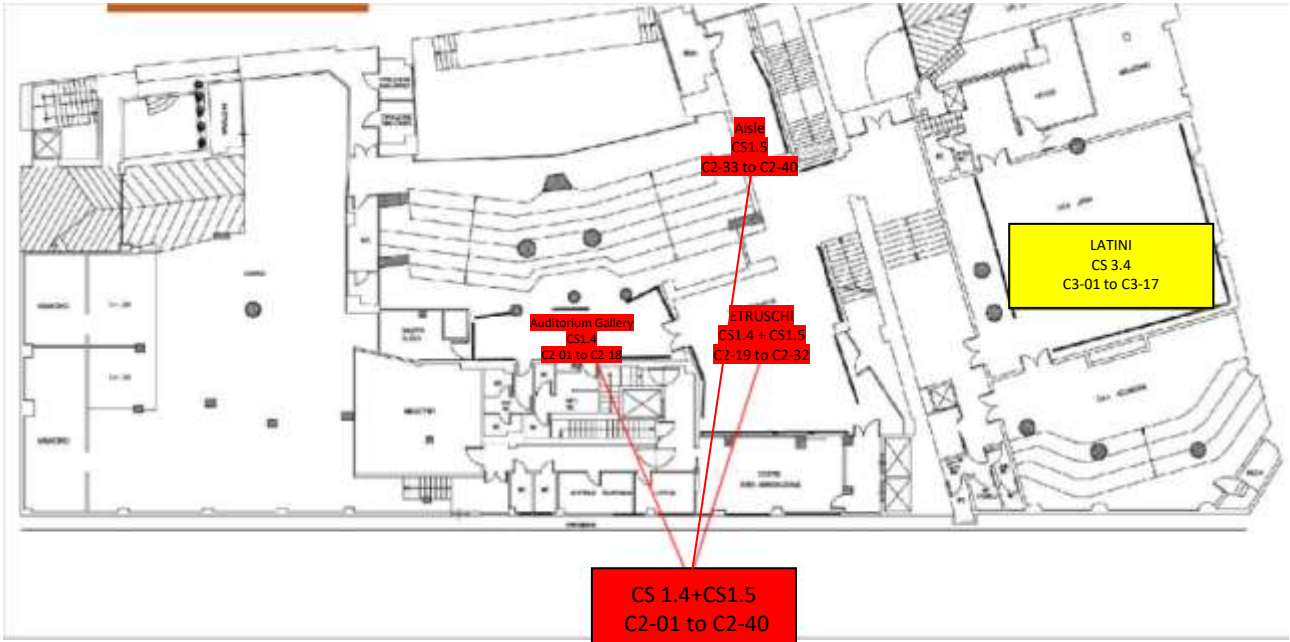
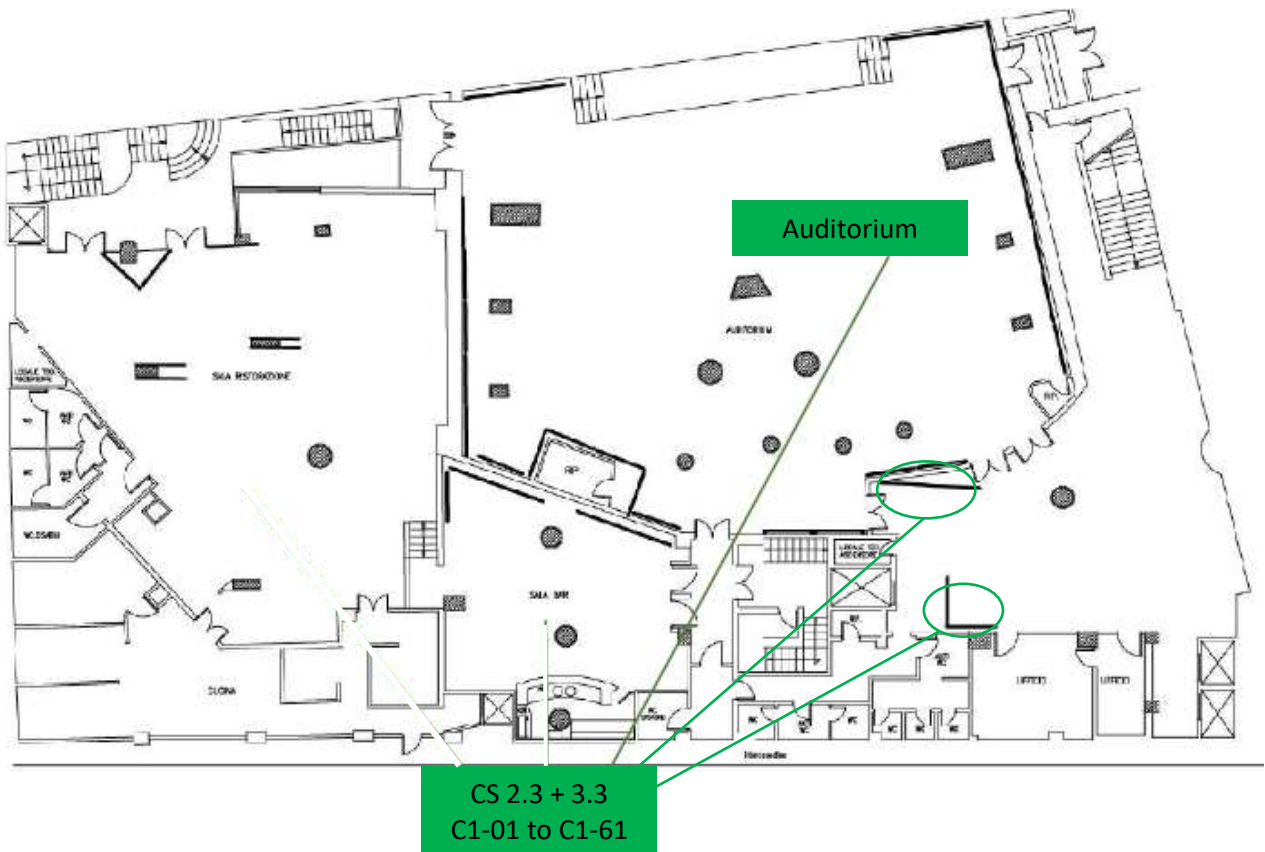


