

9th ASM conference on *Candida* and candidiasis

Jersey city, New Jersey, USA, March 24-28, 2008.

The 9th ASM *Candida* and Candidiasis conference was held at the Hyatt Regency, Jersey City on the 24th-28th March 2008. The hotel was on the bank of the Hudson River, with spectacular views of Manhattan and the Statue of Liberty, especially from the Manhattan Ballroom where all the social events were held.

The main organisers of the 9th *Candida* and candidiasis conference were Aaron Mitchell (Columbia University) and Judy Berman (University of Minnesota). It became obvious that the *Candida* research field remains an expanding one, with a record number of delegates registered for this meeting (more than 400).

The conference had a slightly altered format this year, with all speakers in the main sessions limited to short presentations, and consisting of a mix of established and younger investigators. Seven of the oral presentations were given by recipients of ASM travel grants for junior scientists, and the other 10 recipients contributed to the 300 excellent posters.

On the first evening the conference kicked off with a session reviewing and discussing the various experimental models available for investigating *Candida* clinical infections, with Scott Filler (UCLA), Bernhard Hube (University of Jena) and Terry Mylonakis (Harvard Medical School) discussing mammalian, *in vitro* and non-vertebrate models. This was then followed by a welcome reception that was a chance to catch up with old friends and colleagues.

The scientific content of the conference consisted of 60 talks, separated into 10 sessions concentrating on different aspects of *Candida* biology: genetics & differentiation, evolution & epidemiology, diagnosis & treatment, host-pathogen interactions, cell surface, biofilms & communities, signalling & responses. There was an additional clinical session and, one evening; three parallel focus sessions discussed antifungal drug development, making the most of fungal genome sequences and cool tools for *Candida* molecular and cell biology.

It would be impossible to mention all of the excellent talks that were presented at this conference in this short review, but I will attempt to mention many that were highlights for me.

Lois Hoyer (University of Illinois) discussed the possibility that wild animals could be a reservoir of *Candida albicans* in central Illinois. However, from multi-locus sequence typing (MLST) of strains it was clearly shown that animals carried different strain types than humans from the same geographical region. Domesticated animals, which live in closer contact with humans, had very low carriage levels of *C. albicans*, but did carry similar strain types as the people in the area. The conclusion reached was that humans are the reservoir of *C. albicans* strains associated with humans, but can pass them to pets.

There were also a number of talks that discussed the interactions of *C. albicans* with other species in biofilms. Brian Peters (University of Maryland) added to our knowledge of *C. albicans* inter-species interactions with his presentation on *C. albicans*-*Staphylococcus aureus* interactions. Using proteomic and Western approaches, this group were able to carry out differential gel electrophoresis of biofilms containing either *C. albicans* alone, *S. aureus* alone, or both species in co-culture. It became obvious from the results of this study that the two species not only co-exist within the biofilm, but actually influence each other.

Phenotypic switching in *C. albicans* remains a popular research area. Kevin Alby (Brown University) discussed the effect that manipulation of cycling expression, hence progression through the cell cycle, had on phenotypic switching rates between white and opaque cells. The switching frequency increased with slightly slower growth, but very slow growth did not alter the frequency. It was hypothesized that the differences in switching were due to alterations in synthesis and accumulation of Wor1p, which would be investigated further.

Neocentromeres and their formation was the subject of the presentation by Carrie Ketel (University of Minnesota). *C. albicans* has been shown to have regional centromeres, which are defined by associated proteins. However, deletion of centromeric DNA, and its replacement with the *URA3* gene, did not decrease stability of the chromosome. This was found to be due to formation of a neocentromere. It was interesting to note that the *URA3* gene was silenced in some of the strains obtained. These Ura3⁻ strains had formed neocentromeres on the *URA3* DNA, whereas non-silenced strains usually had neocentromeres formed adjacent to the *URA3* gene.

Putative methods of host immune system evasion were mentioned in presentations by Manuel Santos (University of Aveiro) and Melanie Wellington (University of Rochester). Manuel Santos revealed how the CTG reassignment could theoretically lead to massive proteome diversity. The CTG codon has been found to be loaded with leucine ~3 % of the time; generating different proteins from the same gene. The rate of leucine incorporation increased up to 5% under stress, and it was suggested that this may allow host immune avoidance through antigenic variation.

Candida suppression of reactive oxygen species (ROS) was presented by Melanie Wellington. Of the different *Candida* species tested, *C. albicans* was the best suppressor of ROS, with *C. krusei* also quite effective. However, neither *C. glabrata* nor *C. tropicalis* were effective suppressors of ROS production. Whole live cells were required for the most effective suppression, but phagocytosis was not required. This was suggested to be another strategy to evade host immune defences.

