

Postdoc position in innovative sequencing technologies to profile DNA and RNA virus populations

For application please check:

<https://www.kuleuven.be/personeel/jobsite/jobs/60012976?hl=en&lang=en>

You are seeking for a postdoc position in an international research team using cutting-edge technologies to study plant virus interactions. This postdoc position is for you.

WORKING ENVIRONMENT

About the Tropical Crop Improvement Lab

The Tropical Crop Improvement Laboratory implements trait improvement approaches for important tropical crops such as banana and cassava. The Tropical Crop Improvement Laboratory has a strong focus on molecular biology, genetics and omics approaches to investigate crop responses to biotic and abiotic stresses. Vanderschuren Lab has worked with several pathosystems including model and crop pathosystems to study geminiviruses.

About the Division of Crop Biotechnics

The Division of Crop Biotechnics performs cutting-edge research on crop and model plant species, integrating knowledge at the cellular, tissue, plant, environment and agro-systems level. The Division consists of several research groups developing various molecular tools and having a strong expertise in molecular biology, plant pathology, tropical crops, genomics, plant hormones, plant nutrition and soil. The Division of Crop Biotechnics provides a very international working environment with opportunities to collaborate with top-ranked universities and international research centers.

[Division website](#)

About KU Leuven

KU Leuven offers a competitive and international working environment with access to cutting-edge technologies and expertise. KU Leuven is the best internationally ranked university in Belgium and ranks amongst the best European universities for research and education. KU Leuven also ranks as the [most innovative university](#) in Europe, building on a very strong tech transfer office.

[KU Leuven website](#)

RESEARCH PROJECT

KU Leuven TCI laboratory is leading a H2020 research on emerging plant viral diseases involving a large European consortium including public partnership (Wageningen University, CSIC, INRAE, Volcani Center, LIST, University of Catania, University of Greenwich, etc.) and private partnership (DCM, Syngenta, Corteva, etc.)

Begomoviruses such as ToLCNDV (Tomato leaf curl new Delhi virus) and tobamoviruses such as ToBRFV (Tomato brown rugose fruit virus) have become a major threat to tomato and cucurbit production in Europe. A better understanding of virus dissemination and evolution is a prerequisite to mitigate viral diseases. The recent surge in virus sequence data has been powered by short-read sequencing technologies. While short-read sequencing has provided invaluable information on new viruses and existing viral sequence diversity, it cannot accurately profile full-length genomes at depth. Viruses are often present in complex

populations of highly similar sequences and accurately assembling virus genomes of several kilo-bases in length using only ~100 base pair reads is challenging. This is a major hurdle in virus genomics and taxonomy. In this project we will establish and take advantage of full viral genome sequencing approaches to better profile virus diversity and study the evolution of viral populations in naturally tolerant or resistant plant genotypes.

We will further optimize the newly established CIDER-Seq method (1,2) to characterize geminiviruses and tobamoviruses in close collaboration with a private partner specialized in bioinformatics pipelines, including adaptation of the CIDER-Seq protocol to generate full viral genome sequences using the ONT Minion technology. In depth analysis of virus samples from a wide European network will be used to generate a Genome Detective platform (3) for geminiviruses and tobamoviruses. The full genome sequencing approaches will be used to profile virus populations in plant genotypes contrasting for virus resistance and characterize evolution of virus populations under selection by host plant resistance/tolerance.

PROFILE

We seek a candidate with a PhD degree in Bioengineering, Biology, Bioinformatics, Biotechnology or other relevant degree for the abovementioned project. The successful candidate should have demonstrated experience in bioinformatics, molecular biology, virology.

The successful candidate will have the following profile:

- creative with a strong interest in innovation
- good academic performance at the MSc and PhD level
- demonstrated capacity to write (scientific writing) and communicate in English
- demonstrated capacity to write project proposals
- eager to learn new techniques
- able to integrate in an international working environment

OFFER

- We offer a full-time postdoc position for 3 years with a possibility for extension
- Excellent guidance by a dynamic multidisciplinary team
- Training for scientific leadership
- Support to submit and lead research proposals
- Opportunities for research stays in partner laboratories
- Opportunities to network with reference laboratories in top-ranked institutions
- Training in bioinformatics
- State of the art research infrastructure
- A challenging job in a young, dynamic environment
- High level scientific training at a top-ranked university
- Being part of a world-class research group
- Remuneration according to the KU Leuven salary scales

APPLICATION

For more information please contact Prof. Hervé Vanderschuren (herve.vanderschuren@kuleuven.be).

The position will remain open until suitable candidate is identified. You can apply via the online application tool.

The successful candidate is expected to start during the second semester of 2021.

KU Leuven seeks to foster an environment where all talents can flourish, regardless of gender, age, cultural background, nationality or impairments. If you have any questions relating to accessibility or support, please contact us at diversiteit.HR@kuleuven.be.

REFERENCES

1. Mehta, D., Cornet, L., Hirsch-Hoffmann, M., Zaidi, S. S.-A., Vanderschuren, H. (2020). *Full-length sequencing of circular DNA viruses and extra-chromosomal circular DNA using CIDER-Seq*. **Nature Protocols**, 15, 1673-1689.
2. Mehta, D., Hirsch-Hoffmann, M., Were, M., Patrignani, A., Zaidi, S. S.-A., Were, H., Gruissem, W., Vanderschuren, H. (2019). *A new full-length circular DNA sequencing method for viral-sized genomes reveals that RNAi transgenic plants provoke a shift in geminivirus populations in the field*. **Nucleic Acids Research** 47, e9–e9
3. Cleemput S., Dumon W., Fonseca V., Abdool W. K., Giovanetti M., Alcantara L. C., Deforche K. & de Oliveira T. (2020). *Genome Detective Coronavirus Typing Tool for rapid identification and characterization of novel coronavirus genomes*. **Bioinformatics**, <https://doi.org/10.1093/bioinformatics/btaa145>.