

Aspergillosis in an augmented Greater Sage-Grouse (*Centrocercus urophasianus*) population in central Utah: a case report

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ABSTRACT.—We present the first known case of aspergillosis found in a wild, augmented Greater Sage-Grouse (*Centrocercus urophasianus*) population. This case was not directly associated with the sage-grouse translocations and is the first documented in wild sage-grouse populations since the mid-1900s. Aspergillosis is a fungal infection of the lungs caused by an inoculation of *Aspergillus* spp. spores. Wild birds that are infected by the pathogen's spores die from the resulting infection. We hypothesize that the *Aspergillus* spp. spores were propagated either in mesic nesting conditions or in residual damp mulch piles created from sagebrush (*Artemisia* spp.) habitat restoration projects and that these spores infected the individual within several days of inhalation. This case may have conservation implications for small, augmented, or reintroduced avian populations, especially those of conservation concern where concurrent habitat restoration projects and other conservation actions may create conditions conducive to the propagation of *Aspergillus* spp. spores and enhance the risk of sage-grouse inoculation.

RESUMEN.—Presentamos el primer caso conocido de aspergilosis encontrado en una población silvestre de urogallo mayor (*Centrocercus urophasianus*). Este caso no se asoció directamente con las translocaciones de urogallo y es el primero documentado en poblaciones de urogallo silvestre desde mediados del siglo XX. La aspergilosis es una infección micótica de los pulmones, causada por la inoculación de esporas de *Aspergillus* spp. Las aves silvestres infectadas por las esporas del patógeno mueren a causa de la infección resultante. Nuestra hipótesis es que las esporas de *Aspergillus* spp. se propagaron, ya sea en condiciones de anidación en un hábitat mésico o en pilas de mantillo húmedo remanentes, creadas a partir de los proyectos de restauración del hábitat de la artemisa (*Artemisia* spp.), que infectaron al individuo varios días después como resultado de la inhalación de esporas. Este caso podría tener implicaciones para la conservación de las poblaciones de aves pequeñas, en aumento o reintroducidas, especialmente aquellas de interés para la conservación donde los proyectos simultáneos de restauración de hábitat y otras acciones de conservación pueden crear condiciones propicias para la propagación de las esporas de *Aspergillus* spp. y aumentar el riesgo de inoculación del urogallo.

In May 2018, we recovered the intact carcass of a radio-marked adult female Greater Sage-Grouse (*Centrocercus urophasianus*; sage-grouse) that had been translocated from south-central Utah to the Sheepprock Mountain Sage-Grouse Management Area (SGMA) in March 2017 as part of an augmentation program to prevent extirpation. At the time we recovered the carcass, we could not confirm that the female was nesting. However, based on her localized movements detected via radiotelemetry, she may have initiated a nest that had failed earlier in the season. The recovered carcass was necropsied by Utah

Veterinary Diagnostic Laboratory personnel (UDVL, Spanish Fork, UT), and the necropsy revealed that the female died from aspergillosis, a fungal infection of the lungs caused by an inoculation of *Aspergillus* spp. spores.

According to the nature of the gross and histological examinations, UDVL personnel concluded that the infection was caused by a recent inhalation of a significant quantity of *Aspergillus* spp. spores in spring 2018. Their examination revealed multiple spherical granulomatous lesions within the left lung and thoracic airsacs, suggestive of subacute aspergillosis. This diagnosis was substantiated upon

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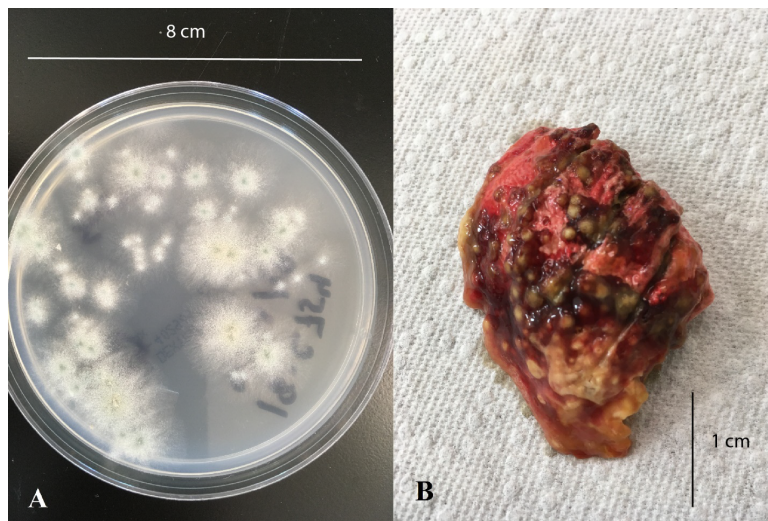


Fig. 1. *Aspergillus* spp. culture (A) taken from a 2018 sample of the lung (B) of an infected female Greater Sage-Grouse (*Centrocercus urophasianus*; sage-grouse), which was an individual translocated into the study area in 2017 as part of an effort to augment the resident sage-grouse population, Sheeprock Sage-Grouse Management Area, Utah, USA.

subsequent culture and histologic examination of the lesions (Figs. 1A, B). Cestodiasis, a severe tapeworm intestinal infestation, was also detected.

