Molecular dissection of the potato virus Y VPg virulence factor reveals complex adaptations to the pvr2 resistance allelic series in pepper

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The virulence properties of potato virus Y (PVY) towards an allelic series at the pvr2 locus in pepper genotypes are related to variations in the genome-linked viral protein (VPg). Eleven amino acid substitutions in the central part of the VPg were identified in strains differing by their virulence properties and were introduced, either singly or in combination, in an infectious PVY clone to get an in-depth genetic analysis of the virulence determinant. The virulence spectrum of these mutants was evaluated by inoculation of four pepper genotypes carrying different alleles at the pvr2 locus. The mutations introduced had complex effects on virulence, including antagonistic epistasis and trade-offs for virulence towards different pvr2 alleles. In addition, several mutants showed new virulence properties that were unknown in the natural environment. Such complex effects of mutations on plant virus virulence are unprecedented. They provide a better understanding of the variable levels of durability of the resistance conferred by the different pvr2 alleles, and have important consequences for a durable management of the resistances.

INTRODUCTION

The efficiency of genetic resistance in plants is impaired by the possible emergence of resistance-breaking pathogen genotypes that can increase in frequency after large-scale growing of cultivars carrying the resistance factors (e.g. Pelham et al., 1970). However, when several resistance genes to a pathogen are available in a host species, their combination (gene pyramiding) can reduce resistance breakdown (Lindhout, 2002). In addition, spatial or temporal management of these resistances could increase their efficiency and durability (Kiyosawa, 1982). Comparing the probability of breakdown of a single gene to sets of genes remains an important challenge for an efficient and durable use of genetic resources.

In pepper (Capsicum annuum L.), several alleles at the pvr2 locus, differing by their resistance spectrum, control recessive resistances to potato virus Y (PVY) (Kyle & Palloix, 1997; Robaglia & Caranta, 2006). All these pvr2 alleles were shown to code for mutants of the eukaryotic translation initiation factor 4E (eIF4E) and differ by a small number of amino acid substitutions (Ruffel et al., 2002, 2004; Fig. 1). The sequence of the genome-linked viral protein (VPg) cistron is the unique virulence determinant towards pvr2. Moury et al. (2004) and Ayme et al. (2006) showed that non-synonymous mutations in a 23-codon-long region in the central part of the VPg cistron of PVY determined virulence towards the three resistance alleles pvr21, pvr22, and pvr23. Note that throughout this paper, virulence is an antonym for avirulence and is defined as the genetic ability of a pathogen to cause a compatible interaction (disease) in a host carrying a genetically determined resistance (Shaner et al., 1992), and pathotype is defined as a subspecies pathogen entity that is controlled by a host gene specific for that entity (Hampton & Provvidenti, 1992). The fact that a few codon positions of the VPg cistron of PVY are subjected to positive selection during their evolution strongly suggests that the encoded protein, and not the corresponding RNA segment (apart from its encoding capacity), determines virulence in pepper (Moury et al., 2004). This hypothesis also fits with functional molecular models that involve eIF4E–VPg physical interaction to determine resistance or virulence properties in plant–virus interactions (Miyoshi et al., 2006; Moury et al., 2004; Robaglia & Caranta, 2006; Whitham & Wang, 2004). It is important to note that, in these plant–virus interactions, resistance is recessive and is the result of incompatibility between virus and plant factors. This is distinct from elicitation of resistances where pathogens trigger host defence responses.

The mechanisms of adaptation of viruses that are confronted with series of alleles of resistance in plants are poorly understood. In this context, two other pathosystems have been explored. The tomato mosaic virus movement protein is the avirulence determinant to the Tm-2 and
Tm-2 resistance alleles in tomato. However, different domains of the protein are involved in adaptation to each resistance (Meski et al., 1989; Weber et al., 1993, 2004) and gain of virulence towards either Tm-2 or Tm-2 does not affect virulence towards the other allele (Fraser, 1985). The coat protein of tobamoviruses is the avirulence determinant to an allelic series of resistances at the L locus in pepper (Berzal-Herranz et al., 1995; Gilardi et al., 2004). In that pathosystem, adaptation of the virus to cultivars carrying the different resistance alleles occurred mainly through replacement of tobamovirus populations belonging to different species, rather than through point modifications of the avirulence gene within a virus species (except for the L3 allele) (Takeuchi et al., 2005). In this context, the pepper–PVY interaction is a unique model to study the adaptation of a virus to a resistance allelic series, notably by evaluating whether PVY can accumulate virulences towards all pvr2 alleles or is specialized to particular pvr2 alleles. To unravel these mechanisms of adaptation, we studied the effect of amino acid substitutions in the central part of the VPg of PVY on its virulence properties towards four pvr2 alleles.

