Aspergillus flavus: human pathogen, allergen and mycotoxin producer

M. T. Hedayati, A. C. Pasqualotto, P. A. Warn, P. Bowyer and D. W. Denning

Aspergillus infections have grown in importance in the last years. However, most of the studies have focused on Aspergillus fumigatus, the most prevalent species in the genus. In certain locales and hospitals, Aspergillus flavus is more common in air than A. fumigatus, for unclear reasons. After A. fumigatus, A. flavus is the second leading cause of invasive aspergillosis and it is the most common cause of superficial infection. Experimental invasive infections in mice show A. flavus to be 100-fold more virulent than A. fumigatus in terms of inoculum required. Particularly common clinical syndromes associated with A. flavus include chronic granulomatous sinusitis, keratitis, cutaneous aspergillosis, wound infections and osteomyelitis following trauma and inoculation. Outbreaks associated with A. flavus appear to be associated with single or closely related strains, in contrast to those associated with A. fumigatus. In addition, A. flavus produces aflatoxins, the most toxic and potent hepatocarcinogenic natural compounds ever characterized. Accurate species identification within Aspergillus flavus complex remains difficult due to overlapping morphological and biochemical characteristics, and much taxonomic and population genetics work is necessary to better understand the species and related species. The flavus complex currently includes 23 species or varieties, including two sexual species, Petromyces alliaceus and P. albertensis. The genome of the highly related Aspergillus oryzae is completed and available; that of A. flavus is in the final stages of annotation. Our understanding of A. flavus lags far behind that of A. fumigatus. Studies of the genomics, taxonomy, population genetics, pathogenicity, allergenicity and antifungal susceptibility of A. flavus are all required.

Introduction

The aspergilli have always been a factor in the human environment. Micheli was the first to distinguish stalks and spore heads, but it was not until the middle of the 19th century that these fungi began to be recognized as active agents in decay processes, as causes of human and animal disease and as fermenting agents capable of producing valuable metabolic products (Raper & Fennell, 1965).

First described by Link (1809), Aspergillus flavus is the name now used to describe a species as well as a group of closely related species. A. flavus is second only to A. fumigatus as the cause of human invasive aspergillosis. In addition, it is the main Aspergillus species infecting insects (Campbell, 1994), and it is also able to cause diseases in economically important crops, such as maize and peanuts, and to produce potent mycotoxins. The purpose of this review is to summarize the current knowledge about this important group of fungi.

Ecology and geographical distribution

Like other Aspergillus species, A. flavus has a worldwide distribution. This probably results from the production of numerous airborne conidia, which easily disperse by air movements and possibly by insects. Atmospheric composition has a great impact on mould growth, with humidity being the most important variable (Gibson et al., 1994). A. flavus grows better with water activity (aw) between 0.86 and 0.96 (Vujanovic et al., 2001). The optimum temperature for A. flavus to grow is 37 °C, but fungal growth can be observed at temperatures ranging from 12 to 48 °C. Such a high optimum temperature contributes to its pathogenicity in humans.

Soil

A. flavus appears to spend most of its life growing as a saprophyte in the soil, where it plays an important role as
nutrient recycler, supported by plant and animal debris (Scheidegger & Payne, 2003). The ability of A. flavus to survive in harsh conditions allows it to easily out-compete other organisms for substrates in the soil or in the plant (Bhatnagar et al., 2000). The fungus overwinters either as mycelium or as resistant structures known as sclerotia. The sclerotia either germinate to produce additional hyphae or they produce conidia (asexual spores), which can be further dispersed in the soil and air.

Outdoor air

A. flavus has been particularly prevalent in the air of some tropical countries (Moubasher et al., 1981; Abdalla, 1988; Gupta et al., 1993; Adhikari et al., 2004). Climatic conditions markedly influence the prevalence of A. flavus in outdoor air. As an example, two Spanish studies revealed very different results. In Barcelona A. flavus and A. niger were the most frequent airborne aspergilli (Calvo et al., 1980) whereas in Madrid A. fumigatus was the most prevalent species (54 %) (Guinea et al., 2005). Comparing Aspergillus species in the air in London, Paris, Lyon and Marseille, Mallea et al. (1972) showed that A. glaucus and A. versicolor group predominated in southern France. On the other hand, A. fumigatus represented more than 35 % of the isolates recovered from Paris and London, whereas A. glaucus group never exceeded 20 % (Mallea et al., 1972). In Brussels, A. fumigatus was the most common Aspergillus species whereas A. flavus represented only 1 % of isolates (Vanbreuseghem & Nolard, 1985).

Home and hospital air

The presence of Aspergillus in the air is a major risk factor for both invasive and allergic aspergillosis (Denning, 1998). Accordingly, several outbreaks of invasive aspergillosis have been associated with construction and/or renovation activities in and around hospitals (Sarubbi et al., 1982; VandenBergh et al., 1993), activities that markedly increase the number of spores in the air. Also, in several studies the link between infection by A. flavus and the contamination of the environment was clearly demonstrated by molecular typing methods (Rath & Ansorg, 1997; Diaz-Guerra et al., 2000) (see below). In two studies from Iran, A. flavus was the most prevalent Aspergillus species to be recovered from the air of hospital wards and homes (Zaini & Hedayati, 1995; Hedayati et al., 2005).

Water

Fungi in drinking water may alter the taste and odours of the water. Health problems are possible, including mycotoxin exposure, direct infection and allergy. More studies are needed on this subject. Surveys of fungi in drinking water have recovered many different taxa, including A. flavus (Gottlich et al., 2002; Goncalves et al., 2006) and in particular A. fumigatus (Warris et al., 2001; Anaissie et al., 2002). Contamination tends to arise from surface reservoirs and not from deep ground wells (Warris et al., 2001). This variation is often attributed to factors such as raw water source (surface versus well), water temperature patterns, treatment patterns and maintenance of distribution systems. Additionally, it was reported that fungi can pass through treatment processes by means of leaks in the system, or from air in contact with water stored in distribution system reservoirs, and can even survive water disinfection with chlorine (Niemi et al., 1982). Interestingly, Paterson et al. (1997) detected aflatoxin in water and identified A. flavus from a cold-water storage tank.

Genome

The sequencing of the A. oryzae genome sequence provides an excellent tool for researchers to gain insight into the basic biology of this organism (Machida et al., 2005; Galagan et al., 2005). The sequencing of A. flavus (NRRL 3357, Geiser Group 1C) is in progress, and will provide a rich source of comparative data. The primary assembly indicates that the A. flavus genome is 36.3 Mb in size and consists of eight chromosomes and 13 071 predicted genes. The mean gene length is 1384 bp (Yu et al., 2005). A. flavus is genetically almost identical to A. oryzae. Comparative genomics will be particularly interesting as A. flavus is a common environmental organism whilst the sequence strain of A. oryzae is a ‘domesticated’ fungus, having been used in soy fermentation for thousands of years, and rarely causes disease.

Taxonomy

Classically, the systematics of Aspergillus and its associated teleomorphs have been based primarily on differences in morphological and cultural characteristics (Raper & Fennel, 1965; Samson et al., 2000). Petromyces alliaceus and P. albertensis are the only two sexually reproducing species (teleomorphs) classified in Aspergillus flavus complex (Table 1) (Frisvad et al., 2005). They were characterized by ascomata produced within closed sclerenchymatous stromata. The genus Petromyces belongs to the family Trichocomaceae of the order Eurotiales of Ascomycetes. Moreover, the taxonomy of the flavus complex group is further complicated by the existence of morphological divergence amongst isolates of the same species (Klich & Pitt, 1988).

