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A/Prof. Wieland Meyer is the chief scientist of the Molecular Mycology Research Laboratory at the Centre for Infectious Diseases and Microbiology, Sydney Medical School - Westmead Hospital, University of Sydney, Sydney, Australia. He graduated in Genetics (1986) and completed his PhD pioneering DNA/PCR fingerprinting for fungi (1992) from the Humboldt University of Berlin, Germany with Prof. T. Börner. He then undertook postdoctoral studies at Duke University Medical Center, Durham, NC, USA (1992-1995) with Prof. T. Mitchell, where he worked at the phylogeny of *Candida* and molecular epidemiology of *Cryptococcus*, before he established the Molecular Mycology Research Laboratory at Westmead Hospital ([www.mycology.org](http://www.mycology.org)) and the Australian National Molecular Medical Mycology Reference Laboratory in 1995. His research focuses on the evolution, phylogeny, speciation, population genetics, molecular epidemiology and typing, especially of the genera *Candida*, *Cryptococcus*, *Scedosporium* and *Pneumocystis*, the development of fast, simple and reliable molecular identification techniques for human/animal fungal pathogens, and the understanding of fungal virulence determinants on a molecular level. He is the curator of the Westmead Hospital Medical Mycology Culture Collection, housing around 8000 strains. He has published 122 peer reviewed papers and 3 books. His research has been cited internationally 2510 times (S.C.I./Web of Science) (H index=29) and is funded by national and international grants (e.g. NH&MRC, Colciencias, etc.). He has established a quality controlled ITS DNA barcode reference database for human pathogenic fungi ([www.mycologylab.org/BioloMICSSequences.aspx](http://www.mycologylab.org/BioloMICSSequences.aspx)) and a number of Multilocus Sequence Typing (MLST) databases ([mlst.mycologylab.org/](http://mlst.mycologylab.org/)). He chaired the Organizing Committee of the 8th International Mycology Congress (IMC8) Cairns, Australia, 2006. He was the Vice- (1998-2002) and President (2002-2005) of the Australasian Mycological Society and the Vice-President of the International Mycological Association (IMA) (2006-2010). He is co-chair of the Council of heads of Australian Collections of Microorganism (CHACM) and a member of the steering committee of the Australian Barcoding of Life Network (ABOLN). He is a member of ISHAM's Global Panel of Opinion Leaders, convener of the ISHAM working group on "Genotyping of *Cryptococcus neoformans* and *C. gattii*" and co-convener of the ISHAM working group on "Barcoding of Medical Fungi". He is associate editor of the journals: Medical Mycology, Personia-Molecular Phylogeny and Evolution of Fungi, Australasian Mycologist and IMA Fungus. He is teaching medical mycology, molecular epidemiology and identification of pathogenic fungi at national and international workshops and supervised numerous postdocs, PhD and honours studies from a diverse range from countries during his scientific career. His vision for ISHAM is to make molecular data for the identification and typing of human/animal pathogenic fungi globally accessible by linking individual quality controlled databases and establishing international data networks to enable a faster identification and a better public health response to emerging highly virulent fungal agents.

### **Selected Peer-reviewed Publications** (selected from 122 peer-reviewed publications)

1. Kidd S, Hagen F, Tschärke R, Huynh M, Bartlett K, Fyfe M, MacDougall L, Boekhout T, Kwon-Chung JK & **Meyer W** (2004) "A rare genotype of *Cryptococcus gattii* caused the Cryptococcosis outbreak on Vancouver Island (British Columbia, Canada)", PNAS 107(49): 17258-17263.
2. **Meyer W**, Aanensen DM, Boekhout T, Cogliati M, Diaz MR, Esposto MC, Fisher M, Gilgado F, Hagen F, Kaocharoen S, Litvintseva AP, Mitchell TG, Simwami SP, Trilles L, Viviani MA, Kwon-Chung J (2009) : Consensus multi-locus sequence typing scheme for *Cryptococcus neoformans* and *Cryptococcus gattii*. Medical Mycology 47(6): 561-574.
3. Ngamskulrungrroj P, Gilgado F, Faganello J, Litvintseva AP, Leal AL, Tsui KM, Mitchell TG, Vainstein MH, **Meyer W** (2009): Genetic diversity of the *Cryptococcus* species complex suggests that *Cryptococcus gattii* deserves to have varieties. PLoS ONE 4(6):e5862.
4. Ngamskulrungrroj P, Price J, Sorrell T, Perfect JR, **Meyer W** (2011): *Cryptococcus gattii* virulence composite: Candidate genes revealed by microarray analysis of high and less virulent Vancouver Island outbreak strains. PLoS One 6(1): e16076
5. Carriconde F, Gilgado F, Arthur I, Ellis D, Malik R, Currie BJ, **Meyer W** (2011): Clonality and  $\alpha$ -a recombination in the Australian *Cryptococcus gattii* VGII population - an emerging outbreak in Australia. PLoS ONE 6(2): e16936