**METHODS**

**Plant genotypes and PVY isolates.** The *C. annuum* inbred lines used in this work were Yolo Wonder (YW), Yolo Y (YY), Florida VR2 (Flo) and HD285. YW, YY and Flo possess, respectively, the pvr2 dominant allele for susceptibility to PVY, the pvr2 and the pvr2 recessive alleles for resistance to PVY, which are the three alleles classically used to define PVY pathotypes (0), (0,1) and (0,1,2) (Gebré Selassie et al., 1985; Kyle & Palloix, 1997). In the pathotype nomenclature, figures correspond to the different pvr2 alleles to which the PVY isolate is virulent (0 stands for virulence to pvr2). YY is isogenic to YW except at the pvr2 locus (Cook, 1961). Flo is closely related to both YW and YY since it differs from them by 4% of around 2000 molecular markers (Lefebvre et al., 2001). HD285 is a doubled haploid line possessing the pvr2 resistance allele and selected for susceptibility alleles in the genetic background with the use of molecular markers (Caranta et al., 1997; Ayme et al., 2006). The pvr2 allele was initially mapped as a major resistance quantitative trait locus (QTL) near the pvr2 locus (Caranta et al., 1997) and was further demonstrated to be an allele at this locus (Ruffel et al., 2004). These four pvr2 alleles were shown to encode eIF4Es differing by a small number of amino acid substitutions (Ruffel et al., 2004 and Fig. 1).

PVY isolates LYE84, SON41p (Moury et al., 2004) and To72 (Gébré Selassie et al., 1985) were collected in *Lycopersicon esculentum* in the Canary Islands in 1984, in *Solanum nigrum* in France in 1982 and in *L. esculentum* in France in 1972, respectively. Isolates CAA21, CAA82, CAA141 and EP03 were obtained from field-infected *C. annuum* plants in Turkey (1994), Israel (1982) and France (1999, 2003), respectively.

**Sequencing of the PVY VPg cistron and mutagenesis of a full-length cDNA clone.** The cDNA corresponding to the VPg cistron of each PVY isolate was cloned and sequenced as previously described (Moury et al., 2004). Based on the sequence diversity of the central part of the VPg sequence, mutants with single mutations or mutation combinations were then produced. The infectious cDNA clone of isolate SON41p (EMBL accession no. AJ439544) (Moury et al., 2004) was mutated using a QuickChange site-directed mutagenesis kit (Stratagene). Cloning experiments were carried out using homologous recombination in yeast as described by Ayme et al. (2006).

**PVY inoculation tests and detection.** Inoculation experiments were carried out under greenhouse conditions or in climatic rooms. Primary inoculations with the different PVY cDNAs were made by DNA-coated tungsten particle bombardments of *Nicotiana clevelandii* or *Nicotiana benthamiana* plants, since direct bombardment of pepper plants is not efficient (Moury et al., 2004). Pepper plants were mechanically inoculated on their two cotyledons approximately 3 weeks after sowing (first leaf stage), using crude extracts from infected *Nicotiana* spp., according to Moury et al. (2004). Detection of the virus in the inoculated plants was performed by the double-antibody sandwich ELISA (DAS-ELISA) as described by Legnani et al. (1995) at various time points after inoculation. The relative concentration of PVY in *Nicotiana* spp. and pepper plants was determined by semi-quantitative DAS-ELISA as described by Ayme et al. (2006). Each experiment involved at least 10 plants per virus clone or isolate and per pepper genotype and was performed at least twice.