Raper & Fennell (1965) considered the A. flavus group to contain nine species and two varieties, including A. flavus, A. flavus var. columnaris, A. parasiticus, A. oryzae, A. oryzae var. effusus, A. zonatus, A. clavato-flavus, A. tamarii, A. flavo-furcatis, A. subolivaceus and A. avenaceus. We have summarized the current species described morphologically in Table 1 (see also supplementary Table S1, available with the online version of this paper, for more data); there appear to be 23 published species or varieties. Despite the growing use of molecular genetic techniques to study the
Table 1. Microscopic features and reported diseases of *Aspergillus flavus* complex

Fuller details are are provided in Supplementary Table S1, available with the online version of this paper.

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<tr>
<td><em>A. flavus</em> Link (1809)</td>
<td>The main agent of acute and chronic invasive and granulomatous <em>Aspergillus</em> sinusitis. Agent of otitis, keratitis, pulmonary and systemic infections in immunocompromised patients, cutaneous aspergillosis and aspergillosis in other vertebrates.</td>
<td>Conidiophores are heavy walled, uncoloured, coarsely roughened, usually less than 1 mm in length. Vesicles are elongate when young, later becoming subglobose or globose, varying from 10 to 65 μm in diameter. Phialides are uniseriate or biseriate. The primary branches are up to 10 μm in length, and the secondary up to 5 μm in length. Conidia are typically globose to subglobose, conspicuously echinulate, varying from 3.5 to 4.5 μm diameter.</td>
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<tr>
<td><em>A. oryzae</em> (Ahlburg) Cohn (1883)</td>
<td>A rare agent of paranasal sinusitis, meningitis, cerebritis, pulmonary infections, ABPA, otomycosis and scleritis. There is one report of involvement in a kidney infection in an albatross.</td>
<td>Conidiophores are up to 4–5 mm in length, colourless, with walls relatively thin, definitely roughened throughout all or most of their length. Vesicles are sub-spherical, stigmata covering the entire surface or the upper three-fourths, up to 75 μm in diameter. Phialides are uniseriate and biseriate, covering the entire surface or the upper three-fourths of the vesicle. Conidia are (sub)spherical to ovoidal, 4.5–8(–10) × 4.5–7 μm, smooth-walled to roughened, greenish to brownish.</td>
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<tr>
<td><em>A. subolivaceus</em> Raper &amp; Fennel (1965)</td>
<td>No documented disease.</td>
<td>Conidiophores are variable in length from 300 to 1300 μm, walls uncoloured, definitely echinulate. Vesicles are subglobose to somewhat elongate, variable in diameter but usually 30–55 μm × 35–60 μm. Phialides are biseriate, primaries 6.5–20.0 × 4.5–7.5 μm, secondaries 7.0–10.0 × 3.3–4.0 μm. Conidia are elliptical and delicately roughened when first formed, becoming smooth or nearly so, predominantly elliptical and mostly 4.0–4.5 × 3.0–3.5 μm.</td>
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<tr>
<td><em>A. thomii</em> Smith (1951)</td>
<td>No documented disease.</td>
<td>Conidiophores are uncoloured, conspicuously roughened or echinulate throughout their entire length, up to 1200–1500 μm long. Vesicles are globose to pyriform ranging from 20–50 μm in diameter. Phialides are typically biseriate, primaries 6–10 × 3.3–4.0 μm, secondaries and uniseriate stigmata 6–9 × 2.2–2.8 μm. Conidia are elliptical and hyaline when first formed, becoming subglobose, brownish yellow and definitely roughened at maturity, varying in diameter from 3.0 to 5.5 μm.</td>
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<tr>
<td><em>A. terricola</em> var. americana Thom &amp; Church (1921)</td>
<td>No documented disease.</td>
<td>Conidiophores are 300–600 μm in length by 6–8 μm in diameter, with walls appearing granulose, uncoloured. Vesicles are globose to subglobose, up to 25 μm in diameter, fertile over the upper two-thirds or three-fourths. Phialides are usually in one series, primaries when present 7.5–9.0 × 4.5–6.0 μm, secondaries 7–10 × 3.3–4.5 μm with tips often phialiform. Conidia are commonly ovate to nearly globose at maturity, mostly 4.5–5.5 × 3.8–5.0 μm, rugulose, brownish yellow.</td>
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<tr>
<td><em>A. parasiticus</em> Speare (1912)</td>
<td>No documented disease.</td>
<td>Conidiophores are variable in length, mostly 300–700 μm long, with walls colourless, smooth or nearly so in some strains, in others smooth below and definitely roughened above. Vesicles are 20–35 μm in diameter. Phialides are in one series, 79 × 3.0–4.0 μm, colourless or in pale yellow-green shades. Conidia are globose, coarsely echinulate, 3.5–5.5 μm in diameter, bright yellow-green.</td>
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<tr>
<td><em>A. sojae</em> Sakaguchi &amp; Yamada (1944)</td>
<td>No documented disease.</td>
<td>Conidiophores are short with walls smooth but sometimes roughened. Vesicles are subglobose to clavate, 10–30 μm. Phialides are definitely uniseriate. Conidia are globose, prominently echinulate, usually 5–6 μm.</td>
</tr>
<tr>
<td><em>A. toxicarius</em> Murakami (1971)</td>
<td>No documented disease.</td>
<td>Conidiophores are roughened, usually less than 1 mm in length. Vesicles are globose to subglobose, 30–40 μm. Phialides are definitely biseriate. Conidia are globose, prominently echinulate, usually 4–5 μm.</td>
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<tr>
<td><em>A. caelatus</em> Horn (1997)</td>
<td>No documented disease.</td>
<td>Conidiophores are hyaline, finely roughened; length variable, mostly 200–800 μm. Vesicles are globose or subglobose, 15–38 μm in diameter, fertile over upper three-fourths. Phialides are 5.0–11.0 × 3.0–6.0 μm. Conidia are globose and thick-walled, with spore body 5.0–6.0 μm in diameter; ornamentation coarse, consisting of tubercles and short bars &lt;1.5 μm high.</td>
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<tr>
<td>Species</td>
<td>Disease</td>
<td>Microscopic features</td>
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<td><em>A. pseudotamarii</em> Ito et al. (2001)</td>
<td>No documented disease.</td>
<td>Conidiophores are hyaline, finely roughened. Vesicles are globose to subglobose, 26–38 μm. Phialides are 4.5–6.1 × 3.1–4.5 μm. Conidia are globose to subglobose, echinulate; variable in diameter, 3.9–9.9 μm.</td>
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<tr>
<td><em>A. corentiformis</em> Bartoli &amp; Maggi (1978)</td>
<td>No documented disease.</td>
<td>Conidiophores are simple or in coremia, straight, up to 1500 μm long by 20–45 μm wide, thick-walled, walls roughened to echinulate, rarely smooth. Vesicles are light to deep tawny, subglobose to elongate, fertile over almost the entire surface, 50–60 × 45–60 μm. In coremia, vesicles are obclavate and spathulate, 90–150 × 85–100 μm. Phialides are biseriate, each series composed of closely packed stigmata, 15–18 × 4–4.5 μm. Conidia are yellowish in mass, very variable in shape, from globose to oval, oblong or cylindrical, more or less encrusted, mostly 6.9–9 μm.</td>
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<tr>
<td><em>A. flavofurcatis</em> Batista &amp; da Silva Maia (1955)</td>
<td>No documented disease.</td>
<td>Conidiophores are erect, usually 1–2 mm in height by 11–20 μm in diameter, uncoloured, delicately granular. Vesicles are flask-shaped to subglobose, mostly 20–45 μm, fertile over most of their surface in large head. Phialides are crowded, biseriate, with both conditions often observed in the same head, 7–15 × 4.5–8.0 μm. Conidia are subglobose to globose at maturity, mostly 6.0–8.0 μm, distinctively demonstrating an olive-brown to dark brown colour change.</td>
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<tr>
<td><em>A. terricola</em> var. <em>indica</em> Mehrrota &amp; Agnihotri (1962)</td>
<td>No documented disease.</td>
<td>Conidiophores are usually short and branched commonly 50–150 × 6.6–10.0 μm, colourless and usually smooth. Vesicles are globose to subglobose, those of smaller heads 9–12 μm in diameter and fertile over the upper half, in larger heads 20–34 μm in diameter and fertile over most of the surface. Phialides are mostly uniseriate, 8.4–9.8 × 5.0–7.0 μm. Conidia are globose, varying from 4.5 to 9.8 μm in diameter, brownish yellow and conspicuously echinulate at maturity.</td>
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<tr>
<td><em>A. terricola</em> Marchal (1893)</td>
<td>No documented disease.</td>
<td>Conidiophores vary in length but reaching 0.5–1.0 mm, uncoloured, smooth or somewhat granulose. Vesicles are subglobose to hemispherical, mostly 20–45 μm. Phialides are uniseriate or biseriate, with both conditions often observed in the same head, 7–15 × 4.5–8.0 μm. Conidia are subglobose to globose at maturity, extremely variable in size, 4.5–9.0 μm, brownish yellow, coarsely echinulate.</td>
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<tr>
<td><em>A. tamarii</em> Kita (1913)</td>
<td>Implicated in a case of eyelid infection.</td>
<td>Conidiophores are usually 1–2 mm in length, hyaline, usually roughened. Vesicles are spherical, 10–50 μm. Phialides are uniseriate and biseriate, covering the entire surface of the vesicle. Conidia are echinulate to tuberculatate, subglobose, 5–8 μm.</td>
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<tr>
<td><em>P. alliaceus</em> Thom &amp; Church (1926)</td>
<td>One report of a chronic otitis externa after surgery.</td>
<td>Conidiophores are smooth-walled, up to 1.2 mm long, hyaline. Vesicles are spherical, occasionally somewhat elongate. Phialides are biseriate or uniseriate, covering at least the upper half of the vesicle. Conidia are ovoidal to subspherical, smooth walled, yellow, 2.5–4 × 2–3.5 μm.</td>
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<tr>
<td><em>P. albertensis</em> Tewari (1985)</td>
<td>No documented disease.</td>
<td>Conidiophores are commonly up to 3500 × 17.6 μm, somewhat sinuous, generally smooth. Vesicles are up to 95 μm, globose to subglobose. Phialides and metulae present in all heads, wedge-shaped, non-septate, 4.6–23 × 2–7 μm, phialides 5.7–9.5 × 1.7–2.5 μm. Conidia are oval to subglobose, smooth 2.3–3.5 × 1.7–3.5 μm.</td>
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<tr>
<td><em>A. lanosus</em> Kamal &amp; Bhargava (1969)</td>
<td>No documented disease.</td>
<td>Conidiophores are commonly 1.5–3 mm, septate with smooth wall, sometimes with true branches. Vesicles are hemispherical to subglobose, 15–30 μm, often fertile over half to two-thirds of surface. Phialides are crowded, biseriate, primaries 8–12 × 3.3–4.4 μm, secondaries 6.5–8.8 × 2.2–2.3 μm. Conidia are smooth, globose to subglobose, 2.2–2.8 μm.</td>
</tr>
<tr>
<td><em>A. robustus</em> Christensen &amp; Kaper (1978)</td>
<td>No documented disease.</td>
<td>Conidiophores are smooth to very slightly roughened, mostly 750–5000 × 10–21 μm. Vesicles are globose to somewhat elongate, thick-walled, fertile over the entire surface, mostly 40–70 μm. Phialides are 9.0–12.6 × 3.4–4.5 μm. Conidia are echinulate, thin-walled ellipsoidal, mostly 3.5–4.5 × 2.8–3.4 μm.</td>
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<tr>
<td><em>A. leporis</em> States &amp; Christensen (1966)</td>
<td>No documented disease.</td>
<td>Conidiophores are extremely variable, commonly 250–1100 μm, echinulate and uncoloured or pale yellow. Vesicles are thick-walled, fertile over three-fourths or more of the surface, globose to subglobose, mostly 20–50 μm. Phialides are biseriate, metula 6.5–16 × 4.5–5 μm. Conidia are globose to subglobose, smooth to delicately roughened, mostly 3–3.5 μm.</td>
</tr>
<tr>
<td><em>A. nomius</em> Kurtzman et al. (1987) (A. zhaoqingensis)</td>
<td>No documented disease.</td>
<td>Conidiophores are uncoloured, echinulate; variable in length, mostly 300–1100 μm. Vesicles are globose to subglobose, 25–65 μm. Phialides are 3.8–6.5 × 7.6–11.3 μm. Conidia are globose to subglobose, echinulate; mostly 4.5–6.5 μm.</td>
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</table>
Species Disease Microscopic features

