

# Application of next-generation sequencing for simultaneous detection of viruses, viroids and phytoplasmas in grapevine & fruit trees

Kerstin Zikeli<sup>1</sup>, Constanze Berwarth<sup>1</sup>, Dennis Knierim<sup>2</sup>, Christoph Hoffmann<sup>3</sup>, Michael Maixner<sup>3</sup>, Stephan Winter<sup>2</sup> and Wilhelm Jelkmann<sup>1</sup>

<sup>1</sup> Julius Kuehn Institute, Institute for Plant Protection in Fruit Crops and Viticulture, Dossenheim

<sup>2</sup> Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures, Braunschweig

<sup>3</sup> Julius Kuehn Institute, Institute for Plant Protection in Fruit Crops and Viticulture, Siebeldingen

E-mail of corresponding author: kerstin.zikeli@julius-kuehn.de

Next-generation sequencing (NGS) technologies have now become an integral part of plant health research. In addition, NGS is applied to a greater extent for detection of plant pathogens in the last years. Thus, it is used for diagnostics of viral and virus-associated diseases of grapevines and fruit trees. RNA sequencing combined with metagenomic analysis enables an unbiased analysis of infected plant samples.

Phytoplasma, viral and viroidal diseases cause severe harvest losses in viticulture and orchards.

Grapevine enation disease (GED), causing formation of enations on the underside of basal leaves and growth depression of infected plants, has been reported in Germany in 2006. The etiology of GED still remains unknown, no correlation of reverse transcription-PCR detected virus species and occurrence of disease has been found so far.

Bois noir, European stone fruit yellows, pear decline and apple proliferation

belong to the most prevalent and economically important phytoplasma diseases of grapevine respectively of fruit trees in Europe.

In this study, a NGS protocol (Illumina MiSeq platform) was applied for detection of viral and phytoplasmic infections of grapevine and fruit tree samples. Symptomatic as well as asymptomatic samples were analysed and subjected to a NGS pipeline starting from total RNA extract for generating an untargeted metagenome dataset. Therefore, untargeted and unknown pathogens may be identified.

Besides viruses and phytoplasmas detected by PCR, further viruses and viroids were found to be present. This NGS approach enabled the detection of low titer infections in tissues (samples were partially tested negatively by normal PCR assay) as well as parallel detection of phytoplasmas, viruses and viroids in a single grapevine or fruit tree sample.



# 11<sup>th</sup> Young Scientists Meeting 2018

14<sup>th</sup> – 16<sup>th</sup> November  
in Braunschweig

- Abstracts -



Berichte aus dem Julius Kühn-Institut

# 200

## **Kontaktadresse/ Contact**

Dr. Anja Hühnlein  
Julius Kühn-Institut (JKI)  
Bundesforschungsinstitut für Kulturpflanzen  
Informationszentrum und Bibliothek  
Erwin-Baur-Straße 27  
06484 Quedlinburg  
Germany

Telefon +49 (0) 3946 47-123

Telefax +49 (0) 3946 47-255

Wir unterstützen den offenen Zugang zu wissenschaftlichem Wissen.  
Die Berichte aus dem Julius Kühn-Institut erscheinen daher als OPEN ACCESS-Zeitschrift.  
Alle Ausgaben stehen kostenfrei im Internet zur Verfügung:  
<http://www.jki.bund.de> Bereich Veröffentlichungen – Berichte.

We advocate open access to scientific knowledge. Reports from the Julius Kühn Institute are therefore published as open access journal. All issues are available free of charge under <http://www.jki.bund.de> (see Publications – Reports).

## **Herausgeber / Editor**

Julius Kühn-Institut, Bundesforschungsinstitut für Kulturpflanzen, Braunschweig, Deutschland  
Julius Kühn Institute, Federal Research Centre for Cultivated Plants, Braunschweig, Germany

## **Vertrieb**

Saphir Verlag, Gutsstraße 15, 38551 Ribbesbüttel  
Telefon +49 (0)5374 6576  
Telefax +49 (0)5374 6577

**ISSN 1866-590X**

**DOI 10.5073/berjki.2018.200.000**



Dieses Werk ist lizenziert unter einer [Creative Commons – Namensnennung – Weitergabe unter gleichen Bedingungen – 4.0 Lizenz](https://creativecommons.org/licenses/by-sa/4.0/).

This work is licensed under a [Creative Commons – Attribution – ShareAlike – 4.0 license](https://creativecommons.org/licenses/by-sa/4.0/).