

ISHAM WORKING GROUP

APPLICATION FORM

1	Name(s) of coordinator(s), including title, proposing the working group Arun Balajee PhD Chief, Molecular Epidemiology Unit Mycotic Diseases Branch Centers for Disease Control and Prevention.
2	Coordinator(s) full contact information, including voice/fax numbers 1600 Clifton Rd, Mailstop G-11 Atlanta GA 30333. Tel 404 639 3337 Fax 404 639 3546 Email: fir3@cdc.gov
3	Names and contact information of working group members

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No.	Participant	Email id
1	Arun Balajee, Mycotic Diseases Branch, CDC, Atlanta, GA – 30333.	fir3@cdc.gov
2	Alejandro Rooney United States Department of Agriculture	Alejandro.Rooney@ARS.USDA.GOV
3	Juan Luis Rodriguez Tudela Mycology Reference Laboratory Majadahonda. Spain	jlrtudela@isciii.es
4	Dr. Gerhard Haase, Institute of Medical Microbiology, University Hospital RWTH Aachen, Pauwelsstr. 30, 52074 Aachen, Germany	ghaase@ukaachen.de
5	Wieland Meyer, Head Molecular Mycology Research Laboratory Centre for Infectious Diseases and Microbiology Westmead Hospital Westmead, NSW 2145, Australia	w.meyer@usyd.edu.au
6	José F. Cano Mycology Unit Medical School 43201 Reus, Spain	josep.cano@urv.cat
7	Cathy Petti, Assistant Professor of Medicine and Pathology University of Utah School of Medicine Medical Director - Infectious Diseases Laboratory, ARUP Laboratories	cathy.petti@aruplab.com
8	Kerry O'Donnell United States Department of Agriculture	Kerry.ODonnell@ARS.USDA.GOV
9	Deanna Sutton Fungus Testing Laboratory Department of Pathology The University of Texas Health Science Center	SUTTOND@UTHSCSA.EDU
10	Aristea Velegraki Asst. Professor, Mycology Vice President International Society for Human and Animal Mycology (ISHAM) University of Athens, Greece.	aveleg@med.uoa.gr
11	Eric Dannaoui Unité de Mycologie Moléculaire, Institut Pasteur, Paris France	dannaoui@pasteur.fr
12	Todd DeSantis, Lawrence Berkeley National Laboratories, U.S. Department of Energy, CA	TDeSantis@lbl.gov
13	M. Ruhnke, Charité Universitätsmedizin Campus Charité Mitte Berlin, Germany	markus.ruhnke@charite.de
14	C. Kibbler, Royal Free Hospital, UK	Christopher.Kibbler@royalfree.nhs.uk
15	Josep Guarro, Professor of Microbiology Mycology Unit, Medical School Rovira i Virgili University, Spain	josep.guarro@urv.cat
16	Manuel Cuenca-Estrella Deputy Director of the Spanish Reference Lab for Mycology	mcuenca-estrella@isciii.es
17	Juergen Loeffler Medizinische Klinik Abteilung II, University of Tuebingen, Otfried-Mueller-Strasse 10, 72076 Tuebingen, Germany. juergen.loeffler@med.uni-tuebingen.de	Loeffler_J@medizin.uni- wuerzburg.de
18	Mary G. Brandt	mbh4@cdc.gov

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4	Please provide a brief description (500-1000 words) of the working group, including its objectives and expected outcomes, with a timeline as to when the outcomes will be met
	<p>Molecular methods for species identification have catapulted fungal species identification into an era where identification formats are more rapid and objective and not subject to interobserver variations. At the same time, clinical microbiology laboratories outside of the research arena are being inundated with availability of a multitude of different genes, numerous commercial and publicly available databases, multiple tools and procedures for species identification. To further the concept of a consensus fungal sequence based identification scheme, a consortium of international excerpts was created. This forum was formed to:</p> <ol style="list-style-type: none">1. Understand the clinical significance of the various species within the species complexes in the genera <i>Aspergillus</i>, <i>Fusarium</i> and for the several genera of <i>Zygomycetes</i> in the Order <i>Mucorales</i>.2. Share research data on multi locus sequence analyses/phylogenetic species recognition pertaining to the above genera.3. Evaluate validity of a single “universal” gene sequence typing strategy for species identification in a clinical laboratory – eg. ITS sequencing to delineate <i>Aspergillus</i> based on data available.4. Explore the possibility of proposing cut-off criteria for species identification using percent identity scores using the above loci5. Explore the use of protein coding locus/ loci (2 or 3) specifically for identification within the species complex –eg. elongation factor for <i>Fusarium</i>6. Understand the utility of molecular phylogenetics to identify/recognize species in a clinical lab setting. Availability / design of such a tool to a clinical microbiology.7. Provide guidelines to compare sequences in public databases for identification and to understand the rationale for maintaining QC strains for id purposes8. Outline “Standard Operating Procedures (SOP)” for implementing such comparative sequencing strategies in routine clinical microbiology laboratories: The SOP document will specify gene regions, primer sets, PCR and cycle sequencing conditions, software necessary to implement such a strategy. Recommend a flow sheet/algorithm that can be used for species identification. <p>Consider potential multicenter studies that will further knowledge in this field.</p>
5	Expected duration of the working group’s operations: 3- 5 years
6	If you are applying for ISHAM funds, could you please provide the names and contact information of professional societies, commercial vendors, private foundations, governmental organizations, etc., from which you have also requested funding for your working groups. N/A

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7 If requesting financial support from ISHAM, please provide a preliminary budget including the initial sum requested and justification for each of the items listed

N/A

8 If ISHAM does provide funding, to whom should the support be directed, e.g., coordinators' internal funds management organization – NOTE – Funds will NOT be transferred to any individual.

N/A

9 Signature of the coordinator(s) – NOTE – electronic signatures are acceptable and only one of the coordinators needs to sign the document:

Date: 08/01/08

S. Arunmozhi Balajee