Persistence of parental age effect on somatic mutation rates across generations in *Arabidopsis*.

Shashi Bhushan[1], Amit Kumar Singh[2], Yogendra Thakur[1] and Ramamurthy Baskar[1]*

1. Department of Biotechnology, Bhupat and Jyoti Mehta School of Biosciences, Indian Institute of Technology-Madras, Chennai 600 036, India.
2. Institut de Biologie Moléculaire des Plantes, UPR2357 CNRS, Université de Strasbourg, 12 rue du Général Zimmer, Strasbourg Cédex, 67084, France.

ABSTRACT

In the model plant *Arabidopsis thaliana*, parental age is known to affect somatic mutation rates in their immediate progeny but it is not clear if this age-associated effect on mutation rates persist across successive generations. Using a set of detector lines carrying the mutated *uidA* gene, we examined if a particular parental age maintained across five consecutive generations affected the rates of base substitution (BSR), intrachromosomal recombination (ICR), frameshift mutation (FS), and transposition. The frequency of functional GUS (blue colored spots) reversions were examined in seedlings as a function of identical/different parental ages across generations. When parental age remained constant, no change was observed in BSR/ICR rates in the first three generations, following which it drops significantly in the 4th and in most instances, is elevated in the 5th generation. On the other hand, with advancing parental age, BSR/ICR rates respectively remained high in the first two/three generations with a striking resemblance in the pattern of mutation rates. We followed a novel approach of identifying and tagging flowers pollinated on a particular day, thereby avoiding possible emasculation induced stress responses, as it may influence mutation rates. By and large there is no correlation in the expression of candidate genes involved in DNA repair to the pattern of reversion events and possibly, the expression patterns may correspond to the genomewide somatic mutations rates. Our results suggest a time component in counting the number of generations a plant has passed through self-fertilization at a particular age in determining the somatic mutation rates.

INTRODUCTION

Adaption during evolution heavily relies on variations occuredwithin DNA sequences (Futuyma, 2013). Stress of different kind experienced by organisms are known to affect the phenotypic traits of the offspring. Such environmental influences are known to be transmitted and termed transgenerational plasticity or parental environmental effects (Tariel et al., 2020)).

In certain situations, plants subjected to a particular stress are known to produce offspring that are better adapted to the same stress (Sultan, 1996; Galloway and Etterson, 2007; Holeski, 2007; Salinas and Munch, 2012). Thus the phenotype of an organism is also determined by the impact of various environmental/growth conditions experienced in earlier generations (Agrawal et al., 1999; Galloway and Etterson, 2007; Salinas et al., 2013).

Unlike animals, in flowering plants, a fraction of somatic mutations are known to be transmitted from reproductive tissues arising later in development (Bilichak and Kovalchuk, 2016). Thus, somatic mutations are also an important source of genetic variation in plants (Otto and Gerstein, 2006; Eyre-Walker and Keightley, 2007), and it is important to understand the frequency and regulators of such events. Spontaneous mutations largely arise as a consequence of impaired proofreading activity and errors occurring during DNA repair (Golubov et al., 2010; Martina et al., 2012). In *A. thaliana,* the single nucleotide mutation (SNM) rate is around 6.95×10^{-9} per site per generation, occurring mostly within transposable elements (TEs) residing in centromeric regions (Weng et al., 2019).

Plants are constantly exposed to biotic and abiotic stresses, triggering different classes of somatic mutations (Molinier et al., 2006). Such experiences are recorded in the somatic cell lineage, affecting the genome stability to confer better adaptation to the same stress in subsequent generations (Molinier et al., 2006; Boyko et al., 2007; Boyko and Kovalchuk, 2010; Bilichak and Kovalchuk, 2016). Thus, any reproductive cell derived from such somatic tissues would also transfer this recorded memory to the subsequent generation (Molinier et al., 2006). This phenomenon of the acquired memory is often referred to as transgenerational inheritance, and is defined as the ability of an organism to 'remember' the environmental conditions of the past at a molecular level, resulting in a subsequent change in the phenotype of the progeny (Tricker, 2015).

The induced somatic mutation rates in *Arabidopsis* are reported to persist for up to 4th generations, (Molinier et al., 2006) however other studies contradict the existence of this phenomenon (Pecinka et al., 2009; Groot et al., 2016). Furthermore, there are also reports suggesting that such transgenerational effects depends on the nature of the stress (Pecinka et al., 2009). Although transgenerational effects are known to be inherited through both the parents in a dominant manner (Molinier et al., 2006), some studies indicate that the influence of maternal gametes on the transgenerational effect is more significant than paternal gametes (Mosher, 2010; Boyko and Kovalchuk, 2010). Transgenerational effects are context-dependent and their reproducibility is reported to be low (Groot et al., 2016). Stochastic responses are part of successful evolutionary adaptations in irregularly changing

environments (Shahrezaei and Swain, 2008). Age-related accumulation of somatic mutations results in the inactivatation of random genes critical for somatic cell function (Failla, 1958; Szilard, 1958; Moorad and Promislow, 2008).

Previously, we reported that parental age of *Arabidopsis* influenced somatic mutation rates in their immediate progeny (Singh et al., 2015) and here demonstrate the persistence of this effect in its transgenerational progenies as well. Parental age at the time of reproduction has a strong influence on the patterns of somatic mutation across generations and this age-dependent information persists for a few generations after which there seems to be resetting of mutation s rates.

RESULTS

Using a set of *Arabidopsis* mutation detector lines (Liu and Crawford, 1998; Li et al., 2004; Azaiez et al., 2006; Auwera et al., 2008), we examined if a particular parental age affected the spontaneous BSR, ICR, FS and transposition rates in the next five consecutive generations. Self-pollinated plants of four different ages (38, 43, 48, and 53 days after sowing (DAS)) were grown, following which the respective reproductive ages were retained in the subsequent generations. (Fig. 1). The mutation rates were examined in two different ways. 1. Counting reversion events in seedlings obtained from plants of the same age set as depicted in Fig. 1. For instance, mutation rates were compared in seedlings of 38 DAS plants in five consecutive generations (comparison of same age (same colors) shown in Fig. 1). 2. Furthermore, we compared the mutation rates as a function of advancing parental age across generations. For eg., the mutations rates were compared across the different ages (colors) of the same generation, i.e. 38, 43, 48, and 53 DAS plants among F1 as in Fig. 1).

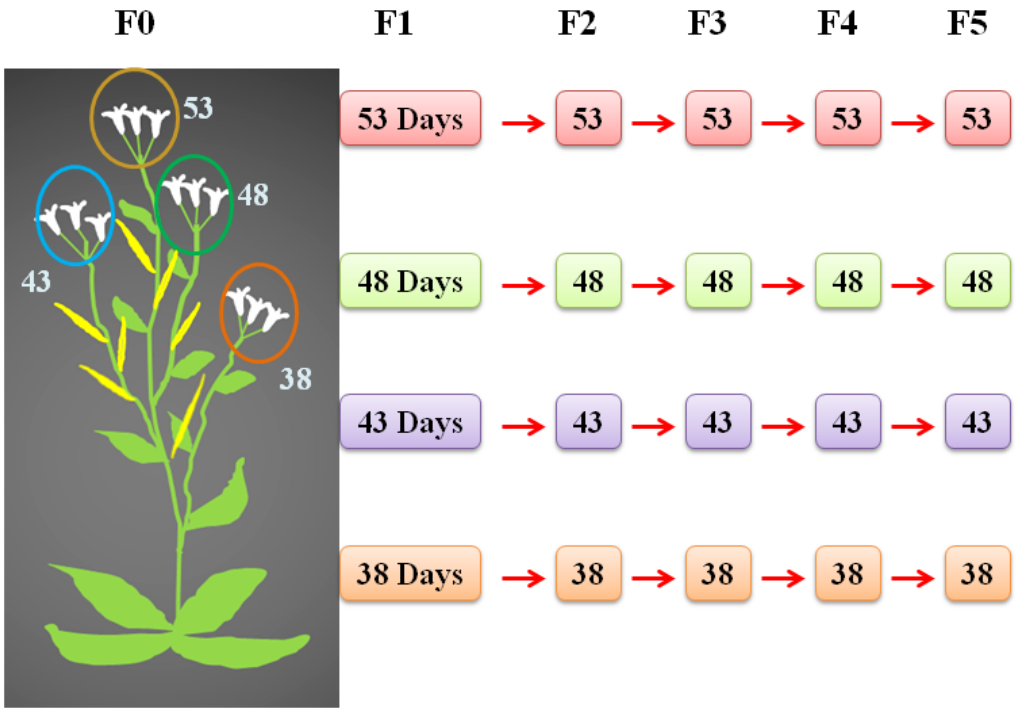


Figure 1. Selfing scheme: Flowers of different DAS were marked with different colored threads and in the subsequent generations also, the self-pollinating age was retained.

Normalization of Mutation Rates after Correcting the Cell Number and Ploidy Levels

Since ploidy levels, cell size, and their number vary significantly from seedlings obtained from plants of different ages (Singh et al., 2015), normalization of mutation rates in required. Plant cells are known to be uneven in size even within a particular tissue (Sugimoto-Shirasu and Roberts, 2003). In the leaf epidermal cells of *Arabidopsis*, a strong correlation exists between the size of the cell and the amount of DNA (Melaragno et al., 1993). Plant cells frequently undergo endoreduplication, resulting in higher ploidy per nucleus which is correlated with increased cell size as well (Sugimoto-Shirasu and Roberts, 2003; Singh et al., 2019). As a result, the individual cell size and their numbers significantly contribute to the overall leaf size (Tsukaya, 2003). Therefore, it is essential to normalize mutation rates, accounting for cell number, cell size, and average ploidy per nucleus in seedlings derived from plants of different ages and generations. As the leaf size is largely determined by the epidermis (Savaldi-Goldstein et al., 2007; Marcotrigiano, 2010), the fourth true leaf (excluding the cotyledons) of Columbia (Col-0) wild type plants were used to determine cell size and number (Singh et al., 2015). We used a scanning electron microscope (SEM) to count the number of adaxial epidermal cells in a specified area of the leaf and measured the cell size.

