

Western North American Naturalist

Aspergillosis in an augmented greater sage-grouse (*Centrocercus urophasianus*) population in central Utah: a case report

--Manuscript Draft--

Manuscript Number:	WNAN-D-20-00013R2
Full Title:	Aspergillosis in an augmented greater sage-grouse (<i>Centrocercus urophasianus</i>) population in central Utah: a case report
Article Type:	Note
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Abstract:	<p>We present the first known case of aspergillosis found in a wild, augmented greater sage-grouse (<i>Centrocercus urophasianus</i>) 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 <i>Aspergillus</i> spp. spores. Wild birds that are infected by the pathogen's spores die from the resulting infection. We hypothesize that the <i>Aspergillus</i> spp. spores were propagated either in mesic nesting conditions or in residual damp mulch piles created from sagebrush (<i>Artemisia</i> spp.) habitat restoration projects and infected the individual within several days of inhaling the spores. 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 <i>Aspergillus</i> spp. spores and enhance the risk of sage-grouse inoculation.</p>
Additional Information:	
Question	Response

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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 infected the individual within several days of inhaling the spores. 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.

NOTE

In May 2018, we recovered the intact carcass of an adult female greater sage-grouse (*Centrocercus urophasianus*; sage-grouse) marked with a radio-transmitter that had been translocated in March 2017 from the south-central Utah to the Sheeprock Mountain Sage-Grouse Management Area (SGMA) 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 radio-telemetry, she may have initiated a nest that had failed earlier in the season. The recovered carcass was necropsied by Utah Veterinary

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4 Diagnostic Laboratory personnel (UDVL; Spanish Fork, UT), and the necropsy revealed that the
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6 female died from aspergillosis, a fungal infection of the lungs caused by an inoculation of
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8 *Aspergillus* spp. spores.
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12 According to the nature of the gross and histological examinations, UDVL personnel
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14 concluded that the infection was caused by a recent inhalation of a significant quantity of
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16 *Aspergillus* spp. spores in spring 2018. Their examination revealed multiple spherical
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18 granulomatous lesions within the left lung and thoracic airsacs, suggestive of subacute
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20 aspergillosis. This diagnosis was substantiated upon subsequent culture and histologic
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22 examination of the lesions (Figures 1 A & B). Cestodiasis, a severe tapeworm intestinal
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24 infestation, was also detected.
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31 Disease occurrences in wild sage-grouse populations are cause for concern because of
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33 documented range-wide population declines (Schroeder et al. 2004). In 2003, the discovery of
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35 the West Nile Virus (WNV; *Flavivirus*), spread by mosquitoes (*Culex* spp.) in sage-grouse,
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37 increased range-wide conservation concerns about the impacts of disease on declining
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39 populations in increasingly anthropogenic and fragmented landscapes (Walker and Naugle
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41 2011). Unlike WNV, *Aspergillus* spp. spores are not spread by an active vector, so there is a low
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43 risk of the pathogen to contribute to extirpation or population declines (MacPhee and Greenwood
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45 2013). However, if environmental factors in areas inhabited by small, isolated sage-grouse
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47 populations create conditions for the pathogen to propagate, the circumstances contributing to
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49 potential outbreaks should be evaluated (Tell et al. 2019).
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55 The documented declines in sage-grouse populations and their distribution as a result of
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57 the loss and fragmentation of sagebrush (*Artemisia* spp.) ecosystems (Schroeder et al. 2004)
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59 resulted in the U.S. Fish and Wildlife Service (USFWS) reviewing the species' protection status
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4 under the U.S. Endangered Species Act (USFWS 2015; ESA). Because of the species'
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6 conservation status, range-wide research and conservation efforts have included the capture and
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8 radio-marking of thousands of sage-grouse within the last two decades as well as efforts to
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10 augment declining populations through translocations to prevent extirpations in many areas
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12 (Stiver 2011). These range-wide efforts were cited in the USFWS in the decision not to provide
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14 sage-grouse ESA protection (USFWS 2015).
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20 Despite this plethora of research and conservation activity, this case is the first
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22 documented occurrence of aspergillosis in a wild sage-grouse since Patterson (1952), who
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24 reported a nesting sage-grouse mortality that he attributed to aspergillosis in a wild population in
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26 Wyoming. This case is also the only documented in a wild, augmented sage-grouse population
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28 further supporting that aspergillosis is not common in sage-grouse (Christiansen and Tate 2011).
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30 In captive-bred populations, Oesterle et al. (2005) reported one incident of aspergillosis in a
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32 population of sage-grouse and noted the high-stress environment where there was heightened
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34 aggression among the captive-bred individuals. Similarly, aspergillosis has also been reported in
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36 wild Gunnison sage-grouse (*C. minimus*) captured and released into captive-breeding facilities
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38 (Apa et al. 2015). However, the source of the infection was attributed to fungal spores
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40 propagated in the dusty conditions of the captive-breeding facilities (Apa et al. 2015).
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47 Aspergillosis occurring in wild populations is infectious and non-contagious, but leads to
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49 fatality of the infected individual because it cannot be treated (Tell 2005, Beernaert 2010). In
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51 wild avian species, it is most commonly found in waterfowl, raptors, upland game birds, and
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53 corvids (Friend 1999, Tell 2005, Kornilowicz-Kowalska and Kitowski 2013, Tell et al. 2019). It
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55 occurs in concentrations of plant and keratinous material and propagates between 30-45°C
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59 (Kornilowicz-Kowalska and Kitowski 2013).
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4 In areas of the United States where woody plant expansion is displacing native
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6 shrublands and grasslands, state and federal land managers are implementing habitat restoration
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8 projects to remove the target species (Miller et al. 2017). Western rangelands specifically are
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10 facing the onset of conifer expansion into sagebrush communities, and managers are working to
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12 mitigate that impact by removing conifers through mastication—grinding down trees where they
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14 stand— as well as other methods (Sandford et al. 2017). The remaining mulch is then left in
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16 place to decompose adding new keratinous material to the landscape. High residual
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18 concentrations of mulch, associated with widespread conifer mastication, in combination with
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20 mesic seasonal micro-climate conditions associated with sage-grouse nests, could facilitate
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22 conditions favorable *Aspergillus* spp. growth and spore propagation (Kornilowicz-Kowalska and
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24 Kitowski 2013).

