

1 Detection of the 'Big Five' Mould Killers of Humans: *Aspergillus*, *Fusarium*, 2 *Lomentospora*, *Scedosporium* and *Mucormycetes*

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7

8 **Abstract**

9
10 Fungi are an important but frequently overlooked cause of morbidity and mortality in
11 humans. Life-threatening fungal infections mainly occur in immunocompromised patients,
12 and are typically caused by environmental opportunists that take advantage of a weakened
13 immune system. The filamentous fungus *Aspergillus fumigatus* is the most important and
14 well-documented mould pathogen of humans, causing a number of complex respiratory
15 diseases, including invasive pulmonary aspergillosis, an often fatal disease in patients with
16 acute leukemia or in immunosuppressed bone marrow or solid organ transplant recipients.
17 However, non-*Aspergillus* moulds are increasingly reported as agents of disseminated
18 diseases, with *Fusarium*, *Scedosporium*, *Lomentospora* and mucormycete species now firmly
19 established as pathogens of immunosuppressed and immunocompetent individuals. Despite
20 well-documented risk factors for invasive fungal diseases, and increased awareness of the
21 risk factors for life-threatening infections, the number of deaths attributable to moulds is
22 likely to be severely underestimated driven, to a large extent, by the lack of readily
23 accessible, cheap, and accurate tests that allow detection and differentiation of infecting
24 species. Early diagnosis is critical to patient survival but, unlike *Aspergillus* diseases, where a
25 number of CE-marked or FDA-approved biomarker tests are now available for clinical
26 diagnosis, similar tests for fusariosis, scedosporiosis and mucormycosis remain
27 experimental, with detection reliant on insensitive and slow culture of pathogens from
28 invasive bronchoalveolar lavage fluid, tissue biopsy, or from blood. This review examines the
29 ecology, epidemiology, and contemporary methods of detection of these mould pathogens,
30 and the obstacles to diagnostic test development and translation of novel biomarkers to the
31 clinical setting.
32

33 **Key words:** *Aspergillus*, aspergillosis, *Fusarium*, *Lomentospora*, *Scedosporium*,
34 mucormycosis, monoclonal antibody, lateral-flow device, fungal diagnostics, mycoses
35

36 **Abbreviations**

37 AFB (acid-fast bacillus); AIDS (acquired immune deficiency syndrome); ABPA (allergic
38 bronchopulmonary aspergillosis); ABPM (allergic bronchopulmonary mycosis); AML (acute
39 myeloid leukaemia); AB (*Aspergillus* bronchitis); AS (*Aspergillus* sensitisation); BALf
40 (bronchoalveolar lavage fluid); CCPA (chronic cavitary pulmonary aspergillosis); CF (cystic
41 fibrosis); CFPA (chronic fibrosing pulmonary aspergillosis); CGD (chronic granulomatous
42 disease); CNPA (chronic necrotising pulmonary aspergillosis); CNS (central nervous system);
43 CPA (chronic pulmonary aspergillosis); COPD (chronic obstructive pulmonary disease); CT
44 (computed tomography); ELISA (Enzyme-Linked Immunosorbent Assay); EORTC/MSG
45 (European Organisation for Research and Treatment of Cancer/Mycology Study Group); EPS
46 (extracellular polysaccharide); FDSC (*Fusarium dimerum* species complex); FOsc (*Fusarium*

47 *oxysporum* species complex); FSSC (*Fusarium solani* species complex); GM (galactomannan);
48 HSCT (haematopoietic stem-cell transplant); IPA (invasive pulmonary aspergillosis); ISHAM
49 (International Society for Human and Animal Mycology); LFA (lateral-flow assay); LFD
50 (lateral-flow device); MRI (magnetic resonance imaging); MAb (monoclonal antibody); MDS
51 (myelodysplastic syndrome); NPV (negative predictive value); NTM (non-tuberculosis
52 mycobacteriosis); PCR (polymerase chain reaction); PET (positron emission tomography);
53 POCT (point-of-care test); PPV (positive predictive value); PSC
54 (*Pseudallescheria/Scedosporium* species complex); PTB (pulmonary tuberculosis); SAIA (sub-
55 acute invasive pulmonary aspergillosis); TAFC (triacetylfulvarinine C).

56

57 **Introduction**

58

59 In 1991, it was estimated that there were 1.5 million species of fungi on the planet
60 (Hawksworth, 1991). With the advent of high throughput sequencing, that estimate was up-
61 graded to as many as 5.1 million species (Blackwell, 2011). Despite this enormous number,
62 in which fungi outnumber plants by at least 6 to 1, only ~700 species have been reported as
63 causing infections in humans (Brown *et al.*, 2012a), while the number that are regularly
64 reported as disease-causing agents in the clinical setting is limited to an even smaller
65 number of species. Nevertheless, that handful of species, which includes yeasts, yeast-like
66 fungi, and moulds, collectively cause enormous but largely unrecognised damage to human
67 health and well-being in the form of superficial infections of the mucosa, skin and nails
68 (Schwartz, 2004), deep infections of the bones and joints (Taj-Aldeen *et al.*, 2015), asthma
69 and allergies (Denning *et al.*, 2014), and life-threatening disseminated infections in already
70 seriously ill patients, amounting to billions of affected people each year (Brown *et al.*,
71 2012a,b).

72 Fungi that cause fatal disseminated infections are typically opportunistic, taking
73 advantage of immune systems weakened caused by primary immunodeficiencies (Lanternier
74 *et al.*, 2013) or AIDS (Limper *et al.*, 2017), haematological malignancies (Pergam, 2017), or
75 the use of potent immuno-suppressive therapies that deplete microbial immunity
76 (Gundacker and Baddley, 2015). The fungi regarded as the most important medically are
77 *Aspergillus*, *Candida*, *Coccidioides*, *Cryptococcus*, *Histoplasma*, *Paracoccidioides*,
78 *Pneumocystis*, and *Talaromyces*. Only one of these, *Aspergillus*, is a true filamentous fungus
79 or mould, the remainder being yeasts, yeast-like, or thermally dimorphic fungi. It is
80 estimated that *Aspergillus* diseases, caused principally by the single species *Aspergillus*
81 *fumigatus*, collectively affect around 9 million people worldwide, with a further 10 million
82 people estimated to be at risk of *Aspergillus* infection. However, because of under-diagnosis
83 and under-reporting of *Aspergillus* diseases, these figures are likely to be under-estimates
84 (Denning *et al.*, 2013). Also under-diagnosed or under-reported, are the diseases caused by
85 other mould pathogens (*Fusarium* spp., species in the *Pseudallescheria/Scedosporium*
86 complex (PSC), *Lomentospora prolificans*, and the mucormycetes comprising, amongst
87 others, *Mucor*, *Rhizomucor*, and *Rhizopus* spp.), despite their increasing frequency as
88 infectious etiologies in the ever-expanding populations of immunocompromised and
89 diabetic patients, and their involvement in polymicrobial diseases following traumatic injury.

90 The aim of this review is to examine the ecology, epidemiology, and methods of
91 detection of these under-reported moulds in the context of human disease. It aims to
92 highlight the paucity of diagnostic tests for these pathogens that, despite repeated calls by

93 learned societies, opinion leaders, and action groups for better access to cheap diagnostics,
94 remain pitifully inadequate, adding to the unacceptably high rates of morbidity and mortality
95 caused by these fungi, and the added financial burden to healthcare providers consequent
96 of delayed or incorrect diagnosis. The reasons for our repeated failure to develop cheap,
97 accurate, and user-friendly diagnostic tests are discussed, as are the steps that might be
98 taken to ‘release the brakes’ on bench-to-bedside translation of diagnostics to the clinical
99 setting, enabling access to point-of-care tests, particularly in poor and developing countries
100 that lack access to well-resourced and well-equipped diagnostic facilities.

101

102 ***Aspergillus* species pathogenic to humans**

103

104 The genus *Aspergillus* comprises between 260 and 837 species of ascomycete fungi, making
105 it one of the most abundant groups of fungi on the planet (Hawksworth, 2011). Despite
106 their abundance, only a small number of species are known to cause diseases in humans,
107 with a single anamorphic species *Aspergillus fumigatus* (teleomorph *Neosartorya fischeri*) in
108 the section *Fumigati* responsible for >80% of recorded infections in humans (Latgé, 1999).
109 Other well-established species capable of causing infections include *A. flavus* (section *Flavi*),
110 *A. terreus* (section *Terrei*), *A. niger* (section *Nigri*) and *A. nidulans* (section *Nidulante*)(Sugui
111 *et al.*, 2015), while a number of sibling species of *A. fumigatus* have emerged as human
112 pathogens over recent years. These rarer species in the section *Fumigati* bare morphological
113 similarities to *A. fumigatus*, but worryingly also exhibit intrinsic resistance to anti-fungal
114 drugs (Sugui *et al.*, 2015; Van der Linden *et al.*, 2011), further complicating detection and
115 treatment with the advent of azole-resistance in clinical strains of *A. fumigatus*
116 (Abdolrasouli *et al.*, 2018). Of these emerging species, *A. udagawae* (*Neosartorya*
117 *udagawae*), *A. lentulus*, and *A. pseudofischeri* (*Neosartorya pseudofischeri*) are the most
118 frequently reported as causing disease in humans. Notwithstanding these, *A. fumigatus*
119 remains the most important pathogen in the *Aspergillus* genus in terms of prevalence and
120 capacity to cause disease in humans. It is almost the most important mould pathogen of
121 humans compared to all other mould species capable of causing life-threatening
122 disseminated infections.

123

124 ***Aspergillus* diseases**

125

126 While *Aspergillus* spp. have recently emerged as the cause of deep-seated tissue infections
127 following combat-related injuries in military personnel (Paolino *et al.*, 2012; Warkentien *et*
128 *al.*, 2012; Tribble and Rodriguez, 2014), they are best known as opportunistic pathogens
129 which cause life-threatening infections in immuno-compromised individuals whose impaired
130 immunity is unable to eliminate the infectious propagules (air-borne spores) inhaled into
131 the lungs. In patients with defective cell-mediated immunity due to cytotoxic chemotherapy
132 or T-cell dysfunction due to corticosteroid or other immunosuppressive therapy, *Aspergillus*
133 spores germinate to produce invasive hyphae which proliferate, leading to the often-fatal
134 disseminated disease invasive pulmonary aspergillosis (IPA). These fungi can also cause
135 allergic and chronic respiratory diseases as a result of an over-zealous host response to
136 saprotrophic colonisation of the lung following inhalation of air-borne spores. The clinical
137 consequences of this are most severe in the context of underlying respiratory disorders such
138 as chronic obstructive pulmonary disease (COPD), post pulmonary tuberculosis (PTB), non-

139 tuberculosis mycobacteriosis (NTM), bronchiectasis, and cystic fibrosis (CF). The role of
140 *Aspergillus* spp. in bronchiectasis in the non-CF lung is less well understood, but *Aspergillus*
141 sensitisation and/or allergic bronchopulmonary aspergillosis (ABPA) is a cause and also a
142 consequence of bronchiectasis (Chotirmall and McElvaney, 2014; Chotirmall and Martin-
143 Gomez, 2018). The sequel to saprotrophic colonisation is infection and the development of
144 chronic pulmonary aspergillosis (CPA), a slowly progressive lung disease, with poor clinical
145 outcome (Denning *et al.*, 2011 and 2013; Takazono and Izumikawa, 2018).

146 The global burden of *Aspergillus* lung diseases is vast (Bongomin *et al.*, 2017). There are
147 an estimated 300,000 cases of IPA per year with approximately 10 million at risk annually
148 (Brown *et al.*, 2012b; Bongomin *et al.*, 2017). The global burden of ABPA in asthma is
149 approximately 4.8 million, ABPA in cystic fibrosis approximately 6,675, CPA approximately 3
150 million (including 1.6 million cases post-tuberculosis), with CPA complicating ABPA
151 approximately 400,000 (Denning *et al.*, 2013). In the United Kingdom, there are estimated
152 to be around 4,000 cases of IPA each year, 178,000 cases of ABPA in people with asthma,
153 and 3600 patients with CPA, based on burden estimates post PTB and in sarcoidosis (Pegorie
154 *et al.*, 2017).

155

156 **Invasive Pulmonary Aspergillosis**

157

158 A fatality due to disseminated invasive pulmonary aspergillosis was first described in 1953
159 following autopsy of a patient with agranulocytosis disease (Rankin, 1953). At that time, IPA
160 was a rare, albeit poorly recognised, disease of immunocompromised patients. It is perhaps
161 ironic that modern advances in the treatment of haematological malignancies, especially
162 remission-induction therapy for acute myeloid leukaemia (AML) or myelodysplastic
163 syndrome (MDS), and the use of highly-effective immune modulating drugs (Kyi *et al.*, 2014;
164 Reinwald *et al.*, 2016), have led to a dramatic increase in the incidence of IPA in
165 immunodeficient patients, such that the mortality rate of IPA exceeds 50% in neutropenic
166 patients, and reaches 90% in haematopoietic stem-cell transplant (HSCT) recipients (Segal,
167 2009; Kousha *et al.*, 2011). The major risk factors for the disease include neutropenia, HSCT
168 and solid organ transplantation, high-dose corticosteroids, haematological malignancy,
169 cytotoxic therapy, advanced AIDS, and chronic granulomatous disease (CGD)(Latgé, 1999;
170 Dutkiewicz and Hage, 2010).

171

172 **Allergic Bronchopulmonary Aspergillosis**

173

174 Of the different yeasts and filamentous fungi able to cause allergic bronchopulmonary
175 mycosis (ABPM) in humans (Chowdary *et al.*, 2014), *A. fumigatus* and allergic
176 bronchopulmonary aspergillosis (ABPA) are the most extensively studied. Allergic
177 bronchopulmonary aspergillosis is one of the most severe *Aspergillus*-related diseases, with
178 the potential to progress into pleuropulmonary fibrosis and respiratory failure (Carsin *et al.*,
179 2017). It occurs almost exclusively in cystic fibrosis or asthmatic patients, and is
180 characterised by a hypersensitivity reaction to *Aspergillus* spp., with diverse clinical and
181 radiological manifestations.