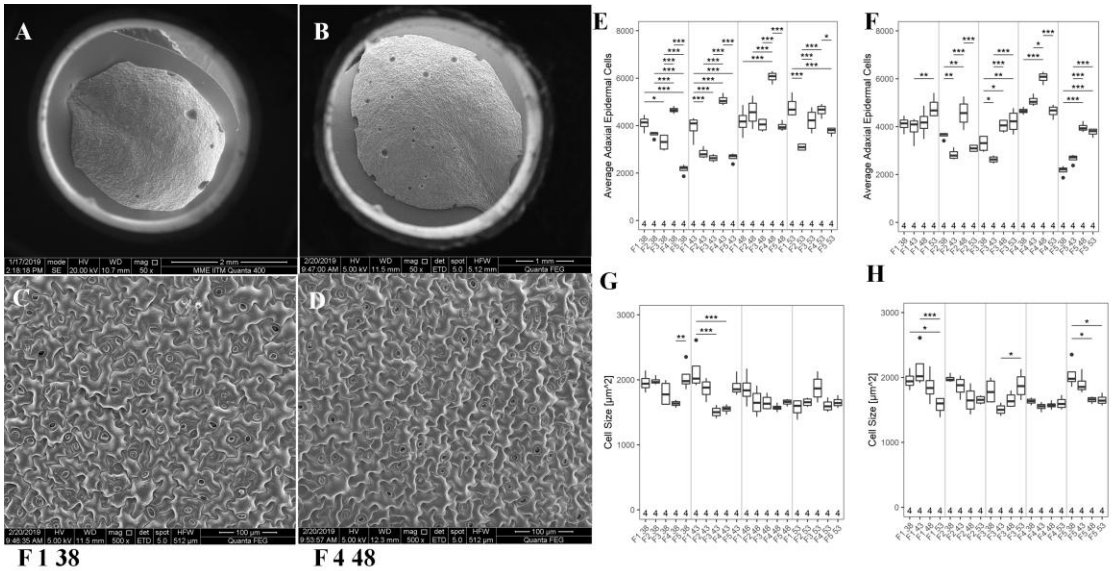


Figure 2. SEM image of the 4th true leaf from seedlings of A. F1 (38 DAS) and B. F4 (48 DAS) generations. Differences in leaf size (A-B) and cell size (C-D) from seedlings of A and B. E-F: The average adaxial epidermal cell number. G-H: The average cell size in three-week-old seedlings derived from parents of (G) identical age sets and (H) different ages. The numbers in X-axis indicates the biological replicates analyzed. *P* values were corrected for multiple testing. No asterisk represents, no significant differences. *, *P* < 0.05; **, *P* < 0.01; *, *P* < 0.001.**

As a function of constant or advancing parental ages, there was wide variation in the epidermal cell number (Fig. 2, E, F), and such differences were not apparent in the context of cell size (Fig. 2, G, H). Interestingly, as a function of fixed parental age, the epidermal cell number increases in the 4th, and drops significantly in the 5th generation (Fig. 2E), although this largely depends on the age group. Except for a few, the percentage of nuclei remained more or less constant in the first three age sets, and remarkably, the percentage of nuclei with 2X ploidy increases in the 4th generation, within a particular age group (Fig. 3, A, B). Depending on age/generation, there were minor differences in ploidy levels per leaf cell nucleus, however, in older ages (53 DAS), the variations in ploidy levels were higher different from one generation to the next (Fig. 3C). Hence, the mutation rates were corrected for heterogeneity as a result of genome numbers and differences in cell numbers (Table 1).

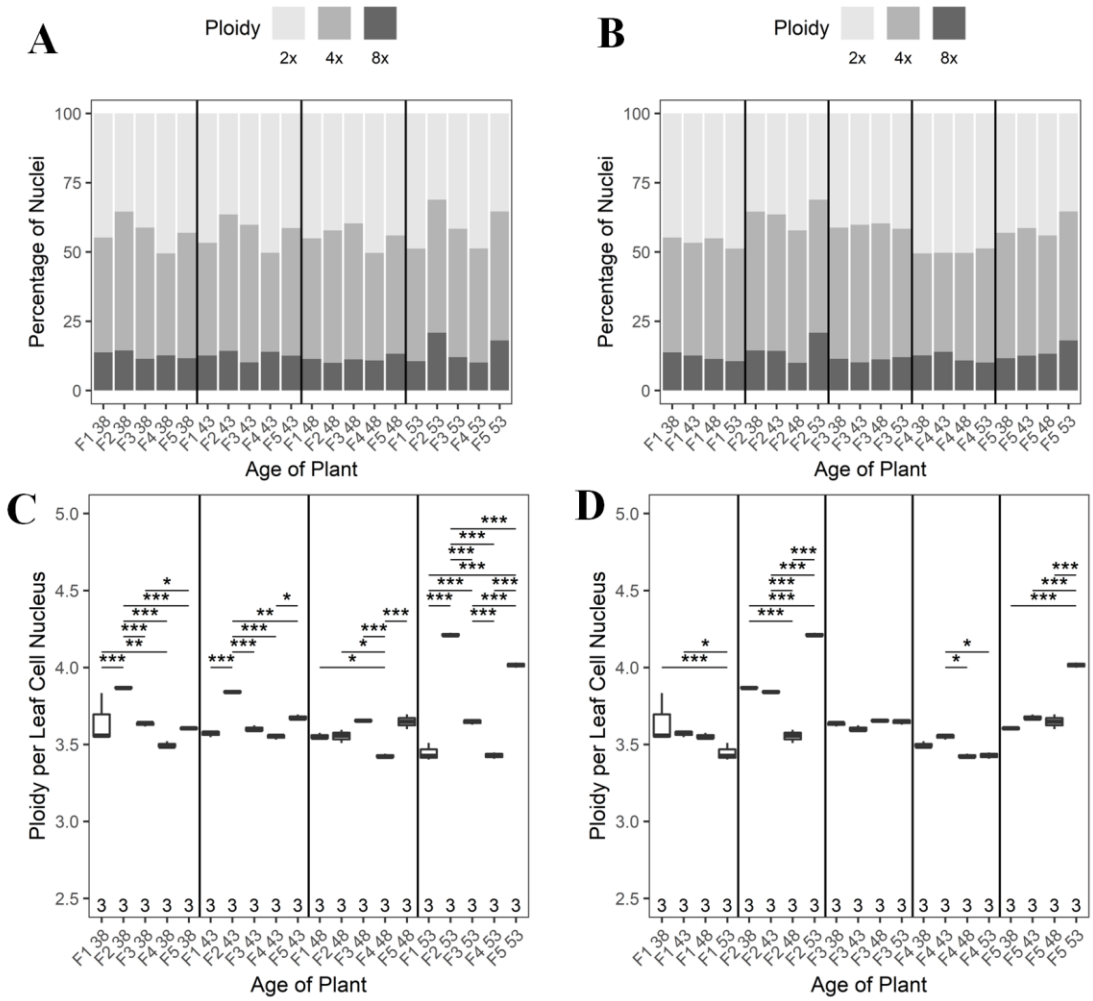


Figure 3. Comparison of ploidy levels across generations. The percentage of diploid, tetraploid, and octoploid nuclei as a function of (A) same and (B) advancing parental ages. Different shades of grey represent changes in ploidy levels. C-D: Ploidy per leaf cell nucleus as a function of C. Constant parental age, D. Different parental ages. The numbers along the X-axis of the graph shows the analyzed biological replicates. *P* values were corrected for multiple testing. No asterisk represents, no significant differences. *, *P* < 0.05; **, *P* < 0.01; *, *P* < 0.001.**

Epidermal Cells					Ploidy per Nucleus				
Age	n	Median	CIQR	Relative Cell No.	n	Median	CIQR	Relative Ploidy	Correction Factor
F1 38	4	4134.841645	0.074743099	1	3	3.557	0.0402	1	1
F1 43	4	4092.023519	0.111139791	0.989644555	3	3.577	0.0056	1.005622716	0.995209
F1 48	4	4175.036919	0.119608416	1.009721116	3	3.544	0.0051	0.996345235	1.006031
F1 53	4	4673.600815	0.120248471	1.130297413	3	3.425	0.0158	0.962890076	1.088352
F2 38	4	3686.811979	0.025377695	0.891645266	3	3.866	0.0013	1.086870959	0.969103
F2 43	4	2791.664624	0.097476684	0.675156358	3	3.841	0.0021	1.079842564	0.729063
F2 48	4	4565.716472	0.165895059	1.104205884	3	3.558	0.0121	1.000281136	1.104516
F2 53	4	3091.480092	0.081892202	0.747665898	3	4.209	0.0026	1.183300534	0.884713
F3 38	4	3310.743566	0.177374671	0.800694162	3	3.639	0.0036	1.023053135	0.819153
F3 43	4	2628.679586	0.078037259	0.635738877	3	3.594	0.0053	1.010402024	0.642352
F3 48	4	4049.544556	0.109844988	0.979371135	3	3.654	0.0027	1.027270171	1.006079
F3 53	4	4223.011129	0.160442252	1.021323545	3	3.651	0.0044	1.026426764	1.048314
F4 38	4	4650.910075	0.02811808	1.12480972	3	3.486	0.0055	0.980039359	1.102358
F4 43	4	5036.341781	0.046995477	1.218025311	3	3.556	0.0048	0.999718864	1.217683
F4 48	4	6083.262136	0.04447478	1.471220099	3	3.42	0.0035	0.961484397	1.414555
F4 53	4	4677.228272	0.066146604	1.131174703	3	3.43	0.0061	0.964295755	1.090787
F5 38	4	2214.953776	0.072334608	0.535680436	3	3.605	0.0025	1.013494518	0.542909
F5 43	4	2718.777308	0.057053435	0.657528762	3	3.668	0.0044	1.031206073	0.678048
F5 48	4	3930.042162	0.049012705	0.950469812	3	3.648	0.0132	1.025583357	0.974786
F5 53	4	3813.991401	0.053696917	0.922403257	3	4.016	0.0042	1.129041327	1.041431

Table 1. The mutation rates were normalized, after correcting the cell number and ploidy per nucleus from plants of various ages/generations. The correction factor was derived from a five-generation study of adaxial epidermal cell count and ploidy per nucleus of leaf cells. The Interquartile Range Coefficient (CIQR) was calculated as a non-parametric variance measurement in the style of the variance coefficient. The relative number of cells and the relative ploidy are the normalization values for generations F2, F3, F4, and F5 compared to F1, and for older ages (43, 48, and 53 DAS), the comparison was with 38 DAS plants. The correction factor was determined by combining the two values for standardization and was introduced before correcting the number of GUS spots. 'n' is the number of plants analyzed and median is the median of measurements.

This work is an extension of the study by Singh et al., (2015) investigating the effect of parental age on mutation rates which relied on manual self pollination. In this study, however, self pollinated flowers of particular DAS were tagged with colored threads to avoid a potential emasculation indued stress response which may distort the mutation rates (Fig. 4).

Comparsion of Reversion Rates after Manual and Natural Selfing

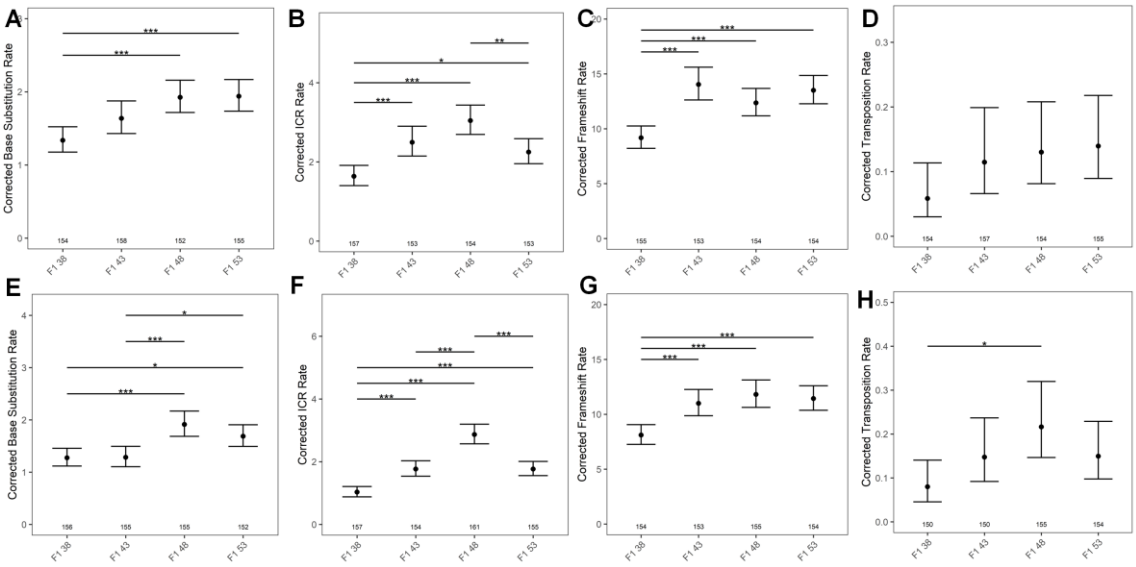


Figure 4. Two methods of selfing and its impact on mutation rates. The top panel represents somatic mutation rates after emasculation followed by manual selfing (A) BSR, (B) ICR, (C) FS and (D) Transposition and the panel below represents somatic mutation rates subsequent to tagging and marking self-fertilized flowers of particular DAS (E) BSR, (F) ICR, (G) FS and (H) Transpotion. The numbers along the X axis shows the number of seedlings analyzed. *P* values were corrected for multiple testing. No asterisk represents, no significant differences. *, *P* < 0.05; **, *P* < 0.01; *, *P* < 0.001.**

We compared the mutation rates following manual self-pollination and simultaneaously after marking self-pollinated flowers of a particular DAS with colored threads to ascertain if there are variations in the observed mutation rates. The pattern of mutation rates after normalization were largely similar, except in the case of frameshift and transposition events within the 43 DAS and 53 DAS respectively (Fig. 4, C, G and Fig. 4, D, H). In both, the mutation rate was slightly higher with manual self-pollination when compared to tagging. Although the pattern of mutations were similar, the rates were higher in seedlings obtained after manual self-pollination than from flowers that underwent natural selfing (Fig. 4A). The elevated mutation rates may possibly be due to emasculation indued stress responses, triggering genome-wide changes or due to physical injury during pollination from flowers of a different plant of the same age (which does not occur during natural selfing).

