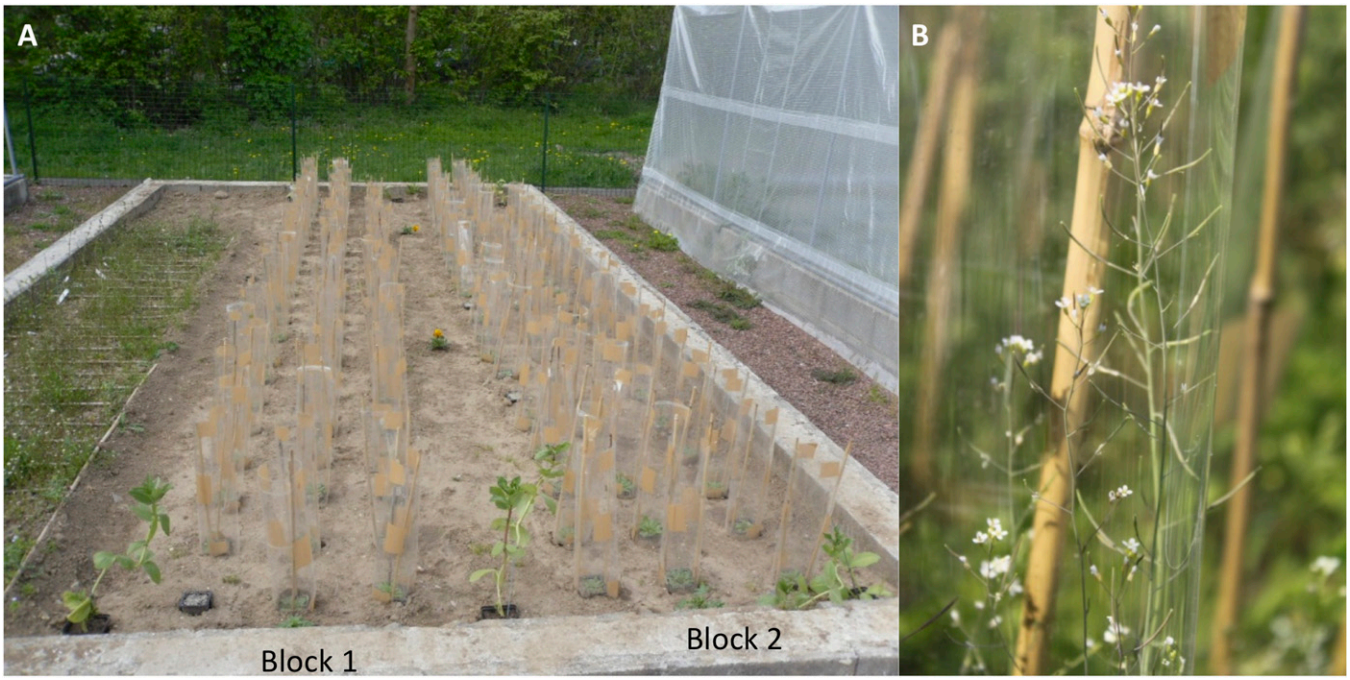

Fig. S4. Seed production of cytolines in a field located at the University of Lille. An experiment of 120 *A. thaliana* plants was organized in two blocks, each one being represented by 60 pots (9 × 9 × 9.5 cm, vol. ~480 cm^3; TEKU MQC) filled with damp standard culture soil (Huminsubstrat N3; Neuhaus). Each block is an independent randomization of 60 plants with one replicate per cytoline (n = 52) and one replicate per parental accession (n = 8). Experimental conditions in the frost-free greenhouse until the transport of pots outside to the field were similar to the conditions for the main experiment described in *SI Text*. (*A*) Overview of the experiment. (*B*) Close view of a $Sha^{cy}Cvi\text{-}0^{nuc}$ plant protected by a plastic tube to avoid out pollination from neighboring conspecifics.