Disease occurrences in wild sage-grouse populations are cause for concern because of documented range-wide population declines (Schroeder et al. 2004). In 2003, the discovery of the West Nile Virus (WNV; *Flavivirus*), spread by mosquitoes (*Culex* spp.), in sage-grouse increased range-wide conservation concerns about the impacts of disease on declining populations in increasingly anthropogenic and fragmented landscapes (Walker and Naugle 2011). Unlike WNV, *Aspergillus* spp. spores are not spread by an active vector, so the risk of the pathogen contributing to extirpation or population declines is low (MacPhee and Greenwood 2013). However, if environmental factors in areas inhabited by small, isolated sage-grouse populations create conditions for the pathogen to propagate, the circumstances contributing to potential outbreaks should be evaluated (Tell et al. 2019).

The documented declines in sage-grouse populations and their distribution as a result of the loss and fragmentation of sagebrush (*Artemisia* spp.) ecosystems (Schroeder et al. 2004) resulted in the U.S. Fish and Wildlife Service (USFWS) reviewing the species' protection status under the U.S. Endangered

Species Act (USFWS 2015; ESA). Because of the species' conservation status, range-wide research and conservation efforts have included the capture and radio-marking of thousands of sage-grouse within the last 2 decades as well as efforts to augment declining populations through translocations to prevent extirpations in many areas (Stiver 2011). These range-wide efforts were cited by the USFWS in the decision not to provide sage-grouse with ESA protection (USFWS 2015).

Despite this plethora of research and conservation activity, this case is the first documented occurrence of aspergillosis in a wild sage-grouse since Patterson (1952), who reported a nesting sage-grouse mortality that he attributed to aspergillosis in a wild population in Wyoming. Our case is also the only one documented in a wild, augmented sage-grouse population, further supporting the case that aspergillosis is not common in sage-grouse (Christiansen and Tate 2011). In captive-bred populations, Oesterle et al. (2005) reported one incident of aspergillosis in a population of sage-grouse and noted the high-stress environment where there was heightened aggression among the captive-bred individuals. Similarly, aspergillosis has also been reported in wild Gunnison Sage-Grouse (*Centrocercus minimus*) captured and released into captive-breeding facilities (Apa and Weichman 2015).

However, the source of the infection was attributed to fungal spores propagated in the dusty conditions of the captive-breeding facilities (Apa and Weichman 2015).

Aspergillosis occurring in wild populations is infectious and noncontagious, but it leads to fatality of the infected individual because it cannot be treated (Tell 2005, Beernaert et al. 2010). In wild avian species, it is most commonly found in waterfowl, raptors, upland game birds, and corvids (Tell 2005, Kornilłowicz-Kowalska and Kitowski 2013, Tell et al. 2019). It occurs in concentrations of plant and keratinous material and propagates between 30 °C and 45 °C (Kornilłowicz-Kowalska and Kitowski 2013).

In areas of the United States where woody plant expansion is displacing native shrublands and grasslands, state and federal land managers are implementing habitat restoration projects to remove the target species (Miller et al. 2017). Western rangelands specifically are facing the onset of conifer expansion into sagebrush communities, and managers are working to mitigate that impact by removing conifers through mastication (i.e., grinding down trees where they stand) as well as other methods (Sandford et al. 2017). The remaining mulch is then left in place to decompose, adding new concentrations of plant material to the landscape. High residual concentrations of mulch (which are associated with widespread conifer mastication) in combination with mesic seasonal microclimate conditions associated with sage-grouse nests could facilitate conditions favorable to *Aspergillus* spp. growth and spore propagation (Kornilłowicz-Kowalska and Kitowski 2013).

In domestic turkeys, an *A. fumigatus* intra-air sac infection causes lesions similar to those found in the recovered female sage-grouse carcass within 72 h postexposure (Kunkle and Rimler 1996). Thus, the female was exposed to the fungal spores in 2018, and exposure was not directly connected to the translocations of 2017. However, the immunosuppressive stressors of the 2017 capture, transport, and release associated with the translocation (Dickens et al. 2010, Parker et al. 2012, Jachowski et al. 2016), in addition to the stressors of the 2018 breeding season and concurrent cestodiasis, likely contributed to a decreased ability of the female to suppress an overwhelming inoculation of fungal spores (Redig et al. 1980, Alley et al. 1999, Tell 2005,

Beernaert et al. 2010, Kornilłowicz-Kowalska and Kitowski 2013).

Further research should examine whether the mulch piles created from conifer removal projects or the plant and keratinous material in sage-grouse nests could propagate *Aspergillus* spp. spores. This research should be conducted in the seasonally mesic environments that are common in spring, when breeding and nesting facilitate higher stress conditions, and where habitat restoration projects may provide novel substrates conducive to the fungus (Kornilłowicz-Kowalska and Kitowski 2013).

As previous literature has suggested with WNV and other diseases (Christiansen and Tate 2011), we recommend that sage-grouse populations continue to be monitored for disease, and that any individuals' carcasses or remains containing airsacs and lungs be sent for necropsy. In areas receiving augmentations, reintroductions, or other conservation translocations, adequate postrelease monitoring is integral not only for movements and demographics but also for disease (IUCN/SSC 2013, Muths and McCallum 2016).

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