As a Function of Constant Parental age, C to T Transitions (BSR) are Stable in First Three Consecutive Generations

To determine the frequency of C to T transitions as a function of constant or differentparental ages across generations, we used the $1390_{T\text{-}C}$ detector line. In the open reading frame of the *uidA* gene, T is mutated to C at the 1390th position (Van der Auwera et al., 2008). In seedlings of 38, 43, and 48 DAS plants, the variation in BSR rates were not significant in the first three generations. However, in the 4th generation, seedlings from 38 and 48 DAS plants exhibited a significant drop in BSR, and thereafter, a significant increase in the 5th generation (Fig. 5A). Similarly, in seedlings from 43 DAS plants, a surge in BSR was observed in the 5th generation (Fig. 5A). Except for the seedlings obtained from the 53 DAS plants, the BSR increased in the 5th generation consistently. Taken together, our results suggest that BSR significantly depends on the number of generations a plant has undergone selfing at a particular age.

Younger Parents Produce Offspings with More BSR

By comparing mutation rates across different ages in five consecutive generations, we particularly observed high BSR in the first three generations of seedlings from 38 DAS plants compared to other ages (Fig. 5B). The BSR dropped significantly in seedlings of 43 DAS plants, and increased thereafter as a function of advancing parental age (48 and 53 DAS). Surprisingly, this pattern was observed only in the first two generations. In the 4th and 5th generations, there was no significant change in BSR, irrespective of parental age (Fig. 5B). These results reiterate the notion that BSR is strongly impacted by the the number of generations a plant has gone through selfing at a particular age.

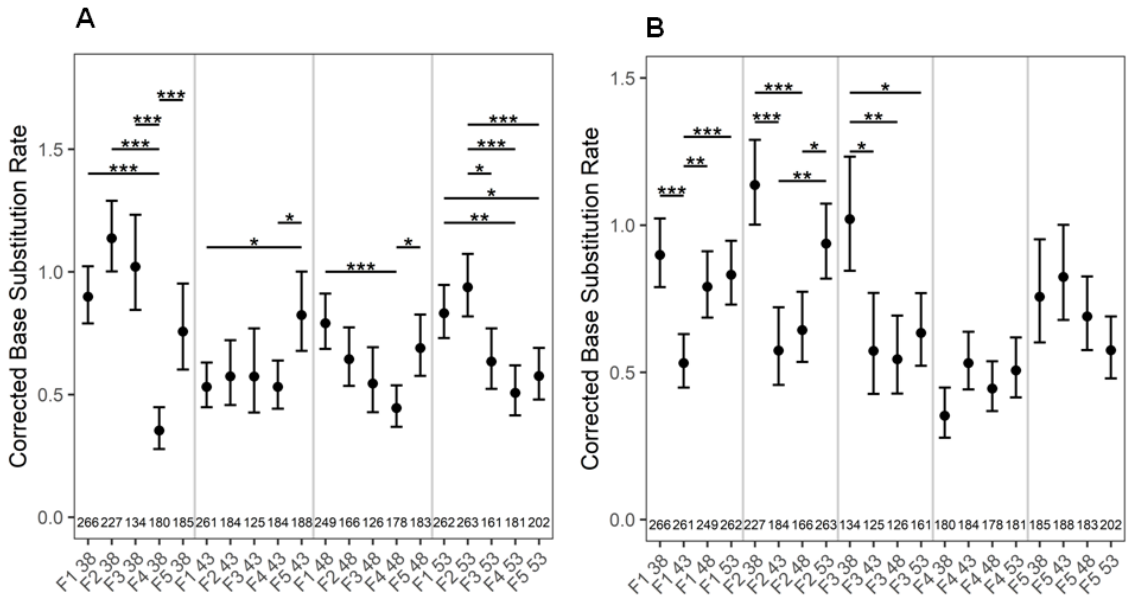


Figure 5. A-B: BSR as a function of A. constant, B. different parental age across different generations. The numbers along the X axis shows the number of seedlings analyzed. *P* values were corrected for multiple testing. No asterisk denotes no significant difference *. *P* < 0.05; **, *P* < 0.01; *, *P* < 0.001.**

ICR Rates are Stable as a Function of Constant Parental Age in Three Consecutive Generations

To examine the effect of reproductive age on ICR rates across generations, we utilized the detector line R2L1, containing two inverted catalase introns within the gene *uidA*. In this system, a recombination event between similar sequences of the catalase intron would result in a functional *uidA* gene, leading to the GUS expression (Li et al., 2004). With a constant age of 38 DAS, there was no significant change in ICR in the first four generations, but the rates significantly increased in the 5th generation (Fig. 6A). However, when the parental age was retained at 43 or 48 DAS, there was no change in ICR rates in the first three generations, following which it decreased in 4th but again surged in the 5th generation. Although such a pattern was also observed in seedlings obtained from 53 DAS plants, the increase in ICR rates was not significant in the 5^{th}generation.

Strikingly, like BSR, ICR rates shoot up in the 5th generation following the aforementioned pattern, and this phenomenon was observed across all ages. This suggests that ICR rates is determined by the number of generations a plant has been previously selfed at a particular reproductive age (Fig. 6A). Interestingly, there is a sigmoidal distribution of mutation rates upon comparison between different age sets across all generations (Fig. 6A).

ICR Rates Increases With Increasing Parental Age but Drops in Very Old Ages

Although, the increase in ICR rates (from seedlings of 38, 43, and 48 DAS) and the drop (in 53 DAS) were apparent in the first three generations, this pattern was not observed in the subsequent two generations (Fig. 6B). Thus, these observations suggest that the influence of advanced age on ICR rates is stronger in the first three generations, following which the influence gets weaker.

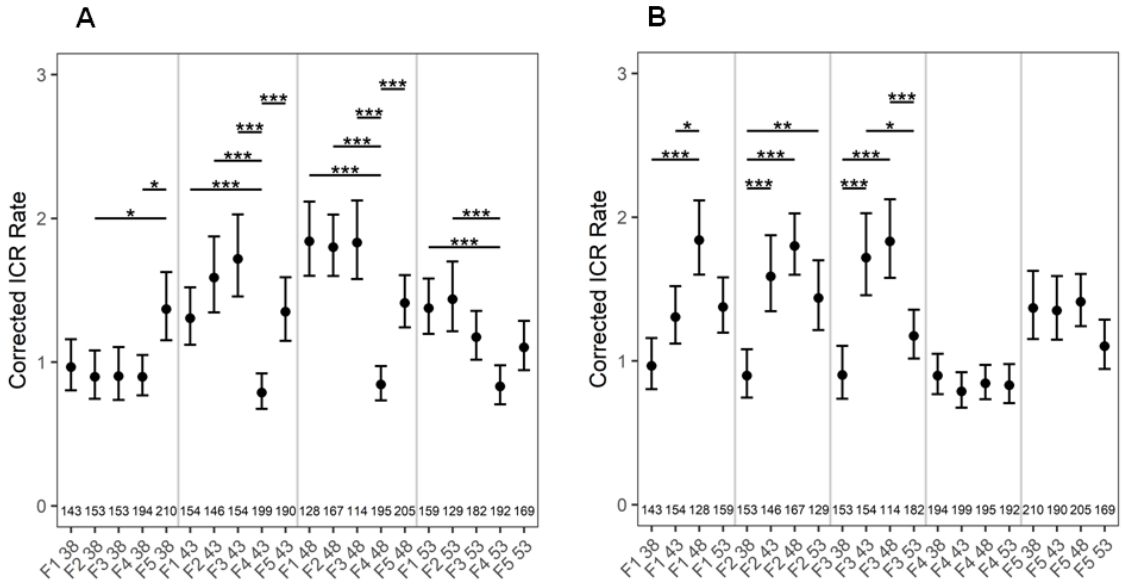


Figure 6. A-B: ICR rates as a function of A. constant, B. increasing parental age across different generations. The numbers at the bottom of the graph show the number of seedlings analyzed. *P* values were corrected for multiple testing. No asterisk represents no significant difference. *, *P* < 0.05; **, *P* < 0.01; *, *P* < 0.001.**

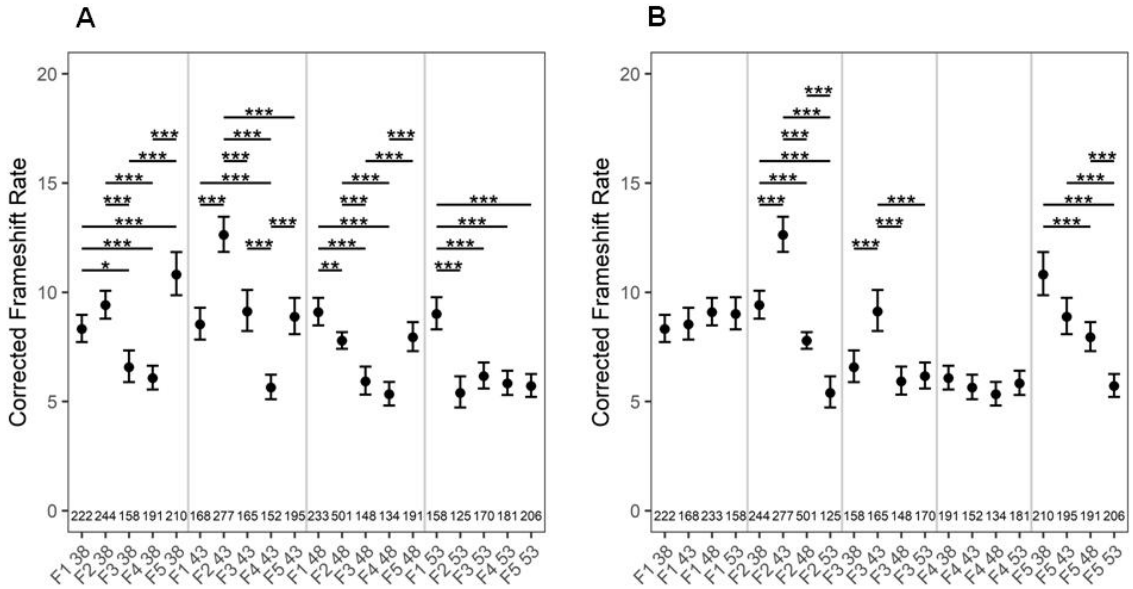


Figure 7. A-B: FS mutation rates as a function of A. fixed, B. increasing parental age across generations. The numbers at the bottom of the graph show the number of seedlings analyzed. *P* values were corrected for multiple testing. No asterisk denotes no significant difference. *, *P* < 0.05; **, *P* < 0.01; *, *P* < 0.001.**

