Editorial

Current Fungal Genomics

Fungi are important to biotechnology including medicine, agriculture and industry fields. Over 100 fungi genome have been sequenced or are being sequenced between 2013/2015 including human and plant pathogens as well as fungi that serve as basic models for molecular and cellular biology. The fungal community working in genomic area is increasing dramatically recently. The obtained data is enabling to understand fungal biology and evolution underlying to fungal impact on different areas. In this way, update the knowledge in the field of fungal genomics in this special issue will have high impact for the general audience of Current Genomics.

This issue covers several areas of Fungal genetics analysis and gene function, particularly, functional genomics and deep sequencing, molecular evolution, developmental biology and system modeling.

The past decades have been marked by a remarkable progress in the genetic engineering of fungi for biotechnology applications as well as high-throughput techniques to gain deep understanding of the life style of these organisms, starting thus the Systems Biology era of fungi. The article by *Gerardo Ruiz Amores* and colleagues review and makes a panorama about new directions to drive future research directed to the construction of high-performance, engineered fungal strains working as microbial cell factories. The review describes relevant topics for those with interest on engineering of fungi for biotechnological applications, as well as construction of synthetic promoters and circuits in industrial strains. It should become a reference manuscript for new comers on the field, in special for those interested on engineered fungal strains.

Dermatophytes are a group of keratinophilic fungi responsible for superficial mycoses in humans and animals. The mechanism of how this group of fungi pathogenesis is established is very little is known. The molecular mechanisms of heat shock proteins in Dermatophytes and the ability of dermatophytes to establish infection and persist in the host are reviewed by Nilce M. Martinez-Rossi and colleagues. This review is combined with research data and focused in gene expression regulation in the *Dermatophytes: Current Advances and Perspectives*. The review reports recent advances in understanding the relationship between structural and functions of the HSPs in dermatophytes, including an evaluation of the broad range of highly conserved HSPs that can be identified in the genomes of different species of dermatophytes. In this study, the authors propose interesting model for the regulation of heat shock protein genes (hsp) in dermatophytes under the action of transcriptional regulators Hsf1, Nuc-1, and PacC. The work adds new knowledge to our understanding of the complexity of fungal metabolism.

Paracoccidioidomycosis is the most prevalent systemic mycosis in Latin America. The article by Fausto Almeida and colleagues is a research article about gene expression modulation in the pathogenic fungus *Paracoccidioides brasiliensis* during cell wall remodeling yeast cells. The article describes the influence of N-glycosylation on the expression of genes involved in cell wall synthesis and degradation during paracoccidioidomycosis. Cell wall remodeling is an important factor for the transition from mycelia to yeast. Interferences in this process might bring new possibilities of therapy strategies. The study presented interesting results to the field.

The article by Amanda Cristina Campos Antoniêto and colleagues describes the role of CRE1 transcription factor in response to sophorose during carbon catabolite repression in the industrial fungus *Trichoderma reesei*. The results are from high throughput RNA seq analysis and bring some interesting insights about gene regulation in *T. reesei*. The article will contribute to the field of biomass degradation was well in the production of enzymes with biotechnology applications.

The article by Mohammed Aiyaz and colleagues is a research article and describes the molecular characterization of *Fusarium* isolated from maize seed samples collected from different agro-climatic regions of India. Genetic diversity among the *Fusarium* isolates based on geographic origin or fumonisin production were also related. The manuscript also used the CD-ELISA method to confirm fumonisin production for *Fusarium* isolates. The findings confirm the importance of molecular studies for species delimitation, and for observing genetic and phenotypic diversity, among the *Fusaria* in India. Although, the experiments and samples is restricted to India, the manuscript is very important to the field, since a lot of seed contamination with this fungus around the world and a lot of losses in crop production is commonly observed.

The last article by Thiago M Mello-de-Sousa is also a research article and adds new pieces of knowledge to regulation of cellulases expression in *T. reesei*. The authors performed analysis of chromatin accessibility in the promoters of three genes related to cell wall degradation in *T. reesei*. The study shows the chromatin accessibility status of the *xyl1*, *cbh1*, and *cbh2* promoter under repressing and inducing conditions in a comparative study between Rut-C30 and the wild-type *T. reesei*.

I believe that the collection of reviews and research article authored by experts in the field presented here will provide a new point of view of recent rapid developments in the field of Fungal Genomics.

R.N. Silva

Roberto N. Silva

Guest Editor

Department of Biochemistry and Immunology
Ribeirão Preto Medical School, University of São Paulo 14049-900
Ribeirão Preto, SP
Brazil