

The role of molecular diagnostics in fungal infections

Lena Klingspor Karolinska Institutet Department of Laboratory Medicine Division of Clinical Microbiology Karolinska University Hospital Stockholm, Sweden

Fungal infections

Pose a diagnostic and therapeutic challenge

Invasive fungal infections (IFI)

- An overall rise in mortality due to IFI
- The absence of reliable diagnostic markers for early identification of IFI

Molecular methods in Clinical Mycology

- Polymerase chain reaction-based techniques and other molecular methods have been proven, in several cases, to be fast, cheap and reliable.
- May provide faster and more sensitive diagnostics
- Can detect fungi which grew slowly (such as dermatophytes)
- Can detect fungi which cannot be cultured (such as Aspergillus in blood)
- Can be automatised!
- PCR offer the potential for improved outcome in patients with IFI such as Aspergillus

Demands of molecular diagnostics in the clinical routine laboratory

- •Easy to use, rapid, automised
- •High sensitivity and specificity
- •Low costs
- •Friendly to the enviroment
- •Faster and/or more sensitive and/or
 - cheaper than conventional tests

The types of clinical specimens most commonly used for molecular diagnostic testing in patients at high risk of IFI include

- serum
- plasma
- whole blood
- bronchoalveolar lavage
- fresh or paraffin-embedded tissue from affected sites
- Other body fluids (such as CSF, pericard fluid, vitreous)

Molecular diagnostics

A range of different DNA extraction protocols and PCR assays:

- Conventional PCR
- Nested PCR
- Nested real-time PCR (LC)
- Real time PCR (TaqMan)
- Real time PCR (LC)

Gene targeted	Specimen	Extraction	Methodology	Micro- organism detected	Number of patients (samples)	Type of patient	Sensitivity/ Specificity/ PPV/NPV (%)	Detection limit	Ref
Cytochr ome b (mtDNA)	Blood, BAL, sputum	Chemical	Real-time PCR (LC)	A. fumigatus, A. clavatus	333 (1012)	HM, HSCT	100/92.6/76.5100 (BAL); 91.7/81.3/49.3/ 98 (Blood)	10 fg	Buchheidt et al. 2004
28S rDNA	Blood	Chemical + Mechanical disruption	Nested real-time PCR (LC)	A. fumigatus, A. flavus, A. nidulans, A.niger	203 (401)	HM, HSCT, Other	92.3/94.6/60/99.3	5 CFU.ml-1	White et al. 2006
18S rDNA	Plasma	Chemical	Real-time PCR (LC)	Aspergillus spp	96 (1251)	HM, HSCT	55/93/40/96	40 copies.ml-1	Kawazu et al. 2004
18S rDNA	Blood, Biopsies, BAL, CSF, sputum, others	Chemical + Mechanical disruption	Real-time PCR (LC)	A. fumigatus, A. flavus, A. nidulans, A. niger, A. terreus	379 (1650)	HSCT, SOT, cancer	ns	2 CFU.ml-1	Klingspor et al. 2006
18S rDNA and mtDNA	Biopsies	Freeze- thaw + Chemical	Nested PCR, Gel electrophoresis	A. fumigatus	21 (ns)	HM, AIDS	n/s	ns	Rickerts et al. 2006

Table 1. Clinical and technical details of studies evaluating the performances of PCR in the diagnosis of IA.

HM, Haematological malignancies; SOT, Solid Organ Transplant; HSCT = haematopoietic stem cell transplant, CSF, Cerebrospinal fluid; BAL, Bronchoalveolar lavage; LC, lightCycler; CFU, colony forming unit; ns, not specified.

Gene targeted	Specimen	Extraction	Methodology	Micro- organism detected	Number of patients (samples)	Type of patient	Sensitivity/ Specificity/ PPV/NPV (%)	Detection limit	Ref
ITS	Biopsies	Chemical	PCR, Gel electrophoresis	Panfungal	62 (75)	Proven IA	ns	ns	Lau et al. 2007
ITS	Blood, BAL, biopsies, CSF, others	Chemical	Real-time PCR (LC)	A. fumigatus, A. flavus, A. nidulans, A. niger, A. terreus	31 (31)	Various malignancies	ns	5-10 CFU/ml (blood), 50 CFU/ml (CSF)	Schaberei ter et al. 2007
Cytochr ome b (mtDNA)	CSF	Chemical	Real-time PCR (LC)	A. fumigatus,	6 (35)	НМ	ns	15 CFU/mI	Hummel et al. 2006
18S rDNA	Blood, biopsies, BAL	Chemical + Mechanical disruption	PCR-ELISA	A. fumigatus, A. flavus, A. nidulans, A. terreus	36 (241)	HM, SOT	41.6/66.6/71.4/ 36.6 (blood), 87.5/58.3/80.7/ 70 (BAL/biopsies)	ns	Lass- Floerl et al. 2004
Alkaline Proteas e and mtDNA	BAL	Chemical	PCR, Southern blot	A. fumigatus, A. terreus, A. flavus, A. niger	249 (ns)	Cancer	80/93/38/99	ns	Raad et al. 2002