**Sequence analysis of viral progeny.** Total RNAs from leaves of systemically infected plants were purified with a TRI Reagent kit (Molecular Research Center Inc.) and used for RT-PCR for amplification of the entire VPg cistron (Moury et al., 2004). Viral progeny of VPg mutants were checked by sequencing RT-PCR DNA fragments produced from at least two plants per virus–genotype combination using the same primers as described by Moury et al. (2004).
RESULTS

Pathotypes and sequence of the VPg of PVY isolates

As a first step to characterize the PVY virulence determinants in relation to the pvr2 alleles in pepper, the virulence properties of seven PVY isolates to four pvr2 alleles were assessed by inoculation of YW, YY, Flo and HD285 pepper plants, homozygous for pvr2 (the reference susceptibility allele), pvr21, pvr22 and pvr23, respectively. Isolates LYE84, CAA21, To72, CAA82 and EP03 were shown to belong to pathotype (0), isolate CAA141 to pathotype (0,1) and SON41p to pathotype (0,1,2) (Ayme et al., 2006; Moury et al., 2004; data not shown; see the Methods section for the pathotype nomenclature). In order to estimate the amino acid diversity of the VPg of these isolates, the VPg cistron of isolates CAA21, To72, CAA82, EP03 and CAA141 was sequenced and compared to that of SON41p and LYE84 (Moury et al., 2004; Table 1). CAA21 had the same nucleotide sequence as LYE84 and differed from SON41p by five amino acids in the central part of the VPg. While To72, EP03 and CAA82 shared identical nucleotide sequences and differed from SON41p by two amino acids (each corresponding to a single nucleotide substitution) (Table 1). CAA141 was relatively distant from SON41p, To72 and LYE84 (six, five and four amino acid substitutions in the central part of the VPg, respectively). Based on these sequences, several VPg mutants of SON41p were created by introducing in SON41p single-nucleotide substitutions corresponding to the observed amino acid differences (Tables 1 and 2). Only mutations Asp119Ser and Ser123Lys, present in CAA141, were not introduced into SON41p. SON41p mutants with combinations of some of these substitutions were also created and five single-nucleotide mutants of SON41p previously selected for virulence towards pvr2 (Ayme et al., 2006) were also included in the study. These are the mutants S101G, T115R, T115K, D119N and S120C (Table 2).

Virulence properties of the VPg mutants

All SON41p mutants were infectious following bombardment of N. clevelandii and N. benthamiana and no differences in their relative accumulation could be revealed in semi-quantitative DAS-ELISA (Ayme et al., 2006; data not shown). These 17 mutants were tested for their virulence towards the four pepper genotypes (Table 2). Since these pepper genotypes essentially differ by their allele at the pvr2 locus (see Methods), virulence differences observed would be caused by specificities of interaction between mutations in the VPg of the virus and the pvr2 alleles in the plants. All the infected plants developed a systemic mosaic (YW, YY and Flo) or systemic necrotic symptoms (HD285) 10–15 days post-inoculation (days p.i.) and yielded high absorbances at 405 nm (A405) in DAS-ELISA tests, while no PVY could be detected by DAS-ELISA in plants that showed no symptoms. For most pepper genotype–PVY mutant combinations, 0 or 100% of the plants became infected, and the VPg sequence of the progeny in infected plants was identical to that of the PVY clone used to prepare the inoculum. In four combinations (T115V/YW, D119H/Flo, H121N/YY and T115M-H121N/YW), only some of the plants were infected and infection was delayed (20 days p.i. or later). Sequencing of the PVY progeny in a random set of these plants (11 out of 29) always revealed additional amino acid substitutions in the central part of the VPg (Table 2). These additional amino acid substitutions were observed at positions shown to be critical for virulence (Ayme et al., 2006) and are presumably involved in PVY adaptation. For the T115V and T115M-H121N mutants in particular, different additional amino acid substitutions were observed depending on the plant analysed (Table 2). For these last two mutants, the virus isolates extracted from the YW plants were back-inoculated to new YW plants. As a control, the original virus populations (from N. benthamiana) were also inoculated to YW plants. All back-inoculated plants, i.e. 9/9 for T115V and 15/15 for T115M-H121N, showed high A405 values in DAS-ELISA and developed systemic symptoms at 10 days p.i., while significantly lower proportions of YW accumulated virus in DAS-ELISA after inoculation with isolates from N. benthamiana (2/9 and 4/15, respectively; P=0.001 and P<0.001, Fisher’s exact tests). We concluded that infection of the YW plants by the initial PVY mutants was the result of a gain of virulence of the original virus that occurred during the resistance tests.

Table 1. Amino acid sequence of the central part of the VPg of PVY isolates or clones

Numbers are amino acid positions in the VPg.

