**GUEST EDITORIAL** 



## Challenges in *Fusarium*, a Trans-Kingdom Pathogen

Anne D. van Diepeningen · G. Sybren de Hoog

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**Abstract** *Fusarium* species are emerging human pathogens, next to being plant pathogens. Problems with *Fusarium* are in their diagnostics and in their difficult treatment, but also in what are actual *Fusarium* species or rather Fusarium-like species. In this issue Guevara-Suarez et al. (Mycopathologia. doi:10. 1007/s11046-016-9983-9, 2016) characterized 89 isolates of Fusarium from Colombia showing especially lineages within the *Fusarium solani* and *oxysporum* species complexes to be responsible for onychomycosis.

**Keywords** Fusariosis  $\cdot$  Refraction to treatment  $\cdot$ Fusarium *taxonomy*  $\cdot$  Human pathogen  $\cdot$  Plant pathogen

*Fusarium* head blight, *Fusarium* ear rot, vascular wilting... Please note that no human diseases are even mentioned here, but plant infections because *Fusar-ium* mostly causes diseases in a wide diversity of cereals and other economically important plant

A. D. van Diepeningen (⊠) · G. S. de Hoog CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands e-mail: a.diepeningen@cbs.knaw.nl

G. S. de Hoog Institute of Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, The Netherlands species, like the devastating epidemics currently swiping across the world decimating our banana trees and crops. These diseases not only diminish yields, but also may spoil the crops by the production of persistent mycotoxins affecting consumer's health [1, 2]. *Fusarium* infections cause billions of dollars of losses and need huge investments in pesticides and other measures to keep them under control and out of the food chain. Every host plant seems to have at least one *Fusarium* pathogen and together they form a very large genus within the fungal kingdom with many plant pathogens (and related species with a saprobic life style).

Even more worrying is that quite a number of fusaria prove capable not only of plant infections but also of trans-kingdom infections in human and animal. Numbers of human infections by Fusarium spp. are rising worldwide due to a better detection, but also due to an increase in the number of susceptible and immunocompromised people [3]. For example, onychomycosis is not a rare condition in healthy humans, but some studies show that up to 10 % of them are caused by Fusarium spp. when etiological agents are typed to species level [4]. Eye infections after trauma with soil or plant material commonly occur in warmer drier climates, while in temperate areas (lack of) lens hygiene appears a common source of keratomycosis [5]. Life-threatening, deep and disseminated infections occur in severely immunocompromised patients, where especially leukemic patients are at risk; a relatively innocent dermatological fusariosis may prove to be the portal of entry [6]. A major problem to all these infections is the fact that *Fusarium* species are relatively insensitive to most available antifungal compounds [7].

Within the large genus Fusarium, it has become customary to cluster closely related sibling species or lineages with little to no morphological differences in so-called species complexes. The opportunists on humans group into seven species complexes: the Fusarium solani, F. oxysporum, F. incarnatum-equiseti, F. fujikuroi, F. clamydosporum, F. dimerum and F. sporotrichioides species complexes [4]. In particular members of the Fusarium solani and F. oxysporum species complexes have been implicated in human infections worldwide [8–10], but local, endemic plant pathogens prove to have virulence to humans as well (e.g., [4]). Many molecular siblings have no binomial designations yet. As it proves that different lineages within one species complex may vary in the antifungal susceptibility [10, 11], it seems advisable to determine etiological agents to species/lineage level.

In this issue Guevara-Suarez et al. [12] characterized 89 isolates of Fusarium from Colombia, the majority having been isolated from onychomycoses. They used multi-locus sequence analysis-the gold standard-to identify known lineages in the F. solani and F. oxysporum species complexes and also identified two new lineages with members capable of human infection. Based on these outcomes, it seems that in the Americas as well as in Europe [12–15] members of these two complexes predominate in onychomycosis, while for instance in Thailand species of the F. incarnatum-equiseti complex are also frequently observed [4]. Interestingly the authors [12] show that pedicure treatment is not a predisposing factor, but rather seems to limit these infections. Most importantly, Guevara-Suarez et al. [12] show that the different lineages vary in susceptibility to antifungal drugs and that the only approved antifungal agent for treating nail infections in Colombia, fluconazole, is exactly the one for which all isolates have minimum inhibitory concentrations higher than 64 µg/ml. This explains the limited success in onychomycosis treatment.

Another problem in addition to the increasing frequency of infections and the problems of treatment, is in diagnostics. A consensus was reached that *Fusarium* was to be the preferred name [16], while a

minority of researchers advocated a subdivision of Fusarium into smaller genera [17]. Diseases are commonly named after the etiologic agent, in this case Fusarium spp. cause 'fusariosis'. When generic names are changed, as a consequence also the disease name is affected. A major problem now lies in the question how large the genus Fusarium actually is and which species are to be regarded as fusarium-like. Clinically relevant are especially the suggested renaming of the Fusarium dimerum species complex as Bisifusarium, and the resurrection of the genus Neocosmospora for the Fusarium solani species complex [17], while the other complexes are currently not in danger of renaming. Clinically, however, all these species give the same type of opportunistic infections ranging from onychomycosis, keratitis, to disseminated infections with necrotic lesions so there it is easiest to describe them all as Fusarium and fusarioses.