A. avenaceus

No documented disease.

Conidiophores are smooth-walled; 300–500 μm long, straight to sinuous, reniform, separate, swollen in the upper part. Vesicles are globose, 30–50 μm, fertile over entire surface. Phialides are biseriate, 6–8 μm in diameter. Conidia are roughened, globose to subglobose, (3.5)–4–7–(8.5) μm in diameter, smooth.

A. beijingensis

No documented disease.

Conidiophores are 100–550 μm long, straight to sinuous, reniform, separate, swollen in the upper part. Vesicles are globose to subglobose, 3.5–6.5 μm in diameter, micro-verrucose. Phialides are 3–4 μm in diameter, fertile over the upper half. Conidia are 3–4 μm long, 4–5.5 μm in diameter, septate, thick-walled, smooth.

A. bombycis

No documented disease.

Conidiophores are 20–50 μm, subglobose, (3.5)–4–7–(8.5) μm in diameter. Conidia are globose to ovoid, 5–6.5(–7) μm in diameter, smooth.

A. caelatus

One report of a maxillary aspergilloma. Conidiophores are 7–12 μm long, fertile over the upper half or three-fourths, often proliferating. Phialides are flask-shaped, 4–5 μm in diameter, fertile over the upper half. Vesicles are globose to subglobose, 3.5–6.5 μm, micro-verrucose.

A. clavatoflavus

One report of a maxillary aspergilloma. Conidiophores are subglobose, 5–6 μm in diameter, fertile over the upper half. Vesicles are globose to subglobose, 3–4 μm long, 4–5.5 μm in diameter, septate, thick-walled, smooth. Conidia are ellipsoid, smooth, mostly 4.0–5.0 μm.

A. flavus

One report of a maxillary aspergilloma. Conidiophores are 6–8 μm long, straight to sinuous, reniform, separate, swollen in the upper part. Vesicles are globose, 30–50 μm, fertile over entire surface. Phialides are biseriate, 6–8 μm in diameter. Conidia are roughened, globose to subglobose, (3.5)–4–7–(8.5) μm in diameter.