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Pathotype</th>
<th>101</th>
<th>105</th>
<th>Amino acid sequence of the VPg</th>
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<tr>
<td></td>
<td></td>
<td>115</td>
<td>119</td>
<td>120</td>
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<tr>
<td>SON41p</td>
<td>(0,1,2)</td>
<td>S</td>
<td>E</td>
<td>V</td>
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<tr>
<td>LYE84</td>
<td>(0)</td>
<td></td>
<td></td>
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<tr>
<td>CAA21</td>
<td>(0)</td>
<td></td>
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<tr>
<td>To72</td>
<td>(0)</td>
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<td>CAA82</td>
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<td>EP03</td>
<td>(0)</td>
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<td>CAA141</td>
<td>(0,1)</td>
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Table 2. Virulence properties of VPg mutants of PVY SON41p towards the pvr2 resistance alleles in pepper

In the case of D119H/Flo and H121N/YY combinations, systemic infections were observed in a small number of inoculated plants (5/30 and 1/39, respectively) and in one of three independent experiments only. Finally, we considered that mutants T115V, D119H, H121N and T115M-H121N belonged to pathotypes (1), (0,1,3), (0,3) and (2), respectively (Table 2). From these data, we could classify the PVY clones into seven pathotypes: (2), (0), (0,1,2), (0,1,3), (0,1,2,3), (1) and (0,3), in addition to pathotype (0,1) defined by CAA141 (see above).

Analysis of the effect of single amino acid substitutions allows to draw a map of virulence determinants towards the different pvr2 alleles in the context of SON41p (Fig. 2). Among single-amino acid mutants, only H121N lost virulence towards pvr2, suggesting that this amino acid is essential for conferring virulence towards this allele to SON41p. For the pvr2 and pvr2 alleles, different

![Map of virulence changes towards alleles at the pvr2 locus conferred by single amino acid substitutions in the VPg of PVY SON41p [pathotype (0,1,2)]. Numbers correspond to amino acid positions in the VPg. Gains and losses of virulence are indicated above or below the line, respectively.](http://vir.sgmjournals.org)
substitutions at the same position modified the virulence properties in an opposite manner. Amino acid substitutions at three positions [I15 (4 of 4), I19 (2 of 2) and I21] abolished virulence towards pvr2, while amino acid substitutions at six positions [I01, I05, I15 (3 of 4), I19 (2 of 2), I20 and I21] resulted in a gain of virulence towards pvr2. Only the single mutant S123N had a pathotype similar to that of SON41p.

**Atypical PVY pathotypes**

All PVY isolates already described in natural infection conditions worldwide belong to pathotypes (0), (0,1) and (0,1,2) (Luis-Arteaga & Gil-Ortega, 1986; Boiteux et al., 1996; Gebré Sélassié et al., 1985; Palloix et al., 1994), since pvr2 was not taken into account in previous works. Through mutagenesis, we generated new pathotypes. One mutant (T115M-H121N) could infect Nicotiana spp. plants, but was unable to infect YW or the other C. annuum genotypes. We do not know whether this mutant has lost the capacity to be infectious in peppers or whether other pepper genotypes would still be susceptible to it. In addition, description of pathotype (1) (T115V mutant) was not expected and provides the first evidence for PVY variants virulent towards pvr2 but avirulent towards pvr2. The poor infectivity of mutants T115V and T115M-H121N in YW is not due to deleterious effects of the mutations introduced into the VPg on fitness, since these mutants accumulated to the same titre as SON41p, T115M or H121N in N. benthamiana or N. clevelandii as measured in semi-quantitative DAS-ELISA (data not shown). Also, mutant T115V accumulated to the same titre as T115M in YY (data not shown). Since YY and YY are isogenic except for the pvr2 locus (Cook, 1961), this is also the first evidence that the pvr2 allele can exert a resistance towards particular PVY variants.

**Trade-offs between virulence properties**

The effect of amino acid substitutions examined on the whole spectrum of virulence rather than on individual pvr2 alleles reveals trade-offs between virulence properties, i.e. situations where an amino acid substitution induces a gain of virulence towards a particular pvr2 allele and simultaneously a loss of virulence towards one or several other pvr2 allele(s). Particularly, among the nine single amino acid mutations that induced the virulence towards pvr2, six induced avirulence towards pvr2 and one also induced avirulence towards pvr2 (Table 2). Trade-offs are, however, conditional to particular mutations, since three single-amino acid mutants (S101G, R105K and S120C) have the ability to infect all pepper genotypes. It should be noticed, however, that two of these two mutants were previously studied (i.e. S101G and S120C) and displayed a poor relative ability to accumulate and to compete in pvr2-carrying peppers (Ayme et al., 2006). This loss of fitness may represent the cost of possessing a wide spectrum of virulence, as hypothesized in theoretical and or experimental studies (Garcia-Arenal & McDonald, 2003; Harrison, 2002).