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185 **Bronchiectasis**

186

187 Bronchiectasis is a chronic respiratory disease characterised by progressive and irreversible
188 dilation of the bronchial lumen, with impaired mucociliary clearance, recurrent infection,
189 and chronic inflammation. *Aspergillus* species are the most common filamentous fungi
190 cultured from respiratory secretions of CF, non-CF, and bronchiectasis patients (Aogáin *et*
191 *al.*, 2018; Máiz *et al.*, 2015, 2018). *Aspergillus fumigatus* is the most frequently recovered
192 species and the species most likely to cause infections, followed by *A. flavus*, *A. niger* and *A.*
193 *terreus* which tend to colonise, rather than infect, the lung (Máiz *et al.*, 2018). These species
194 also differ in their geographical distributions, with a higher prevalence of *A. niger* and *A.*
195 *terreus* in Japan, and *A. flavus* in India and China (Máiz *et al.*, 2018).

196

197 **Chronic Pulmonary Aspergillosis**

198

199 Chronic pulmonary aspergillosis (CPA) is a semi-invasive disease (Chan *et al.*, 2016), lying
200 somewhere in between allergic and invasive forms of aspergillosis (Sehgal *et al.*, 2018). It
201 comprises a number of lung diseases that are long-term sequelae to pulmonary tuberculosis
202 (PTB), namely *Aspergillus* nodule, simple pulmonary aspergilloma, chronic cavitary
203 pulmonary aspergillosis (CCPA; presence of one or more cavities with or without
204 aspergilloma, accompanied by pulmonary and systemic symptoms), chronic fibrosing
205 pulmonary aspergillosis (CFPA; cavitation and fibrosis involving two or more lobes), and sub-
206 acute invasive pulmonary aspergillosis (SAIA)(Denning *et al.*, 2016) also called chronic
207 necrotising pulmonary aspergillosis (CNPA)(Kaymaz *et al.*, 2016) leading to progressive
208 destruction of the lung (Ohba *et al.*, 2012). CCPA is the most common form of CPA (Denning
209 *et al.*, 2003), with most cases of CPA occurring in South-East Asia, Western Pacific, and
210 Africa, where prevalence of PTB is the highest. In high-income settings, COPD appears to be
211 the most important pre-disposing condition for the disease (Smith and Denning, 2011).
212 Unlike IPA, CPA occurs in immunocompetent patients after treatment for TB, leading to
213 weight loss, intense fatigue, severe shortness of breath and life-threatening haemoptysis.
214 *Aspergillus fumigatus* is the most frequently identified species in negative acid-fast bacillus
215 (AFB) sputum smears from sub-Saharan Africans following treatment for PTB. Indeed, CPA is
216 an important differential diagnosis for what appears to be smear-negative tuberculosis
217 (Denning *et al.*, 2011).

218

219 **Detection of *Aspergillus* diseases**

220

221 Detection of *Aspergillus* lung diseases remains a significant clinical challenge. Clinical
222 manifestations of *Aspergillus* lung infection or colonisation are non-specific, as are
223 radiological abnormalities seen on X-rays or on computed tomograms of the chest (chest-
224 CT). Despite this, anomalies on a chest-CT are used in some centres to initiate antifungal
225 drug treatment in at-risk patients. However, the burgeoning costs of antifungal treatments
226 (Schumock *et al.*, 2016) and prolonged hospitalisation for patients with suspected, but often
227 unproven, pulmonary mycosis, has turned the spotlight on diagnostics and the need for
228 improved detection methods that enable the implementation of antifungal stewardship
229 programmes which have the potential deliver significant savings in antifungal drug
230 expenditure (Nwankwo *et al.*, 2018).

231 Diagnostic-driven approaches to antifungal treatment have been shown to be more
232 effective than empirical treatment, driving down costs, and improving outcomes for
233 patients (Barnes, 2013). The emergence of triazole resistance in clinical strains of *A.*
234 *fumigatus* and other *Aspergillus* spp. (Rivero-Menendez *et al.*, 2016; Abdolrasouli *et al.*,
235 2018; Zoran *et al.*, 2018), driven by a multiplicity of factors including widespread use of
236 azole fungicides in agriculture (Fisher *et al.*, 2018; Mortensen *et al.*, 2010; Verweij *et al.*,
237 2009), anti-fungal prophylaxis (Fisher *et al.*, 2018), evolution of resistance in infecting strains
238 in the lung during or after long-term (sometimes life-long) therapy with the same antifungal
239 drug (Howard *et al.*, 2009; Verweij *et al.*, 2016), and sub-therapeutic dosing of patients (van
240 der Elst *et al.*, 2015), is a serious cause for concern. Up to 12% of *Aspergillus* infections are
241 estimated to be resistant to antifungal drugs (Rivero-Menendez *et al.*, 2016), with up to 7%
242 of *Aspergillus* strains from stem cell and solid organ transplant patients found to be
243 resistant (Baddley *et al.*, 2009; Kontoyiannis *et al.*, 2010; Pappas *et al.*, 2010).

244 Diagnostics has an important part to play in guiding patient treatment, by restricting
245 the use of antifungal drugs to those that truly need them. It is important to note that a
246 combination approach to diagnostics is more likely to be effective than a single test
247 approach, despite pressures to cut healthcare costs. No single test fits all, especially where
248 an organism such as *A. fumigatus* is capable of causing a number of different diseases of the
249 lung. For this reason, abnormalities in a chest-CT that raise the suspicion of a fungal lung
250 infection in an at-risk patient should be accompanied by complementary biomarker tests
251 that add additional layers of proof. Biomarker tests such as ‘pan-fungal’ assays for fungal
252 (1→3)-β-D-glucan, and the Bio-Rad *Platelia*® ELISA for *Aspergillus* galactomannan (GM-
253 ELISA) in serum are FDA-approved and are included in the EORTC/MSG and ESCMID-ECMM-
254 ERS guidelines for disease detection (De Pauw *et al.*, 2008; Ullmann *et al.*, 2018), while
255 others such as the point-of-care *Aspergillus* lateral-flow device (*AspLFD*) have been recently
256 CE-marked and are now available commercially for IPA detection. These assays, and other
257 commercial or experimental tests currently in development, are discussed in the context of
258 allergic (ABPA), semi-invasive (CPA), and invasive (IPA) *Aspergillus* lung diseases.

259

260 **Invasive Pulmonary Aspergillosis**

261

262 **Invasive diagnostic procedures**

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264 Bronchoscopy and culture

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266 Diagnosis of IPA at the onset of disease is of paramount importance as prognosis worsens
267 significantly over time. Detection of circulating biomarkers in blood such as *Aspergillus*
268 galactomannan, fungal (1→3)-β-D-glucan, and *Aspergillus* DNA would indicate that the
269 disease is already well progressed. Early detection of *Aspergillus* lung infection is only
270 achievable by using tissue biopsy or bronchoalveolar lavage fluid (BALF) recovered during
271 invasive bronchoscopy, which allow culture of the pathogen or detection of biomarkers of
272 infection, respectively. The ‘gold standard’ test for diagnosis of IPA is culture of *Aspergillus*
273 from a sterile lung biopsy, with associated necrosis of tissues due to presence of hyphal
274 elements. There are a number of problems with culture, including the need for invasive
275 tissue sampling, slow growth or no growth of isolates from cultured material, and difficulties
276 in differentiating *Aspergillus* spp. from other agents of hyalohyphomycoses (e.g. other
277 hyaline septate moulds such as *Fusarium* and *Scedosporium* species) in the absence of

278 characteristic spore-bearing structures. This leads to lengthy turnaround times, and overall
279 poor sensitivity of culture-based detection compared to biomarker tests (Prattes *et al.*,
280 2014). A major benefit of culture is the recovery of isolates for antifungal susceptibility
281 testing and molecular detection of resistance mutations (Postina *et al.*, 2018), especially
282 given the increasing prevalence of triazole resistance in *A. fumigatus* isolates (Abdolrasouli
283 *et al.*, 2018).

284
285 Biomarker detection in BALf

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287 *Lateral-flow technology*

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289 The advantage of assaying BALf for *Aspergillus* biomarkers, is that it allows increased
290 sensitivity and speed of detection compared to culture. The *Aspergillus* lateral-flow device
291 (*AspLFD*), a point-of-care test (POCT) that incorporates a monoclonal antibody (mAb), JF5,
292 which detects a biomarker of active growth (Thornton, 2008; Thornton, 2014), allows rapid
293 near-patient diagnosis of IPA, with confirmatory detection of disease using laboratory-based
294 GM-ELISA, (1→3)-β-D-glucan, or polymerase chain reaction (PCR) tests of BALf samples.
295 Combination biomarker testing adds considerable power to IPA diagnosis, with a number of
296 studies demonstrating improvements in diagnostic sensitivity when these assays are used in
297 combination (Hoenigl *et al.*, 2014; Johnson *et al.*, 2015; Eigl *et al.*, 2017). There have been
298 numerous studies conducted with the prototype *AspLFD* test, with two meta-analysis
299 studies (Pan *et al.*, 2015; Zhang *et al.*, 2019) evaluating its diagnostic performance in
300 combination with GM-ELISA or (1→3)-β-D-glucan tests. The more recent study by Zhang *et*
301 *al.* (2019), which undertook a meta-analysis of 13 previously-published studies of the
302 prototype *AspLFD*, showed that a positive GM-ELISA and a positive (1→3)-β-D-glucan or
303 *AspLFD* test provided a confirmatory diagnosis of IPA.

304 The *AspLFD* was CE-marked in May 2018 for use with both serum and BALf, with
305 Mercier *et al.* (2019a) reporting the performance of the CE-marked test in a retrospective
306 evaluation of BALf samples from haematology patients across four centres in the
307 Netherlands and Belgium. In this multicentre study, the CE-marked test had a good
308 performance for the diagnosis of proven IPA versus controls (no IPA), with a specificity of
309 86% and sensitivity of 82%. Two follow-up studies (Jenks *et al.*, 2019; Mercier *et al.*, 2019b)
310 have compared the *AspLFD* with the newly developed *sōna* galactomannan lateral-flow
311 assay (GM-LFA) produced by IMMY. In the study by Jenks *et al.* (2019), both the *AspLFD* and
312 GM-LFA were highly sensitive and specific for probable/proven IPA versus no IPA in patients
313 with haematological malignancies, with specificities of close to 90% for both the *AspLFD* and
314 GM-LFA when read at 15 min, and with 100% sensitivity for the *AspLFD* when read at 25
315 min. In patients at risk for IPA but without neutropenia or underlying haematological
316 malignancy, the GM-LFA and *AspLFD* tests showed sensitivities ranging from 58% to 69%,
317 with specificities between 68% and 75% (Jenks *et al.*, 2018). When the two tests were
318 combined, sensitivity increased to 81% while specificity remained around 60%, making this a
319 reasonable approach for IPA diagnosis in non-neutropenic patients.

320 In the study by Mercier *et al.* (2019b), which retrospectively tested 235 BALf samples of
321 adult haematology patients from four centres on behalf of the Dutch-Belgian Mycosis Study
322 Group (DB-MSG), performance of the *AspLFD* and GM-LFA for proven IPA were similar. In
323 cases of proven and probable IPA, the tests had identical specificity, but a higher sensitivity
324 and a better NPV for the GM-LFA. However, a very faint test line is discernible in the GM-

325 LFA with BALf samples from patients with no IPA, and is also present with the sample
326 running buffer (i.e. strictly negative tests). This means that a comparator is required in cases
327 where a weak test line is evident in order to determine whether this is due to non-specific
328 binding (NSB), or due to an actual but weak line. Because of this ambiguity, a reading card is
329 included in the IMMY test against which test line intensities are compared. Any test line
330 considered fainter than a line of semi-quantitative intensity 1 is considered to be negative.
331 Alternatively, plain running buffer can be used to create a negative control LFA against
332 which clinical samples can be compared. Any test line more intense than the negative
333 control can be considered positive. However, this procedure introduces additional
334 uncertainty, variability, and cost, since a negative control must be included for every sample
335 run.

336 While the GM-LFA and *Asp*LFD are both relatively easy to use, the *Asp*LFD is somewhat
337 simpler, and does not suffer from NSB unlike the IMMY test. For the *Asp*LFD, no sample pre-
338 treatment is required with non-bloody, non-viscous BALf, which can be applied directly to
339 the test, with results available within 15 minutes. In the case of bloody or viscous BALf,
340 heating with a buffer (3 minutes) followed by centrifugation (5 minutes) is required, with a
341 total test time of approximately 25 minutes. For the GM-LFA, all samples must be pre-
342 treated with heating for 6-8 minutes and centrifugation for 5 minutes, bringing the total test
343 time to roughly 45 minutes. Notwithstanding this, Mercier and co-workers (2019a,b)
344 conclude that both tests show a good performance for diagnosis of IPA in haematology
345 patients using BALf. Both tests can be used for fast screening of patients, although
346 confirmation using an adjunct test such as GM-ELISA, PCR or culture is merited.

347

348 *Cytokines*

349

350 An important limitation of biomarker tests is that sensitivity may decrease during antifungal
351 prophylaxis or empirical therapy of patients with haematological malignancies (Eigl *et al.*,
352 2015; Prattes *et al.*, 2015). To mitigate this loss of test sensitivity, alternative signature
353 molecules in BALf have recently been explored which might act as adjunct biomarkers of the
354 disease. Gonçalves *et al.* (2017) investigated the alveolar cytokine profiles of patients at high
355 risk of developing IPA. The cytokines IL-1 β , IL-6, IL-8, IL-17A, IL-23, and TNF- α were
356 significantly increased among patients with the disease. However, IL-6, IL-8, and IL-23 best
357 differentiated between cases of IPA and controls, whereas the remaining cytokines
358 displayed an inconsistent contribution to discrimination. The cytokine IL-8 was the dominant
359 discriminator, with alveolar levels of ≥ 904 pg/ml predicting IPA with a sensitivity of 90%, a
360 specificity of 73%, and a negative predictive value of 88%.

