Introduction

Animals are frequently more susceptible to certain mycoses than humans, possibly as a result of their proximity to contaminated soil or plant material, or behavior that encourages infection such as digging by dogs, scratching by cats, and occupation of tree hollows by koalas. This makes them ideal sentinels for emerging fungal disease in humans. There are many examples of situations where fungal infections have been observed in areas previously thought to be non-endemic in animals before they have been documented in humans. For example, the emergence of coccidioidomycosis in Washington state followed discovery of the organism in a dog without travel history. Dogs have shed light on risk factors for blastomycosis in humans in the upper midwest of the United States, although one recent study suggested that canine blastomycosis was not a risk factor for human disease in dog owners.

Cryptococcosis

Cryptococcosis is the most common systemic mycosis of cats, which are approximately 10 times more susceptible than dogs. Cryptococcosis is most commonly caused by two encapsulated yeast species that are dimorphic, basidiomycetous fungi of the genus Cryptococcus, Cryptococcus neoformans and Cryptococcus gattii. C. gattii is considered an emerging pathogen of immunocompetent humans in the north-western United States, in contrast to C. neoformans, an opportunistic pathogen in humans. Occasionally, outbreaks of infection in humans and animals occur as a result of exposure to common environmental sources. Cryptococcus spp. were initially classified into 4 serotypes, A, B, C and D, based on antigenic differences in the cryptococcal polysaccharide capsule, and a hybrid serotype AD was also identified. C. neoformans contains serotypes A and D, and C. gattii contains serotypes B and C. With the introduction of a variety of genotyping methods, considerable genetic diversity has been identified within these serotypes. The results of PCR fingerprinting using microsatellite M13 or minisatellite (GACA)4 primers, or amplified fragment length polymorphism (AFLP) analysis, have shown that the Cryptococcus species complex can be divided into at least 8 molecular types. To some extent, the types correlate with Cryptococcus species and serotypes, and consist of VNI/AFLP1 and VNII/AFLP1A/1B (C. neoformans var. grubii, serotype A); VNIII/AFLP3 (AD hybrid); VNIIV/AFLP2 (C. neoformans var. neoformans, serotype D), and VGI/AFLP4, VGII/AFLP6, VGIII/AFLP5 and VGIV/AFLP7 (C. gattii, serotypes B and C). Interspecies hybrid strains (AB and BD serotypes) have also been reported. There is currently some discussion of renaming molecular types of C. gattii as separate species, but this has been controversial. Differences in epidemiology, pathogenicity, clinical features and drug susceptibility have been associated with the species, variety, and molecular types.

C. neoformans has a worldwide distribution. The major environmental niche for C. neoformans is believed to be weathered bird (especially pigeon) guano. It can also be found in decaying plant matter in hollows of certain trees. C. neoformans passes through the gastrointestinal tract of pigeons, but systemic infection of pigeons is rare. Pigeon guano provides an environment rich in many nitrogen-containing compounds including creatinine that favor cryptococcal growth. The vast majority of human cryptococcal infections in human immunodeficiency virus-infected patients result from infection with C. neoformans, especially C. neoformans var. grubii. Interestingly, the majority of dogs with cryptococcosis in North America are purebred dogs that are infected with C. neoformans, whereas infection of cats with this species appears to be rare. This supports the notion that C. neoformans causes disease in individuals with specific severe immune compromise states.

Originally thought to be a tropical or subtropical pathogen, C. gattii has also emerged as an important pathogen in temperate regions following outbreaks of disease in apparently immunocompetent individuals in British Columbia, Canada, and the Pacific Northwest of the United States. The outbreaks of disease in Canada and the Pacific Northwest have been associated with certain highly virulent molecular types of Cryptococcus gattii, primarily VGIIa, and to a lesser extent, VGIIb. At the same time the disease was recognized in humans, a variety of animal species were also found to be affected, including dogs, cats, ferrets, alpacas, and marine mammals, and study of the epidemiology of the disease in animals yielded insights into risk factors for the disease in humans. Identification of molecular type VGIIa in a dog from Oregon supported expansion of the Vancouver Island outbreak into the Pacific Northwest. In northern California, almost all cats with cryptococcosis have been infected with C. gattii genotype VGIII. Following the discovery of this molecular type in cats in California, the same molecular type was recognized in humans from southern California. In contrast, the prevalence of C. gattii infection is lower in cats from southeastern Australia, with most C. gattii isolates belonging to VGI. VGII predominates in southwestern Australia and the Northern Territory. C. gattii
Histoplasmosis

