Determinants of host species range in plant viruses
Benoît Moury, Frédéric Fabre, Eugénie Hébrard, Rémy Froissart

To cite this version:
Benoît Moury, Frédéric Fabre, Eugénie Hébrard, Rémy Froissart. Determinants of host species range in plant viruses. 13. International plant virus epidemiology symposium, Jun 2016, Avignon, France. 165 p. hal-02738870

HAL Id: hal-02738870
https://hal.inrae.fr/hal-02738870
Submitted on 2 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.
DETERMINANTS OF HOST SPECIES RANGE IN PLANT VIRUSES


(1) INRA, UR407 Pathologie Végétale, F-84140 Montfavet, France
(2) INRA, UMR1065 SAVE, F-33882 Villenave d’Ornon, France
(3) UMR186, IRD-Cirad-UM, Laboratory "Interactions Plantes Microorganismes Environnement", Montpellier France
(4) UMR385, INRA-CIRAD-SupAgro, Laboratory «Biologie des Interactions plantes-parasites», Campus international de Baillarguet, F-34398 Montpellier, France
(5) UMR5290, CNRS-IRD-UM1-UM2, Laboratory «Maladies Infectieuses & Vecteurs : Ecologie, Génétique, Evolution & Contrôle», Montpellier France

BACKGROUND and OBJECTIVES
Prediction of pathogen emergence is an important issue, both in human health and agronomy. Strikingly, most studies of pathogen emergence have focused on the responsible ecological or anthropogenic factors rather than on the role of intrinsic pathogen properties.

MATERIAL and METHODS
By focusing on a plant virus database (Brunt et al. 1996), we looked at the relationships between different virus characteristics (genome type, number of segments, type of vertical and horizontal transmissions, vector type, vector type) and the virus plant species range breadth.

RESULTS
We found that four main viral characteristics were strongly linked to virus host range breadth. Viruses (i) with single-stranded genomes (either RNA or DNA), (ii) with bipartite or tripartite genomes, (iii) that were seed transmitted and/or (iv) transmitted by nematodes presented a broader host range than others.

CONCLUSIONS
Viruses harboring these characteristics thus seem to be more prone to emerge in new host species. A statistical model was built that predicts host range breadth based on these four characteristics and could be used to focus quarantine processes and surveillances.

REFERENCES
Building bridges between disciplines for sustainable management of plant virus diseases

13th International Plant Virus Epidemiology Symposium
6-10 June 2016, Avignon, FRANCE

Programme and Abstracts