361

362 *Siderophores*

363

364 Iron is essential for the growth of *Aspergillus fumigatus*, and targeting its acquisition blocks
365 infection by the pathogen (Leal *et al.*, 2013). In iron-poor environments such as serum, the
366 pathogen produces low-molecular-weight siderophores to scavenge ferric iron from the
367 host (Haas, 2003; Hass *et al.*, 2015). One of these, the extracellular siderophore
368 triacetylfusarinine C (TAFC), is produced following spore germination, and is detectable in
369 serum from patients with proven or probable IPA (Carrol *et al.*, 2016). The siderophore is
370 also detectable in BALf, and an evaluation by Orasch *et al.* (2017) of BALf samples from
371 patients with haematological malignancies (of which 73% received antifungal prophylaxis or

372 empirical treatment at the time of bronchoscopy) showed that diagnostic sensitivities of the
373 GM-ELISA and *Asp*LFD tests could be increased when used in combination with TAFC
374 detection, in line with previous BALf GM-ELISA/*Asp*LFD combination testing (Hoenigl *et al.*,
375 2014; Prattes *et al.*, 2015).

376

377 *Polymerase chain reaction*

378

379 *Aspergillus* polymerase chain reaction (PCR) has been shown for many years to be a
380 promising diagnostic procedure for IPA detection, especially when combined with other
381 diagnostic biomarker tests (White *et al.*, 2013; Buchheidt *et al.*, 2017). Despite the
382 widespread use of ‘in-house’ tests, PCR was not included in the 2008 EORTC/MSG diagnostic
383 criteria for IPA (De Pauw *et al.*, 2008) due to a lack of assay standardisation and validation.
384 However, PCR will be included in the latest iteration of the guidelines, following systematic
385 review of the evidence for its clinical use in comparison with antigen testing (White *et al.*,
386 2015). The availability of commercial PCR tests has aided assay standardisation (Rath and
387 Steinmann, 2018), with three PCR assays specifically tailored to *Aspergillus* detection, and
388 which have been evaluated using BALf or respiratory samples. The MycAssay *Aspergillus*[®]
389 assay is a real-time PCR which detects *A. fumigatus* and other *Aspergillus* spp., with a
390 sensitivity of 80% to 94.1%, and a specificity of 87.6% to 98.6%, in non-haematology and
391 mixed patient groups (Torelli *et al.*, 2011; Guinea *et al.*, 2013; Orsi *et al.*, 2015). The
392 AsperGenius[®] test comprises two PCR assays, one for the detection and differentiation of
393 *Aspergillus* spp. (AsperGenius Species multiplex[®]), and the other (AsperGenius Resistance
394 multiplex[®]) for the detection of four azole resistance markers within the Cyp51A gene of *A.*
395 *fumigatus* (L98H, TR34, T289A, Y121F). The AsperGenius Species multiplex[®] assay contains a
396 probe for the *A. fumigatus* complex (*A. fumigatus* and the emerging sibling pathogens *A.*
397 *lentulus*, *A. udagawae*, and *A. viridinutans*), and a probe for *Aspergillus* spp. (the *A.*
398 *fumigatus* complex and *A. flavus*, *A. terreus*, and *A. niger*). Using BALf, the AsperGenius[®]
399 test has a sensitivity of 68.4% to 84%, and a specificity of 80% to >92% (Chong *et al.*, 2016;
400 Guegan *et al.*, 2018). In a study of 91 patients with GM-ELISA positive BALf samples, 79%
401 were positive for *A. fumigatus* or *Aspergillus* spp. DNA, with the azole resistance mutation
402 TR₃₄/L98H detected in 8 of the cases, and T289A/Y121F mutations in a further 3 cases
403 (Schauwvlieghe *et al.*, 2017). The MycoGenie[®] assay detects *A. fumigatus* and the
404 TR₃₄/L98H mutation, and has a test sensitivity of 71.1% and specificity of >92% when used
405 with BALf samples (Guegan *et al.*, 2018). Notwithstanding improvements in PCR
406 standardisation, the Infectious Diseases Society of America (ISDA) currently recommends
407 that *Aspergillus* PCR be used in individual cases if combined with other diagnostic and
408 clinical data (Misch and Safdar, 2016; Patterson *et al.*, 2016; Lass-Flörl, 2019).

409

410 **Semi-invasive and non-invasive diagnostic procedures**

411

412 Biomarker detection in serum

413

414 *ELISA, PCR, (1→3)-β-D-glucan, and LFD tests*

415

416 The literature on the relative specificities and sensitivities of fungal (1→3)-β-D-glucan tests,
417 Bio-Rad *Platelia*[®] GM-ELISA, in-house PCR assays, and prototype *Asp*LFD test, for serum-
418 based diagnosis of *Aspergillus* diseases is capacious, and has been reported extensively

419 elsewhere (Held *et al.*, 2013; White *et al.*, 2013; Pan *et al.*, 2015; Held and Hoenigl, 2017;
420 Rath and Steinmann, 2018; Ruhnke *et al.*, 2018; Patterson and Donnelly, 2019).

421 To date, there have been no studies evaluating the diagnostic performance of the CE-
422 marked *Asp*LFD when used with serum samples. However, an ELISA (GP-ELISA) which
423 employs the same mAb (JF5) used in the *Asp*LFD (and also in the experimental *Aspergillus*
424 proximity ligation assay (Mercier *et al.*, 2018)) has recently been developed and CE-marked
425 by Euroimmun Medizinische Labordiagnostika AG, and its performance compared to the
426 *Platelia*[®] GM-ELISA for IPA diagnosis using serum samples from immunocompromised
427 patients (Dichtl *et al.*, 2019). While the specificities of the GM-ELISA and GP-ELISA were 99%
428 and 96%, respectively, both assays demonstrated low sensitivities. When tests were
429 extended to all sera available in the time frame of 7 days before to 7 days after the day of
430 proven diagnosis, 47% and 56% of the cases were detected by the GM-ELISA and GP-ELISA,
431 respectively. The low sensitivities of both tests underline the need for serial tests when
432 using patient serum.

433

434 Molecular imaging using mAb JF5 and siderophores

435

436 Abnormalities in a chest-CT as diagnostic indicators of IPA (defined as dense, well-
437 delineated, nodular infiltrates with and without ground glass attenuation (the so-called
438 'halo sign'))(De Pauw *et al.*, 2008) are not disease-defining, with other pathologies (non-
439 *Aspergillus* lung infections, and neoplastic and inflammatory processes) giving similar
440 anomalies. Furthermore, these radiological indicators are transient in neutropenic patients,
441 or are rare in non-neutropenic patients (Prattes *et al.*, 2014). While magnetic resonance
442 imaging (MRI) provides unrivalled spatial resolution and soft tissue contrast, and can be
443 used as a detection aid for *Aspergillus* cerebral and central nervous system infections
444 (Starkey *et al.*, 2014; Marzolf *et al.*, 2016), its utility as an imaging modality for lung
445 infections is limited due to the lack of detectable protons in air-filled spaces and potential
446 artefacts between air-tissue interfaces.

447 For these reasons, attempts have been made to improve the accuracy of radiology for
448 diagnosis of IPA by combining positron emission tomography (PET) with CT and MRI
449 (Thornton, 2018). The *Aspergillus*-specific mAb, JF5, when conjugated to the radionuclide
450 ⁶⁴Cu, has been used in immunoPET/MRI as a disease-specific tracer ([⁶⁴Cu]NODAGA-JF5),
451 and allows accurate and sensitive non-invasive detection of *A. fumigatus* lung infections *in*
452 *vivo* (Rolle *et al.*, 2016; Davies *et al.*, 2017). Furthermore, humanisation of JF5 (Davies *et al.*,
453 2017) has allowed translation of the imaging technology to the clinic. A first-in-human
454 clinical trial commenced in 2018, with successful detection of IPA in a neutropenic
455 haematology patient, corroborated by BALf detection using the *Asp*LFD, GM-ELISA, and
456 culture (Thornton, pers. comm.).

457 Alternative approaches to the molecular imaging of IPA include the use of *Aspergillus*
458 siderophores in PET. When coupled to ⁶⁸Ga, a positron emitter with complexing properties
459 similar to those of Fe(III), the iron-chelating siderophore TAFC showed accumulation in the
460 lungs of immunosuppressed rats with IPA, with uptake correlating with severity of
461 *Aspergillus* infection (Petrik *et al.*, 2010 & 2012a,b). While still at the pre-clinical stage of
462 development, a [⁶⁸Ga]TAFC tracer for molecular imaging of *Aspergillus* lung infections *in*
463 *vivo*, holds enormous diagnostic potential, alongside antibody-guided PET/MR imaging
464 (immunoPET/MRI), for non-invasive detection of IPA in humans.

465

466 Biomarker detection in urine

467

468 *GM antigenuria*

469

470 Evidence for the presence of *Aspergillus* carbohydrate biomarkers in urine was first shown
471 in counter-immunodiffusion assays with urine from rabbits experimentally infected with *A.*
472 *fumigatus* (Lehman and Reiss, 1978). Antiserum used in the assay was prepared from an
473 immunosuppressed and infected rabbit (rather than an animal immunised with an *A.*
474 *fumigatus* antigen preparation), and showed that a carbohydrate antigen was detected in
475 the urine of the experimentally infected rabbits. Detection of the antigen was not found in
476 uninfected animals or in animals infected with *Candida albicans*. While human urinary
477 antigen was not investigated, and the identity of the carbohydrate was not established, this
478 early study was the first to demonstrate the excretion of *A. fumigatus* carbohydrate
479 antigen(s) into the urine of animals with IPA.

480 The identity of a carbohydrate antigen in the urine of experimentally infected
481 rabbits, and in the urine of patients with IPA, was subsequently demonstrated by Dupont
482 and co-workers (Dupont *et al.*, 1987). Galactomannan (GM) was detected in animal and
483 human urine samples using a sandwich ELISA employing rabbit antiserum raised against
484 purified GM. Using this assay, urinary GM was detectable throughout the course of lethal
485 aspergillosis in all 16 experimentally infected animals, in concentrations of 24 to 1,900 ng
486 GM/ml urine, with antigen excretion roughly paralleling the extent of disease.
487 Galactomannan was detected in the urine of 7 of 13 patients with IPA, with concentrations
488 of 1 to 83 ng GM/ml urine. A contemporaneous study by Bennett *et al.* (1987) showed that
489 within 24 hours after intravenous injection, 35% of galactomannan was excreted into the
490 urine of immunocompetent rabbits. Galactomannan detection in urine was also investigated
491 as a means of diagnosing experimental and spontaneous aspergillosis in cattle (Jensen *et al.*,
492 1993a). An inhibition ELISA using a GM-specific mAb EB-A1 (Stynen *et al.*, 1992), reacted
493 positively with urine samples from normal cattle, and so could not be used to detect
494 systemic bovine aspergillosis. The same mAb was used by Haynes *et al.* (1990) to detect GM
495 in the urine of neutropenic patients undergoing bone marrow transplantation or remission
496 induction therapy for leukemia. In immunoblotting studies, EB-A1 showed diffuse staining
497 (indicative of carbohydrate) in urine samples from patients with IPA, but no staining with
498 urine from patients without evidence of the disease.

499 The development of a commercial latex agglutination test for *Aspergillus* GM (Pastorex
500 *Aspergillus*, Sanofi Diagnostics Pasteur, France) using another GM-reactive rat mAb, EB-A2,
501 also developed by Stynen *et al.* (1992), enabled standardised testing of GM antigenemia in
502 the serum of IPA patients as a means of diagnosing IPA. The test was also investigated as a
503 diagnostic tool for IPA using GM antigenuria in bone marrow transplant recipients (Ansorg
504 *et al.*, 1994). After modification of the assay for urine testing, it had a detection limit in
505 native urine of approximately 20 ng GM/ml. Antigen was found in 79 (36.4%) of 217 serial
506 urine samples, compared to 40 (11.8%) of 340 serum samples. Overall, antigenuria
507 preceded antigenemia, and was more persistent. The sensitivity, specificity, PPV and NPV of
508 antigenuria for autopsy-proven aspergillosis and clinically-suspected *Aspergillus* infection
509 were 57%, 53%, 31% and 77%, respectively, while those of antigenemia were 43%, 53%,
510 25% and 71%, respectively. It was therefore concluded that urine testing was more reliable
511 than serum testing for the detection of *Aspergillus* GM.

512 Refinement of the latex agglutination test led to the development of a quantitative
513 sandwich ELISA for GM detection in patient serum, and which forms the basis of the
514 commercial Bio-Rad *Platelia*[®] ELISA for GM detection in patient serum and BALf samples.
515 The ELISA, which detects less than 1ng GM/ml sample, was also investigated as a urine test
516 for GM in patients with IPA (Stynen *et al.*, 1995). When GM was detected in urine, it was
517 always lower than in matched serum samples. In addition, GM was always detected earlier
518 in serum than in urine. The maximal number of days separating patient death and the first
519 detection of GM in patient serum and urine were ≥ 39 and ≤ 12 , respectively. Therefore, in
520 contrast to a previous report (Rogers *et al.*, 1990), it was recommended that serum rather
521 than urine be used for the detection of GM, because of the later diagnosis obtained with
522 urine samples.

