Title: Descendants of primed Arabidopsis plants exhibit resistance to biotic stress

Authors and affiliation:

Ana Slaughter¹, Xavier Daniel¹, Victor Flors², Estrella Luna³, Barbara Hohn⁴, Brigitte Mauch-Mani¹

¹ Université de Neuchâtel, Institut de Biologie, Laboratoire de Biologie Moléculaire et Cellulaire, 2009 Neuchâtel, Switzerland
² Plant Physiology Section, Universitat Jaume I, Spain
³ Centre for Sustainable Pest and Disease Management, Rothamsted Research, UK
⁴ Friedrich Miescher Institute, Basel, Switzerland
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Present address: Xavier Daniel, Facultas Teknobiologi Raya Kalitungkut, Surabaya 60293, Indonesia.

Corresponding author: Brigitte Mauch-Mani, brigitte.mauch@unine.ch
**Abstract**

An attack of plants by pathogens or treatment with certain resistance-inducing compounds can lead to the establishment of a unique primed state of defense. Primed plants show enhanced defense reactions upon further challenge with biotic or abiotic stress. Here, we report that the primed state in *Arabidopsis thaliana* is still functional in the next generation without additional treatment. We compared the reactions of Arabidopsis plants that had been either primed with β-amino-butyric acid (BABA) or with an avirulent isolate of the bacteria *Pseudomonas syringae pv tomato* (*PstavrRpt2*). The descendants of primed plants showed a faster and higher accumulation of transcripts of defense-related genes in the SA-signaling pathway and enhanced disease resistance upon challenge inoculation with a virulent isolate of *Pseudomonas syringae* (*Pst*). In addition, the progeny of primed plants was also more resistant against the oomycete pathogen *Hyaloperonospora arabidopsidis*. When transgenerationally primed plants were subjected to an additional priming treatment, their descendants displayed an even stronger primed phenotype, suggesting that plants can inherit a sensitization for the priming phenomenon. Interestingly, this “primed to be primed” phenotype was much reduced in the Arabidopsis BABA-priming mutant *ibs1*. Our results demonstrate that the primed state of plants is transferred to their progeny and confers improved protection from pathogen attack as compared to the descendants of unprimed plants.
INTRODUCTION

Plants have developed sophisticated mechanisms to protect themselves against biotic and abiotic stresses (Jones and Dangl, 2006; Hirayama and Shinozaki, 2010). An impressive amount of information is available on the genes and signaling pathways involved in the plants’ reaction following exposure to a given stress situation (Feys and Parker, 2000; Thomma et al., 2001; Kunkel and Brooks, 2002; Turner et al., 2002; Fujita et al., 2006 Hirayama and Shinozaki, 2007). Triggering of the defensive state of a plant can lead to acquired resistance in the case of biotic stresses or to acclimation for abiotic stresses (van Loon, 1997).

In numerous plant species acquired resistance functions against a wide array of pathogens (Kuc, 2001). Interestingly, acquired resistance can spread systemically throughout the plant. When the induction of resistance is due to non-pathogenic rhizobacteria in the rhizosphere it is referred to as induced systemic resistance (ISR; van Loon 1997). Induced resistance resulting from a natural induction with a pathogen or the induction with chemical inducers is referred to as systemic acquired resistance (SAR; Ryals et al., 1996; Sticher et al., 1997). The manifestation of SAR is tightly correlated with the local and systemic activation of defense-related genes such as genes coding for pathogenesis-related (PR) proteins (Ryals et al., 1996). As during pathogen stress, defense pathways can also be up-regulated by applied chemical stimuli. Resistance induced by the non-protein amino acid BABA leads to a substantial induction of PR genes only upon challenge inoculation (Zimmerli et al., 2000). Based on Northern blots it was originally described that BABA does not induce the expression of PR genes by itself (Zimmerli et al., 2000; Ton et al., 2005) but the availability of more sensitive technologies such as microarrays and PCR revealed that BABA-treatment itself leads to an induction of PR genes, although to much lower levels than observed after pathogen attack (Zimmerli et al., 2008).

When a treatment puts a plant in a state of increased alertness with no or only minimal gene induction it is called sensitizing or priming (Jakab et al., 2001; Conrath et al., 2002; Prime-a-plant group et al., 2006). Priming of defense responses confers a fitness advantage over direct induction of resistance as observed in traditional SAR responses which infer high costs in absence of pathogens (van Hulten et al., 2006). An overview on molecular mechanism(s) possibly underlying priming for defense was recently presented by Conrath (2011). There is increasing evidence that plants have a memory of encountered stress situations that allow them to better adapt to changing conditions. In addition, several studies have shown the relevance of epigenetic mechanisms underlying
plant defense responses (Alvarez-Venegas et al., 2006; Walley et al., 2008; March-Diaz et al., 2008; Jaskiewicz et al., 2011). Furthermore, the relation between PR gene expression and functionality of the SNI1 protein has also been linked to epigenetic regulation of somatic DNA recombination. SNI1 represses PR gene transcription by modifying levels of histone H3 acetylation and histone H3K4 di-methylation (Mosher et al., 2006). Better understanding of how and in what situations plants can use this memory is of great scientific as well as applied interest.