Ground Floor



Floor (-1)



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**Concurrent Session 1.4 Genome, Chromatin, epigenetic**

P. Code	Name	Surname	Title
C2-01	Lucia	Gomez Gil	Structural dynamics of chromosomes and its role in genome plasticity of <i>Fusarium oxysporum</i>
C2-02	Saskia	du Pre	A genetic transformation method for the mycetoma-causing agent <i>Madurella mycetomatis</i>
C2-03	Tünde	Kartali	Detection and molecular characterization of novel dsRNA viruses isolated from different <i>Zygomycete fungi</i>
C2-04	Jovan	Komlusi	Functional dissection of the meiotic drive of female-inherited accessory chromosomes in <i>Zymoseptoria tritici</i>
C2-05	Ting-Fang	Wang	<i>Trichoderma reesei</i> Rad51 can tolerate mismatch sequences to promote interhomolog recombination and chromosome synapsis during hybrid meiosis
C2-06	Lisa	Wise	Identification and characterization of the poly(ADP-ribose) glycohydrolase of <i>Aspergillus nidulans</i>
C2-07	Ramon	Ramos Barrales	Control of virulence by sirtuins in <i>Ustilago maydis</i>
C2-08	Michael	Habig	Temperature and histone modifications affect the mutation rate in the wheat pathogen <i>Zymoseptoria tritici</i>
C2-09	Justine	Colou	Role of Kmt6, a histone methyl transferase, in plant pathogenicity of the necrotrophic fungus <i>Alternaria brassicicola</i>
C2-10	Ying	Huang	<i>Schizosaccharomyces pombe</i> Mti2 and Mti3 function together in mitochondrial translation initiation
C2-11	Pedro	Talhinhas	Flow cytometry as the state of the art tool for fungal nuclear DNA quantification: genome size measurement and nuclear cycle analysis
C2-12	Roland	Martzy	Interaction of a fungal lncRNA with a transactivator enhances cellulase production in <i>Trichoderma reesei</i>
C2-13	Frederick	Witfeld	Genomic analysis and intraspecific diversity of a new heat resistant basidiomycetous fungal species
C2-14	Lauren	Dineen	Functional analysis of the tRNA-ome of <i>Aspergillus fumigatus</i>
C2-15	Shay	Covo	Developmentally-regulated oscillations in the expression of UV repair genes in a soilborne plant pathogen dictate UV repair efficiency and survival
C2-16	Minji	Park	Genomic Analysis of Ketoconazole Resistance in the Dandruff-associated Pathogenic Fungus <i>Malassezia restricta</i>
C2-17	Kap-Hoon	Han	Complete mitochondrial genome sequences of <i>Aspergillus luchuensis</i> , <i>Aspergillus parasiticus</i> and <i>Aspergillus pseudoglaucus</i>
C2-18	Takayuki	Araoz	Ectopic recombination between solo-long terminal repeats triggered pathogenic changes and genome rearrangement in the rice blast fungus
C2-19	Mathu	Malar	The genome of <i>Geosiphon</i> : an arbuscular mycorrhizal fungus that forms symbioses with cyanobacteria
C2-20	Lucía	Ramírez	Mitochondrial dysfunction in <i>Pleurotus ostreatus</i> progeny: a matter of genome conflict.