523 Since the pioneering work in the 1990s, there has been limited interest in GM
524 antigenuria as a detection method for IPA due to reports of its limited utility and high rates
525 of false positivity, which vary between 8% and 47% (Klont *et al.*, 2004). However, since the
526 introduction of the *AspLFD* POCT, which has revolutionised point-of-care testing for the
527 disease, there has been renewed interest in GM detection in urine, due to its non-invasive
528 nature and the applicability of lateral-flow technology to urine biomarker testing. Dufresne
529 *et al.* (2012) recently reported the development of a new GM-reactive mAb (mAb476), and
530 demonstrated the feasibility of using the mAb in an immunochromatographic assay for
531 detection of GM-like antigens in urine. Further development of the assay into a dip-stick
532 format has demonstrated the potential of the test to detect proven or probable IPA in
533 patients at high-risk for the disease (patients with haematological malignancy, and
534 recipients of solid organ or HSCT). Per-patient sensitivity and specificity in the overall cohort
535 was 80% and 92%, respectively, and the urine assay correlated with serum galactomannan
536 indices (Marr *et al.*, 2018). While the test uses non-invasive urine samples for GM detection,
537 the requirement for sample pre-treatment means that it is unlikely to be a point-of-care test
538 for IPA. Nevertheless, it demonstrates the applicability of lateral-flow technology to urine
539 testing for *Aspergillus* diagnostic biomarkers, and for urine-based detection of other fungal
540 pathogens of humans such as *Cryptococcus* (Drain *et al.*, 2019) and *Histoplasma* (Libert *et*
541 *al.*, 2018).

542 543 *Urine siderophores*

544
545 In addition to cell wall carbohydrates such as GM, *A. fumigatus* and other *Aspergillus*
546 species produce proteins that are detectable in urine. These include the iron-scavenging
547 siderophores TAFC and ferricrocin. In a rat model of experimental aspergillosis, TAFC and
548 ferricrocin (FC) were quantified in urine and serum with matrix-assisted laser desorption
549 ionisation (MALDI) (Luptáková *et al.*, 2017). The limits of detection of the ferri-forms of TAFC
550 and FC in rat serum were 0.28 and 0.36 ng/ml, respectively, while in urine the limits of
551 detection were 0.02 and 0.03 ng/ml, respectively. The mean concentrations of TAFC and FC
552 in urine were 0.37 and 0.63 $\mu\text{g/ml}$, respectively. In a rat model of IPA, ferricrocin and TAFC
553 detection in urine using mass spectrometry therefore appeared to provide a non-invasive
554 means of detecting *Aspergillus* lung infections.

555 The siderophore TAFC has also been evaluated as a urine biomarker of IPA in humans
556 using mass spectrometry (Hoenigl *et al.*, 2019). Urine TAFC, normalised to creatinine, was
557 determined in 44 samples from 24 patients with underlying haematological malignancies
558 and probable, possible or no IPA, and compared to GM antigenuria using the Bio-Rad

559 *Platelia*[®] ELISA. Matched blood samples were also tested for GM, and for (1→3)-β-D-glucan
560 using the Fungitell test. The TAFC/crea index determination in urine samples showed a
561 promising performance for diagnosis of IPA, with sensitivities and specificities comparable
562 to those reported for GM in serum and BALf, and superior to GM antigenuria
563 determinations. Compared to TAFC detection in human BALf and serum samples (Carroll *et*
564 *al.*, 2016; Orasch *et al.*, 2017), the diagnostic performance of TAFC levels in urine seems to
565 be superior, which may be due to accumulation in the bladder as shown in recent animal
566 models (Petrik *et al.*, 2014 and 2015).

567

568 **Allergic Bronchopulmonary Aspergillosis (ABPA)**

569

570 Diagnosis of ABPA is extremely difficult, reflected in a number of different diagnostic
571 definitions of the disease. To unify diagnosis and therapy of ABPA, the International Society
572 for Human and Animal Mycology (ISHAM) produced consensus-based guidelines in 2013
573 (Agarwal *et al.*, 2013). Isolation of *A. fumigatus* from sputum samples can sometimes be
574 useful, but is not included in the guidelines due to its poor sensitivity and specificity. As with
575 other *Aspergillus* lung diseases, consolidation seen in a chest-CT is non-pathognomonic and
576 may indicate another pulmonary infection such as pulmonary tuberculosis. Nevertheless,
577 radiographic pulmonary opacities consistent with ABPA (Agarwal *et al.*, 2013) are included
578 under 'other criteria', of which there should be at least two of three present in a patient
579 with bronchial asthma or cystic fibrosis (the other two being presence of precipitating IgG
580 antibodies against *A. fumigatus* in serum, or total eosinophil count >500 cells/μl in steroid
581 naïve patients). These additional criteria should accompany both of the 'obligatory criteria'
582 which are (1) a positive Type I skin test (immediate cutaneous hypersensitivity to *Aspergillus*
583 antigen) or elevated IgE levels against *A. fumigatus*, and (2) elevated total IgE levels (>1000
584 IU/ml).

585 The heavy reliance on serology to include or exclude ABPA has led to efforts to improve
586 test reproducibility since production of IgG and IgE antibodies to *Aspergillus* spp. is usually
587 determined using a crude antigen extract with inherent variability and cross-reactivity with
588 other fungal antigens (Reed, 1978; Cramer *et al.*, 2009). The cloning of genes that encode
589 allergenic proteins of *A. fumigatus* enabled improvements in the reliability of serological
590 diagnosis of ABPA using recombinant antigens (Cramer *et al.*, 1998a,b; Fricker-Hidalgo *et*
591 *al.*, 2010). A recent study by Alghamdi *et al.* (2019) of CF patients with ABPA, *Aspergillus*
592 sensitisation (AS), or *Aspergillus* bronchitis (AB) showed that patients with ABPA had
593 significantly greater IgE reactivity to the allergenic proteins Asp f1, f2, f3, and f4 compared
594 to patients with AS. Patients with AB expressed higher IgG positivity to Asp f1 and Asp f2
595 compared with those with ABPA. There were very low IgE antibody levels against all
596 recombinant antigens in AS patients. Asp f1 IgG reactivity in ABPA patients correlated with
597 positive sputum culture. It was concluded that the use of multiple recombinant allergens
598 may improve the diagnostic accuracy in CF complicated with ABPA or AB. Furthermore, Asp
599 f1 reactivity might be a useful marker for guiding antifungal therapy in ABPA.

600 The role of fungi in bronchiectasis not due to CF is poorly defined. Aogáin *et al.* (2018)
601 characterised for the first time the mycobiome in bronchiectasis, assessing its clinical
602 relevance in two geographically distinct cohorts from the CAMEB study, an international
603 multicentre cross-sectional Cohort of Asian and Matched European Bronchiectasis patients.
604 The mycobiome was determined in 238 patients by targeted amplicon shotgun sequencing
605 of the 18S-28S rRNA internal transcribed spacer regions ITS1 and ITS2. The bronchiectasis

606 mycobiome profiles were dominated by *A. fumigatus* in Singapore/Kuala Lumpur, and by *A.*
607 *terreus* in Dundee, the latter associated with exacerbations. High frequencies of *Aspergillus*-
608 associated disease including sensitisation and ABPA were detected. This study showed that
609 the mycobiome is of clinical relevance in bronchiectasis, and screening for *Aspergillus*-
610 associated disease should be considered even in apparently stable patients.

611

612 **Chronic Pulmonary Aspergillosis (CPA)**

613

614 Symptoms of CPA (taken here as CCPA, CFPA, and SAIA/CNPA) are non-specific and, as with
615 other *Aspergillus* lung diseases, diagnosis of the disease based on culture of fungi from
616 respiratory specimens lacks sensitivity, with culture positivity as low as 11.8% (Takazono and
617 Izumikawa, 2018). Radiological findings on a chest-CT are variable and overlapping and
618 depend on the state and stage of the disease. Diagnosis of a simple pulmonary aspergilloma
619 in an immunocompetent individual is based on detection of a single lung cavity with no
620 progression over at least 3 months of observation, while an *Aspergillus* nodule is defined by
621 the presence of one or more nodules without cavitation (Denning *et al.*, 2016; Muldoon *et al.*,
622 2016). The diseases CCPA and SAIA share the similar characteristics of one or more
623 cavities with or without fungal ball, accompanied by radiological progression such as
624 expanding thick-walled cavities and pericavitary infiltration (Denning *et al.*, 2016). They
625 differ in that SAIA also involves hyphal invasion of the lung parenchyma (Hope *et al.*, 2005).
626 This subtle difference creates a diagnostic dilemma, especially when histopathology is
627 lacking. The time course of radiological progression (CCPA >3 months; SAIA 1-3 months) and
628 process of cavitory formation (CCPA typically occurs in pre-existing cavities, while SAIA
629 cavities are formed during *Aspergillus* infection) are therefore needed for disease
630 differentiation, but are reliant on serial radiography. The syndrome CFPA is defined by
631 cavitation and fibrosis involving two or more lobes leading to a major loss of lung function,
632 and is generally regarded as the end result of untreated CCPA (Denning *et al.*, 2003 and
633 2016).

634 Galactomannan-ELISA of serum has limited diagnostic value for CPA detection, with low
635 sensitivity and specificity even when the threshold index value for test positivity is reduced
636 from ≥ 1.5 (the manufacturer's recommended threshold index value for serodiagnosis of IPA
637 (Maertens *et al.*, 2007)) to ≥ 0.5 (Kitasato *et al.*, 2009). Galactomannan-ELISA of BALf showed
638 relatively higher sensitivity (77.2%) and specificity (77.0%), when the index threshold value
639 for test positivity was reduced further to ≥ 0.4 (Izumikawa *et al.*, 2012). In a more recent
640 study (Salzer *et al.*, 2018), the GM-ELISA was evaluated alongside the *Asp*LFD and levels of
641 cytokines for diagnosis of CPA (Salzer *et al.*, 2018). Sensitivity and specificity of the GM-
642 ELISA with a cut-off of ≥ 0.5 was 41% and 100%, respectively. When the cut-off was
643 increased to ≥ 1.0 , the sensitivity decreased to 30% while specificity remained at 100%. The
644 *Asp*LFD was positive with only 7% of patients. Therefore, based on test sensitivities, both
645 the GM-ELISA and *Asp*LFD showed insufficient performance for diagnosing CPA. However,
646 their high specificities provide high positive predictive values, which may help identify semi-
647 invasive or invasive disease. In this study, the cytokine profiles of CPA patients did not differ
648 significantly from patients with other respiratory disorders, but showed significantly higher
649 levels of IFN- γ , IL-1b, IL-6, IL-8, and TNF- α compared to healthy controls.

650 Further evaluation of the *Asp*LFD test using serum and BALf samples from CPA patients
651 has shown improved diagnostic performance (Takazono *et al.*, 2019). In this study, the
652 diagnostic performance of the *Asp*LFD was compared to the GM-ELISA and (1 \rightarrow 3)- β -D-

653 glucan tests using samples from patients with SAIA, simple pulmonary aspergilloma, and
654 respiratory disease controls (PTB, NTM, COPD, interstitial pneumonia, prior lung surgery,
655 lung cancer, and bacterial infection (pneumonia, lung abscess)). The sensitivity and
656 specificity of the *Asp*LFD using serum were 62.0% and 67.7%, respectively, while serum GM-
657 ELISA (cut-off index value of ≥ 1.5) showed a sensitivity of 22% and a specificity of 92.3%,
658 respectively. Plasma (1 \rightarrow 3)- β -D-glucan tests (cut-off value of 19.3 pg/ml), had a sensitivity
659 of 48% and a specificity of 90.8%, respectively. Using BALf samples, the sensitivity and
660 specificity of the *Asp*LFD were 66.7% and 69.2%, respectively, while the GM-ELISA (cut-off
661 index value of ≥ 0.6) had a sensitivity of 72.7% and specificity of 83.1%. *Aspergillus*
662 precipitating antibody had a test sensitivity of 70%. Given these results, it was concluded
663 that the performance of the *Asp*LFD serum test was acceptable for the diagnosis of CPA as a
664 POCT.

665 As with ABPA, detection of *Aspergillus*-specific IgG plays an important role in the
666 diagnosis of CPA (Richardson and Page, 2018). There are a number of *Aspergillus*-specific
667 IgG tests available commercially (Page *et al.*, 2016; Takazono *et al.*, 2019). In a study
668 comparing six of these assays (Page *et al.*, 2016), the automated ImmunoCAP fluoroenzyme
669 immunoassay and Immunolite ELISA variant (Page *et al.*, 2015) were significantly superior to
670 the other assays (Dynamiker, Genesis, and Serion) in diagnosing CPA, with identical
671 specificities (both 96%) and sensitivities (both 98%). Precipitin testing performed poorly, as
672 did a recently introduced quantitative serum *Aspergillus fumigatus*-specific IgM assay (Yao
673 *et al.*, 2018a). Questions remain concerning the optimum cut-off values for IgG test
674 positivities, with values provided by manufacturer's appearing to be sub-optimal for
675 diagnosis of the disease (Page *et al.*, 2016, 2019; Sehgal *et al.*, 2018). Despite this, it appears
676 that serial serum testing for *Aspergillus*-specific IgG may provide a useful means of
677 monitoring treatment response and outcome since serum IgG levels decrease during
678 antifungal treatment and resolution (Yao *et al.*, 2018b).

679 The limitations of the commercial *Aspergillus*-specific IgG tests are their specificity for
680 *A. fumigatus*, their expense, and their reliance on automation. Approximately 40% of CPA
681 cases are caused by non-*fumigatus* spp. (e.g. *A. niger* and *A. versicolor*), which these tests
682 would not detect (Tashiro *et al.*, 2011). The cost of the tests and their reliance on
683 automated procedures makes them unsuitable for resource-limited settings. While most
684 CPA (and ABPA) patients are diagnosed in high-income countries, prevalence of these
685 diseases is believed to be higher in low- to middle-income countries (Denning *et al.*, 2011).
686 Consequently, a test for CPA that requires minimal laboratory equipment, akin to the
687 *Asp*LFD test for IPA, is needed. This need appears to have been met by a novel anti-
688 *Aspergillus* antibody LFA manufactured by LDBIO Diagnostics, with other LFAs for *Aspergillus*
689 immunoglobulins in development (Richardson and Page, 2018). The LDBIO Diagnostics LFA
690 or immuno-chromatographic test (ICT) has recently been evaluated in a multicenter
691 comparison of assays for CPA diagnosis (Piarroux *et al.*, 2019). The sensitivity and specificity
692 of the ICT were 88.9% and 96.3%, respectively, compared to 93.1% sensitivity and 94.3%
693 specificity for an anti-*Aspergillus* IgG immunoblot assay. Since the ICT displays good
694 diagnostic performance and complies with the ASSURED (Affordable, Sensitive, Specific,
695 User-friendly, Equipment-free, and Delivered) criteria, it is appropriate for diagnosis of CPA
696 in resource-limited settings. Marked improvements in IPA detection have been met through
697 combination diagnostic testing. As advocated previously (Kobayashi and Thornton, 2014), a
698 similar approach may prove beneficial for CPA diagnosis. A combination of serological and

699 biomarker tests such as the LDBIO ICT and OLM *Asp*LFD might allow rapid, simple, cheap,
700 but accurate diagnosis of the disease.