## References

- Summerell BA, Laurence MH, Liew ECY, Leslie JF. Biogeography and phylogeography of *Fusarium*: a review. Fungal Divers. 2010;44:3–13.
- van der Lee T, Zhang H, van Diepeningen A, Waalwijk C. Biogeography of *Fusarium graminearum* species complex and chemotypes: a review. Food Addit Contam Part A Chem Anal Control Expo Risk Assess. 2015;32:453–60.
- Dalyan Cilo B, Al-Hatmi AM, Seyedmousavi S, Rijs AJ, Verweij PE, Ener B, de Hoog GS, van Diepeningen AD. Emergence of fusarioses in a university hospital in Turkey during a 20-year period. Eur J Clin Microbiol Infect Dis. 2015;34:1683–91.
- van Diepeningen AD, Feng P, Ahmed S, Sudhadham M, Bunyaratavej S, de Hoog GS. Spectrum of *Fusarium* infections in tropical dermatology evidenced by multilocus sequencing typing diagnostics. Mycoses. 2015;58:48–57.
- 5. van Diepeningen AD, Al-Hatmi AMS, Brankovics B, de Hoog GS. Taxonomy and clinical spectra of *Fusarium* species: where do we stand in 2014? Curr Clin Microbiol Rep. 2014;1:10–8.
- Nucci M, Anaissie E. Cutaneous infection by *Fusarium* species in healthy and immunocompromised hosts: implications for diagnosis and management. Clin Infect Dis. 2002;35:909–20.
- Guarro J. Fusariosis, a complex infection caused by a high diversity of fungal species refractory to treatment. Eur J Clin Microbiol Infect Dis. 2013;32:1491–500.
- O'Donnell K, Sutton DA, Rinaldi MG, Gueidan C, Crous PW, Geiser DM. Novel multilocus sequence typing scheme reveals high genetic diversity of human pathogenic members of the *Fusarium incarnatum-F. equiseti* and *F.*

chlamydosporum species complexes within the United States. J Clin Microbiol. 2009;47:3851–61.

- 9. O'Donnell K, Gueidan C, Sink S, Johnston PR, Crous PW, Glenn A, Riley R, Zitomer NC, Colyer P, Waalwijk C, Lee T, Moretti A, Kang S, Kim HS, Geiser DM, Juba JH, Baayen RP, Cromey MG, Bithell S, Sutton DA, Skovgaard K, Ploetz R, Corby Kistler H, Elliott M, Davis M, Sarver BA. A twolocus DNA sequence database for typing plant and human pathogens within the *Fusarium oxysporum* species complex. Fungal Genet Biol. 2009;46:936–48.
- O'Donnell K, Sutton DA, Fothergill A, McCarthy D, Rinaldi MG, Brandt ME, Zhang N, Geiser DM. Molecular phylogenetic diversity, multilocus haplotype nomenclature, and in vitro antifungal resistance within the *Fusarium solani* species complex. J Clin Microbiol. 2008;46:2477–90.
- Al-Hatmi AM, van Diepeningen AD, Curfs-Breuker I, de Hoog GS, Meis JF. Specific antifungal susceptibility profiles of opportunists in the *Fusarium fujikuroi* complex. J Antimicrob Chemother. 2015;70:1068–71.
- 12. Guevara-Suarez M, Cano-Lira JF, de Garcia MCC, Sopo L, De Bedout C, Cano LE, García AM, Motta A, Amézquita A, Cárdenas M, Espinel-Ingroff A, Guarro J, Restrepo S, Celis A. Genotyping of *Fusarium* isolates from onychomycosis in Colomobia: detection of two new species within the *Fusarium solani* species complex and in vitro antifungal susceptibility testing. Mycopathologia. 2016;. doi:10.1007/ s11046-016-9983-9.
- Castro López N, Casas C, Sopo L, Rojas A, Del Portillo P, Cepero de García MC, Restrepo S. *Fusarium* species detected in onychomycosis in Colombia. Mycoses. 2008;52:350–6.

- Migheli Q, Balmas V, Harak H, Sanna S, Csherm B, Aoki T, O'Donnell K. Molecular phylogenetic diversity of dermatologic and other human pathogenic fusarial isolates from
- 2010;48:1076–84.
  15. Ninet B, Jan I, Bontems O, Léchenne B, Jousson O, Lew D, Schrenzel J, Panizzon RG, Monod M. Molecular identification of *Fusarium* species in onychomycoses. Dermatology. 2005;210:21–5.

hospitals in Northern and Central Italy. J Clin Microbiol.

- 16. Geiser DM, Aoki T, Bacon CW, Baker SE, Bhattacharyya MK, Brandt ME, Brown DW, Burgess LW, Chulze S, Coleman JJ, Correll JC, Covert SF, Crous PW, Cuomo CA, De Hoog GS, Di Pietro A, Elmer WH, Epstein L, Frandsen RJ, Freeman S, Gagkaeva T, Glenn AE, Gordon TR, Gregory NF, Hammond-Kosack KE, Hanson LE, Jímenez-Gasco Mdel M, Kang S, Kistler HC, Kuldau GA, Leslie JF, Logrieco A, Lu G, Lysøe E, Ma LJ, McCormick SP, Migheli Q, Moretti A, Munaut F, O'Donnell K, Pfenning L, Ploetz RC, Proctor RH, Rehner SA, Robert VA, Rooney AP, Bin Salleh B, Scandiani MM, Scauflaire J, Short DP, Steenkamp E, Suga H, Summerell BA, Sutton DA, Thrane U, Trail F, Van Diepeningen A, Vanetten HD, Viljoen A, Waalwijk C, Ward TJ, Wingfield MJ, Xu JR, Yang XB, Yli-Mattila T, Zhang N. One Fungus, One Name: defining the genus Fusarium in a scientifically robust way that preserves longstanding use. Phytopathology. 2013;103:400-8.
- Lombard L, van der Merwe NA, Groenewald JZ, Crous PW. Generic concepts in Nectriaceae. Stud Mycol. 2015;80:189–245.