C2-21	Ioannis	Papaioannou	Genome evolution in the new model yeast species <i>Saccharomycodes ludwigii</i> : trade-off between meiotic recombination and epigenetic inheritance

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THURSDAY, FEBRUARY 20th

Room: Auditorium Gallery + ETRUSCHI + AISLE

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Concurrent Session 1.5 Omics and Bioinformatics

P. Code	Name	Surname	Title
C2-22	Gabriel	Vignolle	Novel method in genome mining and transcriptome analysis reveal undiscovered RiPPs in <i>Trichoderma</i> spp.
C2-23	Diem	Nguyen	Comparative genomics of transposable elements and Repeat-Induced Point (RIP) mutation landscapes in <i>Neurospora</i> species
C2-24	Elodie	Drula	Capturing biochemical information in the CAZy database
C2-25	Lena	Steins	Comparative genomics of smut fungi indicate ability of meiotic division and sexual reproduction in the genus <i>Pseudozyma</i>
C2-26	Mao	Peng	CreA regulation was observed at low free monosaccharide level during <i>Aspergillus niger</i> grown on crude plant biomass
C2-27	Areejit	Samal	A blueprint of the protein secretion machinery in <i>Neurospora crassa</i>
C2-28	Areejit	Samal	Prediction and analysis of the secretome of an opportunistic fungal pathogen
C2-29	Atsushi	Sato	Comparative genomics between an industrially important species, <i>Aspergillus sojae</i> , and harmful one, <i>Aspergillus parasiticus</i>
C2-30	Marie-Noëlle	Rosso	Conserved white rot enzymatic mechanism for wood decay in the <i>Basidiomycota</i> genus <i>Pycnoporus</i> explored by genomics and proteomics
C2-31	Danielle	Weaver	Uncovering long non-coding RNA associated with drug response in <i>Aspergillus fumigatus</i>
C2-32	Arpad	Csernetics	Development of single and multitargeted gene deletion methods in the inky-cap fungus <i>Coprinopsis cinerea</i>
C2-33	Celine	Petersen	In-house long read sequencing yields affordable superb fungal genome assemblies
C2-34	Masahiro	Hayashi	Effects of nitrogen deficiency on lipid synthesis and metabolic profiling of xylose assimilating thraustochytrid
C2-35	Ayako	Matsuda	Xylose adaptation and metabolic profiling of heterotrophic thraustochytrid for microbial production of biofuels
C2-36	Reem	Aboukhaddour	Draft genome assemblies of a global collection of <i>Pyrenophora tritici-repentis</i> , the causal agent of tan spot disease of wheat
C2-37	Marina	Collina	Genome sequence of <i>Stemphylium vesicarium</i> , the causal agent of Brown Spot disease of Pear
C2-38	Ekaterina	Shelest	Application of comparative promoter analysis for understanding of secondary metabolism regulation in non-model fungi
C2-39	Rita Milvia	De Miccolis Angelini	New genomic resources for the brown rot fungal pathogens <i>Monilinia fructicola</i> , <i>Monilinia laxa</i> and <i>Monilinia fructigena</i>
C2-40	Raphaela	Georg	<i>Trichoderma harzianum</i> aluminum tolerance is mediated by a large change in gene expression profile