Table 1. Clinical and technical details of studies evaluating the performances of PCR in the diagnosis of IA.

HM, Haematological malignancies; SOT, Solid Organ Transplant; CSF, Cerebrospinal fluid; BAL, Bronchoalveolar lavage; LC, lightCycler; CFU, colony forming unit; n/a, ns, not specified.

PCR methods in Clinical Mycology

The implementation of this technique, has been hampered by

- a lack of standardisation of molecular targets, specimens, extraction protocols, and PCR platforms
- and is therefore urgent that a consensus is reach on the type of specimen, molecular target and technique to be used

The choice of specimen has a great influence on the extraction methodology

Easy to obtain: Serum and blood Which blood fraction is best to test?

- Serum/plasma : Circulating DNA?
- Blood : yeast cells, hyphael elements, circulating DNA?
- EDTA- blood (Avoid citrate and heparin)

More difficult to obtain and to repeat

- BAL
- CSF
- Pleura
- Biopsi material

PCR recommendations

The current status of the technical and clinical validation of PCR for *Candida* and *Aspergillus* in blood and other fluids does not allow for a recommendation for clinical use.



White PL, Bretagne S, Klingspor L, Melchers WJ, McCulloch E, Schulz B, Finnstrom N, Mengoli C, Barnes RA, Donnelly JP; Juergen Loeffler on behalf of the European Aspergillus PCR Initiative.

Aspergillus PCR: one step closer towards standardisation J Clin Microbiol. 2010 Feb

EAPCRI concensus regarding Aspergillus

A consensus has been reached concerning the best blood fraction to test, blood volume, how to break the fungal cell wall and for DNA extraction

- >3 * whole-blood in EDTA tubes, in order to have access to both the free- and the cell-associated DNA
- white cell lysis buffer
- bead -beating
- either spin columns or an automated DNA extraction method can be performed
- Internal control
- DNA should be eluted < 100ul

*As the fungal load in the circulation of a patient may be less than 1 genome per ml

Which PCR assay is most suitable?

White et al. 2006 compared

- two primer sets (28S and 18S) and three machines
- Light Cycler (Roche)
- TaqMan (Applied Biosystem)
- Rotor-Gene (Corbett Research)

The sensitivity, specificity, NPV, PPV, were higher with the 28S than the 18S primer set

- The platforms influenced the assay
- Sensitivity and NPV were 100% with the Taqman machine
- Specificity and PPV were 100% with the Rotor-Gene system

Which PCR assay is most suitable ?

- The sensitivity of PCR assays with blood samples from healthy donors spiked with Aspergillus conidia might not reflect the sensitivity of the assay whith clinical blood samples
- we do not know if conida, hyphal fragments or free circulating DNA are detected
- Genomic DNA from bacteria and virus and parasites may be present

There are certain questions to be addressed using those assays

- The frequency of prospective sampling (2-3 times per week?)
- The number of positive results of a PCR assay required to initiate antifungal therapy is not known (2 consecutive PCR results*)
- How to interpret a single positive test? (A transient presence of fungal DNA might be possible but an infection cannot be excluded)

Klingspor L, Loeffler J. Med Mycol. 2009
Florent, M., et al., J Infect Dis, 2006
Buchheidt, D., et al., Br J Haematol, 2004
Kawazu, M., et al., J Clin Microbiol, 2004
Hebart, H., et al., J Infect Dis, 2000.

