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Article Sub-Title					
Article CopyRight	Springer Science+Business Media B.V. (This will be the copyright line in the final PDF)				
Journal Name	Arthropod-Plant Interactions				
Corresponding Author	Family Name	Sauge			
	Particle				
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	Email				
	Received	27 July 2010			
Schedule	Revised				
	Accepted	7 June 2011			

Abstract	In gene-for-gene host–enemy interactions, monogenic plant resistance results from pathogen recognition that initiates the induction of plant defense responses. Schematically, as the result of the on/off process of recognition, phenotypic variability in enemy virulence is expected to be qualitative, with either a failure or a success of host colonization. We focussed on a major gene from peach conferring avoidance resistance against the green peach aphid <i>Myzus persicae</i> . Measurements of herbivore density and time-dependent aspects of resistance induction were examined, as well as variability in the aphid's ability to exploit the resistant host. Varying densities of infestation did not provoke differences in the aphid's tendency to leave a plant, and a single aphid was sufficient to elicit a response. Similarly, the duration of infestation did not affect the aphid response. A brief aphid feeding time of 3 h triggered induced resistance, which became effective between 24 and 48 h after the initial attack. Induced resistance decayed over time in the absence of additional infestation. Thirty aphid genotypes collected from natural populations were tested in the laboratory. No clone could colonize the resistant host, suggesting that all of them triggered the induction of effective plant defense responses. However, we detected significant quantitative variation among clones in the tendency of aphids to leave plants. These results improve our understanding of induced resistance as a dynamic phenomenon and suggest that the potential for aphids to adapt to a major plant resistance gene may depend on factors other than the mere capacity to evade recognition.
Keywords (separated by '-')	Adaptation - Density dependence - Gene-for-gene plant-insect interactions - Induced resistance - <i>Prunus persica</i> - Timing of induction
Footnote Information	Handling Editor: Michael Smith.

Journal: 11829 Article: 9141



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ORIGINAL PAPER

Resistance induction and herbivore virulence in the interaction between *Myzus persicae* (Sulzer) and a major aphid resistance gene (*Rm2*) from peach

5 Marie-Hélène Sauge · Jean-Luc Poëssel ·
6 Thomas Guillemaud · Laurent Lapchin

Received: 27 July 2010/Accepted: 7 June 2011 © Springer Science+Business Media B.V. 2011

9 Abstract In gene-for-gene host-enemy interactions, 10 monogenic plant resistance results from pathogen recog-11 nition that initiates the induction of plant defense respon-12 ses. Schematically, as the result of the on/off process of 13 recognition, phenotypic variability in enemy virulence is 14 expected to be qualitative, with either a failure or a success 15 of host colonization. We focussed on a major gene from 16 peach conferring avoidance resistance against the green 17 peach aphid Myzus persicae. Measurements of herbivore 18 density and time-dependent aspects of resistance induction 19 were examined, as well as variability in the aphid's ability 20 to exploit the resistant host. Varying densities of infestation 21 did not provoke differences in the aphid's tendency to 22 leave a plant, and a single aphid was sufficient to elicit a 23 response. Similarly, the duration of infestation did not 24 affect the aphid response. A brief aphid feeding time of 3 h 25 triggered induced resistance, which became effective 26 between 24 and 48 h after the initial attack. Induced 27 resistance decayed over time in the absence of additional

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infestation. Thirty aphid genotypes collected from natural 28 populations were tested in the laboratory. No clone could 29 colonize the resistant host, suggesting that all of them 30 triggered the induction of effective plant defense responses. 31 However, we detected significant quantitative variation 32 among clones in the tendency of aphids to leave plants. 33 These results improve our understanding of induced 34 resistance as a dynamic phenomenon and suggest that the 35 potential for aphids to adapt to a major plant resistance 36 gene may depend on factors other than the mere capacity to 37 evade recognition. 38

Keywords Adaptation · Density dependence ·	40
Gene-for-gene plant-insect interactions ·	41
Induced resistance · Prunus persica · Timing of induction	42