Frameshift Rates Show a Stochastic Pattern As a Function Of Constant Parental Age Regardless Of Generation To score FS mutations as a function of constant or advancing parental ages, transgenic Col-0 plants containing out-of-frame guanine repeats (G10) in the *uidA* reporter gene (Azaiez et al., 2006) were used. The *uidA* gene function is restored either by the addition of two or deletion of one guanine nucleotide. FS rates from the 3rd generation dropped significantly, and this trend persists across subsequent generations or undergoes further reduction in later generations within seedlings obtained from 38, 43, or 48 DAS plants. However, the FS rates always increased in the 5th generation (Fig. 7A). An exception to this pattern was from the seedlings of 53 DAS plants, where FS rates dropped significantly from the 2nd and lasted till the 5th generation (Fig. 7A). Like BSR/ ICR, FS rates also shoots up significantly in the 5th generation, suggesting a time component in counting the number of generations a plant has passed through self-fertilization. If FS rates were compared as a function of advancing parental age across generations, the rates remained almost constant (38/48 DAS), or gradually declined with advancing age (53 DAS) (Fig. 7B).

Wide Fluctuation in Transposition Rates Across Same or Different Ages/ Generations

To score transposition rates as a function of constant/advancing parental age across different generations, transgenic *Arabidopsis* plants containing the transposable element *tag1* between a 35S promoter of Cauliflower mosaic virus (CaMV) and the *uidA* gene were used (Liu and Crawford, 1998). *tag1* excision allows the expression of *uidA* gene, resulting in blue colored spots upon a histochemical assay. Although transposition rates as a function of constant parental age exhibited a pattern of a increase succeeded by a decrease, the differences were insignificant, with few exceptions (Fig. 8A). The transposition rates were random compared to other classes of mutations (Fig. 8A, B).

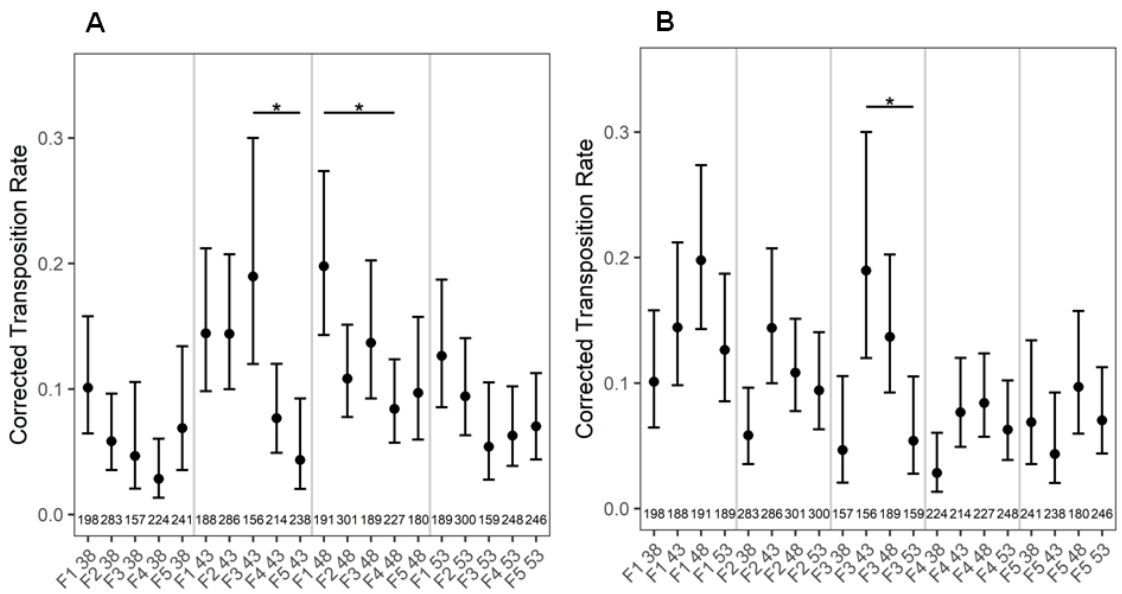


Figure 8. A-B: Transposition rates as a function of A. constant B. increasing parental age across different generations. The numbers at the bottom of the graph show the number of seedlings analyzed. *P* values were corrected for multiple testing. No asterisk represents no significant difference. *, *P* < 0.05.

Irrespective of Age/Generation, Somatic Mutations Falctuate particularly in Fourth and Fifth Generations.

We further wanted to ascertain if the shift in the mutation rates is significant within a certain generation, irrespective of age or conversely, if a significant change occurs at a certain age regardless of the generation. To this end, we combined the mutation rates across all ages in a particular generation (for a particular class of mutation type) and also independently combined the mutation rates across all five generations within a particular age/particular class of mutations.

BSR, ICR, and FS rates followed similar trends wherein rates underwent a small increase in the 2nd, a drop in the 3rd, followed by a significan reduction in the 4th generation and a subsequent increase in the 5th generation (Fig. 9 A, B, and C). Transposition rates also decresed significantly in the 4th but did not show a similar surge in 5th generation (Fig. 9 D). This strengthens our previous observation, where different classes of somatic mutations decreased in the 4th and increased in 5th generation except transpostions.

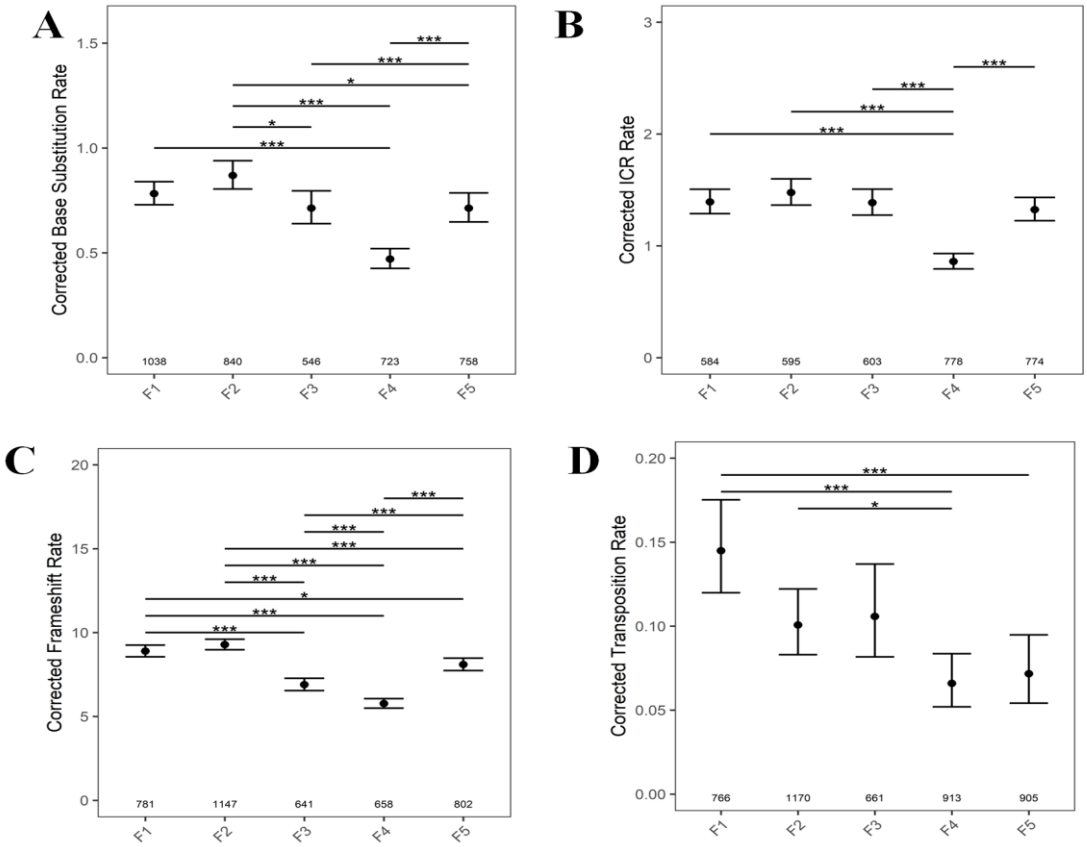


Figure 9. Sum total of mutation rates across generations (A) BSR, (B) ICR, (C) FS rates (D) Transposition rates in F1-F5 generation. The numbers along the X axis, show the numers of seedlings analyzed. *P* values were corrected for multiple testing. No asterisk represent no significant difference. *, *P* < 0.05; *, *P* < 0.001.**

The average ploidy, the cell number, and its size also show a significant change in the 4th generation. The average ploidy is highest in 2nd, significantly decreased in 4th and surged in 5th generation (Fig. 10A). The observed leaf surface area (Fig. 10C) and adaxial epidermal cell number (Fig. 10D) were highest in the 4th and reduced drastically in the 5th generation. In contrast, there was no change in cell size in the first three generations, but a significant reduction in 4th and subsequent increase in the 5th generation was observed.

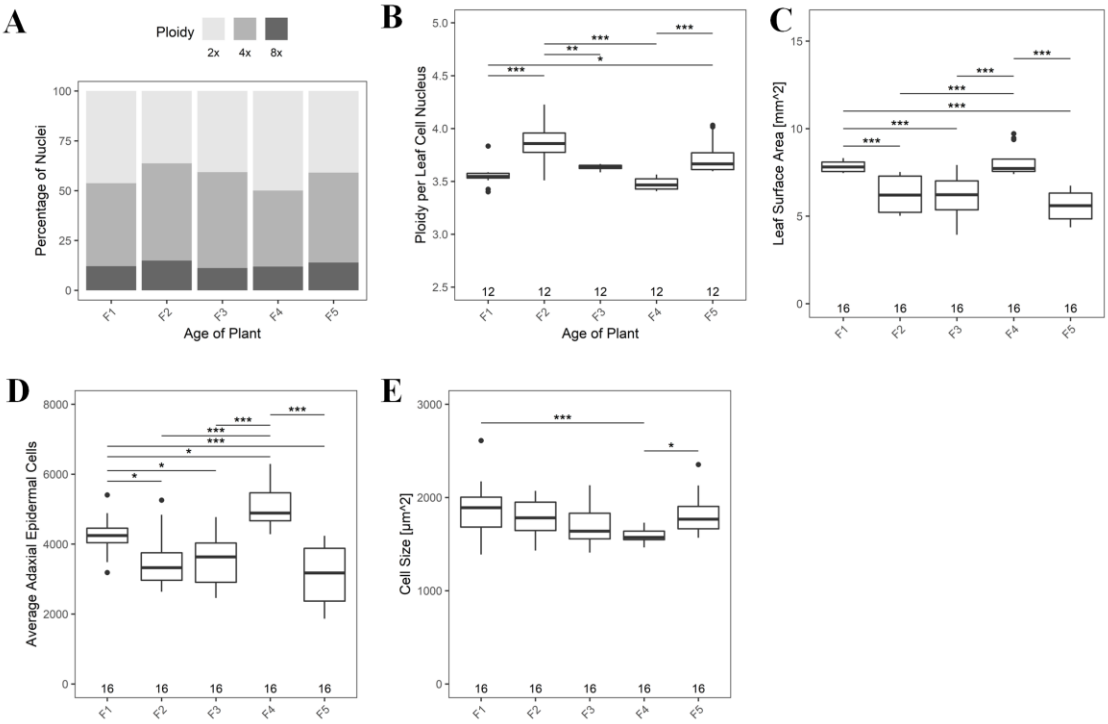


Figure 10. The graph representing the generation wise comparison of (A) total percentage of 2X, 4X and 8X nuclei, (B) Average ploidy per leaf per cell nucleus. (C) Total leaf surface area. (D) Cell size of leaf. (E) Average adaxial epidermal cell numbers. No asterisk represent no significant difference. *, *P* < 0.05; **, *P* < 0.01; *, *P* < 0.001.**