A. lactarius

One report of a maxillary aspergilloma. Conidiophores are 3–4 μm long, 4–5.5 μm in diameter, septate, thick-walled, smooth. Conidia are ellipsoid, smooth, mostly 4.0–5.0 μm.

A. nomius

One report of a maxillary aspergilloma. Conidiophores are 7–12 μm long, fertile over the upper half. Vesicles are globose to subglobose, 3.5–6.5 μm, micro-verrucose. Conidia are 3–4 μm long, 4–5.5 μm in diameter, septate, thick-walled, smooth.

A. oryzae

One report of a maxillary aspergilloma. Conidiophores are 7–12 μm long, fertile over the upper half. Vesicles are globose to subglobose, 3.5–6.5 μm, micro-verrucose. Conidia are 3–4 μm long, 4–5.5 μm in diameter, septate, thick-walled, smooth.

A. parasiticus

One report of a maxillary aspergilloma. Conidiophores are 7–12 μm long, fertile over the upper half. Vesicles are globose to subglobose, 3.5–6.5 μm, micro-verrucose. Conidia are 3–4 μm long, 4–5.5 μm in diameter, septate, thick-walled, smooth.

A. flavus

Restriction fragment length polymorphism (RFLP) has been used to distinguish between A. flavus and A. oryzae and to infer phylogenetic relationships (Bruns et al., 1991; Montiel et al., 2003). Moody & Tyler (1990) demonstrated that restriction profiles of purified mitochondrial DNA can distinguish A. flavus Link, A. parasiticus Speare and A. nomius Kurtzman et al. However, for routine identification of Aspergillus isolates it is desirable to detect mitochondrial DNA RFLP without first separating the mitochondrial DNA from the nuclear DNA (Bruns et al., 1991).

Wang et al. (2001) described the use of partial sequences of the mitochondrial cytchrome b gene (402 bp) to differentiate 77 isolates in the Aspergillus flavus complex into seven DNA types (D-1 to D-7). A. sojae were defined as D-1, A. parasiticus as D-2, A. flavus and A. oryzae were grouped together as D-4, A. tamarii was defined as D-5 and A. nomius as D-7. Furthermore, D-3 was found to be closely related to A. parasiticus (D-2), also including one strain that had been deposited as A. flavus var. flavus. DNA type D-6 included one strain that was identified as A. flavus and was closely related to A. tamarii. Peterson (2000) differentiated 17 type strains in the Aspergillus flavus complex based on rDNA sequence analysis. These included A. flavus, A. oryzae, A. parasiticus, A. sojae, A. terricola var. americana, A. subolivaceus, A. kambarenosis, A. flavus var. columnaris, A. thomii, A. tamarii, A. caelatus, A. leporis, A. nomius, Petrozymes alliaceus, A.avenaceus, A. zonatus and A. clavatoflavus (Table 1). The author also indicated that A. zonatus and A. clavatoflavus were not phylogenetically part of the flavus complex.

Single-strand conformation polymorphism of internal transcribed spacer (ITS) regions has also been used as a genetic approach to differentiate species in the flavus complex (Kumeda & Asao, 1996). This complex seems to comprise distinct clades (Rigo et al., 2002). The three main clades (P. alliaceus, A. flavus and A. tamarii) could also be distinguished based on colony colour and their ubiquinone system. Based on ITS sequences A. robustus, A. caelatus, A. lanosus, A. albenteris, A. coremiformis, A. flavoverticat, A. toxicarius, A. terricola var. indica, A. terricola and the species mentioned by Peterson (2000) were all located in Aspergillus flavus complex. In addition, A. pseudotamarii and A. bombycis were found to be closely related to A. caelatus and A. nomius, respectively (Table 1). Rigo et al. (2002) suggested that A. zonatus and A. clavatoflavus should be excluded from Aspergillus flavus complex, a suggestion previously made by Kozakiewicz (1989), based on scanning electron microscopic studies. Recently, Frisvad et al. (2005) found that A. toxicarius resembles A. parasiticus but differs in at least three sequence differences in the ITS regions, as compared to four strains of A. parasiticus. Usually, the presence of three or more sequence
differences in ITS regions is an indication of a different species. *A. zhaoqingensis* was considered the same as *A. nomius* in this study (Frisvad et al. 2005).

**Identification**

Accurate species identification within *Aspergillus flavus* complex remains difficult due to overlapping morphological and biochemical characteristics (Table 1). In general, *A. flavus* is known as a velvety, yellow to green or brown mould with a goldish to red-brown reverse (Fig. 1). The conidiophores are variable in length, rough, pitted and spiny. They may be either uniseriate or biseriate. They cover the entire vesicle, and phialides point out in all directions (Fig. 2). Conidia are globose to subglobose, conspicuously echinulate, varying from 3.5 to 4.5 μm in diameter. Based on the characteristics of the sclerotia produced, *A. flavus* isolates can be divided into two phenotypic types. The S strain produces numerous small sclerotia (average diameter, 400 μm). The L strain produces fewer, larger sclerotia (Cotty, 1989). Within the S strain, some isolates, termed SB, produce only B aflatoxins, whilst others, named SBG, produce both B and G aflatoxins (Cotty, 1989). The S strain isolates have been referred to as atypical (Nozawa et al., 1989), microsclerotium producing (Saito & Tsurata, 1993) and *A. flavus* var. *parvisclerotigenu* (Geiser et al., 2000). The microsclerotial strains differ from *A. flavus* and therefore it has been suggested that they represent a taxon separated from *A. flavus* (Geiser et al., 2000; Frisvad et al. 2005). Molecular phylogenetics suggests that SB isolates are closely related to the *A. flavus* type culture and other L strain isolates (Egel et al., 1994).

**Molecular typing**

Phenotypic methods to discriminate *A. flavus* showed only a moderate discriminatory power for distinguishing isolates (Rath, 2001). Genotypic methods that have been used for typing *A. flavus* isolates include RFLP (Moody & Tyler, 1990; James et al., 2000), RAPD (Rath, 2001; Heinemann et al., 2004) and microsatellite polymorphism analysis (Guarro et al., 2005). Restriction endonuclease analysis of total cellular DNA has not proven to be a suitable method for discrimination of strains of *A. flavus* (Buffington et al., 1994). James et al. (2000) evaluated a DNA fingerprinting procedure that used a repetitive DNA sequence cloned from *A. flavus* var. *flavus* to probe RFLP of genomic DNA. The discriminatory power was 0.9526. However, RFLP analysis with Southern blotting may be tedious and labour intensive. RAPD analysis is the most frequently applied method, although lack of reproducibility is a well-known limitation of this technique. Buffington et al. (1994) combined the products from RAPD analysis and RFLP analysis of a tester strain of *A. flavus* to produce a DNA probe for Southern blot analysis. Although a high degree of discrimination amongst strain types was achieved, the probe and target sequences remain undisclosed.

Microsatellites are short tandemly repeated DNA sequences with a repetitive motif of 26 nt, forming tracts up to 100 nt long. Given the extensive polymorphism of microsatellites, they have proved to be epidemiologically useful for typing *A. fumigatus* (de Valk et al., 2005). Guarro et al. (2005) used random amplified microsatellites (RAMS) to type isolates of *A. fumigatus* and *A. flavus* obtained from a supposed outbreak. RAMS combines microsatellite and RAPD analysis. A discriminatory power of 0.9489 was obtained with the combination of two different primers. A full understanding of population(s) of *A. flavus* and the discriminatory power of these and other typing systems awaits a full population genetics study.

