



HAL
open science

Natural variation and functional analyses provide evidence for coevolution between plant eIF4E and potyviral VPg

Carine Charron, Maryse Nicolai, Jean-Luc J.-L. Gallois, Pascale Sanchez, Christophe Robaglia, Benoît Moury, Alain Palloix, Carole Caranta

► To cite this version:

Carine Charron, Maryse Nicolai, Jean-Luc J.-L. Gallois, Pascale Sanchez, Christophe Robaglia, et al.. Natural variation and functional analyses provide evidence for coevolution between plant eIF4E and potyviral VPg. 12. Rencontres de Virologie Végétale, Jan 2009, Aussois, France. hal-02751888

HAL Id: hal-02751888

<https://hal.inrae.fr/hal-02751888>

Submitted on 3 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



12^{èmes} rencontres de virologie végétale

Moulins
12/01/09



Aussois du 18 au 22 janvier 2009



Natural variation and functional analyses provide evidence for coevolution between plant eIF4E and potyviral VPg

Carine Charron¹, Maryse Nicolai¹, Jean-Luc Gallois¹, Pascale Sanchez¹, Christophe Robaglia³, Benoît Moury², Alain Palloix¹ and Carole Caranta¹

¹ INRA-UR1052, Génétique et Amélioration des Fruits et Légumes, Dom. St Maurice, BP94, F-84143 Montfavet, France,

² INRA, Pathologie Végétale, Dom. St Maurice, BP94, F-84143 Montfavet, France, and

³ Laboratoire de Génétique et Biophysique des Plantes, CEA-CNRS-Université Aix-Marseille II, Faculté des Sciences de Luminy, F-13009 Marseille, France

Amino acid substitutions in the eukaryotic translation initiation factor 4E (eIF4E) result in recessive resistance to potyviruses in a range of plant species, including *Capsicum* spp. Correspondingly, amino acid changes in the central part of the viral genome-linked protein (VPg) are responsible for the potyvirus's ability to overcome eIF4E-mediated resistance. A key observation was that the physical interaction between eIF4E and the VPg is required for viral infection while eIF4E mutations causative of resistance prevent VPg binding and inhibit the viral cycle. In this study, polymorphism analysis of the *pvr2-eIF4E* coding sequence in a worldwide sample of twenty five *C. annuum* accessions identified ten allelic variants with exclusively non-synonymous variations clustered in two surface loops of eIF4E. Resistance and genetic complementation assays demonstrated that *pvr2* variants, each with signature amino acid changes, corresponded to potyvirus resistance alleles. Systematic analysis of the interactions between eIF4E proteins encoded by the ten *pvr2* alleles and VPgs of virulent and avirulent *Potato virus Y* (PVY) and *Tobacco etch virus* (TEV) strains demonstrated that resistance phenotypes arose from the disruption of the interaction between eIF4E and VPg, and that viral adaptation to eIF4E-mediated resistance resulted from the restored interaction with the resistance protein. Complementation of an eIF4E knock-out yeast strain by *C. annuum* eIF4E proteins further shows that amino acid changes did not impede essential eIF4E functions. Altogether, these results argue in favour of a coevolutionary arms race between *Capsicum* eIF4E and potyviral VPg.