New Disease Reports

Vicia faba, *V. sativa* and *Lens culinaris* as new hosts for *Pea necrotic yellow dwarf virus* in Germany and Austria

Y. Gaafar [1], S. Grausgruber-Gröger [2] and H. Ziebell [1]*

[1] *Julius Kuehn-Institute, Institute for Epidemiology and Pathogen Diagnostics, Messeweg 11-12, 38106 Braunschweig, Germany*; [2] *Austrian Agency for Health and Food Safety, Institute for Sustainable Plant Production, Spargelfeldstrasse 191, 1220 Vienna, Austria*

*E-mail: heiko.ziebell@julius-kuehn.de

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Pea necrotic yellow dwarf virus (PNYDV) was identified in green peas (*Pisum sativum*) in Germany in 2009 (Grigoras *et al*., 2010). In subsequent years, sampling of symptomatic green peas showed that PNYDV was restricted to Saxony and Saxony-Anhalt (Ziebell, 2015). In Austria, PNYDV was detected in 2010, also in *P. sativum* (Grigoras *et al*., 2014).

A countrywide outbreak of virus-like disease symptoms on faba beans (*Vicia faba*) was reported in Germany in 2016. Many fields had large patches of yellowish and dwarfed plants (Fig. 1). More than 460 samples of *P. sativum* (green and protein peas) and *V. faba* showing virus-like symptoms (Fig. 2) were analysed using ELISA for *Alfalfa mosaic virus*, *Cucumber mosaic virus*, *Pea enation mosaic virus* (PEMV), *Red clover vein mosaic virus*-like carlaviruses, and luteo-/poleroviruses, nanoviruses and potyviruses. PEMV was the predominant virus found (70.5% of samples) but infection with luteo-/poleroviruses (26.7%), potyviruses (4.6%) and carlaviruses (0.9%) was confirmed. More importantly, 54.7% of samples tested positive with an ELISA designed for broad detection of nanoviruses (Grigoras *et al*., 2010; Abraham *et al*., 2012). The same samples did not react with an ELISA designed to detect only *Faba bean necrotic stunt virus* and *Faba bean necrotic yellows virus*, indicating infection with PNYDV. Using PCR with PNYDV-specific primers priPeaSdir (5′- AACCTCCGGATATCACCAGAT-3′) and priPeaSrev (5′-CCGGAGGTTTTATTTCAAAACCAAC-3′) targeting the coat protein-encoding component S of the genome (T. Timchenko, pers. comm.), PNYDV infection was confirmed for a subset of 18 samples. Sequencing of amplicons showed 98.7 to 99.9% nucleotide identity with PNYDV (GenBank Accession No. JN133279). Three lentil (*Lens culinaris*) samples from a field trial in central Germany also tested positive for PNYDV using differentiating monoclonal antibodies with confirmation by PCR and sequencing. Sequences from this study can be accessed under accession numbers KY191024 - KY191044.

In Austria, nanovirus symptoms appeared first in *P. sativum* in early June 2016 and shortly after in faba bean. In mid-late June, nearly every *V. faba* crop showed typical symptoms of nanovirus infection. In many faba bean and pea crops infection caused significant yield losses (Fig. 3). Typical symptoms of stunted growth, chlorosis and poorly developed pods were also found in lentils and vetch (*V. sativa*). Thirty-two samples of *L. culinaris*, *P. sativum*, *V. faba* and *V. sativa* from Burgenland, Styria and Upper and Lower Austria were tested for nanovirus infection using PCR primers designed by Kumari *et al.* (2010). The samples consisted of leaves pooled from several symptomatic plants from each field. Twenty-seven samples were positive for nanovirus infection. Representative amplicons from faba beans, lentils, peas, and vetch were sequenced (KY191009 - KY191023) and had 99.6 to 100% identity to PNYDV (KC979043).

This is the first report of *L. culinaris*, *V. faba* and *V. sativa* as natural hosts of PNYDV in Austria and Germany. Due to changes in government policy, the area of legumes grown in Germany doubled from 2012 to 2015 (Table 1) with further increases expected. However, limited host range experiments on peas and faba beans have not identified PNYDV-resistant accessions in Austria or Germany suggesting that legume production in central Europe is threatened by PNYDV infection.

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Figure 1

Figure 2

Figure 3

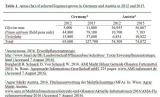

Figure 4

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