Double Strand DNA Damage Increases With Increasing Parental Age in All Generations

As age is known to increase the mutation rates we examined by employed a COMET assay to determine if double-strand DNA (ds-DNA) breaks increase in seedlings derived from parents of all ages. In this assay, damaged DNA forms a comet-like structure during migration in an electrophoresis gel (Moorad and Promislow, 2008). ds-DNA breaks were found to gradually increase with advancing parental age, reaching a maximum in the seedlings of 53 DAS plants. The pattern of DNA double-strand breaks was similar (Fig. 11A) in the 1st, 2nd, and 5th generations and also similar between the 3rd and 4th generations. DNA damage was higher in age 48 and 53 DAS and when parental age was fixed across generations, no significant change was observed (Fig. 11B).

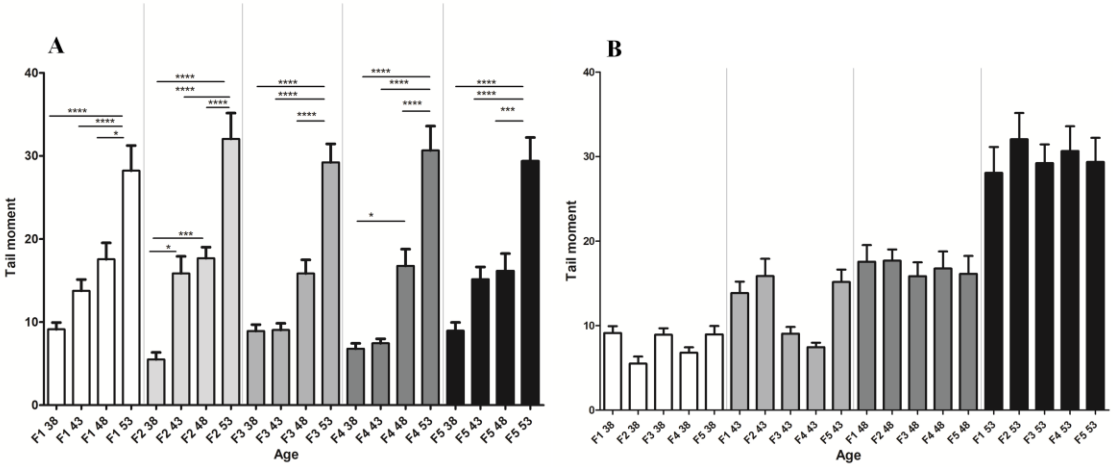
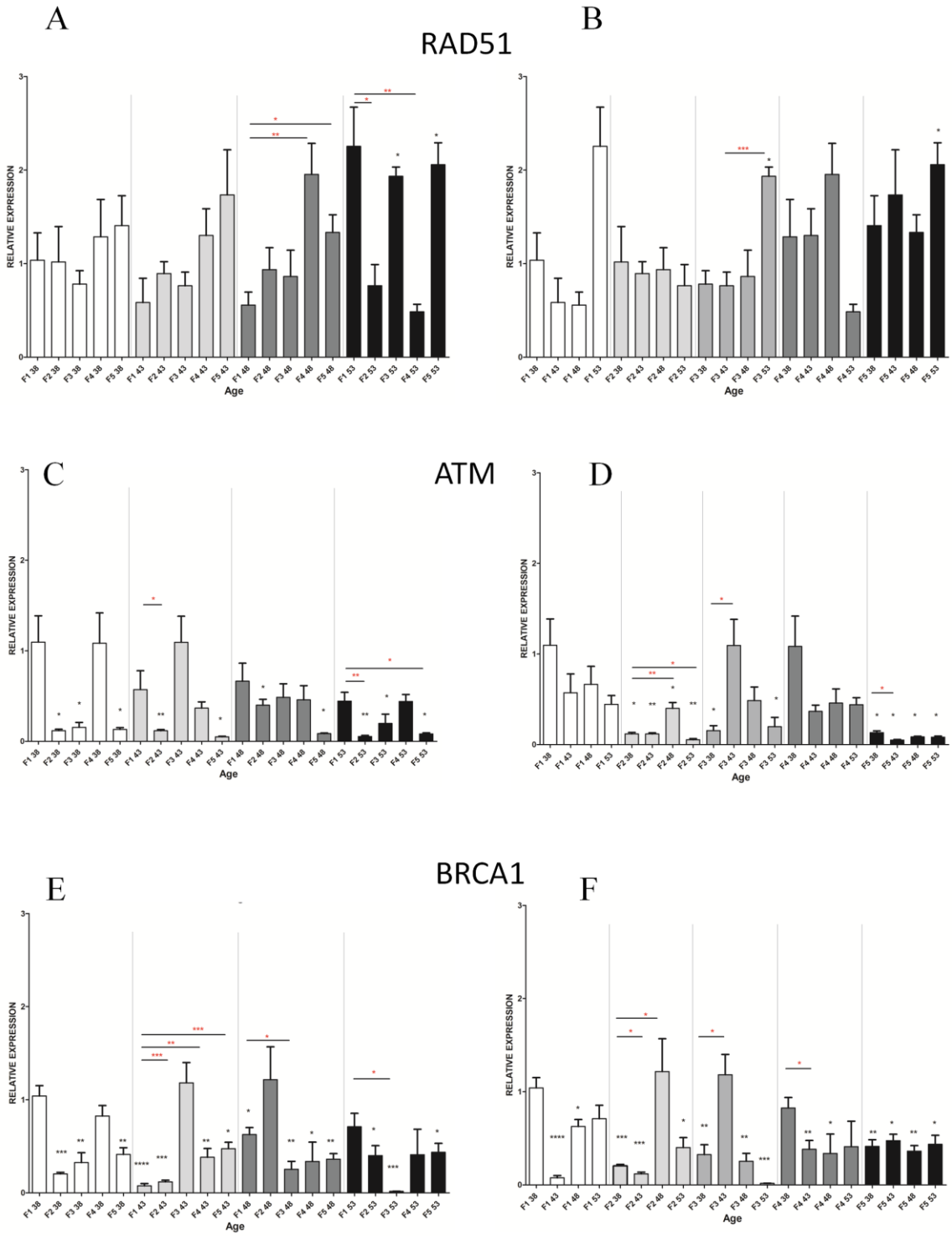


Figure 11. The DNA double-strand break as measured by a COMET assay. (A) Represents the DNA double-strand break with respect to increasing parental age in different generations. (B) Represents the DNA double-strand break with respect to fixed parental age in different generations. No asterisk denotes no significant differences *, *P* < 0.05; *, *P* < 0.001; ****, *P* < 0.0001.**

Wide Variation in the Expression Levels of Genes Involved in DNA repair in First Four Generations but Relatively Stable Expression in the 5th Generation

We examined if there exists a correlation between somatic mutation rates and expression of candidate genes involved in DNA repair such as *ATM, BRCA1, RAD 51* (Friesner et al., 2005; Bleuyard et al., 2005). Methylation levels are also known to impact somatic mutations (Graaf et al., 2015), and hence, the expression of candidates genes like *DDM1, MET1* (Tan et al., 2018; Zubko et al., 2012) were also analyzed together with *5.8S rRNA* (McStay and Grummt, 2008; Simon et al., 2018) by quantitative real-time PCR.


A
RAD51
B
C
ATM
D
E
BRCA1
F
RELATIVE EXPRESSION
Age

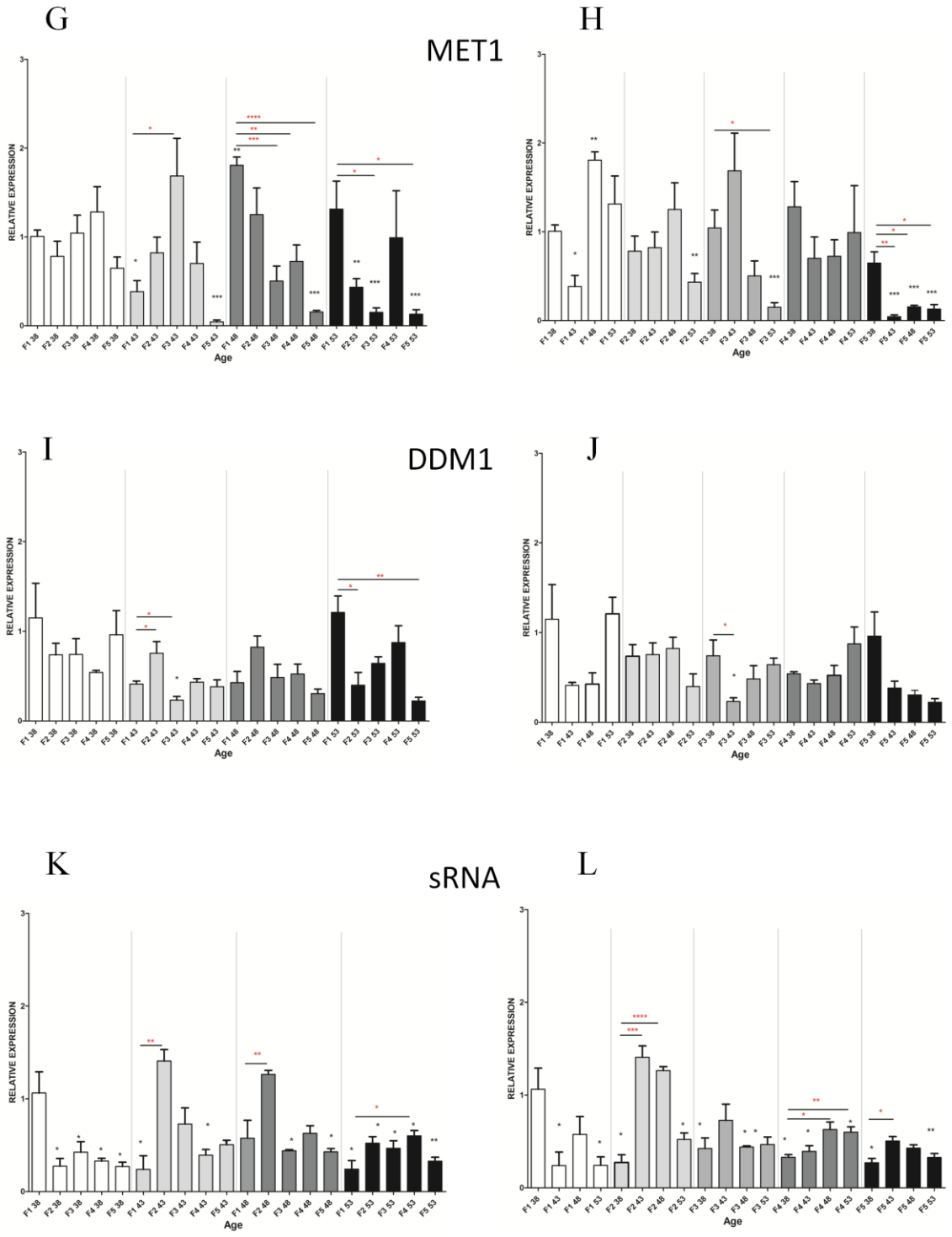


Figure 12. The relative expression of *RAD51* (A), *ATM* (C), *BRACA1* (E), *MET1* (G), *DDM1* (I), small RNA 5.8 (K). The black star represents a significant change in expression in comparison to F1 38 (*) and the significance between same age groups /generations are represented by a red star (*). The graph on the left panel represents gene expression analysis from same-aged parents across different generations. The graph showing the relative gene expression of *RAD51* (B), *ATM1* (D), *BRACA1* (F),

