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Review

Occurrence of indoor wood decay basidiomycetes in Europe

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ABSTRACT

Brown-rot fungi are considered to be the most important wood-inhabiting fungi economically, as they also deteriorate the wood that has been used in buildings. In the northern hemisphere, coniferous wood is the main source of interior structural timber. White-rot fungi, which degrade lignin and preferentially attack hardwood, are less common. Emphasis is usually placed on *Serpula lacrymans* or *Coniophora puteana*, which are the most common indoor basidiomycetes found in buildings in Europe. In this review, we summarize available data on the occurrence of wood decay fungi in the Czech Republic, Poland, Germany (both former East and West), Belgium, France, Norway, Denmark, Finland, Latvia, Estonia, Romania and Albania reported in the past few decades. The total number of occurrences was near 20,000; original data were collected between 1946 and 2008. The most abundant basidiomycetes were *S. lacrymans* and *C. puteana*, with the exception of Norway, where the genus *Antrodia* was the most frequent.

1. Introduction

Indoor wood decay fungi cause many problems worldwide; fungi that invade roofs, walls, ceilings, etc., represent a group of various basidiomycetes that are in many cases resistant to currently used fungicides. These fungi attack and damage wooden houses and other wooden constructions, and the most well-known of these, *Serpula lacrymans* (often regarded as the "cancer of buildings"), is responsible for many millions of USD of damage each year (Palfreyman, 1995). For example, the cost of fungal damage in France was estimated to be approximately € 30 million yearly (Maurice *et al.* 2011), and in the UK, the cost of repairing fungal damage to timber used in construction amounted to £ 3 million per week (Rayner and Boddy 1988). The dry rot remediation business in the UK was estimated to be worth an excess of £ 400 million (Krzyzanowski *et al.* 1999).

The decay of wood and wood-based products usually begins when the spores or mycelial fragments adhere to the wood surface. Wood moisture and temperature are the most important features in terms of the "building habitat". Humphrey and Siggers (1933) previously studied the effect of temperature on the growth rate of 56 wood-decay fungi and found that none would grow below 12 °C and that most would not grow above 40 °C. According to many authors and guidelines for the protection of wood and wood products from attack by decay fungi, it is important and necessary to keep wood or wooden constructions at a moisture content below

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20 % (Carll and Highley 1999). Schmidt (2007) reported minimum and maximum humidity requirements for fungi identified by means of ITS sequencing (to avoid unreliable data for incorrectly identified species; Table 1). As stated by Carll and Highley (1999), the spores of wood decay fungi do not germinate and fungal hyphae do not grow at moisture levels much below the fibre saturation point, which is at approximately 30 % moisture. However, only the part of water that is not bound by dissolved substances (salts, sugars) is available to fungi; a detailed description of the optimum conditions for wood decay in terms of water activity (aw), water potential or relative air humidity (RH) can be found, e.g., in the above-mentioned review of Schmidt (2007). However, data on fungal development under fluctuating moisture conditions that are more common in nature are not yet available. Other factors, such as wood species, local climate, design details, exposure conditions (esp. in roofs and trusses, cellars, and door frames) and coatings might have an indirect effect on wood decay (e.g., Thybring 2017, Meyer and Brischke 2015). Under ideal moisture and temperature conditions, fungal growth may occur even within days.

In theory, wood decay fungi need free water as a diffusion medium for their extracellular digestive enzymes. In the case of brown-rot (or dry-rot) fungi, other factors in addition to enzymatic processes are involved in wood degradation. Low molecular weight compounds, such as oxalate, veratryl alcohol, variegatic acid and others (Goodell *et al.* 1997; Eastwood *et al.* 2011; Watkinson and Eastwood 2012), contribute to lignocellulose decay, as do Fe and most likely other bivalent ions. These chemicals generate hydroxyl, peroxyl and hydroxylperoxyl radicals in Fenton and Fenton-like systems. Inorganic elements play an important role in the physiology and control of at least *S. lacrymans* growth (Schilling 2010; Watkinson and Eastwood 2012). As has been demonstrated (Low *et al.* 2000), *S. lacrymans* removes calcium, silicon and iron from sandstone and calcium, sulphur and iron from traditional plaster. The sequestered elements are located in its hyphae, particularly in the form of calcium oxalate.

2. Detection and identification of decay fungi

Fruiting bodies are normally preferentially used for field identification (e.g., Abrego and Salcedo 2015, Nicolotti *et al.* 2010). Some species rarely fructify in buildings but form mycelial strands (cords). Frankl (2014) found vital mycelia or active fruiting bodies only in only 7 % of his observations (but the remains were found in 95 %). Many studies address the diagnostics of wood decaying fungi based on their macromorphology and micromorphology; i.e., the typical shape and colour of fruiting bodies or spores, cell wall thickness of hyphae, type of branching, presence of dolipore septa, clamp connections or aggregates on the surface or inside the cells, etc. Typical visible properties (brown or white discolouration, eventually cracking into roughly cubical pieces) of degraded wood are also very important. Following the crucial work of Falck (1912), newer diagnostic keys including drawings or colour photographs have been published, e.g., by Domański (1972), Stalpers (1978), Hanlin (1998), Schmidt (2006), Huckfeldt and Schmidt (2006), Buchalo *et al.* (2009) and Stancheva *et al.* (2009).

Precise molecular methods were not available for the identification of indoor wood decay fungi until the 1980s. These methods include species-specific priming PCR (SSPP), rDNA ITS region sequence analysis, restriction fragment length polymorphism analysis (RFLP), random amplified polymorphic DNA analysis (RAPD), amplified fragment length polymorphism analysis (AFLP) and sequence-specific oligonucleotide probe analysis (SSO). For more information, see the work of Maurice *et al.* (2011) or the recent paper by Raja *et al.* (2017) and references cited herein. Methods based on DNA analyses can provide efficient, sensitive and rapid diagnostic tools for the detection and identification of wood decay fungi without requiring a prior fungal isolation step (Glaeser and Lindner 2011, Gonthier *et al.* 2015). In the case of wood decay basidiomycetes, methods based on ribosomal DNA (ITS 1 or 2 rDNA region) sequencing have been established as routine techniques for the identification of fungi to the species level, esp. for those that are hardly or not at all distinguishable by species, such as *Antrodia*, *Coniophora* and *Leucogyrophana* (Schmidt 2006, Jarosch and Besl, 2001; Binder and Hibbett, 2006, Coetzee *et al.*, 2003; Schmidt *et al.*, 2012). In the last ten years, sequencing technologies have changed dramatically, offering multiple options in throughput, accuracy and cost for answering different biological questions.

Some other alternative techniques are based on the production of typical volatile organic compounds (VOC) by fungi (e.g., Schmidt and Kallow, 2005). In addition to 1-octen-3-ol (Ewen *et al.* 2004), which causes the typical smell of mushrooms, several other compounds typical of fungi have been described (e.g., Anton *et al.* 2016, Konuma *et al.* 2015, Korpia

Table 1 – Humidity requirements (wood moister content; %) of selected fungi with respect to the colonization and decay of wood (after Schmidt 2007).

Species	Minimum for colonization	Minimum for decay	Optimum for decay	Maximum for decay
Serpula lacrymans	21	26	45–140	240
Leucogyrophana pinastri	30	37	44–151	184
Coniophora puteana	18	22	36–210	262
Antrodia vaillantii	22	29	52–150	209
Donkioporia expansa	21	26	34–126	256
Gloeophyllum abietinum	20	22	40–208	256
Gloeophyllum sepiarium	28	30	46–207	225
Gloeophyllum trabeum	25	31	46–179	191