Introduction

Models of antagonistic coevolution between host plants 44 45 and their enemies have been largely based around two major hypotheses. Ehrlich and Raven's (1964) theory was 46 that the evolution of insect specialization on host plants is 47 constrained by the diversity of the plant secondary 48 metabolites involved in the relationship. In this arms race 49 metaphor, plants accumulate constitutive chemicals, 50 regarded as biochemical defenses if they have negative 51 52 effects on the herbivores (Wittstock and Gershenzon 2002). Herbivores have in turn evolved behavioral or biochemical 53 strategies for avoiding plant toxins (Després et al. 2007). 54 55 Host defense chemicals and herbivore ability to metabolize 56 plant defensive compounds (virulence) across populations may display continuous heritable variation with a high 57 degree of correspondence between host and herbivore 58 59 phenotypes (Berenbaum and Zangerl 1998).



Journal : Large 11829	Dispatch : 15-6-2011	Pages : 9
Article No. : 9141	□ LE	□ TYPESET
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60 The gene-for-gene concept proposed by Flor (1955) states that a pathogen is able to infect a host unless the host 61 62 carries a specific resistance (R) gene that matches a specific 63 pathogen avirulence (Avr) gene. Major R genes act at the 64 earliest stages of pathogen detection by triggering a sig-65 naling cascade that culminates in activation of strong defenses. Schematically, pathogens adapt to an R gene 66 67 because altered or deleted Avr genes allows them to evade 68 recognition (Bent and Mackey 2007). Gene-for-gene 69 coevolution, first defined in plant-pathogen associations, 70 was also an inspiration for several interactions between 71 plant and piercing-sucking insects (Kaloshian and Walling 2005; Smith and Boyko 2007). The genetics of the inter-72 73 action between wheat and the Hessian fly, Mayetiola 74 destructor (Say) (Diptera: Cecidomyiidae), have been 75 generally recognized to fit this model. The interaction is 76 typically manifested as a binary response, i.e., either a 77 resistant plant and dead fly larvae or a susceptible plant and 78 living larvae (Harris et al. 2003). In many interactions 79 between plants and aphids, resistance is controlled by 80 major genes, some of which encode or show tight linkage 81 with plant R proteins conferring resistance to microbial 82 pathogens (Rossi et al. 1998; Klingler et al. 2005; Dogi-83 mont et al. 2007). Aphid biotypes that can overcome these 84 forms of resistance have appeared commonly among pop-85 ulations and have been designed on the basis of their 86 qualitative pattern of virulence with respect to these genes 87 (e.g., Alston and Briggs 1977; Porter et al. 1997; Burd et al. 88 2006).

89 The distinction between Ehrlich and Raven's hypothesis 90 and the gene-for-gene concept has proven to be useful to 91 understand ecological and evolutionary patterns of varia-92 tion in resistance and virulence at the population level. In 93 particular, the gene-for-gene concept may help explain the 94 nature of the local adaptation of enemy to host that is 95 difficult to reconcile with the arms race view of coevolu-96 tion (Kniskern and Rausher 2001). Considering the mode 97 of host-enemy coevolution can also have practical ramifi-98 cations in agricultural systems, insofar as the type of 99 genetic constraints exerted by resistant crop varieties affects the manner in which herbivorous insects evolve and 100 101 thus impact resistance durability (Gassmann et al. 2009). It 102 was recently demonstrated that the breakdown of mono-103 genic plant resistance occurred less frequently when the 104 R gene was combined to partial resistance quantitative trait 105 loci (Palloix et al. 2009; Brun et al. 2010).

We previously found within the genus *Prunus* (Rosaceae) genetic variation in induced resistance to the green peach aphid *Myzus persicae* (Sulzer) (Hemiptera: Aphididae), a polyphagous aphid species, which represents a threat for many crops in the world (Sauge et al. 2006). This genetic system establishes a useful framework for ecological studies of plant–aphid relationships. Moreover, some of these peach [Prunus persica (L.) Batsch] genotypes are 113 used in breeding programmes. This is the case for the 114 cultivar Rubira that confers strong avoidance resistance 115 causing aphids to leave the plant within a few days (Sauge 116 et al. 2002). The question of resistance durability repre-117 sents a critical issue in cultivated fruit trees, since the 118 119 management of resistance genes in time and space remains limited. Thus, we aim to produce information that could 120 help determining to which of the two modes of coevolution 121 the Rubira-M. persicae interaction approximates. 122

