

## Metagenomics-based detection of viruses infecting cowpea in Burkina-Faso

Essowè Palanga<sup>1,2,4</sup>, Emmanuel Fernandez<sup>3</sup>, Denis Filloux<sup>3</sup>, Romain Ferdinand<sup>3</sup>, James Bouma Neya<sup>1,2,4</sup>, Mahamadou Sawadogo<sup>2</sup>, Oumar Traore<sup>2,4</sup>, Michel Peterschmitt<sup>3</sup> and Philippe Roumagnac<sup>3</sup>

<sup>1</sup> Laboratoire de Génétique et Biotechnologies Végétales, Université de Ouagadougou, 03 BP 7021 Ouagadougou, Burkina Faso

<sup>2</sup> Laboratoire de Virologie et de biotechnologies végétales, INERA, 01 BP 476 Ouagadougou, Burkina Faso

<sup>3</sup> CIRAD-INRA-SupAgro, UMR BGPI, TA A - 54 / K, Campus International de Baillarguet, 34398 Montpellier Cedex 5, France

<sup>4</sup> LMI Patho-Bios, 01 BP 476 Ouagadougou, Burkina Faso

Viral geometagenomics studies, which combine next-generation sequencing (NGS) methods with new possibilities to trace individual sequences to geo-referenced locations and/or hosts are currently providing high resolution qualitative data on plant viral diversity. A viral geometagenomics study of the cowpea (*Vigna unguiculata* (L.) Walp) virome in Burkina Faso was carried out in 2013. Three hundred and twelve cowpea leaf samples were collected from three agro-climatic zones of the country, including 66, 142 and 104 samples from Sahel, Sudan-Sahel and Sudan zones, respectively. Sequence-independent NGS of virion-associated nucleic acids was used for detection and identification of viruses present within the collected leaf samples.

Several viruses previously reported from cowpea were detected. They belong to the family *Potyviridae* [Cowpea aphid-borne mosaic virus, Bean common mosaic virus and Bean common mosaic necrosis virus (BCMNV)], *Tombusviridae* (Cowpea mottle carmovirus), *Bromoviridae* [Cowpea chlorotic mottle virus (CCMV)] and to the genus *Sobemovirus* (Southern cowpea mosaic virus and Southern bean mosaic virus). BCMNV, CCMV and both sobemoviruses were detected for the first time in Burkina Faso. Members of family *Potyviridae* were detected in 64% of the sampled plants whereas viruses of the other three groups were detected in less than 2% of the plants. Viral isolates of family *Potyviridae* and *Tombusviridae* were detected in the three regions whereas representatives of *Bromoviridae* and the genus *Sobemovirus* were detected only in one or two regions, respectively. The Sudan zone is the only area where representatives of the four groups were detected. According to the incidence of members of *Potyviridae* family, the infection pressure is the lowest in the Sahel zone.

The geometagenomics approach proved to be useful to detect new viruses of cowpea, including a new polerovirus (*Luteoviridae* family) detected in all agro-climatic zones except Sahel. Its incidence of 3.5% was higher than that of most of the previously reported viruses. This virus will be further characterized for its economic impact and its biological features including its transmission by insect vector and possibly by seed.

**Mots-clés :** Virus discovery, deep sequencing, Sahel and Sudan agro-climatic zones, Luteoviridae.