Here, we analyze inheritance of priming. We compare the resistance of same generation-primed plants and their descendants towards virulent Pst DC3000 and virulent isolates of the oomycete Hyaloperonospora arabidopsidis. To this end, Arabidopsis plants either mock-treated, treated with BABA, or inoculated with avirulent Pst and the progeny of these plants was analyzed for primed expression of defense-related PR genes and disease resistance. We found that when challenged with a pathogen, the progeny of primed plants showed strongly enhanced expression of defense-related genes and enhanced disease resistance compared to the progeny of non-primed plants.

RESULTS

To study a possible transgenerational inheritance of priming and induced resistance, Arabidopsis lines that had been subjected to specific treatments with the goal of inducing resistance and/or priming were generated (Figure 1). The role of BABA was tested in Arabidopsis accession Wassilewskija (Ws-0) and in the priming mutant ibs1 (in the Ws-0 background; Ton et al., 2005). The parental lines Ws-0 and ibs1 were treated once with water as a control or with BABA solution in water. The plants were grown to seed set and the resulting selfed progeny (S₁ progeny) was called WsH and ibs1H, respectively, in the case of water(H)-treated plants, and WsB and ibs1B, respectively, for BABA(B)-treated plants. Plants from the S₁ progeny (WsB and ibs1B) were again either treated with water or with BABA, respectively. They were grown to seed set thus giving rise to the S₂ progeny. S₂ plants derived from S₁ WsB and S₁ ibs1B plants and treated with water were called WsBH and ibs1BH, respectively. S₂ plants derived from S₁ WsB and S₁ ibs1B plants and treated with BABA were called WsBB and ibs1BB, respectively.

Arabidopsis plants accession Columbia (Col-0) were inoculated with avirulent bacteria carrying the avirulence gene avrRpt2 and were tested for a possible transgenerational effect (Figure 1). Col-0 parental plants were either mock inoculated giving rise to a S₁ progeny called ColM or inoculated with a suspension of avirulent Pst in buffer yielding S₁ progeny seeds called ColP (P standing for Pseudomonas). ColP was sown and again
either mock-inoculated with buffer or inoculated with a suspension of avirulent *Pst* in buffer. The seeds harvested from these plants (S\textsubscript{2} progeny) were called ColPM and ColPP, respectively.

The priming state induced by BABA is transferred to the next generation

A transient accumulation of transcripts of SA-dependent marker genes is a hallmark of BABA-IR and priming (Zimmerli et al., 2000, Ton et al., 2005). Therefore, we studied *PR1* expression, over a time course of 48 hours, in five-week-old plants of WsH, *ibs1*H, WsB, *ibs1*B, WsBH, *ibs1*BH, WsBB and *ibs1*BB that were soil-drenched with 25 ppm BABA or with water as a control, respectively. (see Figure S1A for experimental design).

BABA treatment induced a transient enhancement of *PR1* transcript levels in WsH plants (Figure 2). Interestingly, transcript levels of *PR1* were 3 fold higher in WsB and 4.6 fold higher in WsBB compared to WsH. In contrast, WsBH plants contained similar transcript levels as WsH (Figure 2A) indicating that priming for gene expression was switched off after one generation. The progeny of the *ibs1* mutant showed a similar pattern although the amplitude of the reaction was much reduced (Figure 2B). Our results show that the progeny of Ws-0 as well as of *ibs1* are sensitized to the priming of *PR1* triggered by BABA, thus displaying a memory of the treatments to which their parents had been subjected to. Furthermore, the facts that *ibs1* lines are severely affected in the induction of *PR1* upon infection and that Ws-0 or *ibs1* descendants do not show induction of *PR1* in the absence of BABA treatments (Figure S2, water treated plants) strongly indicate that this phenomenon is related to priming of defense. The results also show that the memory had to be rescued, as in the absence of further priming treatments the level of *PR1* transcripts was not elevated. This is consistent with the transient nature of the priming activity.

Resistance against *Pst* DC3000 is more effective in the progeny of BABA-treated plants

Parent Ws-0 and *ibs1* plants and descendants as shown in Figure 1 were either treated by soil-drench with 25 ppm BABA or water, respectively. Forty-eight hours after treatment (Time 0; Figure S1a), plants were inoculated with virulent *Pst* DC3000. Bacterial growth was monitored by qRT-PCR using *Pst* DC3000-specific primers over a time course of 72 hours after inoculation.

Descendants of BABA-primed plants (WsB, WsBB and WsBH) showed enhanced resistance against *Pst* DC3000 compared to WsH (Figure 3 and S3). In addition, the level
of resistance of the descendants was stronger according to the number of treatments accumulated through previous generations. Furthermore, a similar pattern of resistance was observed after BABA treatment prior to infection, resulting in a more pronounced resistance in the progeny of primed Arabidopsis (Figure 3B). BABA-treated *ibs1* progeny also showed transgenerational enhanced resistance against *Pst* DC3000 although they lacked the improved capacity to expressing BABA-IR observed in wild-type progeny plants.

Priming efficiency, expressed as the quotient of bacterial growth between 2 generations varied from 1.6 to 1.9 in BABA-treated Ws-0 lines. This quotient was between 1.1 and 1.4 for BABA-treated *ibs1* lines, water-treated *ibs1* lines and for water-treated Ws-0 lines (Table S1).