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Room: **Auditorium**

### Concurrent Session 2.3 Antifungal and fungicides

P. Code	Name	Surname	Title
C1-01	Lina	Qin	Deciphering the antifungal mechanism of HSAF using the model filamentous fungus <i>Neurospora crassa</i>
C1-02	Hagiwara	Daisuke	Characterization of azole resistant <i>Aspergillus fumigatus</i> strains isolated from imported tulip bulbs that were purchased in Japan
C1-03	Saskia	du Pre	The mechanism behind the intrinsic resistance of <i>Madurella mycetomatis</i> to the echinocandins
C1-04	Carmen	Limon	Improvement of a lux-system that detect new antifungals
C1-05	Gayan	Abeyasinghe	Exploring the variety of interactions between Fungi and Bacteria
C1-06	Madison	Covington	Increase of reactive oxygen species contributes to growth inhibition by fluconazole in <i>Cryptococcus neoformans</i>
C1-07	Sayoko	Oiki	Cellular response to farnesol and the role of nitric oxide production in <i>Aspergillus fumigatus</i>
C1-08	Mónica	Gandía	Role of the MAPK signaling pathways and chitin synthases of the phytopathogenic fungus <i>Penicillium digitatum</i> in sensitivity to antifungal proteins.
C1-09	Paloma	Manzanares	Comparison of the production pattern and antifungal activity of three antifungal proteins from the phytopathogenic fungus <i>Penicillium expansum</i>
C1-10	Sabine	Fillinger	Amplicon-deep sequencing using Oxford-Nanopore® technology to quantify multi-drug-resistant strains in <i>Zygozoaria tritici</i> populations
C1-11	Anant	Kakar	Antifungal potential of the Temporin B-derived synthetic peptide TB_KKG6K
C1-12	Dejana	Kosanovic	<i>In vitro</i> study of <i>Agaricus bisporus</i> proteomic response to <i>Trichoderma aggressivum</i> f. <i>europaeum</i> supernatant
C1-13	Irene Maja	Nanni	Sensitivity monitoring of <i>Plasmopara viticola</i> to oxathiapiprolin, a new member of piperidinyl thiazole isoxazoline fungicides
C1-14	Alessandra	Di Francesco	Alternative control system of <i>Pleurotus ostreatus</i> against green mold disease
C1-15	Clay	Wang	Discovery of the biosynthetic pathway for the antifungal hymeglusin in <i>Scopulariopsis candida</i>
C1-16	Hajer	Alshraim	A rapid CRISPR-mediated Tet-Off system reveals the phosphoinositide kinases Stt4 and Mss4 are essential for viability of <i>Aspergillus fumigatus</i>
C1-17	Jian	Zhang	Azaphilones biosynthesis in <i>Trichoderma harzianum</i> benefits fungal survival to oxidative stress
C1-18	Amelia	Barber	Comparative genomics of <i>Aspergillus fumigatus</i> and the influence of agriculture on ecology and azole resistance
C1-19	Hamama Imène	Lammari	Sensitivity of Algerian <i>Pyrenophora teres</i> population to QoI and SDHI fungicides as revealed by Pyrosequencing
C1-20	Khaled	El-Tarabily	Molecular identification and disease management of stem canker of royal poinciana caused by <i>Neoscytalidium dimidiatum</i> in the United Arab Emirates
C1-21	Antonio	Moretti	Selection, genetic characterization and aflatoxin production of <i>Aspergillus flavus</i> strains resistant to SDHI boscalid
C1-22	Jelena	Loncar	Activity of oligosaccharides derived from Trimesan on aflatoxin inhibition in <i>Aspergillus flavus</i>
C1-23	Valeria	Scala	Signals in pathogen and host sensing: free fatty acid and oxylipins

