FINAL REPORT (OTKA PD-112468) (period: 1 Sept 2014 – 31 Aug 2017)

With permission from the National Research, Development and Innovation Office (NKFI), the project was suspended from 1 Sept 2015 to 31 Aug 2017, and then closed as the principal investigator was absent on maternity leave until 20 July 2018. As the principal investigator spent a considerable time on sick leave during the first year of the project, activities during this reporting period have consisted mostly of completing work previously commenced on powdery mildew fungi, though not necessarily included in the original work plan. The main results of this work and the papers published are summarised below.

ASCOSPORIC INFECTION IN THE WHEAT POWDERY MILDEW FUNGUS BLUMERIA GRAMINIS F. SP. TRITICI

Although *Blumeria graminis*, the powdery mildew fungus of cereal crops, is one of the most intensively studied plant pathogens, an important part of its life cycle, namely the way ascospores (sexual spores) initiate primary infections, has not been described in detail so far. The studies performed in this project explored this process in *B. graminis* f. sp. *tritici* for the first time, from the germination of ascospores to their penetration into the plant epidermal cells and early colony development, using light and confocal laser scanning microscopy (CLSM).

The results showed that all the germinated ascospores produced a single germ tube type, while the number and position of the germination sites were variable both *in vitro* and on host plant surfaces. In contrast to conidia (asexual spores), the development of primary germ tubes was not observed on the ascospores, so the ascosporic and conidial germination patterns were found to be markedly different in this fungus. As the germ tubes elongated, the germinated ascospores developed septate hyphae, which were usually swollen towards the tips. This was followed by the production of a penetration peg and the formation of a haustorium (fungal feeding structure) inside the penetrated epidermal cell of the host, as also known in the case of conidial infections, after which the septate hyphae continued to grow, initiating the formation of young colonies.

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The field experiments confirmed earlier studies reporting that *B. graminis* chasmothecia (sexual fruiting bodies) collected from the field during the growing season do not contain mature ascospores, only asci filled with protoplasm. The ascospore differentiation in chasmothecia remaining on leaf debris is induced by moist conditions and the ascospores serve as inocula for the infection of volunteers or winter wheat seedlings in late summer or autumn. The ascospores quickly became morphologically differentiated and able to infect their hosts, indicating that their morphological and physiological maturation is a rapid process compared to that of other powdery mildews.

Although the conidial stage of powdery mildews has been intensively studied from many aspects for a long time, very little is known about ascosporic infection in these plant pathogens. To date, the morphology of germinating ascospores has only been studied in detail in three of the approximately 850 powdery mildew species known worldwide. Therefore, the research paper on the direct observation and detailed description of ascosporic infection in *B. graminis* f. sp. *tritici*¹ may contribute to the understanding of the life cycle of powdery mildews, particularly that of their sexual stage. A three-dimensional CLSM image of the early steps of powdery mildew infection initiated on a wheat leaf by a *B. graminis* f. sp. *tritici* ascospore² was accepted as the cover illustration of the journal Phytopathology.

¹ <u>Jankovics, T.</u>, Komáromi, J., Fábián, A., Jäger, K., Vida, G., Kiss, L. (2015): New insights into the life cycle of the wheat powdery mildew: direct observation of ascosporic infection in *Blumeria graminis* f. sp. *tritici. Phytopathology*, 105:797-804. (IF: 3.011)

² http://apsjournals.apsnet.org/page/phyto_cover_6-15

IDENTIFICATION OF THE PATHOGEN CAUSING TOMATO POWDERY MILDEW IN SOUTH AFRICA

Powdery mildew infections caused by *Oidium neolycopersici* have become a problem in tomato production since the late 1980s in many parts of the world, including Europe, Asia and North America. In Africa, this fungus was not found to be associated with significant economic loss until autumn 2013, when tomatoes with typical symptoms of powdery mildew infection were detected for the first time in South Africa. The objective of this study was to precisely identify the causal agent of these infections.