**Transgenerational priming for defense is supported by SA marker gene sensitization**

The priming state of the plants was reflected at the molecular level in the Ws-0 lines and *ibs1* lines upon inoculation with *Pst* DC3000. *PR1* (Figure 3C) and *PR2* and *PR5* transcript accumulation (Figure S4A and B) remained low in all inoculated water controls. In BABA-treated plants inoculated with *Pst* DC3000, *PR1* accumulation peaked at 24 hours post inoculation (hpi) in WsH. WsB plants reacted earlier and stronger and the reaction was even more pronounced in WsBB (Figure 3C). WsBH plants displayed similar kinetics and intensity of *PR1* transcript accumulation as the WsH plants.

In the *ibs1* lines the accumulation of *PR1* transcripts was delayed and attenuated compared to the corresponding Ws-0 line. *ibs1H* plants displayed a low relative expression level peaking at 24 hpi while in *ibs1B* the expression level was twice as high but only at 48 hpi. *ibs1BB* peaked at 24 hpi with 3-fold higher level than *ibs1H*. As for WsBH, in *ibs1BH* *PR1* accumulation levels reverted to *ibs1H* level.

The same trend was observed for *PR2* and *PR5* transcript accumulation (Figure S4A and B). These results show that although all plants reacted to BABA-treatment with an induction of *PR* gene transcripts following inoculation with *Pst* DC3000, the reaction was much more pronounced in the priming-competent Ws-0 lines than in the priming-impaired *ibs1* lines.

**Transgenerational inheritance of priming induced by avirulent *Pst***

In order to demonstrate that transgenerational priming is not only observed following chemical induction, we performed a set of experiments using a natural priming
phenomenon. Since preliminary tests had shown that S₁ descendants of both Ws-0 and
Col-0, respectively, showed transgenerational priming (data not shown), we decided to use
Col-0 plants for this experiment to demonstrate that transgenerational priming was also not
bound to a specific Arabidopsis accession. Leaves of accession Col-0 were infiltrated with
avirulent *Pst* leading to a localized hypersensitive reaction. An overview of treatments and
generations is shown in Figure 1.

Challenge-inoculation of the various Col-0 lines with virulent *Pst* DC3000 showed that
transgeneration priming is also observed following an inducing inoculation of parent plants
with avirulent *Pst*. At all time points post inoculation, the ColP and ColPP plants supported
less bacterial growth compared to ColM plants (Figure 4A). The restriction in bacterial
growth correlated with reduced disease symptoms; ColM and ColPM-plants showed more
severe disease symptoms than the ColP and the ColPP plants (Figure 4B and C).

Therefore, our data show that Arabidopsis plants exposed to same-generation priming by
a necrotizing infection with avirulent bacteria transfer the experience of the encountered
stress situation to their descendants. Interestingly, ColPM plants showed no significant
reduction of disease symptoms and the same *PR1* transcript levels compared to ColM
(Figure 4B). As it was observed with BABA-treated progeny, transgeneration priming did
not last after a priming-free generation, suggesting that BABA- and *PstavrRpt2*- induced
transgenerational resistance may be temporarily maintained via similar mechanisms.

The differences in basal levels of resistance among the studied lines correlated with levels
of transcript accumulation of *PR1* (Figure 4D), *PR2* (Figure S5A) and *PR5* (Figure S5B).

Transgenerational inheritance of priming against *Hyaloperonospora arabidopsidis*

The results described above demonstrate that transgeneration priming is associated with
the sensitization of the SA-dependent response. In order to test whether this phenomenon
was also effective against other SA-sensitive pathogens, we inoculated BABA- and water-
treated progeny, as well as the progeny of plants mock- or avirulent *Pst* inoculated, with
virulent strains of the obligate biotrophic oomycete *H. arabidopsidis* (isolate Noco for Col-0
and isolate Emwa for Ws-0). Disease severity was assessed at 7 dpi in trypan-blue-
stained leaves (Figure 5). The leaves were classified into 5 categories according to their
degree of colonization (Figure 5A). The control lines ColM and WsH (Figure 5) plants
consistently showed a higher degree of colonization by the oomycete than the primed
descendants WsB and WsBB (Figure 5B), ColP and ColPP (Figure 5C). Second
generation descendants whose parents were not subjected to an additional priming
treatment in the S₁ generation reverted to a more susceptible infection phenotype (Figure
These results show that the progeny of Arabidopsis plants exposed to same-generation priming with avirulent bacteria or with BABA in the parental generation are more resistant to *H. arabidopsidis*.

**Priming in the progeny of BABA-treated plants is not due to transfer of BABA to the next generation through the seeds.**

To assess whether the priming observed in the progeny of BABA-treated plants might be due to a transfer of BABA to the next generation through the seeds, we measured BABA concentrations in untreated plants and plants soil-drenched to a final concentration of 40 ppm (Figure S6A) and 25 ppm BABA (Figure S6B), respectively. No BABA was present in untreated plants. The highest concentration of BABA was detected within days after treatment. Traces of BABA were found in the flowers of BABA-treated plants and in the derived S₁ seeds (Figure S6A). We also analyzed BABA content in 7 day old S₁ seedlings and 5 weeks old S₁ rosette stage descendants of BABA-treated Col-0 plants. The traces of BABA detected (< 2.2 µg/g dry weight) were considerably below the concentration threshold for resistance induction which corresponds *in planta* with 50 µg/g dry weight (calculated empirically from experiments performed over the years in our lab). Hence, the BABA level in the progeny of BABA-treated plants is far too low to be responsible for the observed transgenerational priming. Our conclusion is further supported by the fact that transgenerational priming is also observed in the absence of BABA in the progeny of plants inoculated with avirulent *Pst*.