**Population genetics**

Two papers have demonstrated that agricultural isolates of *A. flavus* can be divided into two taxonomically distinct groups (Geiser et al., 1998, 2000). After analysing 314 Australian *A. flavus* isolates taken from agricultural soils,
Geiser et al. (1998) found 16 different genotypes effectively forming two genetically distinct groups, namely I and II. All isolates of A. oryzae analysed appeared to be members of group I and almost no variation was observed amongst them. Isolates belonging to group II appeared to be more homogeneous than those in group I, implying clonal dissemination. It is unknown whether clinical isolates are members of only one or both groups. It is also unclear whether these taxonomic groupings have clinical significance in terms of mode of infection, drug resistance or virulence. The sequenced isolate NRRL 3357 aligns with group IC when the omt12 sequence is used in a phylogenetic alignment according to the parameters described by Geiser et al. (1998) (P. Bowyer, unpublished observations).

Although A. flavus is known to reproduce exclusively asexually in the laboratory, these populations are highly polymorphic in nature. In the phylogenetic study performed by Tran-Dihn et al. (1999) two distinct major profiles for the A. flavus isolates were observed by RAPD. In comparison to isolates belonging to the A. flavus group, RAPD profiles seemed to be considerably less variable within the groups of A. parasiticus isolates. Molecular typing of a larger global collection of A. flavus clinical isolates may contribute to a better understanding of whether there are differences in pathogenicity in the flavus complex. If we consider the fact that most of the outbreaks of A. flavus infection were caused by a single strain, it is possible that subspeciation and detailed population genetics in the flavus complex might be of great clinical relevance.

**Outbreaks**

Outbreaks of aspergillosis involving the skin, oral mucosa or subcutaneous tissues are more often associated with A. flavus than other species (Myoken et al., 2003; James et al., 2000; Heinemann et al., 2004; Vandecasteele et al., 2002; Allo et al., 1987; Grossman et al., 1985; Singer et al., 1998). This is quite distinct from what is observed for outbreaks caused by A. fumigatus, i.e. life-threatening pulmonary or sinuses diseases in severely immunocompromised patients. In fact, clusters of invasive sinusitis or invasive pulmonary infection caused purely by A. flavus are fairly unusual. In a recent review that aimed to summarize the data from all nosocomial Aspergillus outbreaks reported to date (Vonberg & Gastmeier, 2006), 53 outbreaks were found, affecting 458 patients. Species identified most often from clinical samples were A. fumigatus (n=154) and A. flavus (n=101). Although superficial skin infections occurred in only 24 patients (5.2 % of the total), A. flavus was reported in almost all of these cases where Aspergillus species were identified to the species level.

Another important difference between outbreaks of aspergillosis caused by A. fumigatus and A. flavus is the level of genetic diversity among outbreak isolates. Molecular studies have revealed that A. fumigatus isolates recovered from epidemics are usually genetically distinct, meaning that every patient tends to be infected by a different strain of A. fumigatus (Guarro et al., 2005). In contrast, most of the outbreaks caused by A. flavus have been associated with a single or a few different strains, indicating a point source outbreak (Myoken et al., 2003; James et al., 2000; Heinemann et al., 2004; Vandecasteele et al., 2002). There seems to be much less genetic diversity amongst clinical isolates of A. flavus in comparison with A. fumigatus.

**A. flavus as a mycotoxin producer**

Mycotoxins are fungal secondary metabolites that are potentially harmful to animals or humans. The word ‘aflatoxin’ came from ‘Aspergillus flavus’ toxin’, since A. flavus and A. parasiticus are the predominant species responsible for aflatoxin contamination of crops prior to harvest or during storage (Yu et al., 2004). The aflatoxins B1, B2, G1 and G2 are the major four toxins amongst at least 16 structurally related toxins (Goldblatt, 1969). Aflatoxin B1 is particularly important, since it is the most toxic and potent hepatocarcinogenic natural compound ever characterized (Bennett & Klich, 2003). Different A. flavus strains may or may not produce either aflatoxins B1 and/or B2. Other toxic compounds produced by A. flavus are sterigmatocystin, cyclopiazonic acid, kojic acid, β-nitropropionic acid, aspertoxin, aflatem, gliotoxin and aspergillic acid (see http://www.aspergillus.org.uk – mycotoxin section). In addition A. flavus may produce some other secondary metabolite such as dihydroxyaflavinine, indole, paspalinine and versicolorin A (see http://www.aspergillus.org.uk – secondary metabolite section). A. parasiticus produces aflatoxin G1 and G2, in addition to B1 and B2, but not cyclopiazonic acid (Bennett & Klich, 2003; Yu, 2004). Aflatoxins are produced by some other species in Aspergillus flavus complex, including A. toxicarius, A. nomius, A. bombycis and A. pseudotomarii. A. pseudotomarii also produces cyclopiazonic acid. A. oryzae has long been used in the Orient to prepare various kinds of food products; it can produce cyclopiazonic acid and β-nitropropionic acid, but does not produce aflatoxin. A. oryzae, A. parasiticus, A. sojae, A. nomius, A. bombycis, A. tamarii, A. caelatus and A. pseudotomarii may produce kojic acid (Varga et al., 2003). Two sexually reproducing species in the Aspergillus flavus complex, P. alliaceus and P. albertensis, produce a high amount of ochratoxin A (50 300 mg ml⁻¹), and are considered to be responsible for ochratoxin A contamination of figs (Bayman et al., 2002).

**Pathogenicity**

A. flavus has been studied in animal models for over 40 years but is still rarely used in comparison to A. fumigatus. Early studies of invasive aspergillosis in non-immunocompromised murine models demonstrated that A. flavus was more virulent than almost all other Aspergillus species, with
only *A. tamarii* having marginally higher virulence (Ford & Friedman, 1967). More recently, studies in both normal and immunocompromised mice have demonstrated that LD$_{90}$ inocula for *A. flavus* are 100-fold lower than those required for *A. fumigatus* (Mosquera *et al.*, 2001; Kamai *et al.*, 2002). Following intravenous administration in non-neutropenic mice of *A. flavus* spores, the infection is rapidly concentrated in the liver and lungs within 4 h. The fungal burden in the lungs rapidly declines by 95% over 24 h whilst the burden in the liver declines more slowly for 5 days following infection. In contrast, the burden in the kidneys and brain increases until a lethal burden develops 5–10 days post-infection (Ford & Friedman, 1967). The precise cause of death in mice with disseminated infection has not been characterized but tissue burdens immediately before death are much lower than occurs in *A. fumigatus* infections. It seems clear that aflatoxin is not a major factor in disease development, as strains which are unable to produce aflatoxin *in vitro* are similarly virulent (Richard *et al.*, 1984); additionally, infections with aflatoxin-producing strains generate infections in which aflatoxin is undetectable in tissues (Richard *et al.*, 1984).