The issues of concern include

- The validation of the techniques in clinical studies
- The correct interpretation of test results

Clinical validity also needs to be established in large scale prospective trials

 designed to determine the performance and utility of the *Aspergillus* PCR with specimens from high risk populations

MycAssay[™] Aspergillus is a molecular diagnostic kit for detection of *Aspergillus* spp. genomic DNA extracted from bronchial samples

This assay offers

- a commercial, standardised assay for the molecular detection of Aspergillus
- fast detection of Aspergillus spp. and the potential for increased sensitivity for Aspergillus spp
- Sensitivity = 94%; Specificity = 91%;
- PPV = 97%; NPV = 83%

Bronchoalveolar lavage is positive by culture in approximately 40% of cases

Comparison of Whole Blood, Serum and Plasma for Early Detection of Candidemia by Multiplex-Tandem PCR

Candida DNA was detected in

- serum (71%)
- plasma (75%)
- whole blood (54%)

Lau A, et al. J Clin Microbiol. 2009



Real-time Fungal PCR assay was developed and established June 2002 at Huddinge

DNA extraction

Chemical + Mechanical disruption + Automatic extraction (MagNaPure LC)

For measuring the DNA concentration

NanoDrop ND-1000 Spectrophotometer

Selection of target : Multicopy gene; 18S rRNA gene

Real-Time PCR LightCycler 2.0

• Klingspor L and Jalal S. Clin Microbiol Infect. 2006:12(8): 745-53.

R-T Fungal PCR assay

A method for detection of Candida and Aspergillus DNA

- in EDTA-blood samples and plasma
- body fluids such as BAL, CSF, bile, pleura, ascites
- in biopsy specimens.



R-T Fungal PCR assay with hybridisation probes

Provides rapid (6 h) and sensitive (2-10 genome) detection of

- Aspergillus and Candida to genus level
- Identification of Candida to species level
 C.albicans, C.glabrata, C. krusei, C.tropicalis,
 C parapsilosis and C.lusitaniae.

Klingspor L ,Jalal S. Clin Microbiol Infect 2006; 12:745-753

Fungal PCR results in tissue from 31 biopsies compared to culture and direct microscopy

- Candida PCR pos 10 / 31
- 4 liver
- 2 colon
- 2 viterous
- 1 lung
- 1 skin
- Sensitivity 100%
- Specificity 100%

- Aspergillus pos 12/31
- 1 cerebri
 1 kidney
- 2 cerebellum 2 pleura
- 2 lung 1 heart
- 1duodenum 1 liver
- 1artery
- Sensitivity 100%
- Specificity 100%

Dermatophytes

Diagnostic

- Fluorescens microscopi
- Culture 3 veeks
- PCR 5h- 1-day



Molecular detection of dermatophyte species directly from clinical specimens

- 1. Multiplex PCR –Gelelectrophoresis (5h) nails
- 2. A PCR-ELISA method (24 h) skin scrapings & nails
- 3. Real-time PCR (4 h after overnight lysis) nail, skin and hair samples

- 1. Brillowska-Dabrowska A, et Med Mycol. 2010
- 2. Beifuss B, et al Mycoses. 2009 Sep
- 3. Bergmans AM ,et al. Clin Microbiol Infect. 2009

The new ISHAM working group

"PCR-based diagnosis of Dermatophyte infections: on the way to a consensus"

just established!

PCR in combination with:

Gelelectrophoresis

•ELISA

Sequencing

- long sequences
- short sequences (Pyrosequencing)

•In sity hybridisation

Identification of yeasts and moulds to species level

Conventional methods

Molecular typing of fungal isolates

- In situ hybridisation
- Pyrosequencing
- Sequencing

Background

- Increasing incidence of blood infections and invasive infections
- Candida species
 - \rightarrow C. albicans (35-65%)
 - \rightarrow Non-Candida albicans:
 - C. glabrata
 - C. parapsilosis
 - C. krusei
 - C. tropicalis







Procedure Overview – Simple & Easy

Prepare Smear



20 min.

- Add drop from BC+
- Fix bacteria/yeast onto slide
 - Heat
 - Methanol, or
 - Flame fixation



Hybridize

30 min.

- Add PNA probe
- Probe enters cells and binds to target rRNA sequence, if present



Wash

30 min.

- Immerse slide in Wash Solution
- Unbound and excess PNA probe removed from cells and slide



Examine

2 min.