Resistance in Rubira is known to be controlled by a 123 major dominant gene (Pascal et al. 2002). This gene, 124 named Rm2, maps at the bottom end of linkage group 1 of 125 an F_2 genetic map derived from Rubira and anchored to the 126 "Texas" × "Earlygold" reference map for Prunus (Lam-127 bert and Pascal 2011). During the last decade much has 128 been discovered about the biochemical interactions that 129 specifically occur during gene-for-gene interactions (Stahl 130 and Bishop 2000; Kaloshian and Walling 2005; Bent and 131 Mackey 2007; Smith and Boyko 2007). By contrast, only a 132 few data are available about Rm2-mediated plant responses 133 to *M. persicae* infestation (Poëssel et al. 2006). In addition, 134 there are currently no aphid genotypes known to exhibit 135 virulence toward Rm2, probably because no resistant 136 commercial variety bearing this gene has been released so 137 far. Since intensive screening for virulence has never been 138 performed to date, we do not know whether there are 139 variants with preadaptive advantages among natural 140 populations. 141

Thereupon, our specific objectives were twofold. We 142 first wanted to determine whether the induced phenotype of 143 resistance, as measured by the tendency of aphids to leave 144 plants, matches the enemy perception and defense induc-145 tion processes involved in R gene-mediated resistance. For 146 that, we investigated aphid density and time-dependent 147 aspects of induction. Second, we looked for genetic vari-148 ation in the aphid response to host resistance among natural 149 populations of *M. persicae* and tested the prediction that 150 qualitative differences in the expression of virulence occur 151 152 among aphid genotypes.

Materials and Methods 15

Plants and aphids

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Prunus persicacv. Rubira (clone S2605) is a cultivar used155as peach rootstock. It was selected in 1980 at the Institut156National de la Recherche Agronomique, France, in a redleaf peach progeny from USA. It is considered to be157leaf peach progeny from USA. It is considered to be158homozygous at most loci, including the *Rm2* locus and is159usually seed-propagated. For all experiments, seedlings160were grown in a greenhouse and surveyed to keep them161

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162 free of enemies. Plants were tested when 6 weeks (42 day)
163 old.
164 Under temperate climate. *M. persicae* host alternates

Under temperate climate, M. persicae host alternates between the peach where sexual reproduction occurs (primary host) and many herbaceous host plants (secondary hosts). In early spring 2002, thirty aphid colonies were collected in three locations of southern France, in peach orchards planted with susceptible varieties (Table 1) (Guillemaud et al. 2003b). Aphids from each sample were assumed to belong to the clonal progeny of a fundatrix, hatched from sexually produced eggs. We believed that each colony represented a distinct genotype, a hypothesis that was verified by genotyping a subset of samples using eight microsatellite loci (result not shown). An avirulent laboratory clone (Mp03) used in previous work (Pascal et al. 2002; Sauge et al. 2002, 2006) was added to the set of field clones and used as a reference. We used one parthenogenetic female from each sample to initiate the rearing of 30 new colonies on individual peach seedlings in a growth chamber with a 16-h day length at 19°C.

Plant resistance in response to varying densities182and timing of aphid infestation183

To characterize the induced phenotype of resistance in 184 relation to (1) the intensity and (2) the timing of aphid 185 feeding stimuli, we carried out four experiments where the 186 two factors were manipulated independently (see Table 2 187 for experimental designs). We asked several questions. 188 What is the threshold density of inducing aphids required 189 to elicit induced resistance and is the level of induced 190 resistance related to the number of inducing aphids 191 (experiment a)? What is the minimum duration after the 192 beginning of feeding by inducing aphids required to detect 193 induced resistance (experiment b)? Is duration of aphid 194 feeding the same or can shorter feeding durations trigger 195 induced resistance as well (experiment c)? Finally, what is 196 the time course of induced resistance in the absence of 197 additional aphid feeding (experiment d)? 198

We conducted the experiments on plants that had been 199 preinfested by *M. persicae* (clone Mp03) or not (control). 200