Morphological studies and the analysis of nrDNA ITS sequences confirmed that *O. neolycopersici* was the causal agent of tomato powdery mildew in South Africa, providing the first evidence that this fungus had appeared in that region³. Before 2013, the occurrence of *O. neolycopersici* on the African continent had only been reported from Tanzania.

³ Lebeda, A., Mieslerová, B., <u>Jankovics, T.</u>, Kiss, L., Van de r Linde, E.J. (2015): First detection of tomato powdery mildew caused by *Oidium neolycopersici* in South Africa. *South African Journal of Botany*, 99:153-157. (IF: 1,244)

GENETIC VARIABILITY OF THE POWDERY MILDEW FUNGI INFECTING PAPAVERACEOUS HOSTS

Recent reports on morphologically indistinguishable powdery mildew anamorphs belonging to the genus *Pseudoidium* on various papaveraceous hosts in European countries drew attention to deficiencies in earlier publications on the identification of the powdery mildew fungi found on these hosts. Herbarium materials and newly obtained samples were studied to reveal the phylogenetic relationship and host range of these pathogens in order to achieve the precise identification and delimitation of their species.

The pathogen infecting *Chelidonium majus* in Europe was clearly identified as *Erysiphe macleayae*. The appearance of chasmothecia on this host, which is reported in this work for the first time in Europe, suggests that *E. macleayae* has probably only recently expanded its area of distribution from Asia to Europe. This study revealed that *E. macleayae* exhibits a specific host range different from that of *E. cruciferarum*, the most common pathogen on papaveraceous hosts in Europe. Inoculation experiments also indicated that *E. macleayae* may be capable of infecting a wider range of hosts than that explored in previous studies.

Based on the nrDNA ITS sequences, the powdery mildew fungi on papaveraceous hosts previously identified as *E. cruciferarum* were found to be

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distinct lineages, suggesting that *E. cruciferarum sensu lato* might represent a species complex consisting of several morphologically indistinguishable lineages specialized to various hosts or groups of hosts. The consistency of the results of morphological observations, molecular analyses and inoculation tests justified revising the taxonomic status of the anamorph infecting *Eschscholzia californica*. Therefore a new species name, *Pseudoidium eschscholzii*, is proposed⁴.

⁴ *Pastirčáková, K., *<u>Jankovics, T.</u>, Komáromi, J., Pintye, A., Pastirčák, M. (2016): Genetic diversity and host range of powdery mildews on Papaveraceae. *Mycological Progress*, 15:36. (IF: 1,616)

*shared first authorship

POWDERY MILDEW RESISTANCE IN WHEAT CULTIVAR MV HOMBÁR IS CONFERRED BY A NEW GENE, PmHo

A new powdery mildew resistance gene designated as PmHo was identified in 'Mv Hombár' winter wheat, bred in Martonvásár, Hungary⁵. It has exhibited a high level of resistance over the last two decades. Genetic mapping of recombinant inbred lines derived from the cross 'Ukrainka'/Mv Hombár located this gene on chromosome 2AL. The segregation ratio and consistent effect in all environments indicated that PmHo is a major dominant powdery mildew resistance gene. The race-specific nature of resistance in Mv Hombár was shown by the emergence of a single virulent pathotype designated as 51-Ho. This pathotype was, to some extent, able to infect Mv Hombár, developing visible symptoms with sporulating colonies. Microscopic studies revealed that, in incompatible interactions, posthaustorial hypersensitivity reaction was the most prevalent but not exclusive plant defense response in Mv Hombár, and fungal growth was mostly arrested during haustorium formation or in the early stages of colony development. The delayed fungal development of the virulent pathotype 51-Ho may be explained by additional effects of other loci that were also involved in the powdery mildew resistance of Mv Hombár. ⁵Komáromi, J., <u>Jankovics, T.</u>, Fábián, A., Puskás, K., Zhang, Z., Zhang, M., Li, H., Jäger, K., Láng, L., and Vida, G. (2016): Powdery mildew resistance in wheat cultivar Mv Hombár is conferred by a new gene, PmHo. *Phytopathology* 106:1326-1334. (IF: 2,896)