**Antagonistic epistasis between mutations**

Complex effects of substitutions can be observed when comparing the virulence spectra of single vs multiple mutants. When two or three amino acid substitutions were introduced simultaneously into SON41p, the virulence spectrum of the multiple mutant usually included only the virulences shared by all corresponding single mutants (R105K-S123N, T115M-D119H, D119H-H121N and T115M-D119H-H121N). In two occurrences, however, the virulence spectrum of the multiple mutant included fewer virulences than those shared by all corresponding single mutants. Single mutants T115M, D119N and H121N infect pvr2 and pvr2-carrying genotypes. However, the double mutant D119H-H121N is avirulent towards pvr2 and the double mutant T115M-H121N is avirulent towards both pvr2 and pvr2 (Table 2), indicating occurrence of antagonistic epistasis, as defined by Wilke et al. (2003), between substitutions within the VPg.

**DISCUSSION**

**Explaining the higher durability of pvr2**

In our study, we focussed on major, qualitative fitness variations (i.e. virulence spectra in pepper genotypes) determined by mutations in the VPg of PVY. Quantitative fitness variations also act on the evolution of PVY populations and may affect resistance durability. Semi-quantitative DAS-ELISA did not reveal any quantitative fitness differences between SON41p and its VPg mutants in N. benthamiana, N. clevelandii or YW (for those mutants virulent to YW) in single infections (data not shown). In the other pepper genotypes, only limited differences in fitness were observed in DAS-ELISA (Ayme et al., 2006; data not shown). Although competition between mutants within plants could potentially reveal more subtle fitness differences invisible in single infections, it should be noted that fitness measurements in single infections fitted experimental data of resistance breaking better than competition fitness measurements from a previous study (Ayme et al., 2006). Moreover, the VPg of potyviruses is not a determinant of plant-to-plant transmission efficiency by the aphid vectors. As a consequence, if these mutants appeared, they would have the potential to spread in pepper fields or in the field environment (weeds).

Our analysis of the effect of mutations in the virulence determinant of PVY towards the pvr2 allelic series in pepper contributes to explain the observed durability of resistances conferred by these alleles and to help manage these resistances. In spite of wide cultivation of pvr2-, or pvr2-carrying pepper cultivars for decades (Greenleaf, 1986), PVY virulence towards pvr2 was rather frequent but not predominant, and virulence towards pvr2 was only
exceptionally observed in the field (Boiteux et al., 1996). This suggests a higher durability of the resistance conferred by the latter allele. The pvr2 allele has not been exploited in pepper hybrid cultivars but is present in landraces grown locally. PVY populations virulent to pvr2 can easily be selected for (Ayme et al., 2006), which suggests a low durability. Three reasons could explain the higher durability of pvr2.

First, fewer amino acid combinations in the central part of the VPg conferred virulence towards pvr2 in comparison to the other pvr alleles. To compare the frequencies of virulence towards pvr2, pvr2 and pvr2, one should first remove the mutants whose virulence is biased towards some of these alleles because of the experimental design, i.e. (i) because the virulence to a particular allele pvr2 was selected during the experiment, (ii) because the original PVY clone used for mutagenesis is virulent towards particular pvr2 alleles but not towards others and (iii) because the isolate whose sequence was used to design the substitutions is virulent towards particular pvr2 alleles but not towards others. As a consequence, to compare the frequencies of virulence towards pvr2 and pvr2, all clones can be used except T115V, because the original clone (SON41p) and the isolate used to design the substitution (CAA141) are both virulent to pvr2 but not to pvr2.

