

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

- Moraal, L.G. Expected impact of climate change on insect pests of forest trees in The Netherlands. Wageningen, Alterra-report 1761. In press.
- Moraal, L.G., Jagers op Akkerhuis, G.A.J.M., Siepel, H., Schelhaas M.J. & Martakis G.F.P., 2004. Verschuivingen van insectenplagen bij bomen sinds 1946 in relatie met klimaatverandering. Met aandacht voor de effecten van stikstofdepositie, vochtstress, bossamenstelling en bosbeheer. Wageningen, Alterra-rapport 856. 52 pp.
- Moraal, L.G. & Jagers op Akkerhuis, G.A.J.M. Population changes of insect pests on trees and shrubs in The Netherlands since 1946 in relation with climate change, forest management and site factors. In prep.

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.*)

References

- Görtz, A., Zuehlke, S., Steiner, U., Dehne, H.W., Waalwijk, C., de Vries, I. & Oerke, E.C. (in preparation). Maize ear rot caused by *Fusarium* spp. in Germany: year-to-year variability in mycotoxin contamination and species profile.
- Waalwijk, C., Kastelein, P., Vries, P.M. de, Kerényi, Z., Lee, T. van der, Hesselink, T., Kohl, J. & Kema, G.H.J., 2003. Major changes in *Fusarium* spp. in wheat in the Netherlands. *European Journal of Plant Pathology* 109: 743-754.
- Ward, T.D., Clear, R.M., Rooney, A.P., O'Donnell, K., Gaba, D., Patrick, S., Starkey, D.E., Gilbert, J., Geiser, D.M. & Nowicki, T.W., 2008. An adaptive evolutionary shift in *Fusarium* head blight pathogen populations is driving the rapid spread of more toxigenic *Fusarium graminearum* in North America. *Fungal Genetics & Biology* 45: 473-484.
- Yang, L.J., Lee, T.A.J. van der, Yang, X.J., Yu, D.Z. & Waalwijk, C., 2008. *Fusarium* populations on Chinese barley show a dramatic gradient in mycotoxin profiles. *Phytopathology* 98: 719-727.
- Zhang, Z., Zhang, H., Lee, T.A.J. van der, Li, C., Arens, P., Xu, J., Xu, J.S., Yang, L.J., Yu, D.Z., Waalwijk, C. & Feng, J. (submitted) Genetic diversity studies of *Fusarium* species on barley in China show a clear substructure associated with their geographic origin.