**Concurrent Session 3.3 Applied and Environmental microbiology**

P. Code	Name	Surname	Title
C1-24	Takeshita	Norio	Fungal highway and bacterial toll
C1-25 (on 19th B2-25)	Lea	Atanasova	Functional diversification of cellobiose dehydrogenases uncovers their involvement in multiple nutritional strategies of the mycoparasite <i>Clonostachys rosea</i>
C1-26	Joske	Ruytinx	Functional and evolutionary genetics of zinc tolerance in <i>Suillus luteus</i>
C1-27	Desirré Alexia	Lourenço Petters	Antifungal potential of endophytes from brazilian medicinal plants against the <i>Colletotrichum abscissum</i> and <i>Phyllosticta citricarpa</i>
C1-28	Lee	Inhyung	Development of an improved menopausal symptom-alleviating licorice ( <i>Glycyrrhiza uralensis</i> ) by biotransformation using <i>Monascus albidulus</i>
C1-29	Jiali	Meng	GalR, GalX and AraR co-regulate D-galactose and L-arabinose utilization in <i>Aspergillus nidulans</i>
C1-30	Adiphol	Dilokpimol	Exoproteome and transcriptome of a potential new fungal cell factory, <i>Penicillium subrubescens</i> : Target specific biomass degrading enzyme production
C1-31	Xinxin	Li	Functional validation of Carbohydrate Esterase family 1 subfamily 1 and 2 by characterization of fungal esterases from uncharacterized branches
C1-32	Roland	Kun	Regulation of wheat bran utilization in the industrially relevant filamentous fungus <i>Aspergillus niger</i>
C1-33	Chengshu	Wang	Release and recovery: Twenty years' evolution of a fungal population after releasing exotic strains to control insect pests
C1-34	Takehito	Nakazawa	Comparative genetic and transcriptome analyses of <i>pex1</i> and <i>gat1</i> single-gene mutants between <i>Ceriporiopsis subvermispora</i> and <i>Pleurotus ostreatus</i>
C1-35	Moira	Kelly	Thriving after host extinction: intraspecific variation and isolate-specific metabolic capacities of <i>Batrachochytrium salamandrivorans</i>
C1-36	Sandra	Garrigues	Combinatorial control of transcription factors involved in sugar beet pulp utilization in the industrially relevant fungus <i>Aspergillus niger</i>
C1-37	Tom	van den Brule	A Genome Wide Association Study reveals genomic insights in conidial heat resistance of <i>Paecilomyces variotii</i>
C1-38	Anna	Gorbushina	Stress tolerance in microcolonial black fungi can be studied with new techniques: presenting a genetic toolbox for <i>Knufia petricola</i>
C1-39	Zhong	Yaohua	Deletion of the target extracellular protease genes identified by secretomics for high-level production of cellulolytic enzymes in <i>Trichoderma reesei</i>
C1-40	Honda	Yoichi	CRISPR/Cas9 in mushrooms without integration of ectopic DNA
C1-41	Jillian	Romsdahl	Directed evolution of melanized fungi to investigate mechanisms of adaptation and resistance to ionizing radiation
C1-42	Kristiina	Hildén	The white-rot fungus <i>Obba rivulosa</i> shows expression of a constitutive set of plant cell wall degradation targeted genes during growth on spruce wood
C1-43	Eero	Kiviniemi	Wood decay fungi studied under fermentative and oxygen-stress conditions
C1-44	Keietsu	Abe	Analysis of self-assembly mechanism of hydrophobin RoA of <i>Aspergillus oryzae</i> using Langmuir-Blodgett method
C1-45	Katsuya	Gomi	Expression profiles of amylolytic genes in the black koji-mold <i>Aspergillus luchuensis</i>
C1-46	Agnese	Seminara	Timing of fungal spore release dictates survival during atmospheric transport
C1-47	Daniele	Lagomorsino Oneto	Optimal strategies for fungal spores liberation
C1-48	Fernando	Pérez-Rodríguez	Bacterium endosymbiosis in <i>Ustilago maydis</i> infecting maize plants in nature
C1-49	Catalina	Landeta	The growth of marine fungi in complex substrates produces hydrophobic proteins with the ability to self-assembling
C1-50	Javier	Ribera	Fungal melanin-based electrospun membranes for heavy metal detoxification of water
C1-51	Inês	Diniz	Integrating field surveys and molecular data to assess the phytosanitary status of cashew in Guinea-Bissau (West Africa)
C1-52	Fuga	Yamasaki	Simultaneous gene mutations in both nuclei of dikaryotic strain of <i>Pleurotus ostreatus</i> using CRISPR/Cas9
C1-53	Andrea	Ceci	A genomic and transcriptomic study on genetic data into mycoremediation strategies
C1-54	Giovanna	Varese	Bioremediation of polluted soils - the role of fungi
C1-55	Giovanna	Varese	Draft genome sequences and annotation of <i>Trichoderma lixii</i> and <i>Trichoderma capillare</i> isolated from PAH-contaminated soil and industrial wastewaters
C1-56	Antonio	Pisabarro	Multi-omics analysis of wood-dependent induction of lignocellulolytic enzyme secretion in cultures of the white-rot basidiomycete <i>Pleurotus ostreatus</i>