A number of talks concentrated on diagnosis, treatment and vaccination against *Candida* infections. Cornelius Clancy (University of Pittsburgh) and Concha Gil (University of Madrid) discussed the use of antibodies against *Candida* proteins as markers of invasive candidiasis. Both groups had taken similar approaches, identifying the *Candida* antigens that patients reacted to. Cornelius Clancy's group found that responses occurred to 15 antigens. However, further analyses revealed that antibodies responses against only four of the antigens (Set1p, Eno1p, Muc1p and Pgl1p) were equally good predictors of systemic disease. The work of Concha Gil's group suggested that a greater number of proteins were targets of the immune response, with anti-Bgl2p and anti-Pgl1p levels predictors of invasive disease. High levels of anti-Eno1p were shown to be a good predictor of recovery from invasive disease. Concha Gil also introduced the concept of the Surfome, the outermost proteins on the cell surface.

In the area of vaccination, Hong Xin (Louisiana State University) discussed the use to glycopeptide vaccines against *C. albicans*. N-terminal peptides (14 aa) from 6 different *C. albicans* proteins were linked to β -1,2-trimannose to produce glycopeptides. These glycopeptides were loaded onto dendritic cells and used to immunize mice. Although all peptides gave similar antibody levels, only three provided good protection and one resulted in more rapid death of the mice. Further work will be carried out in this area.

One of the newest therapies to be discussed at the meeting was the development of antifungal β -peptides, presented by Amy Karlsson (University of Wisconsin). These peptides contain β -amino acids, rather than α -amino acids, and are more stable molecules in biological environments.

The *C. albicans* ALS gene family remained a hot topic, with two speakers presenting on the roles of ALS3 during growth and infection. Yue Fu (UCLA) examined the contribution of ALS3 to virulence in systemic disease by expressing the gene in *C. glabrata*. Whilst the *C. albicans als3* null mutant showed no difference in virulence, expression of the gene in *C. glabrata* increased adherence and endocytosis by endothelial cells. However, in *C. glabrata* virulence tests there was no difference in organ burdens at early times, with differences only seen at day 14 post-infection.

Ricardo Almeida (University of Jena) examined the role of *C. albicans* ALS3 in the acquisition of iron in the form of ferritin. Expression of *Ca ALS3* in *Saccharomyces cerevisiae* allowed ferritin binding, which did not occur with expression of either ALS1 or ALS5. This was suggested to be a source of iron for *Candida in vivo*.

Although the majority of talks focussed on *Candida albicans*, there was a marked increase in talks and posters focussing on other *Candida* species, especially *Candida glabrata* and *Candida dubliniensis*. Both Thomas Edlind (Drexel University) and Kyoko Niimi (University of Otago) discussed drug resistance in *C. glabrata*, concentrating on echinocandins. However, the hot topics for *C. glabrata* were silencing of gene expression and adhesin genes. Eefje Kraneveld (University of Amsterdam) had analyzed the *C. glabrata* genome, identifying 67 putative adhesins that were divided into seven families. A large proportion of the adhesion genes were found in sub-telomeric regions, and expression of genes was found to be both growth phase and strain dependent. Alejandro de las Penas (Mexico) followed on by discussing silencing and the *Epa1* gene, and Estelle Mogensen (Institute Pasteur) discussed chromatin remodelling and silencing. In the Cool Tools session Mike Snyder (Yale University) gave us a taste of things to come with his presentation on protein microarrays. Although not yet available for *C. albicans*, these have been used for a variety of different assays in other systems. Martine Raymond (University of Montreal) then went on to describe how ChIP-chip technology had been used for transcription factor gene discovery in *Candida albicans*, identifying ~ 250 transcription factors.

Representatives of both CandidaDB (<http://genodb.pasteur.fr/CandidaDB>) and CGD (<http://www.candidagenome.org>) spoke in the session “making the most of fungal genome sequences”. Both databases were demonstrated to show how they could be utilised and updates/improvements were highlighted. The *Candida* community were also requested to provide feedback and support for the CGD website, with details of how this could be done found on their website.

The final evening of the conference was filled with the conference dinner, and dancing until late. I know that I am looking forward to the next ASM *Candida* and candidiasis conference to see how advances in technologies and approaches will have broadened our knowledge and understanding of *Candida* species biology and diseases caused by them.

Donna MacCallum

Aberdeen Fungal Group, School of Medical Sciences,
University of Aberdeen, Foresterhill,
Aberdeen, AB25 2ZD Great Britain
d.m.maccallum@abdn.ac.uk