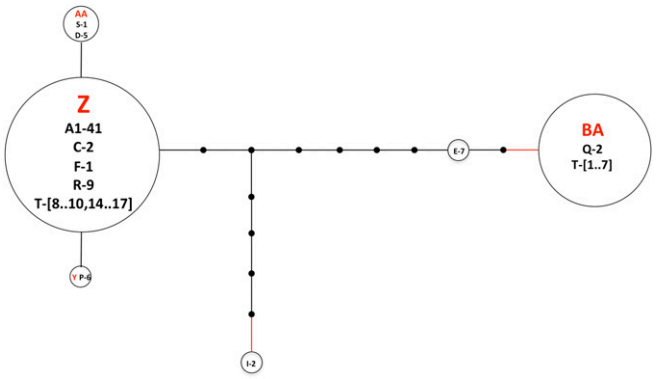

Fig. S5. Network of cytotypes found in the local metapopulation TOU. Each described cytotype is represented by a circle whose size is proportional to the number of individuals observed for this cytotype. Black dots represent hypothetical intermediates cytotypes that have not been observed in this study. The two red segments represent identical polymorphisms, whose distribution could lead to a reticulation of the network. Each segment between circles or dots represents one chloroplast or mitochondrial polymorphism. Capital red letters stand for cytotypes that were previously observed in ref. 2.

Table S1. Identification numbers and genomic composition of cytolines

Cytoplasm donor	Sha	Sha	Sha	Sha	Sha	Sha	Oy-0	Oy-0	Oy-0	Oy-0	Oy-0	Oy-0	Jea	Jea	Jea	Jea	Jea	Jea	Cvi-0
Nucleus donor	Blh-1	Bur-0	Ct-1	Cvi-0	Jea	Oy-0	Sha	Blh-1	Bur-0	Ct-1	Cvi-0	Jea	Blh-1	Bur-0	Ct-1	Cvi-0	Oy-0	Sha	Blh-1
Versailles Id	36CV	37CV	38CV	39CV	41CV	42CV	43CV	44CV	45CV	46CV	47CV	49CV	50CV	51CV	52CV	53CV	55CV	56CV	64CV
Inf. SNPs	139	143	123	112	136	130	131	144	153	139	134	132	148	130	123	121	133	127	159
MSAT	5	6	10	14	8	10	10	11	7	48	15	8	6	9	8	9	7	9	8
Cytoplasm donor	Cvi-0	Cvi-0	Cvi-0	Cvi-0	Cvi-0	Ct-1	Ct-1	Ct-1	Ct-1	Ct-1	Ct-1	Bur-0	Bur-0	Bur-0	Bur-0	Bur-0	Bur-0	Blh-1	Blh-1
Nucleus donor	Bur-0	Ct-1	Jea	Oy-0	Sha	Blh-1	Bur-0	Cvi-0	Jea	Oy-0	Sha	Blh-1	Ct-1	Cvi-0	Jea	Oy-0	Sha	Bur-0	Ct-1
Versailles Id	65CV	66CV	68CV	69CV	70CV	71CV	72CV	73CV	75CV	76CV	77CV	78CV	79CV	80CV	82CV	83CV	84CV	85CV	86CV
Inf. SNPs	139	125	127	136	138	140	140	128	118	144	118	174	138	133	134	123	139	159	143
MSAT	9	10	9	13	7	10	8	9	10	48	11	8	10	11	9	7	6	8	10
Cytoplasm donor	Blh-1	Blh-1	Blh-1	Blh-1	Ita-0	Ita-0	Ita-0	Ita-0	Ita-0	Ita-0	Ita-0	Blh-1	Bur-0	Ct-1	Cvi-0	Jea	Oy-0	Sha	
Nucleus donor	Cvi-0	Jea	Oy-0	Sha	Blh-1	Bur-0	Ct-1	Cvi-0	Jea	Oy-0	Sha	Ita-0	Ita-0	Ita-0	Ita-0	Ita-0	Ita-0	Ita-0	
Versailles Id	87CV	89CV	90CV	91CV	92CV	93CV	94CV	95CV	96CV	97CV	98CV	99CV	100CV	101CV	102CV	103CV	104CV	105CV	
Inf. SNPs	154	154	142	118	148	89	140	77	139	146	140	146	116	121	90	134	144	141	
MSAT	10	5	12	9	7	16	11	15	7	7	10	7	12	13	16	7	8	10	

The resource is available at the Versailles *Arabidopsis* Stock Center. The number of informative SNPs (Inf. SNPs) and microsatellite (MSAT) markers used to assess fixation of the recurrent parent nucleus are given. Details are available on the Versailles *Arabidopsis* Stock Center website (publiclines.versailles.inra.fr/).

