

Phylloxera: genomics sheds light on the history of the invasion of French vines and unveils new family of genes

Grape phylloxera, an insect related to aphids, devastated French vineyards in the 19th century after the pest accidentally made its way to Europe. The serious risk the insect poses today is under control, thanks to tolerant rootstocks, but phylloxera is ever-present and little-known. Researchers at INRAE have coordinated an international consortium to sequence and annotate the phylloxera genome. Their findings were published in this year's xx June issue of *BMC Biology*. They reveal that the pest comes from North America, most likely along the upper Mississippi River. Genomic analyses also show the existence of the largest gene family ever identified in a genome to date, probably involved in the interaction between the pest and its host plant. These new findings are opening up new avenues of scientific research into how to improve viticulture, and more broadly about the risks involved in introducing exotic species into territories.

The scientific consortium on the phylloxera (*Daktulosphaira vitifoliae*) genome was created in 2011 with the goal to shed new light on the invasion that caused the phylloxera crisis in Europe in the 19th century, and to better understand the potential the insect has to adapt thanks to the deciphering of its genome. The consortium piloted by INRAE brought together more than 70 scientists from eight countries including several research units from CNRS in France. The Institute mobilised complementary skills to coordinate the research, calling upon experts in diseases of the vine, insect genomes, and bioinformatics. Researchers also benefited from technical support from the INRAE BIPAA platform (Bioinformatics Platform for Agro-ecosystems Arthropods) which gave them access to genomic resources on insects associated with agro-ecosystems, and enabled them to carry out extensive analyses.

Unlocking the history of an invasion

The researchers organised sampling campaigns of the pest in Europe and the United States and carried out genomic analyses on individual insects. Their findings shed light on the 19th-century infestation and confirmed that *Vitis riparia*, a wild type of American vine, is indeed the source of the phylloxera that invaded Europe. More specifically, wild varieties located along the Mississippi River are believed to be responsible for introducing the pest into French vineyards. It is these populations that made their way to Europe that are believed to have then spread to the rest of the world. The phylloxera crisis destroyed half of French vines, putting a lasting dent in the economy and geography of viticulture. Ultimately, it was resistant vine rootstock from the US that saved viticulture and allowed it to flourish once again in Europe.

Ground-breaking discoveries on the biology of an insect

Genomic analyses have allowed science to unveil the existence of a new family of genes, the biggest ever identified to date in a genome. Indeed, it includes nearly 2 700 genes (large gene families known to science rarely exceed 200), which represents more than 10% of the entire phylloxera genome. These genes are believed to be essential to interactions between phylloxera and grapevines. They code for small secreted proteins, called "effectors", which are

thought to intervene in de-activating the basic defences of the plant. In its indigenous region, the co-evolution between plant and pest is believed to have allowed the plant to resist attack, whereas in Europe, cultivated vines did not have an adapted system of defence to ward off this new pest and its lethal cocktail of effectors.

These new findings have shed much light, for example on the evolution of insects, especially aphids, and on the genetics and selection of rootstock that are resistant to phylloxera. Both topics are being studied at INRAE. This new knowledge also serves to improve our understanding of biological invasions and their potentially disastrous consequences on agriculture and therefore on society and the economy.

Reference:

Claude Rispe, Fabrice Legeai, *et al.* *The genome sequence of the grape phylloxera provides insights into the evolution, adaptation and invasion routes of an iconic pest*, BMC Biology (BMCB-D-19-01125R2) – 23 juillet 2020

DOI : <https://doi.org/10.1186/s12915-020-00820-5>

Scientific contacts:

François DELMOTTE

T. +33 5 57 12 26 14 or francois.delmotte@inrae.fr

Joint Research Unit for Vine Health and Agroecology (SAVE) INRAE – Bordeaux Sciences Agro

Plant Health and Environment Division

INRAE Nouvelle-Aquitaine Bordeaux research centre

Denis TAGU

T. +33 2 23 48 51 65 or denis.tagu@inrae.fr

Institute for Genetics, the Environment and Plant Protection (IGEPP) INRAE – Agrocampus Ouest Rennes - Université

Rennes 1

Plant Health and Environment Division

INRAE Brittany-Normandy research centre

Press Contact

INRAE Press Office - +33 1 42 75 91 86 – presse@inrae.fr

Created on January 1, 2020, the French National Research Institute for Agriculture, Food, and Environment (INRAE) is a major player in research and innovation. INRAE carries out targeted research and resulted from the merger of INRA and IRSTEA. It is a community of 12,000 people with 268 research, experimental research, and support units located in 18 regional centres throughout France. Internationally, INRAE is among the top research organisations in the agricultural and food sciences as well as in the plant and animal sciences. It also ranks 11th globally in ecology and environmental science. It is the world's leading research organisation specialising in agriculture, food, and the environment. INRAE's main goal is to be a key player in the transitions necessary to address major global challenges. Faced with a growing world population, climate change, resource scarcity, and declining biodiversity, the institute is developing solutions that involve multiperformance agriculture, high-quality food, and the sustainable management of resources and ecosystems.