Immunocompromised rats and rabbits have also been used as hosts of disseminated, invasive pulmonary and sinus *A. flavus* infections (Kaliamurthy *et al.*, 2003). Infection results in death between 7 and 10 days post-infection, with the highest tissue burden recovered from the lungs→liver→brain→kidneys (this is in stark contrast to the tissue burdens in mice following *A. fumigatus* infection). Rabbits have been used as a model of paranasal sinus mycoses caused by *A. flavus* following direct injection into the sinus. In these studies the rabbits were not immunocompromised but required a very high inoculum (up to $10^8$ spores) to reliably establish an infection (Chakrabarti *et al.*, 1997). Domestic chickens, geese and turkey pouls are all susceptible to *A. flavus* without immunosuppression. Infections occur naturally in domestic flocks and can also be established following aerosol exposure.

### Human diseases

*A. flavus* causes a broad spectrum of disease in humans, ranging from hypersensitivity reactions to invasive infections associated with angioinvasion. After *A. fumigatus*, *A. flavus* is the second leading cause of invasive and non-invasive aspergillosis (Denning, 1998; Morgan *et al.*, 2005). The primary route of infection is inhalation of fungal spores. The bigger size of *A. flavus* spores ($25 \mu m$ in diameter in comparison to $23 \mu m$ for *A. fumigatus*) favours their deposition in the upper respiratory tract. Maybe this is one of the reasons why *A. flavus* is a common aetiological agent of fungal sinusitis and cutaneous infections, but not invasive fungal pneumonia. Possibly surface characteristics of the spores other than size are also important determinants of localization (Morrow, 1980).

As mentioned before, climate and geographical factors are important determinants of the local prevalence of *A. flavus* infections. In countries like Saudi Arabia and Sudan, with semi-arid and arid dry weather conditions, *A. flavus* is the main aetiological agent of invasive aspergillosis (Khairallah *et al.*, 1992; Kameswaran *et al.*, 1992). *A. flavus* is also one of the main pathogens responsible for pulmonary aspergillosis in Africa (Mahgoub & el-Hassan, 1972). For unknown reasons, the frequency of infections caused by *A. flavus* is also elevated in some hospitals, in different locales. Even though the clinical features of aspergillosis are generally identical for all of *Aspergillus* species, some particularities regarding *A. flavus* infections are described below.

### Chronic cavitary pulmonary aspergillosis (CCPA) and aspergillosis

*A. fumigatus* causes the vast majority of cases of CCPA and aspergillosis (Denning *et al.*, 2003). For unknown reasons, *A. flavus* has rarely been associated with CCPA (Liao *et al.*, 1988; Staib *et al.*, 1983). Approximately 10 cases have been reported so far, mostly from regions with hot and dry climate. Systemic oxalosis has mostly been associated with *A. niger* aspergillomas in diabetic patients, and it is rare with *A. flavus* (Dogan *et al.*, 2004).

### Allergic bronchopulmonary aspergillosis (ABPA) and allergens

Although *A. fumigatus* is responsible for the vast majority of ABPA cases, *A. flavus* has also been implicated in some series (Khan *et al.*, 1976; Chakrabarti *et al.*, 2002), mostly in studies from India. In addition, ABPA caused by *Aspergillus flavus* complex can also occur as an occupational disease. Many reports from Japan have shown that exposure to high concentrations of *A. oryzae* spores during the production of soybean products can lead to ABPA (Akiyama *et al.*, 1987; Kurosawa *et al.*, 1990). The vast majority of patients with ABPA have asthma; however, interestingly, some of these patients did not.

Several species of *Aspergillus* have been shown to be allergenic, including *A. fumigatus*, *A. niger*, *A. flavus* and *A. oryzae*. Over 20 allergens have been characterized in *A. fumigatus*, two from *A. flavus* (Asp fl 13 and Asp fl 18) and a further four from the closely related *A. oryzae* (Asp o 13, Asp o 21, Asp o lactase and Asp o lipase) (Mari & Riccioli, 2004; http://www.allergome.org/). Recent genome sequencing projects have made it possible to survey the allergens present in *Aspergillus* species. Table 2 shows predicted *A. flavus* allergen homologues by comparison with allergens from other *Aspergillus* species. It can be seen that many allergens present in *A. fumigatus* are present at high levels of homology in *A. flavus*. Proteins with $>50\%$ identity to allergen proteins are likely to be immunologically cross-reactive (Bowyer *et al.*, 2006). Asp o 21 and Asp o 13 allergens from the closely related *A. oryzae* are present at 98 and 100% identity respectively and are likely to function as allergens in *A. flavus*. Additionally Asp f 1, Asp f 5, Asp f 12, Asp f 13, Asp f 18, Asp f 22 and Asp f 23 are all present...
in the \textit{A. flavus} genome at \textgreater{}90 \% identity and are likely to be allergenic in this species. Thus it is likely that \textit{A. flavus} will produce many more allergenic proteins than the two currently known and may possess an allergen complement similar to that of \textit{A. fumigatus}.

**Keratitis and endophthalmitis**

Fungal keratitis occurs predominantly in tropical and warm climates, and various case series have been published from Africa (Gugnani et al., 1978; Cheikh-Rouhou et al., 2001), the Middle East (Khairallah et al., 1992), South Asia (Wong et al., 1997) and some parts of the USA (Rosa et al., 1997). Amongst keratitis cases caused by \textit{Aspergillus} spp., \textit{A. flavus} accounted for 80 \% of the total \textit{Aspergillus} infections (Khairallah et al., 1992). The major predisposing condition to \textit{A. flavus} keratitis is trauma, generally with plant material (Gugnani et al., 1978; Khairallah et al., 1992; Wong et al., 1997; Cheikh-Rouhou et al., 2001). In some cases \textit{A. flavus} keratitis was reported after laser and cataract surgery (Sridhar et al., 2000; Mendicute et al., 2000). Fungal endophthalmitis has rarely been associated with \textit{A. flavus} (Lance et al., 1988; Demicco et al., 1984; Cameron et al., 1991).

**Cutaneous infection**

Most cases of cutaneous aspergillosis are caused by \textit{A. flavus} (van Burik et al., 1998; Chakrabarti et al., 1998). Skin involvement can be classified as either (i) primary, following direct inoculation of \textit{Aspergillus} at sites of skin injury (e.g. intravenous catheter sites, traumatic inoculation, occlusive dressings, burns or surgery), or (ii) secondary, from haematogenous spread, most commonly following a pulmonary portal of entry, or from contigous extension from a neighbouring cavity such as the maxillary sinus. The clinical presentation of cutaneous aspergillosis by \textit{A. flavus} is characterized by the presence of violaceous macules, papules, plaques or nodules, haemorrhagic bullae, ulcerations with central necrosis with or without eschar formation, pustules or subcutaneous abscesses.

**Wound infection**

\textit{A. flavus} is a particularly important species in wound aspergillosis, accounting for 41 \% of cases confirmed by culture (Pasqualotto & Denning, 2006). Many studies have linked the occurrence of postoperative aspergillosis with the dissemination of \textit{Aspergillus} spores in the operating room (Pasqualotto & Denning, 2006). Diaz-Guerra et al. (2000) reported the simultaneous isolation of one \textit{A. flavus} isolate from the aortic prosthesis of a heart surgery patient, and another two isolates were recovered from a dual-reservoir cooler-heater used in the operating room where this patient was operated on. Genetic typing of these isolates by RAPD revealed identical genotypes, indicating the nosocomial origin of the strain. \textit{Aspergillus} infection should always be considered in the differential diagnosis of slowly progressive but destructive wound infections, culture-negative pleural effusion and culture-negative mediastinitis after cardiac surgery.