Table 1	Geographical	origin and	number (n) of Myzi	ıs persicae	genotypes	collected	from peach	orchards in southern France
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Location	Date	п	Longitude	Latitude	Genotype label
Gotheron	25 February 2002	8	4°57′É	44°58′N	Got 1–8
Carros	27-28 March 2002	16	7°11′E	43°47′N	Car 1–16
Avignon	2 April 2002	6	4°48′E	43°56′N	Avi 1–6

The distance between the sampled orchards is given in Guillemaud et al. (2003a)

Table 2 Experimental design used to characterize the expression of plant resistance in	Experiment	Number of inducing aphids	Total time from beginning of feeding by inducing aphids to testing for induced resistance (h) $[1] + [2]$		
response to varying densities (experiment a) and timing of aphid preinfestation (experiments b, c, and d)	R		Duration of feeding [1]	Time between the end of feeding and testing for induced resistance [2]	[1] + [2]
(experiments b, e, and d)	a (<i>n</i> = 10)	1	48	0	48
		5	48	0	48
		10	48	0	48
		20	48	0	48
	b $(n = 6)$	20	6	0	6
		20	12	0	12
)	20	24	0	24
		20	48	0	48
	c $(n = 9-10)$	20	3	45	48
<i>n</i> represents the number of plant		20	6	42	48
replicates, with 10 aphids per		20	9	39	48
plant	d (<i>n</i> = 10)	20	48	0	0
Each experiment included		20	48	24	72
control plants that were not preinfested		20	48	48	96

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201 Inducing adult aphids were placed on their preferred 202 feeding site (the terminal growing shoot) of each plant of 203 the preinfested group; they were not restricted from dis-204 persing. At the end of the preinfestation period, we 205 removed all aphids. In experiment a, we fixed the duration 206 of preinfestation at 48 h, a sufficient duration to trigger 207 induced resistance. In experiments b, c, and d, we fixed the 208 number of inducing aphids at 20 to ensure a reasonable 209 aphid density (Sauge et al. 2002). To measure the level of 210 induced resistance, we placed 10 test adult aphids (clone 211 Mp03) on each control and preinfested plant. In the case of 212 preinfested plants, we installed test aphids on the same 213 shoot as the one used for preinfestation. The number of 214 aphids remaining on plants was counted 6 times during the 215 first 48 h after their installation. The few offspring pro-216 duced were removed at each inspection. We adopted a 217 short counting period because the longer this period, the 218 higher the probability for an induction by test aphids to 219 occur on control plants. We performed 6-10 plant repli-220 cates for each treatment.

221 Genotypic variation in aphid virulence

222 To determine whether there was variation in the response 223 of *M. persicae* to plant resistance among natural popula-224 tions and, if so, whether the level of virulence differed 225 qualitatively or quantitatively, we exposed clones collected 226 from several orchards (planted with susceptible peach 227 varieties) to Rubira plants. We placed 25 synchronized 228 adult aphids on each caged plant. Aphids remaining on 229 plants were counted twice a day at 9.00 and 17.00 h until 230 no more aphids were left. The few offspring produced were 231 not taken into account as a parameter of virulence since 232 they all died on plants before completing the final molt. We 233 evaluated the 30 field clones and the reference clone Mp03. 234 We performed two replicates for each clone.

235 Statistical analysis

236 All statistical analyses were performed using the R soft-237 ware (R Development Core Team 2010). Since avoidance 238 resistance can be characterized by the time at which the 239 aphid leaves the plant, we used survival analysis, a statis-240 tical method to study time-to-event variables. It is com-241 monly utilized in biomedical research and is also applied in 242 ecological entomology to predicting the foraging behavior 243 of parasitoids (e.g., Haccou et al. 1991) or modeling pop-244 ulation dynamics (Ma and Bechinski 2008). We adopted a 245 Cox's proportional hazards model (Cox 1972) to quantify 246 the plant-leaving tendency of aphids. The model describes 247 the influence of covariates on the instantaneous probability 248 that the aphid leaves the plant, given that it is still on it, 249 according to the equation:

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$h(t) = h_{\rm o}(t) \exp\beta^{x}$,