Histoplasmosis is caused by Histoplasma capsulatum, a dimorphic, soil-borne fungus that is found worldwide, but especially in the Mississippi and Ohio river valleys of the USA as well as in Latin America. Eight clades of the organism have been identified by genetic analysis: North American (class 1 and class 2), Latin American (group A and group B), and one each of Australian, Indonesian, Eurasian and African, which appear to vary in virulence. All except the Eurasian clade, which is derived from the Latin America group A clade, may represent distinct phylogenetic species.

Histoplasma capsulatum can be found in the intestinal tract and guano of bats, which constitute the primary reservoir of the organism and serve to disseminate it geographically. Bat caves maintain the perfect conditions for growth of H. capsulatum. Although H. capsulatum can be found in high concentrations in decaying avian guano (especially around blackbird or starling roosts and chicken coops), it is not found in fresh feces or shed in the feces of birds. Cats appear to be as susceptible, or slightly more susceptible to histoplasmosis than dogs. The most common organs affected are the lungs and tracheobronchial lymph nodes. When infection disseminates, it often involves the eye, spleen and liver in cats; and the gastrointestinal tract in dogs.

Although histoplasmosis has appeared sporadically in dogs and cats from northern California for many years, increasing numbers of cases in the last 3-5 years in both northern and southern California suggests that the disease may be emerging to a greater extent in California. This has correlated with appearance of human disease in the region. Understanding risk factors for the disease in cats and dogs in California may provide important insights into human risk factors.

Sporotrichosis

Organisms that belong to the Sporothrix schenckii species complex are dimorphic, saprophytic fungi that cause sporotrichosis, a subacute to chronic disease that most often results from cutaneous or subcutaneous inoculation of the organism through a puncture wound, but can also follow inhalation. Sporotrichosis has been described in cats, dogs, humans, and a variety of other domestic and wild animal hosts that include horses, ruminants, swine, rats, mice, hamsters, armadillos, domestic fowl, chimpanzees and dolphins.

Sporothrix species thrive in warm, humid conditions. They prefer moist soil that is rich in decaying vegetation, as well as sphagnum moss, wood, thorns or hay. The fungus is distributed worldwide in tropical and temperate zones, but is most prevalent in tropical or subtropical regions of the Americas. Although all Sporothrix isolates have in the past been grouped into one species, multiple genotypes exist that vary in virulence and geographic distribution. As a result, a S. schenckii species complex has been identified, which includes at least 6 species: S. schenckii sensu stricto, S. brasiliensis, S. globosa, S. mexicana, S. albicans and S. luriei. S. brasiliensis appears to be limited to Brazil. S. schenckii, S. brasiliensis and S. albicans have been isolated from cats, and S. schenckii and S. luriei have been isolated from dogs.

Cats are more susceptible to sporotrichosis than dogs and facilitate distribution of organisms in the environment. Contaminated claw or bite wounds are thought to be important modes of transmission. In Rio de Janeiro, a large outbreak of sporotrichosis has been described over the last decade, which has involved more than a thousand humans and thousands of cats. Of isolates made from affected humans in the outbreak, most have been S. brasiliensis, but S. schenckii sensu stricto and S. globosa have also been isolated. An understanding of the epidemiology of the disease in cats has yielded insight into risk factors for sporotrichosis in humans. As with Cryptococcus, antifungal drug resistance emergence in animal isolates may provide early warning of resistance in human isolates.

References