MET1* (H), *DDM1* (J), *small RNA 5.8* (L) representing comparative gene expression with increasing parental age in every generation (with *GAPDH* as a reference gene). Error bars represent SEM of biological replicates (n =3–6). Student's *t*-Test *, *P* < 0.05; **, *P* < 0.01; ***, *P* < 0.001; *, *P* < 0.0001.**

Although few interesting patterns in gene expression across different ages/generations were observed, this did not correlate with mutation rates. For instance, in seedlings obtained from 48 DAS plants, *RAD51* expression increased in the 4th and dropped in the 5th generation, while in contrast, seedlings from 53 DAS plants exhibited low expression in the 2nd and 4th generation, but increased significantly in the 5th generation (Fig. 12A). With increasing parental age, *RAD51* expression was significantly upregulated in seedlings from 53 DAS plants from the 3rd and 5th generation compared to F1 38 DAS plants (Fig. 12B) but we found no correlation between the expression pattern and the observed mutation rates. Although *ATM* expression was consistently down-regulated, the drop in expression was significant in the 2nd and the 5th generation in all age groups (Fig. 12C). However, with increasing parental age, *ATM* was down-regulated significantly in 2nd, 3^{rd,} and 5th generations, compared to F1 38 (Fig. 12D). *BRCA1* expression was significantly down-regulated across all ages (Fig. 12E) and with advanced parental ages, this pattern was observed only in the 4th (2.7 fold) and 5th (2.51 fold) generations compared to 38 DAS of the 1st generation (Fig. 12F). While there was considerable heterogeneity in *MET1* expression levels across all ages/generation, the fold change (7.74 to 23.4) of *MET1* expression was striking across all ages in the 5th generation alone (Fig. 12G). Plants of advancing ages (53 DAS) bred at the same age for five generations show an interesting *DDM1* expression pattern of an initial high, drop in 2nd, gradual increase thereafter, and another drop in the 5th generation. Except for a few, there was no change in *DDM1* expression as a function of increasing parental age (Fig. 12J). *sRNA* shows contrasting expression patterns depending on the parental age. For instance, in 38 DAS, the expression was high initially then dropped for the latter four generations, while in older (53 DAS) plants, the expression was initially low in the 1st generation, and underwent an increase in subsequent generations (Fig. 12K). The wide variation in gene expression levels of different candidates analysed in the first four generations and relatively stable expression in the 5th generation may have a combinatorial effect on mutation rates, which requires further investigation. It is likely that the wide fluctuations in expression correlates with overall somatic mutations ocuring throughout the genome.

DISCUSSION

Possible reasons for the differences in the mutation rates between the work of Singh et al., (2015) and this study.

To avoid or at least minimize an emasculation-induced stress response, we identified flowers which just undwerwent pollination at various DAS, following which the seeds were harvested. Furthermore, unlike the previous study, we took into account the influence of seed age, and harvested the seeds and plated them immediately at maturity. Ideally, storing the seeds from plants of different ages/generations and staining all the seedlings at the same time will remove any bias from the resultant data, due to uniform variation in staining across all seedlings. However, this approach would also strongly bias the results since seed storage is a strong determinant of mutation rates, even upon storage at 4^0C (Thakur et al., data not published). In earlier work of Singh et al., (2015), for each parental age, emasculation was carried out from a set of flowers from independent plants while in contrast, we identified all the self-pollinated flowers of a particular age following anthesis from the same plant as this could also bias mutation rates. Lastly, the number of times a plant has passed through self-fertilization would also affect mutation rates, and thus, the collective effect of the individual variables may account for the observed differences in mutation rates.

By comparing the whole genome sequence of *A. thaliana* derived from a single seed descent, somatic mutation rates were estimated in two widely separated generations. In *A. thaliana*, somatic mutations were found to be biased toward G:C to A:T and are concentrated in transposable elements, pericentrometic/centromeric zones (Weng et al., 2019). However, it was not known if the fertilization age was retained across successive generations in that study. Although such an approach is insightful, it would miss crucial spatial information regarding the localizaiton of the mutations. Our results strongly suggest that somatic mutation rates follow a specific pattern that significantly depends on the number of generations a plant has gone through selfing at a particular age. Although the number of generations we analysed is small, the data strongly indicates that that somatic mutation rates follow a pattern, robustly influenced by function of parental age and generation time.

The expression pattern of genes involved in DNA repair such as *RAD51*, *ATM*, and *BRCA1* and *sRNA* was random in the first four generations but became relatively stable in the 5th generation (Fig. 12). The number of generations may be counted by fluctuations followed by stable gene expression impacting the mutation rates as in every 5th generation there is a surge in C to T transition rates. In *C. elegans*, for example, changes in histone methylation expression are stochastic for the first four generations, and thereafter becames stable in the 5th

(Greer et al., 2011). If such changes are conserved in *Arabidopsis* also, it would likely have an impact on gene expression and mutation rates. An increase in C→T base substitution events is related to cytosine methylation, and methylcytosine is susceptible to deamination (Mugal and Ellegren, 2011). High degree of DNA methylation, possibly leads to low gene expression (Moore et al., 2013) and such genes transcribing at reduced levels are likely to have low mutation rates as well (Park et al., 2012). DNA methylation levels are known to be higher in older compared to younger plant tissues (Bitonti, 2002; Fraga et al., 2002; Sun et al., 2015) but some studies have also reported contradictory findings (Monteuuis et al., 2009; Meng et al., 2012; Michalak et al., 2015). Cytosine DNA methylation is important for maintaining genome stability and regulating gene expression (Vanyushin and Ashapkin, 2011) but is also known to increase neighborhood mutations in somatic cells of *Arabidopsis* (Kusmartsev et al., 2020). This suggests a context-dependent methylation event during development (Ambrosi et al., 2017; Baker et al., 2018). Our results show higher C→T transition rates in seedlings obtained from younger and older, but not from middle-aged parents. *DDM1* and *MET1* are required for CG methylation. In support of a role for *DDMI* in higher C→T transitation from younger and older parents, a correlation was observed between *DDM1* expression (Fig. 12J) and mutation rates in seedlings from middle-aged parents (43 and 48 DAS) of 1st and 3rd generations and similar mutation rates in 4th and 5th generation (Fig. 5B).

Our results show increased ICR events in seedlings of 38, 43, and 48 DAS plants, but not from seedlings of 53 DAS plants (Fig. 6B). Although DSBs increased with parental age, we still observed low ICR rates in seedlings obtained from 53 DAS plants, which may be due to increased non-homologous end-joining (NHEJ) with plant age (Boyko et al., 2006). The expression of Ku70 protein in particular, known to be involved in NHEJ was identified to increase with plant age (Golubov et al., 2010). This state resulting in a decline within ICR rates in older parents may be transmitted to the next generation, which would also explain the observed increase in DSBs in the offspring of older parents.

Plants with long life may have low cell division rates and, as a consequence, are also possess low mutation rates (Watson et al., 2016). It is also possible that the cell division rates in the reproductive meristem may not be uniform across different ages. Furthermore, DNA replication is known to be independent of life span, suggesting that older plants may not be passing on more mutations to their offsprings relative to younger plants (Watson et al., 2016). Therefore, epigenetic inheritance, possibly mediated by DNA methylation or small RNAs,

may be a key mechanism underlying the observed transgenerational effects (Herman and Sultan, 2011; Holeski et al., 2012; Zhang et al., 2013; Amtmann et al., 2013).

MATERIAL AND METHODS

Plant Growth Conditions

Prior to planting, *Arabidopsis thaliana* (Columbia) seeds were surface sterilized with 70% (v/v) ethanol followed by 0.5% (v/v) bleach treatment for 3 min. The seeds were washed thrice with sterile water and plated on autoclaved MS medium (with 3% [w/v] Suc), pH 5.7, and containing 0.05% (v/v) Plant Preservative Mixture (Biogenuix Medsystem Pvt. Ltd.) and kept at 4°C for 48 h in the dark for synchronized seed germination. The plates were transferred to plant growth chambers (Percival, USA) that had a uniform light intensity of 8,000 lux (under a 16-h-light/8-h-dark cycle). The temperature of the growth chamber (Percival CU-36L6) was maintained at 22°C throughout, and the humidity was set to 80%. Three-week-old seedlings were transferred from MS plates to soil and grown again in a growth chamber (Percival AR-36L3). The soil consisted of equal proportions of garden soil, peat, perlite, and vermiculite. Plants were grown in a randomized manner in the growth chambers and at frequent intervals, their positions were changed.

Somatic Mutation Detector Lines

The base substitution detector line $1{,}390_{T\rightarrow C}$ was a gift from Anna Depicker, University Ghent University, Ghent, Belgium (Auwera et al., 2008). Transgenic ICR lines (R2L1) carrying inverted catalase introns (418 bp) in the *uidA* gene and the frameshift detector line (G10) were a gift from Francois Belzile, Universite´ Laval, Quebec, Canada (Li et al., 2004; Azaiez et al., 2006). The detector line harboring the *Tag1* element was a gift from Nigel M. Crawford, University of California, San Diego, USA (Liu and Crawford, 1998).

Identification of Self Pollinated Flowers From Plants of Different DAS

Self-pollinated flowers were identified on 38, 43, 48, and 53 DAS from the same plant and marked with different colored threads after anthesis. Matured seeds were harvested and germinated on MS plates.

Histochemical Staining for GUS Activity

GUS staining was performed in 3-week-old seedlings as described by Jefferson et al., (1987) in three biological replicates. The total number of seedlings analyzed is indicated in the Figures. The blue colored GUS reversions were counted using a stereozoom microscope (Leica KL300, Germany).

Estimating Correction Factors to Calculate Mutation Rates

The mutation rates were corrected considering the changes in the number of adaxial epidermal cells of the fourth true leaf. The ploidy per nucleus in 3-week-old seedlings (derived from F2, F3, F4 and F5 generations of 43, 48, and 53 DAS) was compared with the ploidy levels in seedlings derived from F1 38 DAS plants. The correction factor was calculated using the formula (Singh et al., 2015).

$$\text{TITER} = (P_H \times C_H) / P_Y \times C_Y$$

Where P_Y is the average ploidy per nucleus. To compare the differences in mutation rates as a function of plant age, seedlings derived from young parents (F1 38 DAS) were considered (Singh et al., 2015). P_H is the average ploidy per nucleus in seedlings from 43, 48, and 53 DAS plants of F2, F3, F4, and F5 generation. C_Y is the average number of adaxial epidermal cells in the fourth leaf of seedlings derived from F1 38 DAS plants. C_H is the average number of adaxial epidermal cells in the fourth leaf of seedlings derived from 43, 48, and 53 DAS plants of F2, F3, F4, and F5 generation.