251 in which h(t) is the plant-leaving tendency (hazard function) 252 after a time t spent on the plant, $h_0(t)$ is the baseline hazard at time t (representing the hazard for an individual with the 253 254 value 0 for all the covariates) and β is the regression coef-255 ficient of the covariate x. If a coefficient β is such that the exponential term (the hazard ratio) is greater than one, then 256 the corresponding covariate x has an increasing effect on the 257 258 plant-leaving tendency. A coefficient β leading to a hazard ratio smaller than one reduces this tendency. 259

We estimated the time taken by an individual aphid to 260 261 leave the plant as the mean time between the last inspection 262 where it was checked and the first inspection where it was missing. We estimated the coefficient β by maximizing a 263 partial likelihood, and we tested the significant effect of the 264 covariates by examining the null hypothesis $H_0 \beta = 0$ by a 265 likelihood ratio statistics. Covariates in the experiments on 266 host resistance were successively the density and duration 267 268 of infestation. The baseline hazard was set to the control. Right-censored data were used to take into account aphids 269 remaining on plants after the period of observation had 270 expired, i.e., 48 h. The covariate in the experiment on 271 herbivore virulence was the aphid genotype. The baseline 272 273 hazard at the mean of all covariates in the model was set to the genotype Got 1. Plant replicates were specified as strata 274 in the model. Strata in a Cox model are regarded as addi-275 276 tional sources of variation that must be accounted for the estimation of the coefficients, but whose effects are not 277 considered of particular interest. In a second step, we tested 278 279 for differences in the survival curves of aphids across 280 groups of preinfestation or aphid genotypes using the log rank test, one of a family of test procedures with parameter 281 ρ defined by Harrington and Fleming (1982). 282

Results

Plant resistance in response to aphid infestation 284

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285 The tendency of *M. persicae* to leave plants of Rubira was affected by preinfestation (Table 3). The amount of dam-286 age needed to elicit induced resistance was extremely low. 287 A preinfestation by a single aphid significantly increased 288 the hazard for subsequent individuals to leave the plant, by 289 a factor of exp (β) = 6.31 on average, that is, by 531% 290 (Table 3a). Higher numbers of inducing aphids did not lead 291 to an increased level of induced resistance within the tested range (log rank test: $\chi^2 = 0.5$, df = 3, P = 0.908), show-292 293 ing that induced resistance was not aphid density-294 dependent. 295

Varying timing of preinfestation differentially affected 296 the plant-leaving tendency of aphids. In experiment b 297

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Experiment	Covariates	β	SE (β)	$\exp(\beta)$	n	χ^2 (df)	Р	Effect on leaving tendency
a	Treatment effect				500	135 (4)	< 0.0001	
	-1 aphid	1.84	0.210	6.31***				+
	-5 aphids	1.71	0.206	5.53***				+
	-10 aphids	1.78	0.208	5.95***				+
	-20 aphids	1.57	0.206	4.80***				+
b	Treatment effect				300	37.2 (4)	< 0.0001	
	6 h	0.339	0.218	0.71				No effect
	-12 h	0.322	0.211	1.38				No effect
	-24 h	0.267	0.215	1.31				No effect
	-48 h	0.911	0.207	2.45***				+
c	Treatment effect				390	24.3 (3)	<0.0001	
	-3 h + 45 h	0.432	0.164	1.54**				+
	-6 h + 42 h	0.610	0.164	1.84***				+
	–9 h + 39 h	0.726	0.162	2.07***				+
d	Treatment effect				400	71.9 (3)	< 0.0001	
	-48 h	1.427	0.201	4.17***			Y	+
	-48 h + 24 h	1.228	0.205	3.41***				+
	-48 h + 48 h	0.494	0.209	1.64*				+

Table 3 Effect of aphid density (experiment a) and timing of preinfestation (experiments b, c, and d) on the plant-leaving tendency of Myzus persicae

Estimated regression coefficients (β), standard errors (SE), and hazard ratios [exp (β)] for the covariates of a Cox proportional hazards model. χ^2 correspond to a likelihood ratio test

*, **, ***, levels of significance as compared to the baseline hazard (uninfested control) for the coefficients at P < 0.05, 0.01 and 0.001, respectively

+ indicates an increasing effect of the covariate on the plant-leaving tendency. The more remote the hazard ratio to zero, the stronger the plantleaving tendency

