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2-year postdoctoral position on population genetics and evolution of a plant virus (Colmar, France)

PROJECT

Grapevine, a perennial plant of high economic value, was domesticated about 11000 years ago. With more than 100 viruses identified, this plant hosts a wide variety of viruses which could be due to the extensive exchange of *Vitis* germplasm on a global scale since its domestication. Some ubiquitous viruses, considered as the background virome, have little or no negative biological impact on the vines. On the opposite, others may be responsible for harmful diseases. In particular, grapevine fanleaf virus (GFLV) is depicted as one of the most severe grapevine viruses causing fanleaf degeneration which engenders serious economic losses. GFLV is a nepovirus (NEmatode-transmitted POlyhedral viruses) worldwide distributed and is endemic in France. In vineyards, it is naturally transmitted in a specific manner by *Xiphinema index* from vine to vine. The genome of GFLV consists of two ss(+) RNA genomic segments. This specialist virus (primarily infecting *Vitis* spp.) shows a high degree of genetic diversity: the nucleotide divergence is at least 12% between most of the GFLV variants, whether RNA1 or RNA2 (within and between plots as well as between countries). Looking at its evolutionary pattern, most of the codons are under negative or neutral pressure. Co-infection by genetically distant variants of GFLV within a single plant regularly occurs in vineyards, leading to the detection of frequent recombinants and reassortants (variants resulting from genomic segments exchanges).

The primary aims of this post-doctoral project are (i) to provide an insight into this **high level of genetic diversity**, (ii) characterize the **structure of GFLV populations** at the intra-/inter- plot level and (iii) study the forces that drive the **evolution of this virus**. More specifically, using numerous RNA-Seq data already available, it aims at:
- determining the genetic diversity and spatial distribution of natural GFLV populations present in six highly diseased commercial plots from Champagne and Burgundy regions, France (a quarter of the plants from each plot, i.e. 50 plants/plot, has already been sequenced)
- estimating the mutation rate, the frequency of recombination and reassortments (100 samples have been collected at different time points, spanning from some grapevines 25 years, on grapevines infected in controlled conditions with only one or two variants)
- studying the evolutionary history of GFLV (in addition to the complete and partial GFLV genome sequences available on GenBank, about a thousand complete consensus sequences obtained by the team will be available). All these data - along with the associated phenotypic data - will eventually be used to identify the genetic determinants of GFLV symptoms on grapevines.

This work will generate fundamental knowledge that will be used to implement cross-protection (a biocontrol method consisting of inoculating mild variants to protect against subsequent infection by severe ones) against fanleaf disease in the vineyards. It should notably enable us to define the sampling effort required to determine the diversity spectrum of challenger variants as well as estimate the genetic stability of the GFLV variants.

This research will be carried out in close collaboration with Emmanuelle Vigne (leader of Vaccivine2 project), Jean-Michel Hily (co-director of LPA VitiVirobiome) and Anne Sicard (ANR ToProtectMe)

CANDIDATE PROFIL

We are looking for a highly motivated candidate enjoying working with a large amount of RNA-Seq data and exploring a unique and original virus. A solid experience in bioinformatic, statistics, phylogenetics, phylogeography is required since the work will mainly focus on data analysis. The candidate is expected to take initiative and collaborate within and outside the group as well as to have good writing and communication skills. This 2-year position is expected to start in January 2025.

LABORATORY PUBLICATIONS RELATED TO THE TOPIC

Hily, J.-M., Poulicard, N., Candresse, T., Vigne, E., Beuve, M., Renault, L., Velt, A., Spilmont, A.-S., & Lemaire, O. (2020). Datamining, genetic diversity analyses, and phylogeographic reconstructions redefine the worldwide evolutionary history of grapevine Pinot gris virus and grapevine berry inner necrosis virus. *Phytobiomes Journal*, *4*(2), 165-177. https://doi.org/10.1094/pbiomes-10-19-0061-r

Hily, J. M., Poulicard, N., Kubina, J., Reynard, J. S., Spilmont, A. S., Fuchs, M., Lemaire, O., & Vigne, E. (2021). Metagenomic analysis of nepoviruses: diversity, evolution and identification of a genome region in members of subgroup A that appears to be important for host range. *Arch Virol*, *166*(10), 2789-2801. https://doi.org/10.1007/s00705-021-05111-0

Joly, A. C., Garcia, S., Hily, J. M., Koechler, S., Demangeat, G., Garcia, D., Vigne, E., Lemaire, O., Zuber, H., & Gagliardi, D. (2023). An extensive survey of phytoviral RNA 3' uridylation identifies extreme variations and virus-specific patterns. *Plant Physiology*, *193*(1), 271-290. https://doi.org/10.1093/plphys/kiad278

Kubina, J., Hily, J.-M., Mustin, P., Komar, V., Garcia, S., Martin, I. R., Poulicard, N., Velt, A., Bonnet, V., Mercier, L., Lemaire, O., & Vigne, E. (2022). Characterization of grapevine fanleaf virus isolates in 'chardonnay' vines exhibiting severe and mild symptoms in two vineyards. Viruses, 14(10), 2303. https://www.mdpi.com/1999-4915/14/10/2303

INRAE

The French National Research Institute for Agriculture, Food, and Environment (INRAE) is a major player in research and innovation. It is a community of 12,000 people with 272 research, experimental research, and support units located in 18 regional centers throughout France. Internationally, INRAE is among the top research organizations in the agricultural and food sciences, plant and animal sciences, as well as in ecology and environmental science. It is the world's leading research organization specializing in agriculture, food and the environment. INRAE's 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 has a major role to play in building solutions and supporting the necessary acceleration of agricultural, food and environmental transitions.

INRAE Grand-Est Colmar

You will work in the research unit entitled UMR SVQV (UMR-1131 – 'Santé de la Vigne et Qualité du Vin') that associates scientists and technicians from the INRAE, Colmar and from the University of Strasbourg. The main goal of SVQV research unit is to gain an understanding of the relationships between grapevine and both its fungal and viral pathogens – including virus vectors – in order to develop innovative solutions for a more environmentally friendly viticulture in the context of global warming. The research conducted in the unit is based on complementary expertise in plant pathology, entomology, genetics and metabolomics. You will be part of the Virology Vection team which focuses more specifically on the (i) development of resistance strategies to the virus responsible of fanleaf disease (*Grapevine fanleaf virus*, GFLV) and (ii) on the identification of the factors involved in virus transmission by different vectors (nematodes, mealybugs and aphids).

INRAE's life quality

By joining our teams, you benefit from (depending on the type of contract and its duration):
- up to 30 days of annual leave + 15 days "Reduction of Working Time" (for a full time);
- parenting support: CESU childcare, leisure services;
- skills development systems: training, career advise;
- social support: advice and listening, social assistance and loans;
- holiday and leisure services: holiday vouchers, accommodation at preferential rates;
- sports and cultural activities;
- collective catering.

↘ Terms and conditions

- Unit: **UMR SVQV 1131 (Team 'Virology and Vection')**
https://eng-svqv.colmar.hub.inrae.fr/presentation2/general-information

- Workplace: **Colmar**

- Contract: **Fixed-term contract**

- Duration: **24 months**

- Starting date: **January 2025**

- Gross month Salary: **3135 to 3559 € (depending on the experience)**

↘ Application process

Submit a single PDF file (CV, cover letter, publication list, contact information for at least two referees) via email to emmanuelle.vigne@inrae.fr

Deadline : 2024, November 15th