**Endocarditis and pericarditis**

\textit{A. flavus} has been reported as a cause of both native and prosthetic valve endocarditis, which is occasionally a manifestation of disseminated aspergillosis (Demaria et al., 2000; Rao & Saha, 2000; Irles et al., 2004). Occasional cases occur in patients with no overt risk factors (Kennedy et al., 1998; Khan et al., 1995). In postoperative \textit{Aspergillus} endocarditis, \textit{A. flavus} accounts for 11.2 \% of cases (Pasqualotto & Denning, 2006). A rare case of fungal endocarditis (\textit{A. flavus}) on a permanent pacemaker has been described (Acquati et al., 1987). Two reports have associated \textit{A. flavus} with pericarditis (Cooper et al., 1981).

**Central nervous system infection**

Case series of craniocebral aspergillosis due to \textit{A. flavus} in immunocompetent hosts have been reported mainly from Pakistan, India, Saudi Arabia, Sudan and other African countries (Rudwan & Sheikh, 1976; Hussain et al., 1995; Panda et al., 1998). Most of these cases occurred as a complication of chronic granulomatous sinusitis, described below. These reports have speculated that tropical environmental conditions (hot and dry weather), bad hygiene and poor socioeconomic status are responsible

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**Table 2. Predicted allergens in the \textit{A. flavus} genome**

<table>
<thead>
<tr>
<th>Allergen</th>
<th>Percentage identity of the \textit{A. flavus} homologue</th>
</tr>
</thead>
<tbody>
<tr>
<td>Asp f 1 Mitogillin</td>
<td>97</td>
</tr>
<tr>
<td>Asp f 2 [Afu4g09580]</td>
<td>65</td>
</tr>
<tr>
<td>Asp f 3 PMP20 [Afu6g02280]</td>
<td>86</td>
</tr>
<tr>
<td>Asp f 4 [Afu2g03830]</td>
<td>56</td>
</tr>
<tr>
<td>Asp f 5 Metalloprotease</td>
<td>95</td>
</tr>
<tr>
<td>Asp f 6 Mn SOD [Afu1g14550]</td>
<td>60</td>
</tr>
<tr>
<td>Asp f 7 [Afu4g06670]</td>
<td>48</td>
</tr>
<tr>
<td>Asp f 8 [Afu2g10100] ribosomal P2</td>
<td>85</td>
</tr>
<tr>
<td>Asp f 9 [Afu1g16190]</td>
<td>64</td>
</tr>
<tr>
<td>Asp f 10 Aspiligoepsin</td>
<td>75</td>
</tr>
<tr>
<td>Asp f 11 Cyclophilin</td>
<td>85</td>
</tr>
<tr>
<td>Asp f 12 HSP90 [Afu5g04170]</td>
<td>94</td>
</tr>
<tr>
<td>Asp f 13 [Afu2g12630] protease</td>
<td>94 (Asp f 13)</td>
</tr>
<tr>
<td>Asp f 17 [Afu4g03240]</td>
<td>42</td>
</tr>
<tr>
<td>Asp f 18 Cell serine protease [Afu5g09210]</td>
<td>92 (Asp f 18)</td>
</tr>
<tr>
<td>Asp f 22 Enolase [Afu6g06770]</td>
<td>93</td>
</tr>
<tr>
<td>Asp f 23 Rpl3 [Afu2g11850]</td>
<td>95</td>
</tr>
<tr>
<td>Asp f 13 (previously Asp f 1)</td>
<td>100</td>
</tr>
<tr>
<td>Asp n 14 β-Xylosidase</td>
<td>64</td>
</tr>
<tr>
<td>Asp n 25 3-Phytase B</td>
<td>31</td>
</tr>
<tr>
<td>Asp n Glucoamylase</td>
<td>68</td>
</tr>
<tr>
<td>Asp o 13 Oryzin</td>
<td>100</td>
</tr>
<tr>
<td>Asp o 21 α-Amylase A</td>
<td>98</td>
</tr>
</tbody>
</table>
Rhinosinusitis

A. flavus is more likely to be recovered from the upper respiratory tract than any other Aspergillus species (Chakrabarti et al., 1992; Hussain et al., 1995; Iwen et al., 1992; Yagi et al., 1992; Yagi et al., 1999). Clinical presentations of Aspergillus rhinosinusitis include acute and chronic invasive, chronic granulomatous and non-invasive syndromes (Hope et al., 2005). For an adequate diagnosis, tissue should be obtained for histopathology (fungal stains are essential), with fungal cultures of surgical specimens. Cultures of the nasal mucus are unreliable for diagnosis because the cultures reflect recent air sampling, rather than disease.

Chronic granulomatous sinusitis is a curious syndrome of chronic slowly progressive sinusitis associated with proptosis that has been also called indolent fungal sinusitis and primary paranasal granuloma. Florid granulomatous inflammation is the histological hallmark of this condition. Interestingly, almost all reports come from the Sudan (Milosev et al., 1969; Gumaa et al., 1992; Yagi et al., 1999), Saudi Arabia (Alrajhi et al., 2001) and the Indian subcontinent (Chakrabarti et al., 1992; Ramani et al., 1994; Panda et al., 2004). There are a limited number of reports in the USA, which appear to affect almost exclusively African-Americans (Currens et al., 2002). Whether this reflects climatic conditions and/or any genetic predisposition is unknown. Curiously, patients appear to be immunocompetent and are infected almost exclusively with A. flavus (Gumaa et al., 1992; Yagi et al., 1999; Alrajhi et al., 2001). Bone erosion is a common finding (Yagi et al., 1999) and tissue destruction occurs as a result of expansion of the mass rather than vascular invasion. Most individuals present with a unilateral proptosis (Milosev et al., 1969). Frequently there is direct spread beyond the confines of the sinuses to invade the brain, cavernous sinus, orbit and great vessels (Hope et al., 2005). Marked regression generally occurs following surgical procedures designed to produce adequate aeration of the sinuses. However, the recurrence rate is high (about 80 %), and some evidence suggests that the use of antifungal drugs may offer benefit (Gumaa et al., 1992).

Allergic fungal sinusitis (AFS) and sinus aspergilloma

Although A. fumigatus seems to be the most frequent Aspergillus organism causing AFS, A. flavus is particularly frequent in some geographical areas, such as the Middle East and India (Taj-Aldeen et al., 2003, 2004; Saravanan et al., 2006; Thakar et al., 2004). Patients with AFS may have co-existent mucosal granulomatous inflammation indicative of fungal tissue invasion (Thakar et al., 2004). In these cases from India, A. flavus was the only pathogen identified (Thakar et al., 2004). Sinus aspergilloma (fungus ball) is also usually caused by A. fumigatus and such infections caused by A. flavus are less frequent in developed countries (Milosev et al., 1969; Stammberger et al., 1984; Ferreiro et al., 1997). Again, A. flavus is more commonly isolated from patients in India, Sudan and other tropical countries (Panda et al., 1998; Yagi et al., 1999; Chakrabarti et al., 1992; Milosev et al., 1969).

Osteoarticular infection

A. flavus seems to be the main aetiological agent of Aspergillus osteomyelitis following trauma (Fisher, 1992), a situation which resembles the elevated frequency at which A. flavus causes primary cutaneous aspergillosis and wound infections.

Urinary tract infection

Urinary tract aspergillosis due to A. flavus is rare, with few cases reported (Khan et al., 1995; Perez-Arellano et al., 2001; Kueter et al., 2002). Usually a unilateral or bilateral fungal bezoar of the urinary pelvis is the presenting problem. Predisposing conditions include diabetes, intravenous drug addiction and schistosomiasis.