298 where the aphid behavior was studied immediately after 299 removing inducing aphids (Table 3b), we found that 300 induced resistance became effective between 24 and 48 h 301 of aphid feeding, since the minimum duration necessary to 302 detect induced resistance was 48 h. At this stage, it was not 303 possible to assess if induction required 24 h or 48 h of 304 feeding, or some combination. Experiment c indicated that 305 very short feeding times (as short as 3 h) were sufficient to 306 elicit induced resistance, provided induction was measured 307 48 h after the beginning of preinfestation (Table 3c). In 308 addition, when the time since the onset of preinfestation 309 was held constant to 48 h, there was no significant effect of 310 the duration of preinfestation on the level of plant avoidance (log rank test: $\chi^2 = 5.1$, df = 2, P = 0.079). 311

312 Induced resistance persisted for at least 48 h after the 313 end of a 48-h preinfestation (Table 3d). However, esti-314 mated hazard ratios decayed as the time elapsed between 315 the end of preinfestation and the measure of induced 316 resistance increased. The hazard to leave the plant was increased by 317% when induced resistance was measured 317 318 immediately after removing the aphids, but only by 241% 319 and 64% when induced resistance was measured, respec-320 tively, 24 and 48 h after the end of the preinfestation.

Differences among groups were highly significant (log rank	321
test: $\chi^2 = 27.8$, $df = 2$, $P < 0.0001$).	322

Genotypic variation in aphid virulence

No aphid genotype sampled in the orchard could establish 324 colonies on Rubira plants. In addition, when looking at the 325 aphid tendency to leave the plant (Table 4), all the clones 326 had a higher estimated hazard ratio than Mp03, the labo-327 ratory reference clone which is known to trigger effective 328 induced resistance (Sauge et al. 2002). Taken together, 329 these results suggest that all clones are avirulent. The fact 330 that Mp03 had the lowest hazard ratio possibly reflects the 331 effects of conditioning (maternal effects), since this labo-332 ratory clone was reared continuously on peach without host 333 plant alternation. Excluding these possible conditioning 334 effects would require to rear Mp03 on a secondary host, 335 such as pepper or potato, before to test it on Rubira. 336 Anyhow, since Mp03 has always been maintained on a 337 susceptible peach variety, it is unlikely to have undergone 338 any selective adaptation to Rubira. 339

340 Despite the fact that all the field clones were avirulent, we detected highly significant variation among them in 341

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Table 4 Effect of Myzus persic leaving tendenc by a Cox propo model (n = 1,5df = 30, P < 0.

<i>icae</i> on the plant- cy as estimated	Covariates	β	SE (β)	$\exp(\beta)$	Effect on leaving tendency
ortional hazards	-Mp03	-0.692	0.205	0.500 ***	_
550, $\chi^2 = 167$, 0.0001)	–Car 16	-0.094	0.202	0.909	No effect
0.0001)	–Car 8	-0.086	0.203	0.917	No effect
	-Car 14	-0.077	0.200	0.926	No effect
	–Car 6	-0.053	0.202	0.948	No effect
	–Avi 5	-0.028	0.200	0.972	No effect
	-Car 11	-0.003	0.201	0.996	No effect
	–Car 3	0.008	0.201	1.009	No effect
	Car 15	0.043	0.204	1.044	No effect
	–Car 2	0.047	0.201	1.048	No effect
	–Got 7	0.122	0.201	1.131	No effect
	–Car 4	0.149	0.200	1.161	No effect
	-Avi 3	0.189	0.201	1.208	No effect
	–Avi 2	0.197	0.200	1.218	No effect
	–Avi 6	0.208	0.201	1.232	No effect
	–Got 4	0.228	0.209	1.257	No effect
	-Got 5	0.242	0.201	1.275	No effect
	-Got 2	0.288	0.200	1.334	No effect
ression	-Car 10	0.288	0.200	1.334	No effect
), standard errors	–Got 8	0.296	0.200	1.345	No effect
rd ratios [exp (β)]	–Avi 1	0.307	0.201	1.360	No effect
tes of the model. to a likelihood	–Car 5	0.365	0.200	1.442	No effect
to a internitood	-Got 3	0.375	0.201	1.456	No effect
els of significance	–Got 6	0.388	0.201	1.475	No effect
o the baseline	–Car 9	0.419	0.201	1.521*	+
Got 1) for the $P < 0.05, 0.01$	-Car 12	0.509	0.201	1.664*	+
pectively	–Car 7	0.639	0.201	1.895**	+
increasing effect;	-Car 13	0.750	0.201	2.119***	+
decreasing effect	–Avi 4	0.942	0.202	2.567***	+
e on the plant-	–Car 1	1.302	0.202	3.679***	+