Among these 17 PVY clones, six were virulent towards pvr2 while 12 were virulent towards pvr2, which is significantly higher (P=0.047, Fisher’s exact test). To compare the frequencies of virulence towards pvr2 and pvr2, one cannot use the five mutants which were selected for their virulence towards pvr2 (i.e. S101G, T115K, D119S, S123N and S126C), or the two mutants which belong to the same pathotype as the original clone SON41p (S123N and R105K-S123N), since they would be expected to induce a bias in favour of the virulence to pvr2 and against the virulence to pvr2 and, for the same reason, SON41p itself. Among the ten remaining mutants, only one was virulent towards pvr2, while significantly more (seven) were virulent towards pvr2 (P=0.008, Fisher’s exact test). No significant differences were observed between the frequencies of virulences towards pvr2 and pvr2. Thus, in the range of variation examined, PVY should accumulate several mutations at precise positions and of precise types to become virulent towards pvr2, whereas numerous possibilities of amino acid combinations confer virulence towards pvr2 or pvr2. Consequently, the probability to gain virulence towards pvr2 or pvr2 is expected to be higher than that towards pvr2.

Second, due to epistatic relationships between mutations, all sequential mutation pathways are not equivalent to accumulate the different substitutions required for virulence towards pvr2. For example, in order to gain virulence towards pvr2, the triple mutant T112M-D119H-H121N has to accumulate the three reverse mutations M115T, H119D and N121H. If we consider the six possible pathways for the sequential acquisition of these three mutations, two of them, beginning with H119D, lead to a ‘dead end’ for the virus, since mutant T112M-H121N is not infectious in all four pepper genotypes. This would contribute to decrease the probability of fixation of these substitutions. These antagonistic epistases between mutations are similar to those mentioned in other viruses by Sanjuan et al. (2004), Burch & Chao (2004) and Bonhoeffer et al. (2004), who evaluated quantitative fitness variations instead of virulence spectra. Sanjuan et al. (2004) showed antagonistic epistasis of mutations chosen at random or of mutations beneficial to the fitness of vesicular stomatitis virus. Burch & Chao (2004) and Bonhoeffer et al. (2004) found evidence for antagonistic epistasis of deleterious mutations in bacteriophage φ6 and human immunodeficiency virus type 1, respectively. In these three examples, there was a clear predominance of antagonistic over synergistic epistatic mutations. In our case, the mutants were confronted with host resistance genes and the effects of antagonistic epistasis on virus fitness are much more drastic since they consist of a lack of virulence towards particular host genotypes.

Third, among the natural isolates analysed so far, those displaying the closest VPg sequence compared to SON41p and its mutants virulent towards pvr2 are To72, CAAB2 and EP03, differing by two amino acids. Since they were collected in France or Israel, from 1972 to 2003, isolates with such VPg sequences seem to be common. In order to gain virulence towards pvr2, these isolates require at least two nucleotide substitutions while they only require a single nucleotide substitution to become virulent to pvr2 or pvr2. Similarly, a high durability of virus resistances has been previously related to the necessity for the virus to accumulate at least two substitutions to gain virulence (Harrison, 2002). This hypothesis could be further explored by gaining insight into the variability of the VPg cistron of field pepper PVY isolates.

Management of pepper cultivars for durable PVY resistance

Accumulating (pyramiding) different resistance genes in a cultivar and temporal or spatial deployment of different resistances are frequently proposed as promising strategies to preserve the durability of plant resistance towards their pathogens. The efficiency of such strategies was demonstrated in several instances (Pink, 2002) and may be due to the difficulties for the pathogen to acquire multiple virulences. Occurrence of trade-offs between virulences towards pvr2 and pvr2 alleles could suggest to alternate temporally and/or spatially cultivars carrying these alleles. However, the occurrence of a few mutants accumulating virulences towards all pvr alleles examined here suggests that these strategies are risky. Moreover, the selective pressures exerted by the pvr2 and pvr2 alleles could act as ‘springboards’ for the acquisition of the virulence towards pvr2, since they could accelerate the fixation of the first mutations required for virulence towards pvr2. Considering the isolates that share a VPg cistron identical
to that of mutant $D_{119}N-H_{121}N$, the use of $pvr2^1$ or $pvr2^3$ could contribute to selection for the reverse mutant $D_{119}N$ (by fixation of the mutation $N_{121}H$), while $pvr2^1$ could select for the reverse mutation $H_{121}N$ (by fixation of the mutation $N_{119}D$) (Fig. 3). These mutants would then need only a single-nucleotide substitution to become virulent towards $pvr2^2$. Growing pepper cultivars carrying $pvr2^2$ or $pvr2^1$ could then represent a threat for the durability of $pvr2^2$.

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