

Postdoc position in plant virus diagnostics and population genetics using NGS technologies – Belgium

Scientific context. The recent developments of high-throughput sequencing (NGS) technologies and bioinformatics have drastically changed the research on viral pathogens, including the ability to decipher the population genetics of any species. In addition, there are now raising a growing interest by scientist, regulatory agencies and diagnostic laboratories for their application in virus diagnostics.

General context. The postdoc position is integrated within ongoing collaborations with European, African and South American teams. The Laboratory of Plant Pathology from Gembloux Agro-Bio Tech (Liège University, Belgium) is currently leading the COST Action FA1407 (www.cost-divas.eu), including more than 125 scientists and focused on the development of NGS technologies for the study and the diagnostic of plant viruses. The laboratory is also the virus diagnostic laboratory for the largest germplasm collection of banana held by Bioversity International (www.bioversityinternational.org).

Research topics. The postdoc position is focused on two forefront topics in plant virology :

1. The development and validation of NGS-based diagnostic protocol for routine indexing of germplasm collection of banana. Two NGS protocols will be applied on routine samples and compared to the classical indexing protocol (including IC-(RT)-PCR and electronic microscopy – work done by a technician). The performance of the protocols will be evaluated and the most promising proposed for extensive validation. This project, developed in the frame of CGIAR activities (www.cgiar.org), will last 6 months from 09/2017. It will be carried out within a team including one technician and one PhD student.

2. Evaluation of the impact of host plant on the population genetics of the barley yellow dwarf virus (BYDV). BYDV is the most damaging virus of cereals, despite the intensive use of insecticide treatments to control its aphid vectors. It can infect more than one hundred *Poaceae* and has a very high mutation rate. Through the transition toward a sustainable agriculture, several modifications of cropping systems are currently developed and may impact the population genetics of BYDV. This project will apply an original approach based on innovative techniques, methodologies and bioinformatics to study the impact of host plant succession and the aphid vectors on the population genetics of BYDV. The work will last 18 months, from 03/2018 and will be carried out within a team including two PhD students with the support of greenhouse technicians.

Techniques used. RNA extraction, classical molecular biology (PCR, RT-PCR), NGS sequencing and bioinformatic analyses, statistical analyses.

Location: Research activities will be performed at Liège University, Gembloux campus in Belgium (35 min by train from Brussels)

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