

Willie Commelin Scholtendag 2004

Op donderdag 22 januari 2004 vond op de Uithof in Utrecht de Willie Commelin Scholtendag plaats. Deze jaarlijks terugkerende bijeenkomst wordt georganiseerd door de sectie voor de Fytopathologie van de Koninklijke Nederlandse Botanische Vereniging en heeft tot doel kennisuitwisseling tussen de fytopathologische onderzoeksgroepen op instituten, proefstations en universiteiten te bevorderen. De bijeenkomst werd bijgewoond door ongeveer tachtig personen. De samenvattingen van de presentaties staan hieronder weergegeven.

De datum voor de volgende WCS dag is vastgesteld op donderdag 20 januari 2005, wederom op de Uithof in Utrecht. U bent allen uitgenodigd om deel te nemen. Het bestuur van de sectie streeft naar een programma waarin alle actoren in het fytopathologisch onderzoek in Nederland vertegenwoordigd zijn en nodigt met name onderzoekers van instituten en proefstations uit een bijdrage te leveren. Voor nadere informatie over de KNBV sectie fytopathologie en de WCS dag kunt u zich wenden tot Guido Bloemberg, secretaris (bloemberg@rulbim.leidenuniv.nl / 071 527 5056) of Francine Govers, voorzitter (francine.govers@wur.nl / 0317 483 138).

Hosts, species and genotypes

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How we define and recognise species is a theme that is central to phytomycolo23gy. For the purpose of this talk, I will briefly discuss the various models currently employed for species recognition and point out the positive and negative aspects of each, using various examples of phytopathogenic fungi. To this end, the recognition of phylogenetic species by employing genealogical concordance appears to be the widely accepted, though the biological and morphological species concepts are still commonly used. In recent years the synergism between plant pathology and phytomycology has largely been lost and hence plant pathology as a science finds itself in a serious predicament. Most plant pathologists work with names that relate to outdated concepts. Few actually work with the organisms named in their grant proposals. In this

talk I will present data to address various issues related to: (a) genomic data vs. the Saccardoan system and the anamorph names it gave rise to; (b) pathogen diagnostics and the value of epitypification; (c) genomic data that will indicate that many of the pathogen names we are currently using need to change; (d) the need of plant pathologists to ensure that they are represented in AToL initiatives; (e) the understanding that clonality, sex and variation mean we have to think about studying populations rather than random strains. Although the pros and cons of various proposed changes remain debatable, the mycological dogma we were taught is changing due to genomics. The biggest advantage to systematics is that these new approaches promise an eventual stability to a science that underpins plant pathology.

Downy mildew genomics: identification and functional analysis of genes encoding secreted proteins

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Downy mildews infect many important crops worldwide. To protect crops from downy mildew disease, natural resistance genes have been introduced into cultivars. However, resistance is usually rapidly overcome by the pathogen. The project 'Downy mildew genomics and plant disease resistance' aims to identify new resistance genes that mediate the recognition of important pathogen proteins and may therefore be more durable. A genomics approach is used to identify downy mildew genes that encode secreted proteins and that are specifically expressed during the infection process. Two downy mildew – plant interactions are studied: *Peronospora parasitica* – *Arabidopsis thaliana* and *Bremia lactucae* – lettuce. Over three thousand Expressed Sequence Tags (ESTs) have been collected from *B. lactucae* and *P. parasitica* conidiospore libraries. These ESTs have been screened for signal peptides and for similarity to genes or proteins in public databases. Microarray technology is being

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