Author Proof

Estimated regre coefficients (β) , (SE), and hazard for the covariate γ^2 correspond to ratio test *, **, *** level as compared to

hazard (clone G coefficients at P and 0.001, resp + indicates an i

 indicates a d of the covariate leaving tendency

plant avoidance (log rank test: $\chi^2 = 122$, df = 29, 342 343 P < 0.0001). Under identical conditions, the hazard ratio 344 estimated for clone Car 1 was on average four times higher 345 than for clone Car 16 (Table 4). We did not detect any 346 influence of the geographical origin of the genotypes on the estimated aphid plant-leaving tendency (Kruskal-Wallis 347 rank sum test: $\chi^2 = 0.940$, df = 2, P = 0.62). 348

Discussion 349

Data from the first part of this study are not sufficient to 350 351 prove that the interaction between the gene Rm2 from 352 Rubira and M. persicae follows a gene-for-gene model, but 353 the results are a first step toward accepting such a model. 354 The phenotypic expression of resistance as characterized 355 by the aphid plant-leaving tendency matches the enemy *R* gene-mediated resistance. A similar behavioral approach 357 358 was adopted for example in the work by Gómez et al. (2009), where inducible change in leaf palatability mea-359 sured by means of choice tests with the cabbage army 360 moth, Mamestra brassicae (L.), was interpreted as a sign of 361 defense activation in white clover, Trifolium repens L. We 362 suggest that induced resistance in Rubira is called an all-or-363 nothing trait, given that its level depends neither on the 364 amount nor on the duration of the aphid feeding stimuli. 365 This qualitative response supports the idea that aphid 366 adaptation might occur because of the loss of pathogen 367 recognition by the plant. 368

perception and defense induction processes involved in

369 Irrespective of the genetic context of our study, the absence of aphid density dependence in induction contrasts 370 with results from research with arthropods with chewing 371 372 mouthparts, in which the intensity of herbivory was found

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373 to influence the magnitude of induced resistance or defense 374 induction (Agrawal and Karban 2000; Underwood 2000; 375 Massey et al. 2007). This difference may be due to the fact 376 that phloem feeders do not remove leaf tissue per se. For 377 example, Zehnder and Hunter (2007) found that in milk-378 weed (Asclepias) species infested by the oleander aphid, 379 Aphis nerii (Boyer de Fonscolombe) (Hemiptera: Aphidi-380 dae), aphid density did not lead to increased induction of 381 plant defensive cardenolides.

382 The speed of responses to enemy attacks may be critical 383 in determining whether the plant or the pest prevails. The 384 time course of *M. persicae*-induced resistance showed a pattern similar to the dynamics of plant defense responses 385 386 in other well-characterized plant-aphid systems that 387 involve resistance derived from major genes (e.g., Gao 388 et al. 2007; Li et al. 2008). In these systems, plant 389 responses were activated as soon as 6 h after infestation and extended periods of aphid probing activated more 390 391 genes, whose number could be finally doubled at 36 or 48 h 392 after infestation. Then, the induction of defense-related 393 genes declined after 24 or 48 h. In Rubira, a very brief 394 aphid feeding duration is required for producing the 395 defense signal. Then, a short time lag between infestation 396 and defense activation ensures rapid and efficient protec-397 tion against the aphid, compared to other M. persicae-398 inducible peach genotypes lacking major resistance gene 399 (Sauge et al. 2006). After peak induction at 48 h, induced 400 resistance decayed over time in the absence of additional 401 infestation. Determining the possible costs and benefits 402 associated with the activation of defensive traits and 403 maintenance of the induction status for prolonged periods 404 of time deserves investigations, because they may influence 405 the evolution of resistance.

