# Analysis of speciation modes in plant RNA viruses

## Sprawozdania

Informacje na temat projektu

**PLANTVIRSPE**

Identyfikator umowy o grant: 322100

Projekt został zamknięty

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# Final Report Summary - PLANTVIRSPE (Analysis of speciation modes in plant RNA viruses)

Understanding the determinants of parasite evolution is a long-standing goal in biology, as it is essential to design more efficient strategies to prevent the emergence of new infectious diseases and to control existing ones. A key aspect of the evolution of viruses is their high potential to generate genetic diversity. This characteristic provides viruses with a high capacity for adaptation to new environments, including new hosts. Adaptation to new hosts may lead to diversification of the virus population, which may result in the emergence of new diseases caused by the appearance of new viral lineages or species: that is, by ‘speciation’ events. Despite its importance, how viruses speciate is still poorly understood.

The main objective of the PLANTVIRSPE project is to gain deeper understanding on the modes and determinants of virus speciation using plant-virus interactions. Specifically, the project focuses on the species of the genus Potyvirus (which makes 25% of all known plant virus species) that infect wild hosts in evergreen oak and riparian forests, two of the most widespread ecosystems in the European Mediterranean Basin. The aspects to be addressed in this project are: 1) Characterization of Potyvirus infection networks in evergreen oak and riparian forests. 2) Analysis of genetic diversity and structure of Potyvirus populations in the selected ecosystems, which is directly linked to virus speciation. 3) Study of ecological factors involved in Potyvirus speciation. 4) Development of a predictive model of Potyvirus speciation.

To achieve these goals, Potyvirus infection networks in five locations of evergreen oak forest and in five locations of riparian forest in the Iberian Peninsula have been characterized. At each of these ten locations, inventories of plant biodiversity have been made; Potyvirus species present have been identified, and their incidence and host range have been determined. Results indicate that evergreen oak and riparian forests significantly differ in plant composition and in plant and host species richness, which is higher in riparian forests. Potyvirus incidence and virus species richness was also higher in riparian forests, the virus species present in each ecosystem being different and some of them not being previously reported. Therefore, Potyvirus infection risk is higher in ecosystems with higher biodiversity. The nucleotide sequences of the coat protein gene of 157 virus isolates collected in the two ecosystems monitored have been obtained. Comparative genomics analyses of these sequences indicated that the genetic diversity of potyviral populations is structured according to the host and geographical location of origin of each virus isolate. These results are compatible with Potyvirus genetic diversification through sympatric speciation. Multivariate model analyses indicated that ecological (biodiversity, plant density) and climatic factors are major determinants of Potyvirus incidence and genetic diversification.

In summary, this is one of the first works in which the infection networks of a plant virus genus have been characterized at such high level of detail in wild ecosystems. This information provides an exceptionally well-characterized natural plant-virus interaction. Using such unique data set we provide compelling evidence that the main mode of Potyvirus speciation is sympatric. Ours is also one of the first analyses that address the role of a wide range of ecological and climatic factors in such speciation processes. This information contributes to better understand how new plant viruses emerge, and may help to control plant viral diseases.

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