**Changes in DNA methylation levels in the PR1 promotor.**

Since the *PR1* gene has been shown to be very responsive to priming and this effect is transferred to the next generation (this paper) we decided to assess the DNA methylation level in the region of the *PR1* promotor where many of the elements possibly involved in such an increased induction are located. To this end we subjected plant DNA to bisulfite treatment and quantified the pattern of methylation of CGN, CHG and CHH sites over a 503 bp long region in the generated clones using the CyMate program (Hetzel et al. 2007). The CyMate output for methylation analysis is depicted in Fig. S7 and S8. This analysis was performed on samples of WsH, WsB, WsBB and WsBH as well as on samples of *ibs1H*, *ibs1B*, *ibs1BB* and *ibs1BH*. As shown in Fig. S9, only minimal changes in overall c-methylation frequency were observed in the sequenced clones. This is also true for the methylation pattern of specific motives (WRKY/W-boxes; TGA binding sites; ERF binding...
site; PR-box and NF-κB binding site) within the PR1 promotor section tested (data not shown).

DISCUSSION

Our results show that subjecting Arabidopsis plants to a treatment with the chemical BABA or an inoculation with avirulent bacteria induces a primed state that is transmitted to the progeny. The progeny of primed plants has a higher basal level of disease resistance and an enhanced capacity to react to additional priming treatments.

In order to study the transmission of the BABA-primed state in WsB, WsBB and WsBH plants, we analyzed levels of transient accumulation of PR gene transcripts upon BABA treatment. Basal levels of PR expression were not altered previous to BABA treatment (Figure 2), however WsB was sensitized to additional BABA treatments resulting in higher PR1 transcript levels compared to the progeny of water-treated plants (WsH). Additional BABA-treatment of the WsB generation further increased the priming capacity in the WsBB generation (Figure 2). Furthermore, the enhanced disease resistance in the progeny of primed lines against Pst DC3000 correlated with increased levels of SA-dependent gene transcripts of PR1, PR2 and PR5 upon infection, indicating general changes in the regulatory mechanisms of defense gene expression (Figure 3). Interestingly, our data also show that priming induced by inoculation with avirulent Pst (PstavrRpt2) can also be inherited by the descendants. The progeny of plants treated with BABA or inoculated with avirulent Pst were significantly more resistant to virulent Pst and H. arabidopsidis, respectively, than the progeny of control-treated plants (Figure 4). Transgeneration priming of PR1 expression was lost in the S2 generation (WsBH) in the absence of new BABA treatments, whereas the resistance phenotype was still partially detected.

Interestingly, BABA-treatment of a parental generation sensitizes its descendants to be primed more effectively: the progeny is “primed to be primed”. In contrast, the ibs1 mutant that is defective in priming (Ton et al., 2005), was compromised in the “primed to be primed” response (Figure 3). Transgenerational enhancement of basal resistance was, however, not affected in ibs1 suggesting the involvement of different underlying mechanisms in the two phenomena.

We had previously shown that BABA was able to prime plants to react faster to biotic and abiotic stress (Zimmerli et al., 2000; Jakab et al., 2005; Flors et al., 2008; Galis et al., 2009) and it is accepted that priming occurs in many plant species and with various priming agents (Agrawal, 2002; Conrath et al., 2002, Prime-a-plant group et al., 2006). Despite numerous reports on the same generation, examples pointing to transgenerational
priming are scarce. Wild radish that had been fed on by Pieris rapae or treated with jasmonate, respectively, yielded progeny that displayed an increase in resistance to herbivores (Boyko et al., 2007). Enhanced virus resistance was reported in the progeny of virus-induced tobacco plants (Boyko et al., 2010; Kathiria et al., 2010). In addition, other studies describe transgeneration effects in the progeny of plants infected with the virulent Pst DC3000 or damaged by herbivory attack, which are mediated by the up-regulation of the SA- or JA-related signaling pathway, respectively (Luna et al., 2011; Rasmann et al., 2011). Therefore, this suggests that the molecular mechanisms underlying induced defense inheritance may depend on the stress or the priming agent to which parental lines were exposed to. The capacity for transgenerational priming on the other hand is clearly not accession-specific since we observed it in both Arabidopsis accessions with Ws-0 and with Col-0 background, respectively.

In our study, for both BABA- and Pst-primed plants the primed state was only upheld in the immediate progeny. Without renewed priming treatment of the parent generation, in the progeny, the disease resistance phenotype and defense gene expression reverted to an “unprimed” state. In contrast, Luna et al. (2011) and Rasmann et al. (2011) demonstrated that transgenerational priming can be maintained over one stress-free generation. However, non-persistent transgenerational adaptive effects to further generations have been described previously (Pecinka et al., 2009). Furthermore, Luna et al. (2011) exposed parental plants to recurrent pathogen stress by Pst DC 3000 whereas our experiments consisted in single inoculations. The timeframe in which transgenerational priming or resistance is upheld seems to be dependent on the inducer and the severity of the disease in the parental generation.