C1-57	Jiang	Siqi	Ecophysiology and applied biodiversity of phyllosphere fungi in tropical and subtropical forests
C1-58	Domenico	Davolos	<i>In silico identification of the oosporein gene cluster in the genome of Victoriomyces antarcticus</i>
C1-59	Banu	Metin	Diversity of <i>Penicillium roqueforti</i> isolates from Turkish mold-ripened cheeses
C1-60	Khaled	El-Tarabily	Biological control of stem canker of royal poinciana caused by <i>Neoscytalidium dimidiatum</i> using endophytic actinobacteria able of producing ACC deamina
C1-61	Veronica	Spinelli	Boosting plant growth: fungal metabolites as biostimulants for growth promotion of <i>Hypericum perforatum</i> (L.)

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**Concurrent Session 3.4 Synthetic biology and Biotechnology**

P. Code	Name	Surname	Title
C3-01	Sandriale	Noriler	Investigation of secondary Metabolite Biosynthetic Pathways in Endophytic Fungi Through Genomic Analysis
C3-02	Olga	Mosunova	Exploring fungal genomes for novel natural products
C3-03	Sandra	Garrigues	CRISPR/Cas9 technology enables the development of the filamentous ascomycete fungus <i>Penicillium subrubescens</i> as a new industrial enzyme producer
C3-04	Wouter	de Bonte	Fungal host strains for the industrial enzyme or protein production
C3-05	David	Peris Navarro	Combining and improving phenotypic traits through the generation of synthetic two- and six-species yeast hybrids
C3-06	Tiziano	Benocci	Deletion of the regulatory gene <i>ara1</i> or metabolic gene <i>xki1</i> in <i>Trichoderma reesei</i> leads to increased CAZyme gene expression on crude plant biomass
C3-07	Joanna	Kowalczyk	Expanding the molecular toolbox for the white-rot fungus <i>Dichomitus squalens</i>
C3-08	Jose F.	Marcos	FungalBraid: A GoldenBraid-based modular cloning platform for fungal synthetic biology
C3-09	Luis	Larrondo	Coupling cell communication and optogenetics: Implementation of a synthetic light-inducible intercellular system in yeast
C3-10	Benedikt	Siebecker	Characterization of gene regulatory networks of <i>Thermothelomyces thermophilus</i> to improve protein production
C3-11	Gregory	Bulmer	Imidazolium-labelled glycosides for the characterisation of enzymatic function during plant biomass degradation
C3-12 (on 19th B2-26)	Jolanda	van Munster	Surface analysis tools identify how <i>Aspergillus niger</i> and its enzymes modify lignocellulose
C3-13	Tabea	Schuetze	Practical guidance for the implementation of the CRISPR genome editing tool in filamentous fungi
C3-14	Zhihua	Zhou	A putative methyltransferase TrMET involved in cellulase induction in <i>Trichoderma reesei</i>
C3-15	Andika	Sidar	Newly designed modular carbohydrate-active enzyme to increase the efficiency of lignocellulose degradation
C3-16	Domenico	Davolos	Draft genome and annotation of <i>Aspergillus affinis</i> (Circumdati): first insights into a biotech perspective
C3-17	Cesar	Terrasan	Biological importance of lytic polysaccharide monoxygenases and cellobiose dehydrogenase in <i>Aspergillus nidulans</i>

