

## RESEARCH CONFERENCES

### ESF-EMBO Symposium

### Comparative Genomics of Eukaryotic Microorganisms: Eukaryotic Genome Evolution

Hotel Eden Roc, Sant Feliu de Guixols (Costa Brava) • Spain  
**20-25 October 2007**

#### List of Accepted Posters

	Surname	First Name	Poster Title
1	Abdul Murad	Abdul Munir	Identification and genome survey sequence of a psychrophilic yeast, <i>Leucosporidium antarcticum</i>
2	Abu Bakar	Farah Diba	Development of <i>Colletotrichum gloeosporioides</i> cDNA libraries and generation of ESTs
3	Almeida	João Manuel	Phenotypic evolution, genomes and ecological speciation in <i>Saccharomyces sensu stricto</i>
4	Aminake	Makoah Nigel	Molecular characterisation of the 437 codon of Pfdhps in gametocytes emerging after treatment with Sulfadoxine-Pyrimethamine, Amodiaquine and combination SP/AQ.
5	Amselem	Joelle	Setting up of a fungal genomic annotation platform
6	Beyne	Emmanuelle	Coherency rules aid collaborative genome annotation
7	Bigey	Frédéric	First whole genome sequencing of a commercial wine <i>Saccharomyces cerevisiae</i> strain: the use of comparative genomics to reveal the adaptation to wine fermentation
8	Carreto	Laura	Comparative gene expression profiling of wild type <i>S. cerevisiae</i> strains
9	Coelho	Marco	Identification of MAT genes in the bipolar basidiomycetous yeast <i>Rhodospodium toruloides</i> - comparison with the homologous genomic region of <i>Sporobolomyces roseus</i>
10	Colón-González	Maritrini	The paralogous genes BAT1 and BAT2 encode for two anaplerotic enzymes that play an important role in the adaptation to the facultative metabolism of <i>Saccharomyces cerevisiae</i>
11	Cushion	Melanie	Sequence of the mitochondrial genome of <i>Pneumocystis carinii</i> : Gene mapping and evidence of linearity
12	Di Rienzi	Sara	Comparative analysis of replication origins using the genome organization of pre- and post-whole genome duplication yeast species
13	Dominguez Del Angel	Victoria	The invaded genome of the Dothideomycete <i>Leptosphaeria maculans</i>
14	Dumas	Bernard	A comparative genomic approach to identify molecular determinants of <i>Aphanomyces euteiches</i> pathogenicity
15	Echavarri Erasun	Carlos	The Ergosterol Pathway: Function and Evolution
16	El-Dorri	Hamza	Structure analysis and glucose-dependent expression of computationally identified hexose transporters genes of the filamentous fungus <i>Trichoderma reesei</i>
17	Feuermann	Marc	The Fungal Proteome Annotation in the UniProtKB/Swiss-Prot knowledgebase

18	Fischer	Gilles	Rates of genome rearrangements in the Kluyveromyces related yeast clades
19	Fokkens	Like	Evolution of protein complexes in eukaryotes
20	François	Jean Marie	MAPYEAST, a WEB-based navigation tool for integration and visualization of biological data from the yeast <i>Saccharomyces cerevisiae</i>
21	Gonçalves	Paula	Phenotypic evolution, genomes and ecological speciation in <i>Saccharomyces sensu stricto</i>
22	Hanna	Bishoy	Structure analysis and glucose-dependent expression of computationally identified hexose transporters genes of the filamentous fungus <i>Trichoderma reesei</i>
23	Kachouri-Lafond	Rym	Search and comparative analysis of non-coding RNAs in hemiascomycetous Yeasts
24	Kazi	Julhash	Bioinformatic prediction and analysis of eukaryotic protein kinases in the rat genome
25	Kensche	Philip	Conservation of gene orientation in fungi
26	Kinsky	Slavomir	Comparative analysis of yeast telomeres: Telomere-associated proteins in <i>Yarrowia lipolytica</i>
27	Lebrun	Marc Henri	Fungal secondary metabolism is an essential component of the complex interplay between rice and <i>Magnaporthe</i>
28	Legras	Jean-Luc	How man history has affected <i>Saccharomyces cerevisiae</i> diversity?
29	Martin	Tiphaine	The Génolevures website is designed around comparative genomic studies of hemiascomycetous yeasts
30	Marvin	Marcus Edward	Comparison of genome sequences between populations of <i>Saccharomyces paradoxus</i> helps determine functional variation in yKu and its role in maintaining genome stability
31	Montanini	Barbara	Phylogenetic and functional analysis of the Cation Diffusion Facilitator (CDF) family: improved signature and prediction of substrate specificity
32	Nishimura	Marie	Mstu1, an APSES transcription factor, is related to appressorial turgor generation in <i>Magnaporthe oryzae</i> .
33	Ozier-Kalogeropoulos	Odile	Promiscuous DNA in the Nuclear Genomes of Hemiascomycetous yeasts
34	Palma	Margarida	Comparative genome-based analysis of sugar porters in yeasts
35	Panabieres	Franck	Characterization, evolution and expression of the ubiquitin gene family in the oomycete plant pathogen <i>Phytophthora parasitica</i>
36	Perez-Torrado	Roberto	Comparative analysis of global expression in winemaking conditions among <i>Saccharomyces cerevisiae</i> , <i>S. kudriavzevii</i> and their hybrids.
37	Sacerdot	Christine	Promiscuous DNA in the Nuclear Genomes of Hemiascomycetous yeasts
38	Santamaria	Monica	Testing barcode markers in ascomycota: intron distribution along mitochondrial genes
39	Stam	Hein	Functional genomics of <i>Aspergillus niger</i>
40	Svetec	Ivan-Krešimir	Genetic duplications as a side-effect of gene replacement in yeast
41	Vandepoele	Klaas	Whole genome analysis provides many novel insights into the evolution of chromalveolates