- Fluorescence microscopy using 60x or 100x oil objective
- Target bacteria/yeast fluoresce

Yeast Traffic Light[®] PNA FISH[®]



C. albicans C. tropicalis C. parapsilosis



C. albicans/C.glabrata PNA FISH®



C. albicans C. glabrata

PNA FISH <u>Peptid Nucleic Acid= PNA</u> <u>Fluorecence In Situ Hybridisering= Fish</u>



Identification of medically important yeasts by the Pyrosequencing[™] technology



Fast - up to 96 samples analysed in less than 6 h

Work flow



<u>Accurate</u> - identification to species level by software against local database

The pyrogram[™]



T GG CC GGG T C A C G A GG CCC TA ...

.....peak height is proportional to the number of incorporated nucleotides

Detailed Report Sample ID: 132 Well: B2 PSQ run: 050105 gold kit Entry ID: samp20 Sequence library: andreys db pr1 (2005-01-28, 11:07) Query sequence: CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG Sc Result: Candida norvegensis (from BLAST, pr. 1) Sc Quality: Good Codd Codd <th></th> <th></th> <th></th>			
Sample ID: 132 Well: B2 PSQ run: 050105 gold kit Entry ID: svamp20 Sequence: CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG Result: Candida norvegensis (from BLAST, pr. 1) Quality: Good 100 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 4 4 5 4			
Sample ID: 132 Wei: gr. PSQ run: cs00105 gold kit Psq run: cs00105 gold kit Sequence library: antrops db pri (2005-01-28, 11:07) Query sequence: CCTCAAAGTAATCGTCCTGGTTCGCCGGCCACAGGGGAGGCTAGCCAGAAGGAAAAG Result: Candida norvegensis (from BLAST, pr. 1) Sc Quality: Good Image: Sample ID: Sc Image: Sample ID: Sc Image: Sample ID: Candida norvegensis (from BLAST, pr. 1) Sc Image: Sample ID:	Detailed Report		
Sample ID: 132 Well: B2 PSQ.run: 050105 gold kit Entry ID: swamp20 Sequence librar: andreys db pri (2005-01-28, 11:07) Query sequence: CCTCAAAGTAATCGTCCTGGTTCGCCGGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG Result: Candida norvegensis (from BLAST, pr. 1) Scr Quality: Good Scr 100 2			
Well: B2 PSQ run: 05015 gold kit Entry ID: svamp20 Sequence library: andreys db pr1 (2005-01-28, 11:07) Query sequence: CCTCAAAGTAATCGTCCTCGCCCCACAGGGGAGGCTAGCCAGAGGAAAAG Result: Candida norvegensis (from BLAST, pr. 1) Quality: Good 100 2 2 2 12 2	Sample I	D: 132	
PSQ run: u 050105 gold kit Entry ID: svamp20 Sequence library: andreys db pr1 (2005-01-28, 11:07) Query sequence: CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG Result: Candida norvegensis (from BLAST, pr. 1) Sca Quality: Good	Well:	82	
Entry ID: svamp20 Sequence library: andreys db pr (2005-01-28, 11:07) Query sequence: CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAGG Result: Candida norvegensis (from BLAST, pr. 1) Quality: Good	PSQ run:	050105 gold kit	
Sequence indray: andreys ab pri (2005-01-28, 11:07) Query sequence: CCTCAAAGTAATCGTCCCGGTCGCCCCCACAGGGGAGGCTAGCCAGAAGGAAAGG Result: Candida norvegensis (from BLAST, pr. 1) Quality: Good Image: Sequence in the security is andreys and the security is and the se	Entry ID:	svamp20	
Quality: Condida norvegensis (from BLAST, pr. 1) So Quality: Good Good 100 2	Sequence lit	irary: andreys db pr1 (2005-01-28, 11:07)	
Result: Candida norvegensis (from BLAST, pr. 1) Sc Quality: Good Good </td <td>Query seque</td> <td>Ince. CETEAAAGTAATEGTEETGGTTEGEEGEECACAGGGGAGGETAGEEAGAAGGAAAAG</td> <td></td>	Query seque	Ince. CETEAAAGTAATEGTEETGGTTEGEEGEECACAGGGGAGGETAGEEAGAAGGAAAAG	
Quality: Good 175 2	Result:	Candida norvegensis (from BLAST, pr. 1)	Scor
Hit 1: Candida norvegensis (from BLAST, pr. 1) Score: 100 Identities: 53/53 (100%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGAGGCTAGCCAGAAGGAAAGG 57 Identities: 48/57 (14%) Score: 81.3 Identities: 48/57 (14%) Score: 81.3 Identities: 48/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAGG 57 Identities: 48/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAGG 57 Identities: 48/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCCCACAGGGGAGGCTAGCCAGAAGGAAG	Quality:	Good	
Hit 1: Candida norvegensis (from BLAST, pr. 1) Score: 100 Identities: 53/53 (100%) Identities: 63/52 (100%) Identities: 48/57 (100%) Identities: 48/57 (10%) Identities: <th></th> <th></th> <th></th>			