701

702 ***Fusarium* species pathogenic to humans**

703

704 The genus *Fusarium* comprises plant, human, and animal pathogenic species with
705 worldwide distribution (Jain *et al.*, 2011; Muraosa *et al.*, 2017). As a group of organisms,
706 they are a major constraint to food security, not only as pathogen of crop plants, but also as
707 producer of mycotoxins contaminating the food chain (Thornton and Wills, 2015). In
708 humans, *Fusarium* spp. cause a spectrum of diseases including nail infections
709 (onychomycosis)(Arrese *et al.*, 1996; Westerberg and Voyack, 2013), bone and joint
710 infections (Koehler *et al.*, 2014), infections of the skin and of burn wounds (Nucci and
711 Annaissie, 2002; Latenser, 2003; Gurusidappa and Mamatha, 2011; Muhammed *et al.*, 2013;
712 Nucci *et al.*, 2013; van Diepeningen *et al.*, 2014), mycotic eye infections (fungal
713 keratitis)(Jurkunas *et al.*, 2009; He *et al.*, 2011), and deep tissue infections following
714 combat-related blast injury (Paolino *et al.*, 2012; Warkentien *et al.*, 2012; Tribble and
715 Rodriguez, 2014). Up until the 1980s, most reported *Fusarium* infections were to the nails
716 and eyes, or were locally invasive infections. Since then, there has been an increase in the
717 number of cases of life-threatening disseminated disease (fusariosis) in patients with
718 haematological malignancies (García-Ruiz *et al.*, 2015), in HIV patients (Esnakula *et al.*,
719 2013), in patients with diabetes and liver cirrhosis (Chen *et al.*, 2017), in solid organ
720 transplant recipients (Muhammed *et al.*, 2013; Mohanty and Sahu, 2014), and most
721 particularly in allogeneic HSCT recipients (Fanci *et al.*, 2013; Scheel *et al.*, 2013; Al-Hatmi *et al.*,
722 2016), reflecting their greater immunosuppression and profound and prolonged
723 neutropenia. Fusariosis is now the second most common mould disease of humans after
724 aspergillosis (Guarro, 2013), multidrug-resistant and refractory to treatment (Fanci *et al.*,
725 2013; Al-Hatmi *et al.*, 2016), with poor prognosis (Tortorano *et al.*, 2014), and with mortality
726 rates reaching 75%.

727 At least 70 species of *Fusarium* are able to cause infections in humans, and are
728 grouped into species complexes (Guarro, 2013). Most infections in humans are caused by
729 only four species; *F. petrophilum* and *F. keratoplasticum* in the *Fusarium solani* species
730 complex (FSSC)(Short *et al.*, 2013), an unnamed species in the *Fusarium dimerum* species
731 complex (FDSC), and a further unnamed species in the *Fusarium oxysporum* species complex
732 (FOSC). Members of these species complexes are readily isolated from environmental
733 samples, including soil and plant material (Thornton and Wills, 2015), air (Scheel *et al.*,
734 2013), and water systems and plumbing fixtures (Dogget, 2000; Anaissie *et al.*, 2002; Mehl
735 and Epstein, 2008; Anaissie *et al.*, 2011; Short *et al.*, 2011). Indeed, contaminated water
736 systems appear to be an important environmental source of pathogenic fusaria in
737 community-acquired and nosocomial outbreaks of fusariosis, with a recent study showing
738 that hospital and communal sink biofilms are heavily colonised by pathogenic species in the
739 FSSC, FDSC, and FOSC complexes (Al-Maqtoofi and Thornton, 2016), and thus a potential
740 source of infectious propagules.

741

742

743

744

745 **Detection of *Fusarium* diseases**

746

747 Radiology, histology and culture

748

749 In countries with high rates of fungal keratitis, confocal microscopy of the eye has proved
750 useful in the non-invasive detection of fungal structures (hyphae, pseudo-hyphae, and
751 yeast-like structures) in the infected cornea (Brasnu *et al.*, 2007). However, direct
752 microscopy is non-specific, and so is unable to discriminate between the various different
753 fungi (*Aspergillus*, *Candida*, *Fusarium*) capable of causing mycotic infections of the cornea.

754 Radiological findings in CT may be useful in raising the suspicion of a *Fusarium* lung
755 infection, but are non-specific, with findings including alveolar and interstitial infiltrates,
756 nodules and cavities that are typical of other mould infections (Marom *et al.*, 2008). In chest
757 CT, nodules and masses were the most common findings, with a halo sign being absent in
758 80% of cases.

759 The ESCMID and ECMM joint guidelines for diagnosis of hyalohyphomycosis strongly
760 recommend histopathology for the diagnosis of fusariosis (Tortorano *et al.*, 2014). However,
761 in tissue, the hyphae of *Fusarium* typically resemble those of *Aspergillus*, with hyaline and
762 septate filaments that dichotomise at acute and right angles (Nucci and Anaissie, 2007).
763 Attempts have been made to improve the accuracy of *in situ* detection of *Fusarium* in
764 tissues, but these remain experimental, relying on immunohistochemical procedures that
765 employ cross-reactive antisera (Fukuzawa *et al.*, 1995; Kaufman *et al.*, 1997; Saito *et al.*,
766 1999), or on molecular detection using in-house PCR assays (Salehi *et al.*, 2016). Definitive
767 diagnosis of invasive *Fusarium* infections therefore relies on culture of the fungus from skin
768 biopsies and other infected tissues (sinuses, lungs) or from the blood. Fusariosis is perhaps
769 unique amongst the invasive mould diseases, in that the pathogens' infectious propagules
770 are spread haematogenously, and can be recovered from the bloodstream in up to 82% of
771 cases (Grossman *et al.*, 2012; Muhammed *et al.*, 2013). In contrast, *Aspergillus* is rarely
772 detected in the blood. Haematogenous spread of *Fusarium* spores accounts for the multiple
773 necrotic skin lesions that develop in 75-90% of disseminated infections (Van Diepeningen *et al.*,
774 2015a), a clinical manifestation uncommon in disseminated aspergillosis. Culture from
775 tissue and blood samples enables identification of *Fusarium* based on the crescent or
776 banana-shaped macroconidia characteristic of this genus. However, identification to species
777 level, which is essential for guiding clinical management (Muhammed *et al.*, 2011), is
778 difficult and relies on nucleic acid-based tests of tissue specimens or axenic cultures.

779

780 Nucleic acid tests

781

782 Ribosomal RNA gene sequences, and sequencing of the internal transcribed spacer (ITS)
783 region, a procedure widely used for the identification of other mould species, is of limited
784 value for identifying and bar-coding *Fusarium* species due to the presence of duplicated
785 divergent alleles in this region. For this reason, molecular identification of clinical isolates
786 relies on three loci; *TEF-1 α* (translation elongation factor-1 α)(García-Ruiz *et al.*, 2015; Zarrin
787 *et al.*, 2016; Muhammed *et al.*, 2018), *RPB1* (the largest subunit of RNA polymerase), and
788 *RPB2* (the second largest subunit of RNA polymerase)(Al-Hatmi *et al.*, 2016). Based on these
789 loci, DNA sequence databases have been constructed, and can be interrogated at
790 FUSARIUM-ID (<http://isolate.fusariumdb.org/guide.php>) and at CBS-KNAW
791 (<http://www.westerdijkinstituut.nl/fusarium/>), for the identification of environmental and

792 clinical isolates. Using a newly generated *Fusarium*-specific monoclonal antibody (ED7) that
793 detects an extracellular antigen (a 200kDa water-soluble carbohydrate), Al-Maqtoofi and
794 Thornton (2016) were able to track pathogenic fusaria in hospital and communal sink
795 biofilms, with FSSC sequence type (ST) 1-a, FO SC ST 33, and FDSC ST ET-gr isolates identified
796 using *TEF-1 α* sequencing of recovered strains. This study demonstrated the specificity of
797 mAb ED7, which might find use in the detection of *Fusarium* infections in humans based on
798 detection of the 200kDa biomarker in patient samples. Multi-locus sequence typing (MLST)
799 is currently regarded as the most robust method for differentiating *Fusarium* species
800 complexes (Wang *et al.*, 2011) or identifying isolates to species level (Tortorano *et al.*,
801 2014), with *TEF-1 α* and *RPB2* employed in many MLST diagnostic regimens (Van
802 Diepeningen *et al.*, 2015b).

803 There are currently no nucleic acid-based detection systems CE-marked or FDA-
804 approved for the diagnosis of human fusariosis, but a number of experimental polymerase
805 chain reaction (PCR) tests have been reported for the detection and quantification of
806 *Fusarium* DNA in murine models of fusariosis, and in human tissue specimens (Bernal-
807 Martínez *et al.*, 2012; Muraosa *et al.*, 2014; Salehi *et al.*, 2016). A duplex RT-PCR using two
808 specific molecular beacon probes targeting a highly conserved region of the rDNA gene was
809 developed for *F. solani* and non-*Fusarium solani* DNA detection, and validated in two mouse
810 models of invasive infection (Bernal-Martínez *et al.*, 2012). Specificity of the assay was
811 100%. While sensitivity of the assay in a *F. solani* infection model was 93.9% for lung tissues
812 and 86.7% for serum samples, its sensitivity in a *F. oxysporum* infection model was 87% for
813 lung tissues and 42.8% for serum samples. A *Fusarium* genus-specific and FSSC-specific RT-
814 PCR system has also been developed, which targets the 28s ribosomal RNA gene (Muraosa
815 *et al.*, 2014). To apply the RT-PCR system to the molecular diagnosis of fusariosis,
816 performance was evaluated using plasma and whole blood samples from a mouse model of
817 invasive *F. solani* infection. The sensitivity of the RT-PCR system was found to be 100% in
818 plasma, but no amplification was detected in whole blood. In a retrospective multicentre
819 study, Salehi *et al.* (2016) reported the discrimination of fusariosis, aspergillosis,
820 mucormycosis, and scedosporiosis in formalin-fixed paraffin-embedded human tissue
821 specimens using multiple real-time quantitative PCR assays. The qPCR assays, targeting the
822 ITS2 region of ribosomal DNA using fluorescently labelled primers, was used to identify
823 clinically important genera and species of *Fusarium*, *Aspergillus*, *Scedosporium*, and
824 mucormycetes, and the molecular identification compared to results from histological
825 examination. *Fusarium oxysporum* and *F. solani* DNA was amplified from five specimens
826 from patients initially diagnosed by histopathology as having aspergillosis. This study
827 demonstrates that histopathological features of moulds may be easily confused in tissue
828 sections, and that qPCR can be used for the rapid and accurate identification of fungal
829 pathogens to the genus and species levels directly from FFPE tissues. Despite this, molecular
830 tests should be used only to supplement conventional laboratory tests (Tortorano *et al.*,
831 2014).

832

833 Antigen tests

834

835 At present, there are no antigen tests available commercially which are specific for *Fusarium*
836 detection. While (1 \rightarrow 3)- β -D-glucan detection can be used to diagnose fusariosis both in
837 animal models (Khan *et al.*, 2008) and in humans, its pan-fungal reactivity means that it
838 lacks specificity. Disconcertingly, cross-reaction of the *Aspergillus* GM-ELISA with *Fusarium*

839 spp. has been reported, with roughly half of patients with fusariosis giving a positive test
840 result with the assay (Tortorano *et al.*, 2012). The reason for this cross-reactivity is
841 uncertain, but may be due to the presence of the β -1,5-linked GalF moieties recognised by
842 the GM-reactive mAb EB-A2 being present in polysaccharide antigens from fungi other than
843 *Aspergillus*, including *Fusarium* spp (Tortorano *et al.*, 2012). Certainly, galactomannan has
844 been found in *Fusarium* culture supernatants (Tortorano *et al.*, 2012; Wiedemann *et al.*,
845 2016). The Platelia *Candida* mannan ELISA has also been reported to cross-react with *F.*
846 *verticillioides*, *F. solani* and *F. oxysporum* (Rimek *et al.*, 2003). These findings call into
847 question the validity of these tests for the specific diagnosis of aspergillosis and candidiasis,
848 respectively. Despite this, the GM-ELISA has been evaluated in humans as a means of
849 diagnosing fusariosis and as a monitoring tool for treatment response (Nucci *et al.*, 2014),
850 but there is little obvious legitimacy for using this assay for fusariosis detection in the clinical
851 setting given the similar patient groups susceptible to candidiasis, aspergillosis and
852 fusariosis.