Table S2. Postharvest storage of seeds used in the phenotyping experiment

Cytoplasm donor	Blh-1	Bur-0	Ct-1	Cvi-0	Ita-0	Jea	Oy-0	Sha	Blh-1	Bur-0	Ct-1	Cvi-0	Ita-0	Jea	Oy-0	Sha						
Nucleus donor	Blh-1	Blh-1	Blh-1	Blh-1	Blh-1	Blh-1	Blh-1	Blh-1	Bur-0	Bur-0	Bur-0	Bur-0	Bur-0	Bur-0	Bur-0	Bur-0						
Versailles Id	180AV	78CV	71CV	64CV	92CV	50CV	44CV	36CV	85CV	172AV	72CV	65CV	93CV	51CV	45CV	37CV						
Nb of days of storage (mean ± SD)	63.8 ± 5.5	61.3 ± 3.6	62.4 ± 3.4	63.9 ± 3.7	63.9 ± 7.3	62.8 ± 4.1	64.3 ± 4.8	60.9 ± 2.0	83.5 ± 3.0	82.8 ± 4.4	84.1 ± 4.9	81.9 ± 6.0	77.0 ± 4.7	85.1 ± 2.8	80.3 ± 4.2	84.1 ± 3.2						
Cytoplasm donor	Blh-1	Bur-0	Ct-1	Cvi-0	Ita-0	Jea	Oy-0	Sha	Blh-1	Bur-0	Ct-1	Cvi-0	Ita-0	Jea	Oy-0	Sha	Blh-1	Cvi-0	Ita-0	Jea	Oy-0	Sha
Nucleus donor	Ct-1	Ct-1	Ct-1	Ct-1	Ct-1	Ct-1	Ct-1	Ct-1	Cvi-0	Cvi-0	Cvi-0	Cvi-0	Cvi-0	Cvi-0	Cvi-0	Cvi-0	Ita-0	Ita-0	Ita-0	Ita-0	Ita-0	Ita-0
Versailles Id	86CV	79CV	162AV	66CV	94CV	52CV	46CV	38CV	87CV	80CV	73CV	166AV	95CV	53CV	47CV	39CV	99CV	102CV	157AV	103CV	104CV	105CV
Nb of days of storage (mean ± SD)	90.9 ± 1.7	89.3 ± 2.5	90.3 ± 1.8	91.2 ± 1.8	90.0 ± 0.8	89.8 ± 0.9	90.8 ± 1.4	90.1 ± 1.3	63.6 ± 6.1	65.7 ± 4.7	83.4 ± 2.7	83.6 ± 2.7	80.5 ± 2.9	80.2 ± 3.1	63.1 ± 3.2	74.3 ± 10.2	81.8 ± 5.5	85.2 ± 3.2	84.0 ± 0.0	78.9 ± 7.6	85.6 ± 3.4	82.0 ± 8.2
Cytoplasm donor	Blh-1	Bur-0	Cvi-0	Ita-0	Jea	Oy-0	Sha	Blh-1	Bur-0	Ct-1	Cvi-0	Ita-0	Jea	Oy-0	Sha	Bur-0	Ct-1	Cvi-0	Ita-0	Jea	Oy-0	Sha
Nucleus donor	Jea	Jea	Jea	Jea	Jea	Jea	Jea	Oy-0	Oy-0	Oy-0	Oy-0	Oy-0	Oy-0	Oy-0	Oy-0	Sha	Sha	Sha	Sha	Sha	Sha	Sha
Versailles Id	89CV	82CV	68CV	96CV	25AV	49CV	41CV	90CV	83CV	76CV	69CV	97CV	55CV	224AV	42CV	84CV	77CV	70CV	98CV	56CV	43CV	236AV
Nb of days of storage (mean ± SD)	79.8 ± 10.4	78.3 ± 9.7	86.5 ± 6.8	79.9 ± 9.8	76.7 ± 7.9	79.8 ± 10.0	79.6 ± 8.6	90.1 ± 1.6	89.4 ± 1.9	90.1 ± 2.1	88.8 ± 4.1	89.3 ± 2.3	89.8 ± 2.7	89.1 ± 3.5	88.7 ± 2.5	83.1 ± 1.8	85.0 ± 3.0	82.8 ± 4.7	82.2 ± 3.2	84.4 ± 3.4	82.4 ± 2.6	80.3 ± 3.6