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**THURSDAY, FEBRUARY 20th**  
Room: **LATINI**  
h: 18:00

<b>Speaker and Affiliation</b>	<b>Title of the flash talk (5 minutes)</b>
<b>Ting-Fang Wang</b> - Academia Sinica Institute of Molecular Biology	Complete genome sequences reveals novel insights into chromosomal organization and evolution of different <i>Trichoderma</i> species
<b>Pedro Talhinhas</b> - Instituto Superior de Agronomia LEAF	Flow cytometry as the state of the art tool for fungal nuclear DNA quantification: genome size measurement and nuclear cycle analysis
<b>Michael Habig</b> , Christian-Albrechts-Universität zu Kiel and Max Planck Institute for Evolutionary	Temperature and histone modifications affect the mutation rate in the wheat pathogen <i>Zygomycetozoria tritici</i>
<b>Atsushi Sato</b> - Kikkoman Corporation Research & Development	Comparative genomics between an industrially important species, <i>Aspergillus sojae</i> , and harmful one, <i>Aspergillus parasiticus</i>
<b>Danielle Weaver</b> - University of Manchester Faculty of Biology, Medicine & Health	Uncovering long non-coding RNA associated with drug response in <i>Aspergillus fumigatus</i>
<b>Celine Petersen</b> - Aalborg University Biotechnology	In-house long-read sequencing yields affordable superb fungal genome assemblies
<b>Clay Wang</b> - University of California-USA	Discovery of the biosynthetic pathway for the antifungal hymeglusin in <i>Scopulariopsis candida</i>
<b>Hajer Alshraim Alshammri</b> - University of Manchester - UK	A rapid CRISPR-mediated Tet-Off system reveals the phosphoinositide kinases Stt4 and Mss4 are essential for viability of <i>Aspergillus fumigatus</i>
<b>Amelia Barber</b> - University of Halle-Germany	Comparative genomics of <i>Aspergillus fumigatus</i> and the influence of agriculture on ecology and azole resistance
<b>Norio Takeshita</b> - Japan, University of Tsukuba Microbiology Research Center for Sustainability (MiCS) Tsukuba	Fungal highway and bacterial toll
<b>Keietsu Abe</b> - Japan, Graduate School of Agricultural Science, Tohoku University	Analysis of self-assembly mechanism of hydrophobin RoIA of <i>Aspergillus oryzae</i> using Langmuir-Blodgett method



<b>Adiphol Dilokpimol</b> - Netherlands, Westerdijk Fungal Biodiversity Institute Fungal Physiology Utrecht	Exoproteome and transcriptome of a new fungal cell factory, <i>Penicillium subrubescens</i> , reveal target specific plant biomass degrading enzyme production
<b>David Peris</b> - University of Oslo Biosciences	Combining and improving phenotypic traits through the generation of synthetic two- and six-species yeast hybrids
<b>Tiziano Benocci</b> -AIT	Deletion of the regulatory gene <i>ara1</i> or metabolic gene <i>xki1</i> in <i>Trichoderma reesei</i> leads to increased CAZyme gene expression on crude plant biomass
<b>Olga Mosunova</b> - Westerdijk Fungal Biodiversity Institute	Exploration of fungal genomes awakens a novel biosynthetic pathway