853

854 ***Pseudallescheria/Scedosporium* species complex and *Lomentospora*** 855 ***prolificans***

856

857 Previously, *Pseudallescheria boydii* was considered synonymous with *Pseudallescheria*
858 *angusta*, *Pseudallescheria ellipsoidea*, and *Pseudallescheria fusoidea* (Rainer *et al.*, 2000),
859 with a subsequent taxonomic study suggesting that *P. boydii* is a complex comprising six
860 species (*P. boydii*, *P. angusta*, *P. ellipsoidea*, *P. fusoidea*, *P. minutispora*, and *Scedosporium*
861 *aurantiacum*)(Gilgado *et al.*, 2005). *Scedosporium apiospermum* along with *Graphium* spp.
862 (*G. capitatum*, *G. eumorphum*, and *G. penicillioides*) were considered to be synanomorpha
863 of *P. boydii* (Rainer *et al.*, 2006), with *S. apiospermum* then shown to be a species distinct
864 from *P. boydii* (Gilgado *et al.*, 2008), challenging previous doctrine that this fungus was the
865 asexual or anamorphic state of *P. boydii*. Currently, *Pseudallescheria* and *Scedosporium* are
866 regarded as a composite of species, the *Pseudallescheria/Scedosporium* complex (PSC)
867 (Luplertlop, 2018), with the genus *Scedosporium* now comprising *S. aurantiacum*, *S.*
868 *desertorum*, *S. minutisporum*, *S. cereisporum*, and *S. dehoogii*, in addition to the *S.*
869 *apiospermum* complex consisting of *S. angustum*, *S. apiospermum*, *S. boydii*, *S. ellipsoidea*,
870 and *S. fusoideum* (Ramirez-Garcia *et al.*, 2018). Prior to the advent of molecular taxonomy,
871 the dematiaceous fungus *Scedosporium prolificans* (formerly *S. inflatum*) was believed to be
872 a member of the genus *Scedosporium*, but has since been shown to be unrelated to
873 *Scedosporium*, and has been re-classified as *Lomentospora prolificans* (Hennebert and Desai,
874 1974) with the genus *Lomentospora* being re-instated for this species (Lackner *et al.*, 2014).

875 The species *S. apiospermum*, *S. aurantiacum*, and *S. boydii* are pathogenic to humans,
876 causing eumycetoma, localised cutaneous infections, muscle, joint and bone infections, and
877 fatal disseminated infections (Cortez *et al.*, 2008; Taylor *et al.*, 2014; Kondo *et al.*, 2018;
878 Ramirez-Garcia *et al.*, 2018), and are consequently the most studied species in the genus.
879 These fungi are soil saprotrophs that appear to have a proclivity for habitats impacted by
880 human activity (Kalteis *et al.*, 2009; Rougeron *et al.*, 2015). However, the evidence for this
881 association is questionable, since these organisms are also readily isolated from habitats
882 such as brackish waters and estuarine muds (Thornton, 2009). Notwithstanding this, the
883 numerous reports of these fungi as agents of disease in near-drowning events and following
884 natural disasters such as tsunamis due to aspiration of soil-laden water (Garzoni *et al.*, 2005;

885 Leroy and Smismans, 2007; Linscott, 2007; Nakamura *et al.*, 2011, 2013; Angelina *et al.*,
886 2013; Nakamura *et al.*, 2013), demonstrates their abundance in the natural environment,
887 and their ability to cause life-threatening central nervous system (CNS) and cerebral
888 infections following traumatic implant of infectious propagules in the lungs (Ramirez-Garcia
889 *et al.*, 2017). Less is known about the ecology of *Lomentospora prolificans*, but it is a soil-
890 and compost-borne fungus (Hennebert and Desai, 1974; Grantina-levina *et al.*, 2013), and is
891 present, alongside members of the PSC, in estuarine muds (Thornton *et al.*, 2015).

892 Pathogens in the PSC complex and *L. prolificans* are persistent colonisers of the lungs of
893 cystic fibrosis (CF) patients, and are the second most frequent moulds after *A. fumigatus* in
894 the sputum of CF patients and those with underlying respiratory diseases (Cimon *et al.*,
895 2000; Cooley *et al.*, 2007; Blyth *et al.*, 2010a,b; Sedlacek *et al.*, 2015; Schwarz *et al.*, 2015;
896 Schwarz *et al.*, 2017; Tomazin and Matos, 2017; Bouchara *et al.*, 2018; Schwarz *et al.*, 2018).
897 While chronic airway colonisation of the lung by these fungi can lead to fatal outcomes in CF
898 patients (Borghi *et al.*, 2010), the role of these fungi in CF exacerbation, other than causing
899 acute obstruction (Padoan *et al.*, 2016), is not fully understood. Notwithstanding this, a
900 trait common to all strains isolated from the CF lung is their high resistance to antifungal
901 drugs, with *L. prolificans* demonstrating multi-drug resistance (Borghi *et al.*, 2010; Sedlacek
902 *et al.*, 2015), and successful treatment of lung infections requiring triple antifungal drug
903 regimes in several cases (Schwarz *et al.*, 2018). Important risk factors for fatal disseminated
904 infections (scedosporiosis and lomentosporiosis) include neutropenia and haematological
905 malignancy (Maertens *et al.*, 2000; Rodriguez-Tudela *et al.*, 2009; Song *et al.*, 2009),
906 advanced AIDS (Tammer *et al.*, 2011), chronic granulomatous disease (Santos *et al.*, 2000),
907 allogeneic stem cell transplantation (Tamaki *et al.*, 2016), and solid organ transplantation
908 (Husain *et al.*, 2005). Malignancy, fungemia, central nervous system (CNS) and lung
909 involvement are prognostic factors predicting worse outcome for scedosporiosis and
910 lomentosporiosis (Seidel *et al.*, 2019). Disseminated infections following lung
911 transplantation are particularly problematic (Vagefi *et al.*, 2005; Morio *et al.*, 2010; Rolfe
912 *et al.*, 2013), with a *S. apiospermum* and *L. prolificans* mixed disseminated infection reported
913 recently (Balandin *et al.*, 2016).

914

915 **Detection of *Scedosporium* and *Lomentospora* diseases**

916

917 Radiology, histology and culture

918

919 *Scedosporium* and *Lomentospora* infections are often clinically indistinguishable from other
920 invasive mould infections, with radiology based on chest CT providing little diagnostic worth
921 due to non-specific indicators of fungal lung infection (Dabén *et al.*, 2008; Holmes *et al.*,
922 2013; Nakamura *et al.*, 2013; Schwarz *et al.*, 2015). In contrast, brain MRI is an important
923 diagnostic modality for detecting disseminated CNS infections in immunosuppressed stem
924 cell and solid organ transplant recipients, and in victims of near-drowning, particularly in
925 cases where antifungal treatment fails to resolve disease, or where a clear spreading focus
926 is absent (Morio *et al.*, 2010; Bhuta *et al.*, 2012; Holmes *et al.*, 2013; Nakamura *et al.*, 2013;
927 Sharma and Singh, 2015; Tamaki *et al.*, 2016; Ramirez-Garcia *et al.*, 2018).

928 Histopathological examination of biopsy material has limited diagnostic utility as it is
929 difficult to distinguish *Scedosporium/Lomentospora*-infected tissues from those infected
930 with other hyaline fungi such as *Aspergillus* and *Fusarium* species (Ramirez-Garcia *et al.*,
931 2018), although the dematiaceous (melanised) hyphae of *L. prolificans* may provide an

932 opportunity for species differentiation. Immunohistological procedures using polyclonal
933 fluorescent antibodies have attempted to improve the accuracy of *in situ* detection
934 (Kaufman *et al.*, 1997), but cross-reaction with antigens from other fungi such as *Aspergillus*
935 hamper their usefulness. For these reasons, diagnosis of scedosporiosis and
936 lomentosporosis relies on the recovery of the etiological agent from clinical specimens and
937 identification using macroscopic and microscopic features (Ramsperger *et al.*, 2014; Luna-
938 Rodríguez *et al.*, 2019) *in vitro*. As with *Fusarium* species, accurate differentiation of species
939 is critical for guiding clinical management due to variable antifungal susceptibilities (Gilgado
940 *et al.*, 2006; Cortez *et al.*, 2008; Box *et al.*, 2018). While *Scedosporium* and *Lomentospora*
941 species can be recovered from sterile sites such as blood, bone and tissue biopsy specimens
942 using standard mycological media, for example Saboraud's dextrose agar (SDA), their
943 frequent occurrence in sputum samples of CF patients (Sedlacek *et al.*, 2015; Chen *et al.*,
944 2017) necessitated the development of selective media that prevent overgrowth by faster
945 growing *Aspergillus*, *Candida* and *Fusarium* species in polymicrobial clinical samples (Rainer
946 *et al.*, 2008; Blyth *et al.*, 2010; Hong *et al.*, 2016). One of the most effective media for
947 selective isolation of *Scedosporium* species is *Scedosporium* Selective agar (SceSel+)(Rainer
948 *et al.*, 2008; Blyth *et al.*, 2010) containing the antifungal agents benomyl and dichloran that
949 limit the growth of *Aspergillus* and *Candida*. *Scedosporium* species and *L. prolificans* can
950 then be further differentiated in culture with the inclusion of cycloheximide that is
951 inhibitory to *L. prolificans* (Ramsperger *et al.*, 2014).

952

953 Nucleic acid tests

954

955 Speciation of isolates within the *Pseudallescheria/Scedosporium* complex and their
956 discrimination from *L. prolificans* based on microscopic features requires considerable
957 expertise and can be problematic. For this reason, a number of molecular methods have
958 been developed for the detection and differentiation of these fungi in axenic culture,
959 sputum, and tissue samples including multiplex PCR (Harun *et al.*, 2011); repetitive
960 sequence-based PCR (rep-PCR)(Steinmann *et al.*, 2011); qPCR, loop-mediated isothermal
961 amplification (LAMP) and PCR-based reverse line blot (PCR-RLB)(Lu *et al.*, 2011a,b);
962 oligonucleotide arrays (Bouchara *et al.*, 2009); DNA sequencing and restriction fragment
963 length polymorphisms (RFLP)(Delhaes *et al.*, 2008; Gilgado *et al.*, 2005, 2008), and Rolling
964 Circle Amplification (RCA)(Lackner *et al.*, 2012). These techniques and their different
965 capabilities are comprehensively reviewed elsewhere (Ramsperger *et al.*, 2014; Ramirez-
966 Garcia *et al.*, 2018). Despite these myriad methods for pathogen detection and speciation,
967 no single technique has been universally adopted nor are any commercial tests currently
968 recommended for this purpose. Current guidelines recommend that nucleic acid-based
969 assays be used in combination with conventional laboratory tests (Tortorano *et al.*, 2014).

970

971 Proteomics and antigen tests

972

973 Matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-
974 TOF/MS) has been investigated as an alternative strategy for identification of fungi within
975 the PSC (Coulibaly *et al.*, 2011), and other pathogenic moulds (Santos *et al.*, 2010; Cassagne
976 *et al.*, 2011; Bader, 2013; Lau *et al.*, 2013). This technique currently lacks the requisite
977 standardisation needed for clinical acceptability in medical mycology, but it nevertheless
978 has the potential to replace gene-sequencing methods for mould identification, as it is

979 accurate, comparatively inexpensive and relatively quick compared to sequencing methods.
980 However, it does require robust online reference databases constructed using similar fungal
981 growth and extraction procedures for interrogation of MS spectra from unknown species.
982 Commercially available MALDI-TOF/MS identification solutions are apparently inadequate
983 for *Scedosporium/Lomentospora* discrimination at present (Ramirez-Garcia *et al.*, 2018).

984 Mass spectrometry (MS) has also recently used by Thornton *et al.* (2015) to identify the
985 antigen bound by a mAb (CA4) specific to *L. prolificans*. This IgG1 mAb is highly specific,
986 binding to an intracellular protein from *L. prolificans*, but not with proteins extracted from
987 members of the PSC or from other unrelated moulds. CA4-reactive peptides in western
988 blots of cell extracts following two-dimensional electrophoresis were identified using MS as
989 fragments of the melanin-biosynthetic enzyme tetrahydroxynaphthalene reductase (4HNR).
990 This enzyme is one of a number of enzymes involved in DHN-melanin production of
991 dematiaceous moulds such as *L. prolificans* (Al-Laaeiby *et al.*, 2016). Confirmation of the CA4
992 antigen as the enzyme 4HNR was established using genome sequencing and targeted
993 disruption of the 4HNR-encoding gene. Mutants lacking the gene, and with abnormal
994 pigmentation (orange-brown spores compared to the black spores of the wild type strain),
995 were enzyme-deficient and no longer reactive with mAb CA4.

996 The study of Thornton *et al.* (2015) further demonstrates the power of hybridoma
997 technology to develop mAbs specific to pathogenic moulds, but the generation of a species-
998 specific mAb to an intracellular antigen is unusual. The majority of genus or species-specific
999 mAbs generated against cell extracts from pathogenic yeasts, yeast-like fungi, and moulds,
1000 bind to carbohydrate moieties on extracellular carbohydrate or glycoprotein antigens
1001 (Thornton *et al.*, 2002; Thornton, 2009; Davies and Thornton, 2014; Al-Maqtoofi and
1002 Thornton, 2016; Davies *et al.*, 2017; Morad *et al.*, 2018). This is the case of mAbs specific to
1003 members of the PSC. Thornton (2009) reported the development of IgG1 (clone HG12) and
1004 IgM (clone GA3) mAbs specific to a heat-stable, water-soluble, 120kDa carbohydrate
1005 present on the surface of conidia and hyphae of *S. apiospermum*, *S. aurantiacum*, and *S.*
1006 *boydii*. The antigen is also readily detectable as an extracellular antigen that is produced in
1007 abundance during active growth of these pathogens. The mAbs do not react with the
1008 related fungus *S. dehoogii*, with *L. prolificans*, or other unrelated human pathogenic fungi.
1009 The copious production of the 120kDa antigen and the availability of highly specific mAbs
1010 for antigen detection, make this an ideal system for the development of a diagnostic test for
1011 members of the PSC. To this end, we have developed a lateral-flow assay (*Sced*-LFA) for PSC
1012 detection that comprises the IgG1 mAb HG12 (Figure 1), and which demonstrates the
1013 feasibility of developing a POCT for rapid detection of pathogens in the PSC. In addition, we
1014 have developed a quantitative sandwich ELISA that combines both mAbs HG12 and GA3.
1015 This ELISA was recently used by Box *et al.* (2018) to determine the pharmacodynamics of
1016 voriconazole in *in vitro* models of invasive pulmonary scedosporiosis. Given the recent CE-
1017 marking and commercial availability of the *Asp*LFD (OLM Diagnostics) and *Aspergillus* GP-
1018 ELISA (Euroimmun AG) which both employ the *Aspergillus*-specific mAb JF5 (Thornton,
1019 2009), the development of complementary qualitative LFA and quantitative ELISA tests for
1020 the diagnosis of scedosporiosis, based on detection of the 120kDa in human BALf and serum
1021 samples, is technically feasible.