Corrected mutation rate = GUS/titer

where GUS is the average number of blue spots per plant.

Statistical Analysis

A total of 3905, 3336, 4027, and 4415 seedlings were examined to detect BSR, ICR, FS, and transpositions, respectively. GUS spots are count data, so we chose a Quasi-Poisson generalized linear model (GLM) with the log link function (Nelder and Wedderburn, 1972). Due to dispersion of the data, a Quasi-Poisson GLM was used. The log of the correction factor for cell number and ploidy per leaf cell nucleus was integrated into the models as a fixed intercept. In all GLMs, the data from the groups were used for multiple comparisons. Correction for multiple testing was done to keep the family-wise error rate at 5% (Gabriel, 1969). *P* values were adjusted with a single-step method that considers the joint multivariate *t*

distribution of the individual test statistic (Bretz et al., 2010). The results are presented with a two-sided *P* value adjusted for multiple comparisons. All the statistical analysis were done using R (R Developmental Core Team, 2010) For multiple comparisions, *P* values were modified by multcomp package R (Bretz et al., 2010). Graphs were produced with ggplot2 (Wickham, 2009).

Cell Size and Cell Number Analysis by Scanning Electron Microscopy

For SEM, a wax impression of plant tissue was prepared according to the protocol of Beermann and Hülskamp (2010). The fourth true leaf of a 3-week old *Arabidopsis* seedling derived from parents of different ages was dissected, and as suggested by the manufacturer, the two components of waxy dental material were deposited on the leaf to generate an impression (Coltene PRESIDENT light body, Coltene AG, Altstatten, Switzerland). After 5 min, when the wax had hardened, the leaves were gently removed. This leaf mould was used for sample preparation with Spurr resin, and the resin with the leaf impression was taken out carefully from mould, and the sample was coated with gold using Polaron Range sputter coater (Quorum Technologies). The coated resins were mounted onto a SEM stub with a double-sided carbon tape to capture the images (FEI Quanta 400-F SEM (FEI Company, USA) under 20kV voltage and 70 Pa pressure). The adaxial leaf surface area was calculated by using the SEM images captured at 50X magnification (Singh et al., 2015). Independently, SEM images were taken at different positions of the leaf at 500X magnification. The average cell size was calculated by dividing the number of cells observed in an area of 500X magnification at different positions of the leaf. To calculate the total number of adaxial epidermal cells, the total area of the leaf was divided by a fixed area of 500X magnification and multiplied by the number of cells present in an area of 500X magnification. ImageJ (NIH, USA) software was used for counting the total number of cells and the total area of the leaf. Four biological replicates were considered to determine the average number of adaxial epidermal cells of the 4th true leaf.

Ploidy Analysis by Flow Cytometry

Ploidy analysis was performed as per the protocol of Doležel et al., (2007). The fraction of nuclei with 2X, 4X, and 8X ploidy were estimated together with the average number of genomes per nucleus from seedlings of different parental ages. Approximately 60 mg of leaf tissue of 3-week-old seedlings was finely chopped with a razor blade in a glass Petri dish

containing 1 mL of ice-cold nuclei extraction buffer (Sysmex CyStain^{TM} PI Absolute P KIT). The chopped tissues were filtered with a 20 µm nylon filter (CellTrics® filters, Sysmex). Three biological replicates were carried out for flow cytometry. To stain the nuclei, 2 ml of staining buffer (provided with the kit) containing propidium iodide and RNase in 1:2 ratio was mixed to the filtrate and kept for an hour at room temperature. A sample derived from Tomato (*Solanum lycopersicum* 'Stupicke') was used as control. After the incubation period, the samples were analyzed using a Partec CyFlow® Ploidy analyser (Sysmex). Data analysis was carried out with CyView Software (Sysmex).

RNA Isolation and Quantitative Real-Time PCR

Using the Trizol reagent (Invitrogen, USA), total RNA was isolated from 21-day old seedlings of wild type Columbia-0 (Col-0) obtained from plants of different ages in five consecutive generations. cDNA was synthesized using 2 µg RNA, random hexamers, and High Capacity cDNA Reverse Transcription Kit (Applied Biosystems, USA). Quantitative real-time PCR was done in triplicate using the DyNAmoTM Flash SYBR Green qPCR kit (QuantStudio (TM) 7 Flex System). The primers for amplifying *ATM*, *BRCA1*, *RAD51*, *DDM1*, *MET1*, and *sRNA* (5.8S *rRNA* and 25S *rRNA* with 18S rRNA fragment) are listed in Table S1. The expression levels of glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) mRNA was used as an internal standard. The relative gene expression in each age and generation was determined by calculating $2^{(-\Delta\Delta Ct)}$ as described previously (Veremeyko et al., 2012).

Neutral COMET Assay

To measure ds DNA breaks, a COMET assay was performed using the Oxiselect Comet Assay Kit from Cell Biolabs, Inc. USA. 3 week old Col-0 seedlings of 38, 43, 48, and 53 DAS from all five generations were chopped using a razor blade in 1 mL of Otto I solution. Subsequently, the sample was filtered with a 20µm nylon filter (CellTrics® filters, Sysmex), and the filtrate was centrifuged at 300 rpm for 5 min. The pellet was dissolved in phosphate-buffered saline (PBS) containing 20 mM EDTA. The dissolved sample was mixed with warm low-melting agarose in a ratio of 2:5 and poured onto a slide coated with normal agarose. The sample was covered with a glass coverslip, stored at 4°C for 15 min and after removing the coverslip, the slides were transferred to a chamber filled with chilled lysis buffer for 30 to 60 min at 4°C. The slides were then transferred to another chamber filled with cold alkaline solution (NaOH and EDTA, pH 10) for 30 min at 4°C in the dark. The slides with the sample

were treated with chilled Tris-borate/EDTA buffer for 5 min and transferred to a horizontal electrophoresis chamber containing the same buffer. Electrophoresis was carried out at 1 V cm^{-1} for 15min. Thereafter, the slides were gently rinsed thrice with deionized water, followed by rinsing with 70% (v/v) ethanol for 5 min. After air drying, the sample was stained with vista green and kept for 15 min in dark at room temperature. Then, the COMETS were observed using an upright fluorescence microscope (Nikon Eclipse 80i) fitted with a fluorescein isothiocyanate (FITC) filter. We analysed around 50-55 Comet using a free online tools available from CaspLab. One way ANOVA with a 95% confidence interval of difference was used for the statistical analysis carried out by prism software (USA).

AUTHOR CONTIBUTION

Conceived and designed the experiments: SB and RB. Performed the experiments and compiled the data: SB and YT . Analysed the data: SB, AKS, and RB. Wrote the paper: SB, AKS, and RB. All authors read and approved the final manuscript.

ACKNOWLEDGMENTS

We gratefully acknowledge Francois Belzile (Université Laval), Anna Depicker (University of Ghent), Nigel M. Crawford (University of California, San Diego), and Barbara Hohn (Friedrich Miescher Institute) for providing reporter line seeds; The Sophisticated Analytical Instruments Facility (SAIF), Indian Institute of Technology-Madras for assistance with SEM analysis; and Rama Shanker Verma (Indian Institute of Technology-Madras, Chennai) for help with flow cytometry.

LITERATURE CITED

Agrawal AA, Laforsch C, Tollrian R (1999) Transgenerational induction of defences in animals and plants. *Nature* **401**: 60–63

Ambrosi C, Manzo M, Baubec T (2017) Dynamics and Context-Dependent Roles of DNA Methylation. *J Mol Biol* **429**: 1459–1475

Amtmann A, Sani E, Herzyk P, Perrella G, Colot V (2013) Hyperosmotic priming of *Arabidopsis* seedlings establishes a long-term somatic memory accompanied by specific changes of the epigenome. *Genome Biol*. **14:** 1-23

Van der Auwera G, Baute J, Bauwens M, Peck I, Piette D, Pycke M, Asselman P, Depicker A (2008) Development and application of novel constructs to score C:G-to-T:A transitions and homologous recombination in *Arabidopsis*. *Plant Physiol* **146**: 22–31

Auwera G Van Der, Baute J, Bauwens M, Peck I, Piette D, Pycke M, Asselman P, Depicker A (2008) Development and Application of Novel Constructs to Score C : G-to-T : A Transitions and Homologous Recombination in *Arabidopsis*. *Plant Physiol* **146**: 22–31

Azaiez A, Bouchard EF, Jean M, Belzile FJ (2006) Length, orientation, and plant host influence the mutation frequency in microsatellites. *Genome* **49**: 1366–73

Baker BH, Berg LJ, Sultan SE (2018) Context-dependent developmental effects of parental shade versus sun are mediated by dna methylation. *Front Plant Sci* **9**: 1–15

Beermann A, Hülskamp M (2010) Dental wax impressions of plant tissues for viewing with scanning electron microscopy (SEM). *Cold Spring Harb Protoc*. **5:** 1-3

Bilichak A, Kovalchuk I (2016) Transgenerational response to stress in plants and its application for breeding. *J Exp Bot* **67**: 2081–2092

Bitonti MB (2002) Distinct nuclear organization, DNA methylation pattern and cytokinin distribution mark juvenile, juvenile-like and adult vegetative apical meristems in peach (Prunus persica (L.) Batsch). *J Exp Bot* **53**: 1047–1054

Bleuyard JY, Gallego ME, Savigny F, White CI (2005) Differing requirements for the *Arabidopsis* Rad51 paralogs in meiosis and DNA repair. *Plant J* **41**: 533–545

Boyko A, Filkowski J, Hudson D, Kovalchuk I (2006) Homologous recombination in plants is organ specific. *Mutat Res - Fundam Mol Mech Mutagen* **595**: 145–155

Boyko A, Kathiria P, Zemp FJ, Yao Y, Pogribny I, Kovalchuk I (2007) Transgenerational changes in the genome stability and methylation in pathogen-infected plants: (Virus-induced plant genome instability). *Nucleic Acids Res* **35**: 1714–1725

Boyko A, Kovalchuk I (2010) Transgenerational response to stress in *Arabidopsis thaliana*. *Plant Signal Behav* **5**: 995–998

Bretz F, Hothorn T, Westfall P (2010) Multiple Comparisons Using R. *CRC Press Boca Raton*, FL.

Doležel J, Greilhuber J, Suda J (2007) Estimation of nuclear DNA content in plants using flow cytometry. *Nat Protoc* **2**: 2233–2244

Eyre-Walker A, Keightley PD (2007) The distribution of fitness effects of new mutations. *Nat Rev Genet* **8**: 610–618

Failla G (1958) the Aging Process and Cancerogenesis. *Ann N Y Acad Sci* **71**: 1124–1140

Fraga MF, Rodríguez R, Cañal MJ (2002) Genomic DNA methylation-demethylation during aging and reinvigoration of *Pinus radiata*. *Tree Physiol* **22**: 813–816

Friesner JD, Liu B, Culligan K, Britt AB (2005) Ionizing Radiation–dependent ? -H2AX Focus Formation Requires Ataxia Telangiectasia Mutated and Ataxia Telangiectasia Mutated and Rad3-related. *Mol Biol Cel*l **15**: 2566–2576

Futuyma DJ (2013) Evolution, THIRD EDITION. *Sunderland*, Massachusetts U.S.A.