The possibility that the transgenerational priming observed in progeny from BABA-treated parents might be due to a direct transfer of BABA through the seeds to the new generation is improbable. Our BABA measurements show that already 3 weeks after treating Arabidopsis with BABA, the remaining quantities of BABA in the plant tissues were far below the threshold needed to induce resistance (Figure S6). BABA was undetectable in the progeny of BABA-treated plants at the time of challenge inoculation.

In order for the offspring to remember a past experience from the parents, the latter have to be able to perceive the specific stress, they have to store this information, retain and transmit it to the descendants. To benefit from this information the descendants have to be able to retrieve the information and translate it into appropriate reactions. Although the molecular mechanisms of same-generation priming have recently started to be better understood (reviewed in Conrath, 2011), the molecular details underlying
transgenerational priming are still under study. However, recent groups have demonstrated that epigenetic mechanisms play a role in plant defense and several review articles comment on the possible involvement of epigenetic mechanisms in transgenerational phenomena (Chinnusamy and Zhu, 2009; Sano, 2010; Alvarez et al., 2010). Histone modifications are examples of epigenetic mechanisms; indeed, such modifications in the promoters of defense genes have been shown to correlate with transgenerational induced resistance in Arabidopsis against abiotic (Boyko et al., 2010) and biotic stresses (Luna et al., 2011). In addition, small RNA molecules (siRNA) are known to be important components of gene regulation (Vaucheret 2006) and have been described that they play a role in transgenerational effects in plants against abiotic stress (Boyko et al., 2010). In agreement with these results, Rasmann et al., 2011 describe that mutants blocked in the enzymatic activity responsible for the biosynthesis of siRNA lacked to express transgeneration enhanced resistance to herbivores. Finally, it has been described that different defense situations such as pathogen infection (Pavet et al., 2006) or chemical treatment with JA and SA (Verhoeven et al., 2010) resulted in changes in DNA methylation patterns. These changes are yet the most likely signal to be transmittable through meiosis. Indeed, Luna et al. (2011) showed that reduced DNA methylation in the drm1drm2cmt3 triple mutant mimics transgenerational priming of SA-dependent defences. In combination with previous findings that P. syringae bacteria induce large-scale hypomethylation in Arabidopsis (Pavet et al., 2006), it is plausible that the transmission of this defence priming is mediated by hypomethylated DNA. Although DNA methylation has long been considered to be stable, spontaneous gain or loss of DNA methylation leading to meta-stable heritable changes in methylated cytosines have been described recently (Schmitz et al., 2011). Such mechanisms might explain why the priming state is not transmitted to a further generation in our system or in the one described by Rasmann et al. (2011) when the priming pressure is not upheld. Since we observed a constant and strong priming of PR1 expression in both BABA- and Pst-primed plants we tested whether demethylation in the PR1 pomotor might explain the priming behaviour in our Ws-0 parental and descendant lines as well as in the corresponding ibs1 lines lacking the strong priming of PR1 expression. Notable changes in DNA c-methylation were found for neither of the lines and treatments in the section of the promotor sequenced nor in the specific motives corresponding to cis-elements known to be important for PR1 expression (Fig. S7, 8, 9). In contrast, Pavet et al., (2006) observed a demethylation of nearly 38 % following infection of Arabidopsis with Pst.
Inheritance of alterations in DNA methylation being the most plausible explanation for the observed transgenerational inheritance of priming, it is tempting to conclude from our results that transgenerational regulation of PR1 expression in this case could be based on the activity of hypomethylated trans-acting elements of transcription factors that regulate the expression of PR1 and related genes. Whether this is the case in our system is currently under investigation.

CONCLUSION

The capacity of a plant to express primed resistance depends on multiple signal transduction pathways (Zimmerli et al., 2000; Jakab et al., 2005; Galis et al., 2009). The emerging picture is that priming improves a plant's ability to cope with a given stress situation. Hence, a plant's capacity for priming is an important survival parameter. Inheritance of the primed state as observed in transgenerational priming is expected to contribute to improved adaptation of the progeny to environmental conditions. Our findings have obvious implications for natural and agronomical ecosystems. Especially in the latter field, transgenerational priming suggests the possibility of producing disease resistant offspring by intentionally exposing parent plants to a priming treatment.

MATERIALS AND METHODS

Biological material

Arabidopsis thaliana accession Col-0, Ws-0 and the ibs1 mutant were grown in Jiffy peat pellets maintained at 20°C day/18°C night temperature with 8 h light (150 µE m⁻² s⁻¹) and 70% RH. About 30 seeds per pot were stratified at 4°C in the dark for 2 days and grown for three weeks before being used for Pst DC3000 bioassays. For the H. arabidopsidis bioassays, two-week-old plants were used. When the seedlings had reached the cotyledon stage, the number was reduced to 15/Jiffy (n = 3 in Figure legends stands for n = 3 Jiffies with each 15 plants). One 4-week-old plant per Jiffy was used for stress induction with Pst avrRpt2 and for BABA priming experiments. Bacterial strains were grown as described (Zimmerli et al., 2000) with the exception that the avirulent strain Pst avrRpt2 was grown with the addition of 25 µg mL⁻¹ kanamycin for selection. H. arabidopsidis strains Noco and Emwa were maintained on A. thaliana Col-0 and Ws-0, respectively.