Resistance to antifungal drugs

Until recent years, the only drugs available to treat aspergillosis were amphotericin B (AmB) and itraconazole, the latter in oral and intravenous formulations. Recently voriconazole, posaconazole and caspofungin have also been approved for the treatment of aspergillosis. Although resistance to antifungal drugs is not as great a concern as resistance to antibacterial agents, there has been an increase in the number of reported cases of both primary and secondary resistance in human mycoses (Denning et al., 1997). Therefore, it seems possible that resistance of the fungus to the drug or an inadequate concentration of the antifungal drug at the site of infection might contribute to the high mortality rate seen for these infections.

Amphotericin B

Although the true rate of AmB resistance is unknown, some investigators have reported isolates of A. flavus resistant to AmB in vitro (Odds et al., 1998; Lass-Florl et al., 1998; Seo et al., 1999; Mosquera et al., 2001; Gomez-Lopez et al., 2003; Sutton et al., 2004; Hsueh et al., 2005), although this is not universally accepted. In a study from Taiwan (Hsueh et al., 2005) isolates of A. flavus and A. fumigatus with reduced susceptibilities to AmB were found (MICs 2 μg ml⁻¹). Among the four species tested, A. flavus was the least susceptible to AmB; the MICs at which 50 % and 90 % of A. flavus isolates were inhibited were twofold greater than those for A. fumigatus and A. niger.

A preliminary report has documented a steady increase in AmB resistance in vitro amongst Aspergillus isolates recovered since 2001 (Sutton et al., 2004). About 20 % of A. fumigatus and A. flavus isolates recovered in 2004 had
minimum lethal concentrations (MLCs) of AmB $\geq 16 \mu g \text{ml}^{-1}$ compared to 0 % in 2001. Some investigators have hypothesized that the extensive use of AmB against fungal infections has led to the emergence of less susceptible species, such as A. terreus and A. flavus (Marr et al., 2002). Recently, Lionakis et al. (2005) found that the proportion of Aspergillus spp. resistant to antifungals (especially AmB) was much higher amongst isolates recovered from cancer patients with prior exposure to AmB or triazoles.

Few data are available regarding correlations between MIC and outcome of treatment with AmB for infections caused by Aspergillus species. In the survey of Odds et al. (1998) the efficacy of AmB at 0.31 mg kg$^{-1}$ was seen in vivo against A. fumigatus (MIC 1 $\mu g \text{ml}^{-1}$) but efficacy was not seen against A. flavus at the same MIC, at any dose tested. In another study (Lass-Florl et al., 1998), AmB MICs of $\geq 2 \mu g \text{ml}^{-1}$ were associated with treatment failure amongst patients with invasive aspergillosis. Mosquera et al. (2001) demonstrated a lack of correlation between susceptibility to AmB in vitro and clinical outcome for A. flavus infections in vivo by using different susceptibility testing methods, including the Clinical and Laboratory Standards Institute (CLSI, formerly NCCLS) M-38A method. Difficulty in treating invasive aspergillosis might relate in part to poor penetration of AmB into infected tissue (Paterson et al., 2003).

Itraconazole resistance in Aspergillus species is presumptively defined as an MIC of $\geq 8 \mu g \text{ml}^{-1}$ (Gomez-Lopez et al., 2003). According to this criterion, Hsueh et al. (2005) found resistance to itraconazole in 4.2 % (4 of 96) of Aspergillus species, including two A. fumigatus and two A. flavus isolates. Similar rates of resistance were found amongst isolates included in previous studies (Gomez-Lopez et al., 2003; Lionakis et al., 2005). In the study by Hsueh et al. (2005), all of the Aspergillus isolates tested were inhibited by $\leq 8 \mu g \text{itraconazole ml}^{-1}$. Recently, Lionakis et al. (2005) showed that 11 % of the A. flavus isolates in their study were itraconazole resistant based on in vitro susceptibility by tests performed by the CLSI method; using the E-test, only 6 % of A. flavus isolates could be classified as itraconazole resistant. Again, in vitro susceptibility test results may not reflect in vivo response, as demonstrated by Mosquera et al. (2001).

Voriconazole

Voriconazole has good in vitro activity against a range of Aspergillus species, including A. flavus (Pfaller et al. 2002; Diekema et al., 2003; Lass-Florl et al., 2001). Hsueh et al. (2005) showed that all of the Aspergillus isolates tested, including A. flavus, were inhibited by $\leq 1 \mu g \text{voriconazole ml}^{-1}$. Voriconazole MICs are slightly higher than those of itraconazole for A. flavus (Maesaki et al., 2000; Gomez-Lopez et al., 2003). The precise inoculum used can alter the MIC, so higher inocula yield higher and potentially resistant end points (Mosquera et al., 2001). Discordance in results with the CLSI and E-test methods with voriconazole is problematic (Lionakis et al., 2005). Since validated methodology and breakpoints for voriconazole have not yet been established, the rate of resistance is not known. However, some Aspergillus isolates seem to show cross-resistance to itraconazole and voriconazole, as demonstrated with A. fumigatus, and this is strain (and presumably mechanism) dependent (Espinell-Ingroff et al., 2001; Pfaller et al., 2002).

Other antifungal agents

Caspofungin, anidulafungin and micafungin are members of the echinocandin group of antifungal agents that target 1,3-$\beta$-glucan synthase, disrupting hyphal growth at tips and branch points. Caspofungin and micafungin are available for the treatment of invasive aspergillosis and hold promise for treatment alone or in combination with triazoles or AmB (Marr et al., 2002; Cesaro et al., 2004). A. flavus would appear to be slightly less susceptible than A. fumigatus to echinocandins, based on in vitro parameters (Oakley et al., 1998; Espinell-Ingroff, 2003) but eradication rates were 20–25 % better for A. flavus infection than A. fumigatus in two salvage studies (Maertens et al., 2004; Denning et al., 2006). Thus, a species difference in susceptibility to echinocandins may exist, but is not obviously clinically relevant, and could reflect the difficulties in interpretation of in vitro results with echinocandins. No isolates of A. flavus have yet been described that are resistant to posaconazole.

Conclusions

A. flavus is the second most important Aspergillus species causing human infections. The importance of this fungus increases in regions with a dry and hot climate. In addition, many A. flavus isolates produce aflatoxin B1, the most toxic and potent hepatocarcinogenic natural compound ever characterized. Small studies of phylogenetic species in A. flavus indicate that the morphological species contains several genetically isolated species, and until a population-based discriminatory molecular typing system is applied, we will not know the full extent of diversity in A. flavus, sensu lato. Population genetics studies on isolates causing disease would be of great interest. Particularly common clinical syndromes associated with A. flavus include chronic granulomatous sinusitis, keratitis, cutaneous aspergillosis, wound infections and osteomyelitis following trauma and inoculation. On the other hand, A. flavus is rarely the aetiological agent of chronic cavitary pulmonary aspergillosis. In frank contrast to A. fumigatus infections, most of the investigated outbreaks caused by A. flavus were due to a single or a few strains, assuming that the typing systems used were sufficiently discriminatory. Finally, A. flavus seems to be more virulent and more resistant to antifungal drugs than most of the other Aspergillus species. Hopefully, recently published information about the
Aspergillus genomes will help us to better understand the pathogenesis of these infections, as well as providing insights into toxin production and allergens.

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