406 Field data suggest that all M. persicae genotypes tested 407 could be reasonably assigned to a discrete class of aviru-408 lence, since no progeny could establish on the plant. It is 409 likely that the matching class of virulence, if it exists, has 410 remained undetected in our sampling scheme because of a 411 low or spatially heterogeneous frequency of virulent 412 genotypes in natural populations. Today, predicting the 413 evolution of resistance conferred by Rm2 is difficult. On 414 the one hand, a previous microsatellite analysis exposed a 415 large spatial and temporal genetic variability in French 416 populations of *M. persicae* (Guillemaud et al. 2003a), 417 theoretically necessary to allow adaptive genes to evolve (but see Lombaert et al. 2009). In addition, M. persicae 418 contains considerable genetic variation for host plant 419 420 adaptation (Weber 1985; Nikolakakis et al. 2003), and insecticide resistance has evolved in the populations from 421 422 which aphids used in the present work were sampled 423 (Guillemaud et al. 2003b). On the other hand, the selection 424 pressure exerted by Rm2 remained very low for more than 425 30 years, a situation that should not favor the evolution of virulence. In orchards, Rubira is planted as rootstock and
thus does not interact with aphid populations. In nursery, it
is cultivated as seedling but under strong insecticidal
pressure that prevents aphid colonization.426
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Finally, the important and intriguing finding of this 430 study was the identification of significant quantitative 431 variation in the aphid plant-leaving tendency within the 432 range of avirulent genotypes tested. The conclusion that 433 can be drawn from this result is that virulence in the Ru-434 bira-M. persicae interaction may not be qualitative and 435 may also evolve according to the chemical coevolution 436 hypothesis. This assertion seems inconsistent with the 437 interpretation of the first series of experimentations, but it 438 adds weight to the idea that plant-aphid interactions 439 involving genes of the R type may exhibit features con-440 sistent with both models of coevolution. There are now at 441 least two cases supporting this hypothesis. The gene Mi-1.2 442 from tomato, Lycopersicon peruvianum (L.) P. Mill. and 443 the gene Vat from melon, Cucumis melo L., are the only 444 two genes of resistance to insects (namely aphids) that have 445 been cloned so far (Rossi et al. 1998; Dogimont et al. 446 2007). Both belong to the so-called NBS-LRR family of 447 R resistance genes. Hebert et al. (2007) found that Mi-1.2 448 differentially affected the population growth of distinct 449 isolates of the potato aphid, Macrosiphum euphorbiae 450 (Thomas) (Hemiptera: Aphididae), all of which were 451 classified as avirulent. In melon, Vat confers both resis-452 453 tance to the melon aphid, Aphis gossypii Glover (Hemiptera: Aphididae), and resistance to nonpersistent viruses 454 transmission by this same aphid species. Lombaert et al. 455 (2009) detected in aphid populations a continuum of per-456 formance response to Vat from complete avirulence to 457 strong virulence, but no variability and no overcoming of 458 Vat resistance were observed for the trait "virus trans-459 mission". This suggests that A. gossypii is effectively 460 recognized by Vat melon plants, even if the trait "plant 461 resistance" is overcome. 462

Large-scale analysis of M. persicae populations col-463 lected from peach genotypes carrying Rm2 in experi-464 mental orchards is now required to get more information 465 about the formal genetics of the interaction. A detailed 466 characterization of the biochemical interactions that occur 467 in Rubira upon aphid attack is also needed to give evi-468 dence for a gene-for-gene interaction. This characteriza-469 tion could also benefit to breeding for durable resistance. 470 471 Genetic variation in induction of plant metabolites has been reported in several systems (Zangerl and Berenbaum 472 1990; Agrawal et al. 2002; Stevens and Lindroth 2005). If 473 474 similar variation exists in plant material derived from Rubira, breeders could select for peach genotypes har-475 boring the highest concentrations in induced defensive 476 compounds, which might improve the efficiency and 477 478 durability of resistance.

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479 Acknowledgments We acknowledge J.P. Lacroze for technical 480 assistance, S. Simon for aphid sampling, and C. Favret for English 481 correction of an earlier draft. Part of this work received financial 482 supports from the Institut Français de la Biodiversité and Départe-483 ment Santé des Plantes et Environnement, Institut National de la 484 Recherche Agronomique.

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