The timing of treatments in the various bioassays is schematically presented in Figure S1.

Generation of first and second progeny of BABA-primed lines and Pst avrRpt2-lines
Tap water (pH 8.2) as a control treatment or an aqueous solution of BABA (pH 8.2; Sigma; final concentration of 25 ppm in the soil) were applied as a soil drench to 4-week-old Ws-0 and ibs1 plants. Each Jiffy stood in a small Petri dish to guarantee that each plant received exactly the same amount of BABA. Flowering was induced by transferring plants to long-day conditions (16 hours of light). S1 plants grown from the seeds of those parent plants were designated as WsB, ibs1B, WsH and ibs1H, respectively (see Figure 1). They were again treated with water or BABA at four-weeks post germination. Seeds of these plants gave rise to the the S2 generation WsBB, ibs1BB and WsBH, ibs1BH lines, respectively.

Pst DC3000 carrying the avirulence gene **avrRpt2** was used to generate the Pst **avrRpt**-lines (Figure 1). Five leaves of four-week-old Col-0 plants were syringe infiltrated with a bacterial suspension of $10^8$ cfu mL$^{-1}$ in 10 mM MgSO$_4$. Mock-infiltrated plants were injected with 10 mM MgSO$_4$ (pH 8.6). Plants were maintained at 100% relative humidity for 1 week. Flowering was induced by transferring plants to long-day conditions. The resulting S1 seeds (ColP and ColM, respectively) were again syringe infiltrated with bacteria or mock-infiltrated to give rise to the S2 generation (ColPP and ColPM, respectively). For the generation of the “transgeneration” seeds we started with 15 mother plants each for every line and treatment; 15 single plants each were randomly chosen to produce the subsequent generation for each treatment.

**Plant inoculation and sample processing**

BABA (25 ppm final concentration in the soil) or water (control) was applied as soil drench to three-week-old plants 2 days prior to inoculation with *P. syringae* (Zimmerli et al., 2000). BABA-treatment (15 ppm final concentration in the soil) or water was applied similarly on two-week-old plants for *H. arabidopsidis* bioassay (Ton et al., 2005). Plants were dip-inoculated with bacteria (Zimmerli et al., 2000) and disease symptoms were scored (Jakab et al., 2005).

Seedlings were spray-inoculated with *H. arabidopsidis* and tissue colonization was quantified (Ton et al., 2005). Colonized leaves were assigned to five different classes based on hyphal proliferation (Figure 5A). Fisher’s exact test using R.2.11.0 software was done to show significant differences between lines and treatments.

**Quantification of Pseudomonas syringae**

Quantification of *Pst* DC3000 growth was performed by qRT-PCR as described (Boachon et al., 2009). Genomic DNA from three-week-old plants was extracted using the
NucleoSpin Plant II kit (Macherey-Nagel) and bacterial growth was quantified as transcript levels of *Psorf* normalized to the transcript level of the Arabidopsis gene *AtTUB4*. This method was used because it allows to accurately process large number of samples in a short time and to have enough material to perform gene expression analyses on the same material.

**Gene expression analyses**

Total RNA was isolated from three-week-old plants using the NucleoSpin RNA Plant kit (Macherey-Nagel) according to the manufacturer’s instructions. cDNA was obtained from 1 µg of total RNA using the PrimeScript RT kit (Takara). qRT-PCR quantification of gene expression was performed in a Rotor Gene 6000 (Qiagen). Gene-specific primer sequences were designed using Primer 3 software. Three biological replicates were collected per time point. The software program Gene-X was used to calculate the mean normalized (to the housekeeping gene *SAND*) expression of the genes (Vandesompele et al., 2002). Ct values ±standard deviation for *PR1, PR2* and *PR5* for all the lines and treatments at time zero can be found in Table S2.

**Determination of BABA levels**

Plants were frozen in liquid nitrogen and lyophilized. Dry plant material was extracted on ice with of a methanol: water mixture (10:9) containing 0.01% formic acid. After centrifugation the supernatant was recovered and filtered through a 0.22 µm cellulose filter. Aliquots were injected into an ultraperformance liquid chromatograph coupled to a triple quadruple mass spectrometer (Aquity TQD, Waters). The amount of BABA in the samples was calculated by using an external calibration curve of BABA by scoring the eluting peaks using a standard C-18 UPLC column. The mass spectrometer transition selected in positive ESI was 104>44 ratio of Ms/z. The gradient, mobile phases and other chromatographic conditions were as described (Flors et al., 2008).

**DNA extractions and bisulphite sequencing**

Total genomic DNA was extracted from three-week-old leaf tissue of each WsH, WsB, WsBB, WsBH, *ibs1H, ibs1B, ibs1BB* and *ibs1BH* lines using the Qiagen DNeasy Plant Kit (Qiagen) according to the manufacturer’s protocol. Approximately 2 µg of genomic DNA were used for bisulphite conversion. Bisulphite modification and desulphonification of
genomic DNA were performed using the MethylDetector Bisulfite Modification kit (Active Motif, www.activemotif.com) according to the manufacturer’s instructions. Based on Johnson et al. (2003), the primer pair used was as follows: 5’-TCGGAGGAGTATATGTATTGCTTAGAATCA-3’ and 5’-TTGTTTCGTATCGGTAGCTTTGCCAT-3’ (PCR conditions are available upon request). This allowed the amplification by PCR of a 672-bp fragment of the PR1 promotor containing as-1-sequences. The PCR products were inserted into pGEM-T Easy vector and at least 8-20 clones for each WsH, ibs1H and their respective transgenerational descendant lines were selected for plasmid isolation. The clones were sequenced (www.macrogen.com) and 503-bp segments of each sequence starting at position -679 relative to transcription initiation site of the PR1 gene were then aligned using CLUSTAL version 1.83. The alignment files were saved, then submitted to CyMATE (www.gmi.oeaw.ac.at/CyMATE) and analyzed with this program.