Hit 1: Candida norvegensis (from BLAST, pr. 1) Score: 100 Score: 100 Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCACAGGGAGGCTAGCCAGAAGGA 53 Hit 2: Candida inconspicua (LOCUS AF201301) Score: 81.3 Identities: 48/57 (84%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGAGGCTAGCCAGAAGGAAAGC 57 Identities: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGAGGCTAGCCAGAAGGAAAGC 57 Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGAGGCTAGCCAGAAGGAAAGC 57 Jidentities: 48/57 (84%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGCAGGCTAGCCAGAAGGAAAGC 57 Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGCAGGCTAGCCAGAAGGAAAGC 57 Jidentities: 48/57 (84%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCCGCCACAGGGCAGGCTAGCCAGAAGGAAAGC 57 Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCCGCCACAGGGCAGGCTAGCCAGAAGGAAAGC 57 Jidentities: 48/57 (84%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCCGCCACAGGGCAGGCTAGCCAGAAGGAAAGC 57 Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCCGCCACAGGGCAGGCTAGCCAGAAGGAAAGC 57 Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCCGCCACAGGGCAGGCTAGCCAGAAGGAAAGC 54 </th <th></th> <th></th> <th></th>			
175 2		3	
Image: Signal	175	<u>^</u>	
150 100 1		2 2 2	
Hit 1: Candida norvegensis (from BLAST, pr. 1) Score: 100 Gaps: 0/53 (00%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAGG 53 Hit 2: Candida inconspicua (LOCUS AF201301) Score: 81.3 Identities: 48/57 (14%) Library 0 CCTCCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAGG 57 Hit 2: Candida inconspicua (LOCUS AF201301) Score: 81.3 Jdentities: 48/57 (14%) Library 0 CCTCCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Hit 2: Candida inconspicua (LOCUS AF201301) Score: 81.3 Query 0 CCTCCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAGG 57 Hit 1: Candida inconspicua (LOCUS AF201301) IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	150		A
125 100 1			Ğ
Image: Description of the second s	125		
Image: 100 Image: 1000 Image: 100 Image: 100 </td <td>L</td> <td></td> <td></td>	L		
Hit 1: Candida norvegensis (from BLAST, pr. 1) Score: 100 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 (57) Identities: 53/53 (100%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 (57) Gaps: 0/53 (0%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 Hit 2: Candida inconspicua (LOCUS AF201301) Score: 81.3 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAGG 57 Identities: 48/57 (84%) Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAGG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGCAGCCAGAAGGAAAGG 57 E-value: 6.93e-055 0 Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGCAGCCAGAAGGAAAGG 49	100-		
Hit 1: Candida norvegensis (from BLAST, pr. 1) Score: 100 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGAGGCTAGCCAGAAGGA 53 (57) Identities: 53/53 (100%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 (57) Gaps: 0/53 (0%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 Hit 2: Candida inconspicua (LOCUS AF201301) CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGCAGGCTAGCCAGAAGGAAAGG 57 Score: 81.3 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGCAGCCTAGCCAGAAGGAAAAGG 57 Identities: 48/57 (84%) Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGCAGGCTAGGCCAGAAGGAAAAGG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGCAGGCCTAGGCCAGAAGGAAAAGG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGCAGGCCCAGGCAGAGGAAAAGG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCCACAGGCAGAGGCAAAGG 54 E-value: 6.93e-055 0 CCTCAAAGTAATCGTCCTGGTCGCCGCCCCCCCCCCCCC	ESA	I T C G A T C	TCGA
Hit 1: Candida norvegensis (from BLAST, pr. 1) Score: 100 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 (57) Identities: 53/53 (100%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 (57) Gaps: 0/53 (0%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 E-value: 7.80e-070 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCCACAGGGGAGGCTAGCCAGAAGGA 53 Score: 81.3 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Identities: 48/57 (84%) Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 F-value: 6.93e-055 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57			
