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Introduction to the special issue of the Revista Iberoamericana de Micología devoted to Fungal Genomes

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Since the first genome sequence for a free-living organism, *Haemophilus influenzae*, was published in 1995 [6], 36 fungal sequencing projects have been started. At present, nine have been completed, 22 are at Whole Genome Shotgun assembly and five are in progress [1]. The complete sequencing of the genome of the baker's yeast, *Saccharomyces cerevisiae*, the first fungal genome sequenced [5], is considered a landmark in Genomics [3] and the deciphering of the fungal genome represents a unique opportunity to enhance the knowledge we have on those organisms as well as opens the door to benefits that were prophesied to include "magic bullet" therapeutics, individualized medicine, and the prediction of disease long before symptoms surface. However, these breakthroughs are not straightforward and we must realize that we must fashion the four-letter code we all share into tools physicians can use, and ensure that these tools are readily available [2].

In this issue of the Revista Iberoamericana de Micología devoted to Fungal Genomes there are a number of papers in which scientists involved in sequencing projects review the impact of the knowledge of the genome of each fungus has or will have on a variety of basic and applied aspects.

The impact of a completed fungal genome sequence on the development of novel therapeutics for human disease may occur in three areas: improved understanding of disease causation at the molecular level, improved diagnosis and disease classification based on genetic profiles, and new therapeutics based on targets identified in the genome. These improvements will require increased physician understanding of genetic principles applied to common diseases.

The current increase in the number of microbes resistant to antibacterial or antifungal agents represents a potential crisis in human and veterinary medicine. Some believe that we are entering a post-antibiotic era where most antibiotics no longer will be efficacious [4]. Therefore, it is important that new antibiotics be developed. However, because of the potential for cross-resistance, new targets for the discovery of antibiotics are needed particularly where resistance does not currently exist. The results obtained from the sequencing of genomes from pathogenic fungal microbes provide an opportunity to ameliorate this problem. Genomic sequence data can be used to identify new genes that could be used as targets for new antifungal discoveries. Viable new target genes might represent those that are widely distributed among fungal pathogens or that have homologs and are essential for the viability of the organism. Novel, non-traditional targets also will be found through the analysis of genome sequences: those that are involved in disease pathogenesis and those that are involved in adaptation and growth in infection sites. The advantage of the non-classical targets is that targeting these sites may not result in the same degree of selective pressure that encourages resistance, and these could have a longer therapeutic life time. The usefulness of the comparative analyses of fungal genomes and molecular research on the discovery of fungal genes associated with putative targets for novel antifungal agents is reviewed in one of the papers of this issue.

The fungal research community has enthusiastically embraced the utilization of genomics technologies to resolve long-standing issues in fungal biology. For example, such technologies have been proposed to study the mechanics of tip growth, photoreception, gene silencing, the molecular basis of conidiation, the pathway leading to sexual reproduction, and mechanisms of pathogenesis [7]. The resulting databases will allow the comprehensive analysis of developmental processes that are characteristic of fungi, including the molecular nature of pathogenicity. DNA databases underpin analyses of the fungal transcriptome, proteome, and metabolome. This combined information will contribute to our basic understanding of not only the mechanics of infection but also the evolution of pathogenicity. The application of genomic approaches such as comparative genomics to identify sequences that contribute to infection and disease and functional genomics and proteomics to analyze global patterns of gene and protein expression involved in fungal pathogenesis and diagnosis are reviewed in one of the papers of this issue.

As stated in the paper “The making of The Genoma Music” by Aurora Sánchez Sousa and co-workers, musical sequences are ordered structures composed of combinations of a small number of musical notes in a way similar to that presented by nucleotides in genetic sequences. This parallelism has inspired these scientists to convert DNA sequences into musical sequences and the musical equivalent of the sequence of a number of genes, either of fungal origin, such as *Candida albicans* or *Sacharomyces cerevisiae* (*SLT2*), or belonging to the human genome (genes involved in Alzheimer syndrome, blindness, deafness such as *Connexine 26* gene) has been obtained and are presented in the accompanying CD.

The Fungal genomes issue of Revista Iberoamericana de Micología is a rich summary of some of the new avenues that are being opened in Mycology. We have shown some of them in this collection of papers and hope to stimulate more. We are pleased to acknowledge the financial support of Pfizer España in producing this issue. As always, the Revista Iberoamericana de Micología carries sole responsibility for all editorial content and peer review.

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