Galloway LF, Etterson JR (2007) Transgenerational plasticity is adaptive in the wild. *Science*. **318**: 1134–1136

Golubov A, Oa PDW, Yao Y, Maheshwari P, Bilichak A, Boyko A (2010) Microsatellite Instability in *Arabidopsis* Increases with plant development. *Plant Physiol***. 154**: 1415–1427

Graaf VDA, Wardenaara R, Neumann DA, Taudt A, Shaw RG, Jansen RC, Schmitz

RJ, Colomé-Tatché M, Johannes F (2015) Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. *Proc Natl Acad Sci U S A* **112**: 6676–6681

Greer EL, Maures TJ, Ucar D, Hauswirth AG, Mancini E, Lim JP, Benayoun BA, Shi Y, Brunet A (2011) Transgenerational epigenetic inheritance of longevity in Caenorhabditis elegans. *Nature* **479**: 365–371

Groot MP, Knoben N, Ouborg NJ, Kooke R, Vergeer P, Keurentjes JJB, Verhoeven KJF (2016) Effects of multi-generational stress exposure and offspring environment on the expression and persistence of transgenerational effects in *Arabidopsis thaliana*. *PLoS One* **11**: 1–16

Herman JJ, Sultan SE (2011) Adaptive transgenerational plasticity in plants: Case studies, mechanisms, and implications for natural populations. *Front Plant Sci* **2**: 1–10

Holeski LM (2007) Within and between generation phenotypic plasticity in trichome density of Mimulus guttatus. *J Evol Biol* **20**: 2092–2100

Holeski LM, Jander G, Agrawal AA (2012) Transgenerational defense induction and epigenetic inheritance in plants. *Trends Ecol Evol* **27**: 618–626

Jefferson RA, Kavanagh TA, Bevan MW (1987) GUS fusions: beta-glucuronidase as a sensitive and versatile gene fusion marker in higher plants. *EMBO J* **6**: 3901–3907

Kusmartsev V, Drożdż M, Schuster-Böckler B, Warnecke T (2020) Cytosine methylation affects the mutability of neighbouring nucleotides in germline and soma. *Genetics* **214**: 809–823

Li L, Santerre-Ayotte S, Boivin EB, Jean M, Belzile F (2004) A novel reporter for intrachromosomal homoeologous recombination in *Arabidopsis thaliana*. *Plant J* **40**: 1007–1015

Liu D, Crawford NM (1998) Characterization of the germinal and somatic activity of the *Arabidopsis* transposable element Tag1. *Genetics* **148**: 445–456

Marcotrigiano M (2010) A role for leaf epidermis in the control of leaf size and the rate and extent of mesophyll cell division. *Am J Bot* **97**: 224–233

Martina MA, Correa EME, Argaraña CE, Barra JL (2012) Escherichia coli frameshift mutation rate depends on the chromosomal context but not on the GATC content near the mutation site. *PLoS One*. **7:** 1-9

McStay B, Grummt I (2008) The Epigenetics of rRNA Genes: From Molecular to Chromosome Biology. *Annu Rev Cell Dev Biol* **24**: 131–157

Melaragno JE, Mehrotra B, Coleman AW (1993) Relationship between endopolyploidy and cell size in epidermal tissue of *Arabidopsis*. *Plant Cell* **5**: 1661–1668

Meng FR, Li YC, Yin J, Liu H, Chen XJ, Ni ZF, Sun QX (2012) Analysis of DNA methylation during the germination of wheat seeds. *Biol Plant* **56**: 269–275

Michalak M, Plitta-Michalak BP, Naskręt-Barciszewska M, Barciszewski J, Bujarska-Borkowska B, Chmielarz P (2015) Global 5-methylcytosine alterations in DNA during ageing of Quercus robur seeds. *Ann Bot* **116**: 369–376

Molinier J, Ries G, Zipfel C, Hohn B (2006) Transgenerational memory of stress in plants. *Nature* **442**: 1046–1049

Monteuuis O, Baurens FC, Gogh DKS, Quimado M, Doulbeau S, Verdeil JL (2009) DNA methylation in acacia mangium in vitro and ex-vitro buds, in relation to their within-shoot position, age and leaf morphology of the shoots. *Silvae Genet* **58**: 287–292

Moorad JA, Promislow DEL (2008) A theory of age-dependent mutation and senescence. *Genetics* **179**: 2061–2073

Moore LD, Le T, Fan G (2013) DNA methylation and its basic function. *Neuropsychopharmacology* **38**: 23–38

Mosher RA (2010) Maternal control of Pol IV-dependent siRNAs in *Arabidopsis* endosperm. *New Phytol* **186**: 358–364

Mugal CF, Ellegren H (2011) Substitution rate variation at human CpG sites correlates with non-CpG divergence, methylation level and GC content. *Genome Biol*. **12**:R58.

Nelder JA, Wedderburn RW (1972) Generalized Linear Models. **135**: 370–384

Otto SP, Gerstein AC (2006) Why have sex? The population genetics of sex and recombination. *Biochem Soc Trans* **34**: 519–522

Park C, Qian W, Zhang J (2012) Genomic evidence for elevated mutation rates in highly expressed genes. *EMBO Rep* **13**: 1123–9

Pecinka A, Rosa M, Schikora A, Berlinger M, Hirt H, Luschnig C, Scheid OM (2009) Transgenerational Stress Memory Is Not a General Response in *Arabidopsis*. *PLoS ONE* **4(4):** e5202

R Developmental Core Team (2010) R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna.

Roach DA, Wulff RD (1987) Maternal effects in plants. *Annu Rev Ecol Syst* Vol **18:** 209–235

Salinas S, Brown SC, Mangel M, Munch SB (2013) Non-genetic inheritance and changing environments. *Non-Genetic Inherit*. **1:** 38–50.

Salinas S, Munch SB (2012) Thermal legacies: Transgenerational effects of temperature on growth in a vertebrate. *Ecol Lett* **15**: 159–163

Savaldi-Goldstein S, Peto C, Chory J (2007) The epidermis both drives and restricts plant shoot growth. *Nature* **446**: 199–202

Shahrezaei V, Swain PS (2008) Analytical distributions for stochastic gene expression. *Proc Natl Acad Sci U S A* **105**: 17256–17261

Simon L, Rabanal FA, Dubos T, Oliver C, Lauber D, Poulet A, Vogt A, Mandlbauer A, Le Goff S, Sommer A (2018) Genetic and epigenetic variation in 5S ribosomal RNA genes reveals genome dynamics in *Arabidopsis thaliana*. *Nucleic Acids Res* **46**: 3019–3033

Singh AK, Bashir T, Sailer C, Gurumoorthy V, Ramakrishnan A, Dhanapal S, Grossniklaus U, Baskar R (2015) Parental age affects somatic mutation rates in the progeny of flowering plants. *Plant Physiol* **168**: 247–257

Singh AK, Yadav BS, Dhanapal S, Berliner M, Finkelshtein A, Chamovitz DA (2019) CSN5A subunit of COP9 signalosome temporally buffers response to heat in *Arabidopsis*. *Biomolecules* **9**: 1–18

Sugimoto-Shirasu K, Roberts K (2003) “Big it up”: Endoreduplication and cell-size control in plants. *Curr Opin Plant Biol* **6**: 544–553

Sultan SE (1996) Phenotypic plasticity for offspring traits in Polygonum Persicaria. *Ecology* **77**: 1791–1807

Sun LF, Liu TJ, Shan XH, Su SZ, Li SP, Yuan YP, Zhang J (2015) Analysis of DNA

cytosine methylation patterns in maize hybrids and their parents. *Biol Plant* **59**: 266–272

Szilard BYLEO (1958) ON THE NATURE OF THE AGING PROCESS. *Genetics* 30–45

Tan F, Lu Y, Jiang W, Wu T, Zhang R, Zhao Y, Zhou DX (2018) DDM1 represses noncoding RNA expression and RNA-directed DNA methylation in heterochromatin. *Plant Physiol* **177**: 1187–1197

Tariel J, Plénet S, Luquet É (2020) Transgenerational plasticity of inducible defences: Combined effects of grand-parental, parental and current environments. *Ecol Evol* **10**: 2367–2376

Tricker PJ (2015) Transgenerational inheritance or resetting of stress-induced epigenetic modifications: Two sides of the same coin. *Front Plant Sci* **6**: 1–6

Tsukaya H (2003) Organ shape and size: a lesson from studies of leaf morphogenesis. *Curr Opin Plant Biol* 57–62

Vanyushin BF, Ashapkin V V. (2011) DNA methylation in higher plants: Past, present and future. *Biochim Biophys Acta - Gene Regul Mech* **1809**: 360–368

Veremeyko T, Starossom SC, Weiner HL, Ponomarev ED (2012) Detection of microRNAs in microglia by real-time PCR in normal CNS and during neuroinflammation. *J Vis Exp* 1–7

Watson JM, Platzer A, Kazda A, Akimcheva S, Valuchova S, Nizhynska V, Nordborg M, Riha K (2016) Germline replications and somatic mutation accumulation are independent of vegetative life span in *Arabidopsis*. *Proc Natl Acad Sci U S A* **113**: 12226–12231

Weng ML, Becker C, Hildebrandt J, Neumann M, Rutter MT, Shaw RG, Weigel D, Fenster CB (2019a) Fine-grained analysis of spontaneous mutation spectrum and frequency in *Arabidopsis thaliana*. *Genetics* **211**: 703–714

Weng ML, Becker C, Hildebrandt J, Neumann M, Rutter MT, Shaw RG, Weigel D, Fenster CB (2019b) Fine-grained analysis of spontaneous mutation spectrum and frequency in *Arabidopsis thaliana*. *Genetics* **211**: 703–714

Wickham H (2009) ggplot2 Elegant Graphics for Data Analysis. Springer, New York

Zhang YY, Fischer M, Colot V, Bossdorf O (2013) Epigenetic variation creates potential for evolution of plant phenotypic plasticity. *New Phytol* **197**: 314–322

Zubko E, Gentry M, Kunova A, Meyer P (2012) De novo DNA methylation activity of METHYLTRANSFERASE 1 (MET1) partially restores body methylation in *Arabidopsis thaliana*. *Plant J* **71**: 1029–1037

Table S1. List of primers used for realtime PCR and their sequence

S. no.	Gene	Primer sequence
1	***RAD51***	FP 5’TCCATAGCTCAGTGATAGAGC3’
		RP 5’GATTAGTGAACTACTTGACGC3’
2	***MET1***	FP 5’TGACGAAAAAACGGACCCGATA3’
		RP 5’TGGTATACTACAGGTGAAACTC3’
3	***DDM1***	FP 5’AAGGGACGACGGAGACGACTGTT3’
		RP 5’CACCAAGAAGAACAGCGAGCGAT3’
4	***BRCA1***	FP 5’CGCAGCACTTGGTTGTTACA3’
		RP 5’GCTGAGAGTGCAGTGGTTCT3’

5	***ATM***	FP 5’GAAGTGGTGGCCAGGAGAAG3’
		RP 5’TCGAAGAAGCGAACCACGAA3’
6	***GAPDH***	FP 5’GGTCACCATGGCTTCGGTTA3’
		RP 5’AGTCTGGAAGGAGACGATGGA3’
7	**5.8S rRNA**	FP 5’GCAACGCCTCGACCTATTCT3’
		RP 5’TTCTAGGTTAGCGCGCAGTT3’

779