Score: 100 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 (57) Identities: 53/53 (100%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 (57) Gaps: 0/53 (0%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 E-value: 7.80e-070 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 Score: 81.3 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Identities: 48/57 (84%) Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCC-ACAGGGGAGGCAGAGGAAAAG 49 E-value: 6.93e-055 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCAGGC	Hit 1:	Candida norvegensis (from BLAST, pr. 1)	
Identities: 53/53 (100%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53 E-value: 7.80e-070 Condida inconspicua (LOCUS AF201301) Score: 81.3 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Identities: 48/57 (84%) Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCACAAGGGCTAGOCAGAAGGAAA-G 49 E-value: 6.93e-055 6.93e-055 0 CCTCAAAGTAATCGTCCTGGTTCGCCACAAGGGCTAGOCAGAAGGAAA-G 49	Score:	100 DIDATE D. COTCAAAGTAATCGTCCTCGCCCCCCACAGGGGGGGGGGG	
Gaps: 0/53 (0%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCACAGGGGAGGCTAGCCAGAAGGA 53 E-value: 7.80e-070 Hit 2: Candida inconspicua (LOCUS AF201301) Score: 81.3 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Identities: 48/57 (84%) Query 0 CCTCAAAGTAATCGTCCTGGTTCGCC-CCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCC-CCTAGCCAGAAGGAAAGG 49 E-value: 6.93e-055 6.93e-055	Identities:	53/53 (100%)	
E-value: 7.80e-070 Hit 2: Candida inconspicua (LOCUS AF201301) Score: 81.3 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCAAGGAAAAG 57 Identities: 48/57 (84%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCAAGGAAAAG 57 Hitting 1 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAAGGAA	Gaps:	0/53 (0%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGA 53	
Hit 2: Candida inconspicua (LOCUS AF201301) Score: 81.3 Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Identities: 48/57 (84%) 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCC ACAAGGGCTAGCCAGAAGGAAA-G 49 E-value: 6.93e-055 6.93e-055 6.93e-055 CCTCAAAGTAATCGTCCTGGTTCGCC CCTAGCCAGAAGGAAA-G 49	E-value:	7.80e-070	
Hit 2: Candida inconspicua (LOCUS AF201301) Score: 81.3 Jdentities: 48/57 (84%) Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Candida inconspicua (LOCUS AF201301) Score: 8/57 (84%) Query 0 CCTCAAAGTAATCGTCCTGGTTCGCCGCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Hit 1 1 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCC ACAAGGGC Constant 1 Gaps: 6.93e-055			
Score: 81.3 Quezy 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Identities: 48/57 (84%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 57 Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCACAGGGGAGGCTAGCCAGAAGGAAAAG 49 E-value: 6.93e-055 6.93e-055 0 CCTCAAAGTAATCGTCCTGGTTCGCCCCACAGGGGAGGCAGGC	Hit 2:	Candida inconspicua (LOCUS AF201301)	
Identities: 48/57 (84%) IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Score:	81.3 Decreta hacen hacen a process of the second concertain and the second seco	
Gaps: 8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCC++++ACAAGGG++++CTAGCCAGAAGGAAA+G 49 E-value: 6.93e-055	Identities:	48/57 (84%) G CETCAAGTATCOTCOTOGTICGCCCCACAGGGAGGCTAGCCAGAGGAAGGAAGG	
E-value: 6.93e-055	Gaps:	8/57 (14%) Library 0 CCTCAAAGTAATCGTCCTGGTTCGCCACAAGGGCTAGCCAGAAGGAAA-G 49	
	E-value:	6.93e-055	

Zygomycosis

- Cultures from infected tissues are often negative
- The identification of a Zygomycet in tissue is difficult
- Different Zygomycetes share simular morphology according to histopathology/direct microscopy



New molecular methods for the identification of Zygomycetes in culture and tissue

Culture:

 The identification to species level of a strain isolated from culture

Some Methods: PCR+ sequencing. Real-time PCR

Tissue:Unfixed fresh/frozen materialFormalin-fixed, paraffin-embedded biopsies

Some Methods : PCR+ sequencing, Real-time PCR , in situ hybridization

- Standardisation of the techniques are needed
- to improve sensitivity for identification in tissue

Dannaoui E. Clin Microbiol Infect 2009

Sequencing ABI prisma[™]

- A technologi for long DNA sekvenses
- 3 4 working days

•To identify fungi from cultures (fungi that are difficult to identify by conventionell methods)



Molecular diagnostics in fungal infections are here to stay....

BUt standardisation of these teqniques are needed

