New Disease Reports

First report of *Xanthomonas phaseoli* pv. *phaseoli* and *Xanthomonas citri* pv. *fuscans* causing common bacterial blight of bean in Belgium

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In late August 2019, symptoms consistent with those of common bacterial blight were observed on mature beans (*Phaseolus vulgaris*) of several varieties in a trial plot in Hesbaye in the centre of Belgium. On leaves, irregular brown spots were surrounded by a yellow halo and progressed to give a burnt appearance (Fig. 1); on pods, water-soaked spots developed into reddish-brown spots (Fig. 2). Symptoms were scattered throughout the plot (approx. 100 m^2), and harvesting was abandoned due to pod infection.

Isolations were made from the margins of lesions. Tissues were crushed in 30 µl of sterile deionised water, streaked on King's medium B agar and incubated at 28°C. A yellowish bacterium grew abundantly and single colonies were visible after 48 hr. Analysis of 42 single colonies or strains was made by MALDI-TOF mass spectrometry (Bruker Maldi Biotyper) with our database containing strains from the EPPO A2 list. The highest identification scores were either *Xanthomonas axonopodis* pv. *phaseoli* CFBP 2534^{PT}, as for strain 2986.1a, or *X. euvesicatoria* CFBP 6864^{T} and *X. perforans* LMG 28258^{T}, as for strain 3002T1.1 (*X. citri* pv. *fuscans* was not in the database). Individual lesions contained only a single type. Pathogenicity was confirmed *in vitro* using a bean pod assay on pods from three different retail sources (Fig. 3). Inoculated strains were re-isolated from the margin of one water-soaked zone for each pod from each source and correctly identified by MALDI-TOF mass spectrometry.

Common bacterial blight of bean is caused by two *Xanthomonas* species representing four genetic lineages (GL): *X. phaseoli* pv. *phaseoli* (GL1; previously *X. axonopodis* pv. *phaseoli*) and *X. citri* pv. *fuscans* (GL2, GL3, GL *fuscans*) (Mhedbi-Hajri *et al*., 2013; Constantin *et al*., 2016; Chen *et al*., 2018). The PCR test of Audy *et al.* (1994) is specific to the four GLs and was positive for 24 Belgian strains isolated from 21 lesions. Parts of the 16S RNA and *gyrB* (Constantin *et al*., 2016) genes were sequenced for strains 2986.1a (MN584919; MN594779) and 3002T1.1 (MN584920; MN594780) (GenomeLab DTCS Quick Start Kit, GeXP) and the sequences of reference strains were retrieved from GenBank. The aligned sequences (AlignX) were analysed for phylogeny (MEGA7). GL1 and 2986.1a had identical 16S sequences (Fig. 4); they had a single nucleotide polymorphism with the other GLs, 3002T1.1, *X. euvesicatoria* and *X. perforans*, which were identical. The four GLs could be differentiated by the *gyrB* sequences (Fig. 5); 2986.1a grouped with GL1 and 3002T1.1 with GL2. Thus 2986.1a belongs to *X. phaseoli* pv. *phaseoli* and 3002T1.1 to *X. citri* pv. *fuscans* GL2.

Common bacterial blight of bean is present in six continents. In the European Union, the pathogens are only regulated on bean seeds (EU Regulations 2016/2031 and 2019/2072); there is no requirement for eradication in the field. In Belgium, an interception on seeds was reported in 2007 (EPPO, 2019) but this is the first report of the disease in a field crop and the pathogens were not eradicated**.** The case has uncertain origins: detection was late in the season, the plot contained several varieties and was near to a plot of *Vicia faba*, which is susceptible to the disease (Singh *et al.*, 2012) but whose seeds are not regulated. Late June and July 2019 were particularly hot with only occasional and local stormy rains. High rainfall in mid-August probably explains the spread of disease. Attention should be given to the disease during hot wet summers, particularly if these conditions occur earlier in June and July.

References

1. Audy P, Laroche A, Saindon G, Huang HC, Gilbertson RL, 1994. Detection of the bean common blight bacteria, *Xanthomonas campestris* pv. *phaseoli* and *X. c. phaseoli* var. *fuscans*, using the polymerase chain reaction. *Phytopathology* **84**, 1185-1192. http://dx.doi.org/10.1094/Phyto-84-1185
2. Chen NWG, Serres-Giardi L, Ruh M, Briand M, Bonneau S, Darrasse A, Barbe V, Gagnevin L, Koebnik R, Jacques M-A, 2018. Horizontal gene transfer plays a major role in the pathological convergence of *Xanthomonas* lineages on common bean. *BMC Genomics* **19**, 606. http://dx.doi.org/10.1186/s12864-018-4975-4
3. Constantin EC, Cleenwerck I, Maes M, Baeyen S, Van Malderghem C, De Vos P, Cottyn B, 2016. Genetic characterization of strains named as *Xanthomonas axonopodis* pv. *dieffenbachiae* leads to a taxonomic revision of the *X. axonopodis* species complex. *Plant Pathology* **65**, 792-806. http://dx.doi.org/10.1111/ppa.12461
4. EPPO, 2019. *Xanthomonas phaseoli* pv. *phaseoli* (XANTPH). Distribution - Last updated 2019-03-15. https://gd.eppo.int/taxon/XANTPH/distribution. Accessed 18 October 2019.
5. Mhedbi-Hajri N, Hajri A, Boureau T, Darrasse A, Durand K, Brin C, Fischer-Le Saux M, Manceau C, Poussier S, Pruvost O, Lemaire C, Jacques M-A, 2013. Evolutionary history of the plant pathogenic bacterium *Xanthomonas axonopodis*. *PLoS ONE* **8**, e58474. http://dx.doi.org/10.1371/journal.pone.0058474
6. Singh D, Sangle UR, Kumar B, Tripathi HS, Singh KP, Gupta AK, 2012. Integrated disease management of Faba bean (*Vicia faba* L.). In: Singh AK, Bhatt BP, eds. *Faba bean (Vicia faba L.): a potential leguminous crop of India.* Patna, India: ICAR Research Complex for Eastern Region, 279-301.

Figure 1

Figure 2

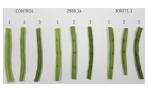

Figure 3

Figure 4

Figure 5

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