

the *Dickeya* biovar 3 variant is taking over from *D. dianthicola*.

In contrast to a biovar 7 *D. dianthicola* strain, the biovar 3 variant efficiently colonizes plant material. Soil infestation with a GFP-tagged strain resulted in a systemic colonization of potato plants within 30 days after inoculation. The biovar 3 variant was also able to colonize roots, stolons and progeny tubers from infected stems.

Spread within a crop may also occur during crop production if bacterial cells of *Dickeya* spp. are disseminated via free water in soil from rotten tubers to tubers of neighbouring plants. We showed that plants adjacent to blackleg diseased plants both within a row and between rows became contaminated after heavy irrigation. *Dickeya* spp. was able to cause disease symptoms even when present in seed at low densities. In field experiments with vacuum-inoculated tubers, a level of 40 cells per gram of potato peel was sufficient to end up with 30 and 15% diseased plants in 2005 and 2006, respectively. Such low levels of infection easily remain unnoticed during seed testing, even if sensitive detection methods are used. As for *Pectobacterium* spp., spread of contamination within and between seed stocks often occurs during harvesting and grading. In an experimental field, contamination with *Dickeya* spp. was spread by mechanical harvesting up to a distance of 80 m behind a zone with rotten tubers, with an average of 12 meter. Hand-harvested tubers from a disease-free crop remained clean.

*Dickeya* spp. seems to act like a biotrophic organism, which needs the host for long-term survival. *D. dianthicola* and the biovar 3 variant survived maximally for only three months in soil. Soil type, temperature and humidity only had a minor effect on survival.

In conclusion, a *Dickeya* spp. has become the dominant blackleg pathogen, probably due to its higher optimal growth temperature and its ability to colonize plant tissue more efficiently compared to *Pectobacterium* spp. The increasing importance of *Dickeya* spp. may be related to the increasing average temperature during the growth season due to global warming.

## Impact of climate change on insect pests of trees

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In The Netherlands, insect pests on trees and shrubs are being monitored continuously since 1946. During these years, almost all insect pest populations showed marked changes, which may be the result of climate change, arrival of new pests, changes in forest management, shifts in forest composition etc.

In an earlier study, we analyzed the number of observations for all pest species in the database on deciduous trees. The results showed that since 1985, pest insects hibernating in the egg stage, numerically exceed insects hibernating as larva, pupa or adult. During the last 2-3 decades, the winters in The Netherlands have become relatively warm and more humid. In literature, it is stated that mild winter temperatures can reduce winter survival of adult, larval and pupal stages more than of the eggs, presumably because the first stages are more vulnerable for entomopathogenic nematodes and fungal activity. This phenomenon may be the cause of our observed increase of egg hibernators (Moraal *et al.* 2004).

In a later study, we have analyzed trends in 61 years of population development of the 91 most abundant species in our database, in such a way that frequently observed species did not bias the results. Of the observed species, only a minority occurred regularly over the entire observation period of 61 years. The remaining species showed population fluctuations that varied from single short-term outbreaks to long-lasting increases or decreases. On coniferous trees, most insect species showed decreasing numbers, while increasing numbers were found most on deciduous trees. In the increasing trend-group of Lepidoptera, more egg hibernating species were observed compared with the decreasing trend-group (Moraal & Jagers op Akkerhuis, in prep).

Future climate change models for our region, predict increasing temperatures, drought periods, and heat waves during the growing season. The European literature on pest outbreaks that followed after the exceptional drought of 2003, give us some indications of the impacts of extreme climatic conditions. Primary pest insects, mostly leaf-consuming larvae, are not dependant on the vitality status of the host trees. Secondary pests, mostly bark-boring species, are dependant on weakened trees e.g. by drought. In literature, some generalized predictions were made, based on current pest distributions and the severity of insect outbreaks in individual regions after the summer drought of 2003. The predictions are that tree mortality due to secon-

dary pest insects may become more important in the future, because dry summers will reduce the resistance of trees. A combination of global trade and a changing climate makes it possible for new invasive species to establish in the EU and The Netherlands. In the absence of specific natural enemies, these species may cause tree mortality on a large scale (Moraal, in press).

There are many interactions and it is extremely difficult to predict the impact of climate change on insect pests in the future, but we may expect an increase of certain primary pests as well as secondary pests and invasive species.

### References

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## Are changes in the composition of the *Fusarium* Head Blight complex caused by climate change?

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*Fusarium* Head Blight (FHB) of wheat and barley is caused by a complex of species. Apart from yield losses, this disease has attracted much attention due to the capacity of many of the species in the complex to produce mycotoxins that are detrimental to humans and animals. In The Netherlands, until the late 1980s / early 1990s, *Fusarium culmorum* was the predominant species on wheat, but since then *F. graminearum* became the most important pathogen. This trend was first detected in 2000 and 2001 (Waalwijk *et*

*al.*, 2003) and was confirmed in other countries in Western Europe. This finding can be explained in several ways, including the expansion of the acreage of maize, which is a good host of *F. graminearum*, but less for *F. culmorum*. Secondly, *F. graminearum* has the capacity to go through sexual development, resulting in airborne ascospores that can travel several hundreds of kilometers; a clear advantage in colonization of crops in virgin soils. Lastly, *F. graminearum* favors higher temperatures than *F. culmorum* and the observed shift might be an indication of changes in climate.

In China, the population structure of FHB pathogens occurring on barley was investigated by sampling at 23 counties along the Yangtze River. In contrast to the situation in Europe or North America, the vast majority of isolates belong to *F. asiaticum*. Analyses of the structure of this population showed a dramatic gradient in the trichothecene mycotoxins produced (Yang *et al.*, 2008). While the production of nivalenol (NIV) was primarily found among isolates collected in the western part of the country, deoxynivalenol (DON) producers were mainly from the eastern provinces. As NIV producers have been reported in Asia in the past, we hypothesized that NIV producers represent the ancient population that is being replaced in the lowlands in the east. The populations in the western parts of China are not (yet) replaced as these counties reside in mountainous areas which are more difficult to become colonized by the DON producers.

A similar gradient was observed in Canada, where populations from the FHB complex in the East appear to overtake the place of those in the West. Phenotypic analyses showed that the 'invading' population consisted of strains that produced more mycotoxin and were more vigorous (Ward *et al.*, 2008). To verify whether a similar situation is currently taking place in China, we analyzed the diversity within and between populations using neutral VNTR markers. Some alleles were observed exclusively in upper valleys of the Yangtze River (Zhang *et al.*) which is in agreement with the occurrence of genetic differentiation along environmental gradients.

These results will be discussed together with data from a novel survey performed in the Netherlands in 2008, to underline the previously observed temporal shifts in the composition of the FHB complex. To put this in a broader perspective, this will be compared with results from surveys in France and Germany, where similar analyses were also performed on maize (Görtz *et al.*)