Table S3. Cytonuclear interactions in specific pairs of parents

	Phenotypic traits																									
Pair of accession	GERM	PGERM4	PGERM5	PGERM6	PGERM13	AREA	PERIM	DIAM	BT	INT	RP	LCYCLE	H1F	HMAX	NBB	NPB	TOTB	FITTOT	FITSTEM	FRUITSTEM	SILSTEM	FITPB	FRUITPB	SILPB	RSTEM	RPB	STERILITY
Blh1/Bur0	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Blh1/Ct1	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Blh1/Cvi0	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Blh1/Ita0	Hom	Hom	NS	NS	NS	NS	NS	NS	NS	NS	NS	Het	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne
Blh1/Jea	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Blh1/Oy0	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Blh1/Sha	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne
Bur0/Ct1	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Bur0/Cvi0	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Bur/0/Ita0	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne
Bur0/Jea	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Bur0/Oy0	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Bur0/Sha	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Ct1/Cvi0	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Ct1/Ita0	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne
Ct1/Jea	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne
Ct1/Oy0	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Ct1/Sha	NS	NS	NS	NS	NS	NS	NS	NS	Het	NS	NS	NS	Het	NS	NS	Het	Het	NS	NS	NS	NS	Het	Het	NS	Hom	Hom	NS
Cvi0/Ita0	Hom	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne
Cvi0/Jea	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Cvi0/Oy0	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Cvi0/Sha	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	Het	Het	NS	Het	NS	NS	NS	NS	NS	NS	Het	NS	NS	Het	NS	NS	Het
Ita0/Jea	Hom	Hom	Het	Hom	Het	NS	NS	NS	NS	NS	NS	NS	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne
Ita0/Oy0	Hom	Hom	Het	Hom	Het	NS	NS	NS	NS	NS	NS	NS	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne
Ita0/Sha	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne	ne
Jea/Oy0	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Jea/Sha	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Oy0/Sha	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS

Significant cytonuclear interactions in a specific pair of accessions are highlighted in red. Hom and Het stand for the error variance chosen to be either homogeneous or heterogeneous, respectively (*Materials and Methods* and *SI Text*). AREA, PERIM rosette surface area and perimeter 28 d after sowing; BT, bolting time; DIAM, rosette diameter at flowering; FITPB, FRUITPB, SILPB, total fruit length, number of fruits, and mean fruit (silique) length on the primary branches; FITSTEM, FRUITSTEM, SILSTEM, total fruit length, number of fruits, and mean fruit (silique) length on the main stem; FITTOT, total fruit length = proxy of total seed production; GERM, germination time; H1F, height from soil to the first fruit on the main stem; HMAX, maximum height; INT, flowering interval; LCYCLE, length of the life cycle; NBB, number of basal branches; ne, not estimated due to (*i*) the missing of one of the following cytolines: Blh-1^{cy}Sha^{nuc}, Bur-0^{cy}Ita-0^{nuc}, Ct-1^{cy}Ita-0^{nuc}, and Ct-1^{cy}Jea^{nuc}, or (*ii*) plants with a Ita-0 nucleus for which postflowering traits were not measured; NPB, number of primary branches; NS, not significant; PGERM4, PGERM5, PGERM6, PGERM13, germination percentage 4, 5, 6, and 13 d after sowing, respectively; RP, reproductive period; RSTEM, RPB, percentage of seeds produced on the main stem and on primary branches; STERILITY, percentage of aborted fruits; SURVIVAL, completion of the life cycle; TOTB, total number of branches.

Other Supporting Information Files

Dataset S1 (XLS)
Dataset S2 (XLS)