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FIGURE LEGENDS

Figure 1. Experimental design. Parent plants: Ws-0 (Wassilewskija wild type plants), ibs1 (a priming mutant in Ws-0 background) and Col-0 (Columbia wild type plants). S₁ progeny: descendants from the selfed parent plants; S₂ progeny: descendants from the selfed S₁ plants. The plants were treated with water = H, BABA = B, mock-treated with buffer = M or inoculated with avirulent Pseudomonas syringae pv tomato containing avrRpt2 = P

Figure 2. Basal PR1 expression levels in the progeny of Ws-0 plants and ibs1 plants (see Figure 1). Four-wk-old plants were soil-drenched with water or a solution of BABA to a final concentration of 25 ppm in the soil. Transcript levels were analyzed with qRT-PCR. Expression was normalized to the sample treated with water at 0 h. PR1 expression in the different Ws-0 lines (A) and in the different ibs1 lines (B) is shown. The values represent means +/- SD of three replicates. Similar results were obtained in three independent experiments.

Figure 3. Descendants of BABA-treated Ws-0 plants are more resistant to virulent Pseudomonas syringae. Three-wk-old plants were treated with BABA (25 ppm final concentration in the soil) or water 2 days prior to inoculation with Pst DC3000 (OD₆₀₀ = 0.08). A, Growth of Pst DC3000 in the water-treated Ws-0 lines (WsH, WsB, WsBB and WsBH) and ibs1 lines (ibs1H, ibs1B, ibs1BB and ibs1BH) at 72 hpi. B, Growth of Pst DC3000 in BABA-treated Ws-0 lines and in ibs1 lines at 72 h post-inoculation. Bacterial growth was quantified by qRT-PCR as transcript levels of Psorf normalized to the transcript level of the Arabidopsis gene AtTUB4. Capital letters indicate statistically significant bacterial growth within the water-treated Ws-0 and ibs1 lines (ANOVA, Student-Newman-Keuls, n = 3, P < 0.05). Small letters indicate statistically significant bacterial growth within the BABA-treated Ws-0 or ibs1 lines. C, qRT-PCR analysis of PR1 gene expression in BABA-treated (circles) and water-treated (squares) Ws-0 and ibs1 lines. Expression was normalized to the corresponding sample treated with water at 0 h. The values represent means +/- SD of three replicates. Similar results were obtained in three independent experiments.

Figure 4. Inheritance of priming induced by avirulent Pseudomonas syringae (PstavrRpt2). Single leaves of 4-wk-old plants were infiltrated with Pst avrRpt2 or mock-infiltrated with buffer. A, Col-0 lines (see Figure 1) were challenge-inoculated with Pst DC3000 and bacterial growth was quantified by qRT-PCR as described for Figure 3. Small and capital
letters above error bars represent statistically significant difference in bacterial growth within Col-0 lines at 48 h and 72 h post-inoculation (ANOVA, Student-Newman-Keuls, \(n = 3\), \(P < 0.001\)). Values represent means +/- SD of 3 biological replicates. B, Quantification of disease resistance of Col lines 5 dpi. Letters represent statistically significant difference in the percentage of leaves with symptoms (ANOVA, Student-Newman-Keuls, \(n = 30\), \(P < 0.05\)). C, Disease phenotype of Col lines. D, qRT-PCR analysis of \(PR1\) gene expression in Col lines. Expression was normalized to the sample treated with water at 0 h. The values represent means +/- SD of three replicates. Similar results were obtained in three independent experiments.

Figure 5. Inheritance of priming against \(H. \text{arabidopsisidis}\). A, Disease ratings were classified based on the percentage of leaf colonization by mycelium. Class I: 0%; class II: 1-25%; class III: 26-50%; class IV: 51-75% and class V: 76-100%. Disease ratings are shown as the percentage of leaves in each resistance class. B, Disease resistance in Ws-0 lines inoculated with the Emwa strain of \(H. \text{arabidopsisidis}\). Asterisks indicate statistically significant differences in the percentage of leaves in the different classes compared to WsH (Fisher test, \(* \ = P < 0.05\); \(* * * = P < 0.001\)). C, Disease resistance in Col lines inoculated with the Noco strain of \(H. \text{arabidopsisidis}\). Asterisks indicate statistically significant differences in the percentage of leaves in the different classes compared to ColM (Fisher test, \(* = P < 0.05\); \(* * * = P < 0.001\)).

Figure S1. Experimental design of resistance tests. A, Schematic representation of the experiments carried out with the Ws-0 and \(ibs1\) lines and their corresponding figures in this study. B, Schematic representation of the experiments carried out with the Co-0l lines and their corresponding figures in this study. C, Schematic representation of the \(H. \text{arabidopsisidis}\) experiments carried out on the Ws-0 and Col-0 lines and the corresponding figure in this study.