1022

1023

1024

1025 **Mucormycete species pathogenic to humans**

1026

1027 Mucormycetes are thermotolerant, fast-growing saprotrophic moulds of the phylum
1028 Zygomycota order Mucorales, which are abundant in a wide range of ecological niches
1029 including soil and compost (Richardson, 2009), food (e.g. cheese where they cause spoilage
1030 (Hymery *et al.*, 2014)), edible crops where they cause post-harvest storage rots (Saito *et al.*,
1031 2016), and household dust (Al-Humiany, 2010). The order Mucorales includes species in the
1032 genus *Apophysomyces*, *Cunninghamella*, *Lichtheimia*, *Mucor*, *Rhizomucor*, *Rhizopus*, and
1033 *Saksenaea*, which are separated from the entomophthoromycetes *Basidiobolus* and
1034 *Condiobolus*, zygomycete fungi that are also capable of causing disease in humans (Binder *et al.*,
1035 2014; Ribes *et al.*, 2000). While mucormycetes such as *Rhizopus oryzae* (syn. *Rhizopus*
1036 *arrhizus*) and *Lichtheimia corymbifera* can cause allergic reactions in humans (Sircar *et al.*,
1037 2015; Rognon *et al.*, 2016), it is the ability of these fungi to cause osteoarticular mycosis
1038 (Taj-Aldeen *et al.*, 2017), and rhino-orbital-cerebral (Arndt *et al.*, 2009; Son *et al.*, 2016), oral
1039 (Hingad *et al.*, 2012), pulmonary (Hung *et al.*, 2015; Wang *et al.*, 2016; Iqbal *et al.*, 2017),
1040 gastrointestinal (Adhikari *et al.*, 2019), cutaneous (Li *et al.*, 2013; Arruebarrena *et al.*, 2016;
1041 Zahoor *et al.*, 2016) or disseminated infections (Walsh *et al.*, 2012) in pre-disposed adult
1042 and paediatric patients (Däbritz *et al.*, 2011) that is of the greatest concern, with a single
1043 species, *Rhizopus oryzae* responsible for >80% of all life-threatening infections (Richardson,
1044 2009; Richardson and Page, 2018; Raghunath *et al.*, 2019). This fungus and other pathogenic
1045 Mucorales (predominantly *Lichtheimia*, *Mucor*, and *Rhizomucor*) differ from other
1046 opportunistic moulds in their ability to infect a broader, more varied population of human
1047 hosts (Richardson, 2009; Gomes *et al.*, 2011).

1048 Cutaneous and deep tissue infections typically occur by direct inoculation during
1049 trauma, such as following combat-related blast injury (Paolino *et al.*, 2012; Warkentien *et al.*,
1050 2012; Tribble and Rodriguez, 2014; Kronen *et al.*, 2017), natural disasters (Andresen *et al.*,
1051 2005; Fanfair *et al.*, 2012), or traffic accidents (Lelievre *et al.*, 2014), but are also
1052 reported in patients with diabetes or haematological malignancies (Arnáiz-García *et al.*,
1053 2009). Reports of disseminated mucormycosis, while rare, are increasing in incidence
1054 particularly in patients with uncontrolled diabetes, iron overload, and ketoacidosis (Binder
1055 *et al.*, 2014; Rammaert *et al.*, 2012), and also in patients with haematological malignancies
1056 and allogeneic stem cell transplants (Petrikkos *et al.*, 2012; Sugui *et al.*, 2011).

1057

1058 **Detection of mucormycosis**

1059

1060 Radiology, histology and culture

1061

1062 The aggressive and rapid course of mucormycete infections makes early detection critically
1063 important for the management both of localised cutaneous, deep-seated, and disseminated
1064 infections (Castrejón-Pérez *et al.*, 2017). This is especially important in the context of their
1065 intrinsic resistance to short-tailed mould-active azole drugs (voriconazole (VCZ) and
1066 fluconazole) due to an evolutionary conserved amino acid substitution in the enzyme
1067 lanosterol 14 α -demethylase responsible for ergosterol biosynthesis (Caramalho *et al.*,
1068 2017). This has led to an increased incidence of breakthrough infections amongst
1069 immunocompromised and high-risk patients receiving VCZ prophylaxis, with the suggestion

1070 that VCZ prophylaxis should be thought of as one of the risk factors for mucormycosis
1071 (Ustun *et al.*, 2007).

1072 As with aspergillosis, fusariosis, and scedosporiosis, abnormalities observed in a chest-
1073 CT consistent with angio-invasive mould infections (nodules, halo signs, cavities, wedge-
1074 shaped infiltrates, and pleural effusions) are not pathognomonic of pulmonary
1075 mucormycosis, and so can only raise the suspicion of mucormycosis in the context of a
1076 patient's clinical history. Despite this, the reversed halo sign in neutropenic patients with
1077 haematological malignancies appears to have high predictive value for mucormycosis
1078 (Legouge *et al.*, 2014; Walsh *et al.*, 2014). Computed tomography has also proven useful in
1079 the differential diagnosis of rhino-orbital-cerebral mucormycosis (ROCM) and bacterial
1080 orbital cellulitis, where the early symptoms of both diseases are similar (Son *et al.*, 2016).
1081 However, it is unable to discriminate between ROCM and aspergillosis in cases of invasive
1082 fungal rhinosinusitis (Arndt *et al.*, 2009). Culture of mucormycetes from biopsy samples
1083 (Hong and Park, 2017b) is problematic due to the fragile nature of mucormycete hyphae
1084 that are aseptate or pauci-septate (Skiada *et al.*, 2013). Growth of mucormycetes in culture
1085 is rapid, but identification to the level of species and even genus requires considerable
1086 mycological expertise (Ziaee *et al.*, 2016). As with other pathogenic moulds, MALDI-TOF/MS
1087 can be used to differentiate species once in axenic culture (Cornely *et al.*, 2014; Cassagne *et al.*,
1088 2011; De Carolis *et al.*, 2012; Schrodler *et al.*, 2012), but more data are needed to
1089 authenticate this technique, and the robustness of reference databases needs to be fully
1090 evaluated.

1091 *In situ* detection of mucormycetes in tissue samples relies on the microscopic
1092 observation of characteristic broad ribbon-like hyphae that can be stained with optical
1093 brighteners such as calcofluor white or with Grocott-Gomori methamine silver (Lass-Flörl,
1094 2009; Antonov *et al.*, 2015; Liao *et al.*, 2015). Sputum and BALf samples can also show the
1095 characteristic broad aseptate hyphae (Glazer *et al.*, 2000), which is a first indicator of
1096 mucormycosis (Al-Abbadi *et al.*, 1997). However, in one case study, only 25% of sputum or
1097 BALf samples were positive pre-mortem (Kontoyiannis *et al.*, 2000). Attempts have been
1098 made to improve the specificity and sensitivity of microscopy by using mucormycete-
1099 reactive antibodies in immunohistochemistry. The production of rabbit hyper-immune
1100 antisera and mAbs to immuno-dominant intracellular antigens of the Mucorales was
1101 reported by Jensen *et al.* (1994, 1996). Jensen *et al.* (1994) demonstrated that heterologous
1102 absorption rendered antisera, raised against *Rhizopus oryzae* somatic antigens,
1103 monospecific by indirect immunofluorescence, whereas heterologous absorption of
1104 *Lichtheimia corymbifera* antiserum did not abolish reactivity with *R. oryzae*. The reactivity of
1105 the heterologously absorbed antisera, and a murine IgG1 mAb (1A7B4) raised against *L.*
1106 *corymbifera*, enabled mucormycetes within bovine lesions to be identified by
1107 immunohistochemistry. In a subsequent study, Jensen *et al.* (1996) showed that a mAb
1108 (WSSA-RA-1), raised against water-soluble somatic antigens from *R. oryzae*, similarly bound
1109 to intracellular homologous antigens of between 14kDa and 110kDa. The high degree of
1110 specificity exhibited by mAb WSSA-RA-1 allowed its use in immunohistochemistry to detect
1111 the pathogen *in situ* in placenta, lymph node and gastrointestinal tract samples of cows with
1112 suspected systemic bovine zygomycosis. In a subsequent study (Jensen *et al.*, 1997), the
1113 same mAb (WSSA-RA-1) was used in immunohistochemistry to improve the sensitivity and
1114 specificity of mucormycosis detection in patients with haematological malignancies.

1115

1116

1117 Nucleic acid tests

1118

1119 Identification of mucoralean fungi in culture based on morphological characteristics is
1120 notoriously difficult, particularly with strains that fail to sporulate. For this reason, nucleic
1121 acid-based procedures have been developed that enable discrimination of Mucorales at
1122 both genus- and species-level, although evidence that identification beyond genus-level aids
1123 treatment is lacking. Unlike *Fusarium*, sequencing of the internal transcribed spacer regions
1124 ITS1 and ITS2 of ribosomal RNA gene (rDNA) has been shown to be a reliable method for
1125 species differentiation in the mucormycetes (Gade *et al.*, 2017), with ITS sequencing
1126 recommended by ISHAM as a first-line method of identification (Balajee *et al.*, 2009).
1127 Numerous in-house molecular assays have been developed for direct detection of
1128 mucoralean DNA in clinical samples (Skiada *et al.*, 2018), including BALF (Lengerova *et al.*,
1129 2014), serum (Millon *et al.*, 2016), and biopsy (skin, lung, stomach mediastine, nose, parotid
1130 gland) samples (Bernal-Martínez *et al.*, 2012). However, their current lack of standardisation
1131 means that they are only moderately supported in the clinical guidelines for the diagnosis of
1132 mucormycosis (Cornely *et al.*, 2014; Skiada *et al.*, 2018). Despite this, PCR has proved useful
1133 in the detection of mucormycete infections, especially in infections that are culture-negative
1134 (Hammond *et al.*, 2011). Lengerova *et al.* (2014) used PCR followed by high-resolution melt
1135 analysis (PCR/HRMA) to detect *Rhizopus* spp., *Rhizomucor pusillus*, *Lichtheimia corymbifera*,
1136 and *Mucor* spp. in BALF samples from immunocompromised patients who were at risk of
1137 invasive fungal disease. Real-time qPCR assays specific to the species identified in the
1138 PCR/HRMA test were used to validate the test. Of the 99 BALF samples collected from 86
1139 patients with pulmonary abnormalities, 91% were negative and 9% were positive in the
1140 PCR/HRMA test, with a sensitivity and specificity 100% and 93%, respectively. By combining
1141 the positive PCR/HRMA results with positive real-time qPCR results, the specificity was
1142 increase to 98%. Due to its high NPV of 99%, the PCR/HRMA test is a fast and reliable
1143 technique for differential diagnosis of pulmonary mucormycosis in immunocompromised
1144 patients caused by the four most clinically important mucormycetes.

1145 Because of the difficulty in obtaining fungal DNA from human fluids, the possibility of
1146 detecting mucormycete DNA in paraffin-embedded and fresh tissues has been investigated
1147 in both an experimental model of disseminated mucormycosis (Dannaoui *et al.*, 2010), and
1148 also in humans (Gade *et al.*, 2017). The universal primers ITS1 and ITS2 were used in PCR to
1149 amplify the ITS1 region from mucormycete DNA in formalin-fixed paraffin-embedded kidney
1150 and brain tissues from mice infected with one of five species (*Rhizopus oryzae*, *Rhizopus*
1151 *microsporus*, *Lichtheimia corymbifera*, *Rhizomucor pusillus*, and *Mucor circinelloides*).
1152 Amplicons were then sequenced for species identification. Using this procedure,
1153 identification of major mucormycete species from formalin-fixed paraffin-embedded could
1154 reach 100%, provided sufficient starting material was available for DNA extraction. Gade *et*
1155 *al.* (2017) investigated the utility of a PCR targeting a 200-300 bp region of the extended 28S
1156 region of rDNA for molecular identification of DNA from mucormycetes and other fungi in
1157 formalin-fixed paraffin-embedded and fresh tissues. They demonstrated this region could
1158 be used to identify all genera and some species of clinically relevant mucormycetes. They
1159 also demonstrated that PCR amplification and direct sequencing of the extended 28S region
1160 of rDNA was more sensitive compared to targeting the ITS2 region, since they were able to
1161 detect and identify mucormycetes and other fungal pathogens in tissues from patients with
1162 histopathological and/or culture evidence of fungal infections that were negative in PCR
1163 using ITS-specific primers.

1164 Antibody and antigen tests

1165

1166 While there are no routine serological tests for diagnosis of disseminated mucormycosis,
1167 ELISA has been used to study the relationship between antibody levels and exposure to
1168 *Rhizopus microsporus* in sawmill workers with allergic alveolitis (Sandven and Eduard, 1992),
1169 while recombinant antigens have been developed for the serodiagnosis of farmer's lung
1170 caused by *Lichtheimia corymbifera* (Rognon *et al.*, 2016). Detection of disseminated
1171 mucormycosis is not possible using tests for (1→3)-β-D-glucan since mucormycetes lack this
1172 carbohydrate in their cell walls (Cornely *et al.*, 2014), but it can be used to rule out IPA, the
1173 most frequent differential diagnosis, or combined *Aspergillus* and Mucorales infections
1174 (Skiada *et al.*, 2013). Early attempts to detect disseminated disease serologically were based
1175 on immunodiffusion (Jones and Kaufman, 1978), electrophoresis and immunoblotting
1176 (Wysong and Waldorf, 1987), and ELISA (Kaufman *et al.*, 1989) of homogenate antigens
1177 challenged with sera from patients with mucormycete infections. However, non-specific
1178 reactivity with the antigen preparations was observed with sera from patients with
1179 aspergillosis and candidiasis also, which meant that the tests were unable to generically or
1180 specifically identify the etiologic agents of mucormycosis.