Figure S2. \(PR1\) expression levels in Ws-0 and \(ibs1\) lines control-treated with water. Four-wk-old plants were treated with water and \(PR1\) expression was analyzed by qRT-PCR. A, \(PR1\) expression in Ws-0 lines. B, \(PR1\) expression in \(ibs1\) lines. Expression was normalized to the values of WsH and \(ibs1\)H, respectively, at -48 h. Values represent means +/- SD of three replicates. Similar results were obtained in three independent experiments.
Figure S3. Descendants of BABA-treated Ws-0 plants are more resistant to virulent *Pseudomonas syringae*. Three-wk-old plants were treated with BABA (25 ppm final concentration in the soil) or water 2 days prior to inoculation with *Pst* DC3000 (OD$_{600}$ = 0.08). A, Growth of *Pst* DC3000 in the water-treated Ws-0 lines (WsH, WsB, WsBB and WsBH). B, *ibs1* lines (*ibs1*H, *ibs1*B, *ibs1*BB and *ibs1*BH) at 0, 48 and 72 pi. C, Growth of *Pst* DC3000 in BABA-treated Ws-0 lines compared to that in D, *ibs1* lines at 0, 48 and 72 hpi. Bacterial growth was quantified by qRT-PCR as transcript levels of *Psorf* normalized to the transcript level of the Arabidopsis gene *AtTUB4*. Capital letters indicate statistically significant bacterial growth at 72 h (ANOVA, Student-Newman-Keuls, n = 3, P < 0.05). Small letters indicate statistically significant bacterial growth at 48 h (ANOVA, Student-Newman-Keuls, n = 3, P < 0.05). E, Disease response of the BABA- or water-treated of *ibs1* lines at 5 days post-inoculation. Small and capital letters above error bars indicate statistically significant differences in the percentage of leaves with symptoms in BABA- and water-treated lines, respectively (ANOVA, Student-Newman-Keuls, n = 30, P < 0.001). F, Visible disease phenotype in the Ws-0 lines. G, Visible disease phenotype in the *ibs1* lines.

Figure S4. qRT-PCR analysis of *PR2* and *PR5* transcript levels in Ws-0 and *ibs1* lines upon inoculation with virulent *Pst*. Expression levels of *PR2* (A) and *PR5* (B) in BABA-treated (circles) and water-treated (squares) Ws-0 and *ibs1* lines. Expression was normalized to the corresponding sample treated with water at 0 h. The values represent means +/- SD of three replicates. Similar results were obtained in three independent experiments.

Figure S5. qRT-PCR analysis of *PR2* and *PR5* transcript levels in Col-0 lines upon inoculation with virulent *Pst*. Expression levels of *PR2* (A) and *PR5* (B). Expression was normalized to the corresponding sample at 0 h. The values represent means +/- SD of three replicates. Similar results were obtained in three independent experiments.

Figure S6. Priming of the progeny of BABA-treated lines is not due to direct transfer of BABA to the next generation. BABA concentrations were determined in untreated plants and in plants soil-drenched with BABA, respectively. A, BABA 40 ppm and B, BABA 25 ppm. S$_1$ = first generation selfed progeny. The horizontal lines at 50 µg BABA/g dw show the threshold concentration for resistance induction.
Figure S7. Graphical output generated by CyMate of the Ws transgenerational lines.

A) Methylation analysis of a 503 bp fragment of the PR1 promotor of Ws and descendants. The location of the cytosines within the sequenced fragment is shown in the ruler at the top of the Figure. Beneath the ruler, the filled symbols represent methylated cytosine residues, whereas the open symbols represent cytosine residues lacking methylation. The red circles stand for mCGN, the blue squares represent mCHG and the green triangles represent mCHH. The uppermost sequence (Ws-0) corresponds to consensus sequence and is followed by individual clones obtained by polymerase chain reaction amplification of bisulfite-treated DNA. The order of the individual sequences is shown on the left.

B) Zoom-in view of the PR1 promotor fragment showing the different motives (WRKY, TGA, ERF, PR-box and NF-κB) identified on the promotor.

Figure S8. Graphical output generated by CyMate of the ibs1 transgenerational lines. Methylation analysis of 503 bp fragment of PR1 promotor of ibs1 and descendants. Filled symbols represent cytosine methylation, whereas open symbols represent lack of methylation. Circles represent mCGN, squares represent mCHG and triangles represent mCHH. The order of the individual sequences is shown on the left.

Figure S9. Bilsulfite sequencing data showing percentage of CGN, CHG and CHH methylation, as computed by the CyMate program, in a 503-bp region of the PR1 promotor of Ws-0 and descendants and ibs1 and descendants, respectively.
Figure 1. Experimental design. Parent plants: Ws-0 (Wassilewskija wild type plants), ibs1 (a priming mutant in Ws-0 background) and Col-0 (Columbia wild type plants). S₁ progeny: descendants from the selfed parent plants; S₂ progeny: descendants from the selfed S₁ plants. The plants were treated with water = H, BABA = B, mock-treated with buffer = M or inoculated with avirulent *Pseudomonas syringae pv tomato* containing avrRpt2 = P.
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