1181 The immunological determinant of mucoralean intracellular glycans has been shown to
1182 comprise linear (1→6)-α-linked mannosyl residues (Miyazaki *et al.*, 1979), with the
1183 cell walls of yeast and hyphal phases of mucoralean fungi containing fucomannopeptide and
1184 mannoprotein (Yamada *et al.*, 1982, 1983). While these antigens have provided useful
1185 targets for direct visualisation of mucoralean hyphae in tissue samples using
1186 immunohistochemistry, their intracellular nature means that they have limited applicability
1187 as circulating biomarkers of mucormycosis in BALf and serum samples. Approaches have
1188 been used to identify extracellular antigens specific to the Mucorales (Hessian & Smith
1189 1982), which might circulate in the bloodstream and therefore be suitable targets for
1190 detection by, for example, ELISA. Extracellular polysaccharides (EPS) of the Mucorales that
1191 appear, using polyclonal IgG antibodies, to be specific to this group of fungi, have been
1192 isolated and characterised (De Ruiter *et al.*, 1991; 1992a,b, 1993, 1994; Notermans and
1193 Soentoro, 1986), and their immunodominant residues shown to comprise 2-O-methyl-D-
1194 mannose (De Ruiter *et al.*, 1994).

1195 Despite these extensive early studies, and despite our improved understanding of the
1196 polysaccharide cell wall architecture of mucoralean fungi (Lecointe *et al.*, 2019), no genus-
1197 or species-specific mAbs are currently available that target immunogenic EPS, and which
1198 might prove suitable for the development of immunoassays for diagnosis of mucormycosis
1199 in humans. Notwithstanding this, somatic antigens diagnostic of systemic *L. corymbifera*
1200 infections have been detected in the urine of cattle (Jensen *et al.*, 1993b), indicating that
1201 biomarkers of mucormycosis circulate in the bloodstream and are excreted. This raises the
1202 possibility of developing a non-invasive test for mucormycosis based on mucormycete
1203 antigenuria, provided that suitable targets can be identified and specific mAbs can be
1204 generated.

1205

1206 **Conclusions and Future Prospects**

1207

1208 One of the main priorities of the Global Action Fund for Fungal Infections (GAFFI) is
1209 availability and access of cheap and effective diagnostic tests for all, particularly those in

1210 poorly-resourced countries. A commendable priority, but one littered with obstacles.
1211 Technically, as this review has shown, it is possible to develop highly specific and sensitive
1212 assays for the detection of some of the most problematic of human pathogens, the
1213 filamentous fungi or moulds. Furthermore, it is possible to demonstrate the clinical utility of
1214 these tests in retrospective or semi-prospective studies. However, the vast majority of these
1215 tests remain at the experimental stage in the laboratory, with little prospect of translation
1216 to the clinic as commercially-available CE-marked or FDA-approved assays. One of the
1217 biggest obstacles to bench-to-bedside translation is the escalating costs for the regulatory
1218 approvals required at each of the different technical and commercial phases of a test's
1219 development, and during its registration as an *in vitro* medical device (IVD).

1220 As Figure 1 and the accompanying text demonstrates, the generation of an
1221 immunoassay, a lateral-flow assay (LFA), that encompasses many of the desirable qualities
1222 of a near-patient point-of-care test for a human pathogenic fungus (short-time to result;
1223 inexpensive equipment/instrumentation; suitable for use by personnel with limited training;
1224 minimal number of steps; uncomplicated interpretation (Kozel and Wickes, 2014; Wickes
1225 and Wiederhold, 2018)) is relatively simple given the availability of a high quality
1226 monoclonal antibody (in this case a well-characterised mAb that detects a water-soluble,
1227 heat-stable, carbohydrate antigen specific to pathogens in the
1228 *Pseudallescheria/Scedosporium* complex (Thornton, 2009)), and the technical know-how of
1229 how to apply it to LFA technology. Production of this demonstration test took a month to
1230 complete, including antibody purification and conjugation, LFA formatting, and
1231 determination of specificity and analytical sensitivity. The limit of detection of purified
1232 antigen is 3.75ng/ml (Figure 1), which is well within the level of analytical sensitivity
1233 required for clinical detection of a circulating antigen in human samples. Despite this, the
1234 demand for a PSC-specific test is insufficient to warrant further commercial development of
1235 the *Sced*-LFA, despite the importance of this group of fungi in human disease.

1236 To take a test such as the *Sced*-LFA from the demonstration phase through to
1237 prototyping and then into test validation and verification with an FDA-approved
1238 manufacturer, requires investment beyond the capabilities of many diagnostic companies,
1239 certainly beyond a small to mid-size enterprise (SME), without a cast-iron guarantee of
1240 financial return and profit within a short period of time post CE-marking or FDA approval.
1241 This guarantee is unlikely to be met with tests for emerging or rare pathogens such as
1242 *Fusarium*, *Lomentospora*, *Scedosporium*, or the mucormycetes, especially given the
1243 investment and time required for CE-marking and FDA approval of an IVD, and subsequent
1244 integration of a novel test into hospital diagnostic workstreams. With every hospital or
1245 regional healthcare authority demanding in-house validation of a test's performance
1246 compared to its own established diagnostic procedures, it can typically take several years
1247 before a test is widely accepted, and is purchased in sufficient numbers so as to justify the
1248 developer's costs for R&D, manufacture, marketing, sales and distribution of the test. These
1249 same principles apply to any diagnostic test, whether it be an antigen test such as the *Sced*-
1250 LFA, or a molecular diagnostic test for fungal DNA (Wickes and Wiederhold, 2018).

1251 If GAFFI's desire for cheap and effective diagnostic tests for all is to be met, there needs
1252 to be a major re-think in the way that we, as a community of medical mycologists,
1253 diagnosticians, and medical practitioners, work together to better support the diagnostics
1254 sector to facilitate the development and translation of novel fungal diagnostics to the
1255 clinical setting. Without this community support, and without much-needed financial
1256 assistance from government funding agencies who have traditionally paid insufficient

1257 attention to human mycoses and their detection, the availability of cheap, easy-to-use, and
1258 effective diagnostic tests will be limited to those pathogens which infect sufficiently large
1259 number of individuals, such as *Aspergillus*, *Cryptococcus*, and *Pneumocystis*, to warrant
1260 diagnostic test development. An exemplar of where community and funding agency support
1261 worked to the patient's advantage was the Aspergillus Technology Consortium (AsTeC) for
1262 aspergillosis clinical laboratory diagnostics. A similar approach needs to be adopted for
1263 other invasive mould diseases.

1264

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1266

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1270

1271 **References**

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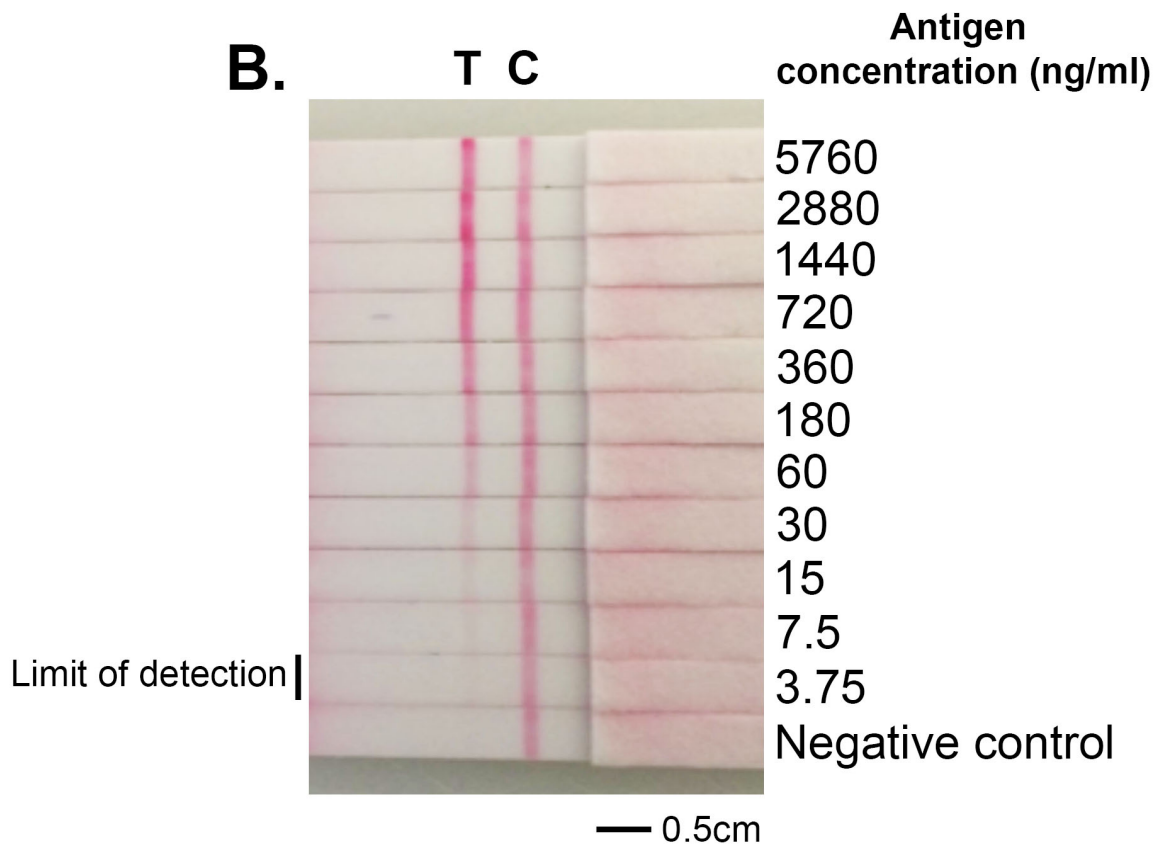
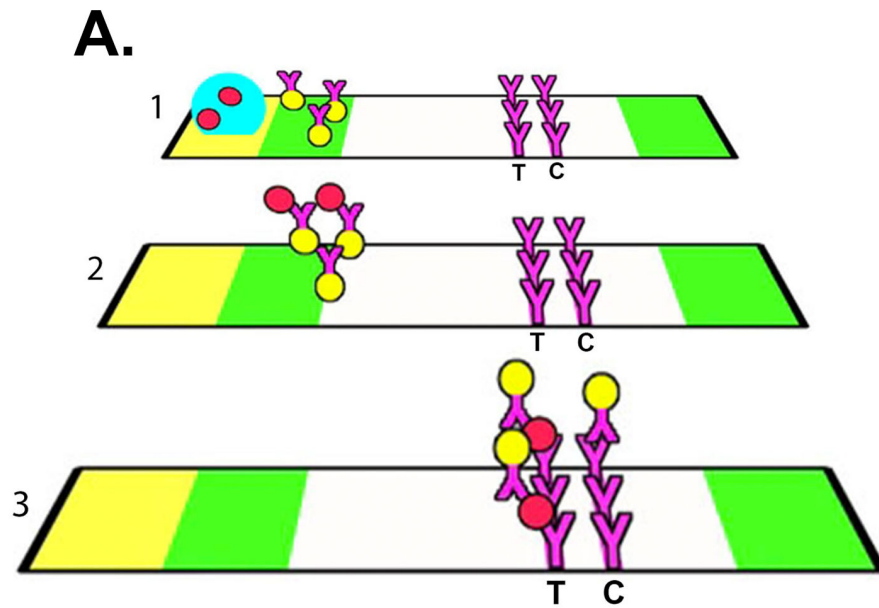
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Thornton Figure 1.



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2375 **Figure 1.** Demonstration lateral-flow assay (*Sced*-LFA) for the detection of pathogens within
2376 the *Pseudallescheria/Scedosporium* species complex. **A.** Schematic diagram showing the
2377 internal workings of the *Sced*-LFA test. The monoclonal antibody HG12 (Thornton, 2009) is
2378 immobilized in the test zone (T) on a porous nitrocellulose membrane. Anti-mouse
2379 immunoglobulin immobilised to the membrane in a separate zone serves as an internal
2380 control (C). On addition of 100µl of analyte (for example bronchoalveolar lavage) to the
2381 release pad (1), mAb HG12 which is conjugated to NanoAct cellulose nanobeads (CNB) in
2382 the release pad (Y-shaped structures with yellow spheres), binds to the diagnostic 120kDa
2383 antigen (red spheres) and the antibody-CNB/antigen complex then moves along the porous
2384 membrane by capillary action (2). The same mAb immobilized in the test zone (T) binds to
2385 the complex (3), resulting in a positive test line. Any mAb-CNB conjugate that migrates
2386 unbound to the target antigen, binds to the internal control (C) indicating that the assay has
2387 run correctly. Where the 120kDa diagnostic antigen is present in the analyte, 2 lines appear
2388 (T and C) indicating infection, but samples that are antigen negative (no infection) result in a
2389 single control line (C) only. **B.** Test results using filtrates from an actively growing culture of
2390 *S. apispermum*, and with mAb HG12 conjugated to red CNB particles. Positive tests results
2391 (T and C both present) are visible for antigen concentrations $\geq 3.75\text{ng/ml}$ filtrate (the limit of
2392 detection). The negative control (antigen-negative culture medium) produces a single
2393 internal control line only. The single-step *Sced*-LFA test is highly specific, quick (taking only
2394 10 minutes to perform from addition of sample to interpretation of result), and is stable for
2395 18 months at room temperature, making it ideal for use in resource-limited settings. The
2396 image shown in B is courtesy of the *Sced*-LFA contract manufacturer LateralDx. Scale bar =
2397 0.5cm.

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