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32 In domestic turkeys, an *A. fumigatus* intra-airsac infection causes lesions similar to those
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34 found in the recovered female sage-grouse carcass within 72 h post-exposure (Kunkle and
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36 Rimler 1996). Thus, the female was exposed to the fungal spores in 2018 and not directly
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38 connected to the translocations of 2017. However, the immunosuppressive stressors of the 2017
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40 capture, transport, and release associated with the translocation (Dickens et al. 2010, Parker et al.
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42 2012, Jachowski et al. 2016), in addition to the stressors of the 2018 breeding season and
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44 concurrent cestodiasis, likely contributed to a decreased ability of the female to suppress an
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46 overwhelming inoculation of fungal spores (Redig et al. 1980, Alley et al. 1999, Tell 2005,
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48 Beernaert et al. 2010, Kornilowicz-Kowalska and Kitowski 2013).

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54 Further research should examine if the mulch piles created from conifer removal projects
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56 or the plant and keratinous material in sage-grouse nests could propagate *Aspergillus* spp. spores.
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58 This research should be conducted in seasonally mesic environments common in spring, when
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4 breeding and nesting facilitate higher stress conditions, and where habitat restoration projects
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6 may provide novel substrates conducive to the fungus (Kornilowicz-Kowalska and Kitowski
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8 2013).
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11 As previous literature has suggested with WNV and other diseases (Christiansen and Tate
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13 2011), we recommend continued monitoring of sage-grouse populations for disease, and that any
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15 individuals' carcasses or remains containing airsacs and lungs be sent for necropsy. In areas
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17 receiving augmentations, reintroductions, or other conservation translocations, adequate post-
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19 release monitoring is integral for not only movements and demographics, but also for disease
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21 (IUCN/SSC 2013, Muths and McCallum 2016).
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27 **ACKNOWLEDGEMENTS**

28
29 We thank the numerous landowners providing access to their lands and the Utah Division of
30
31 Wildlife Resources, Bureau of Land Management, U.S. Forest Service, Utah Public Lands Policy
32
33 Coordinating Office, and Yamaha Outdoor Access Initiative for their support. We also thank the
34
35 several technicians and volunteers who have helped with the translocations and field work.
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Figure:

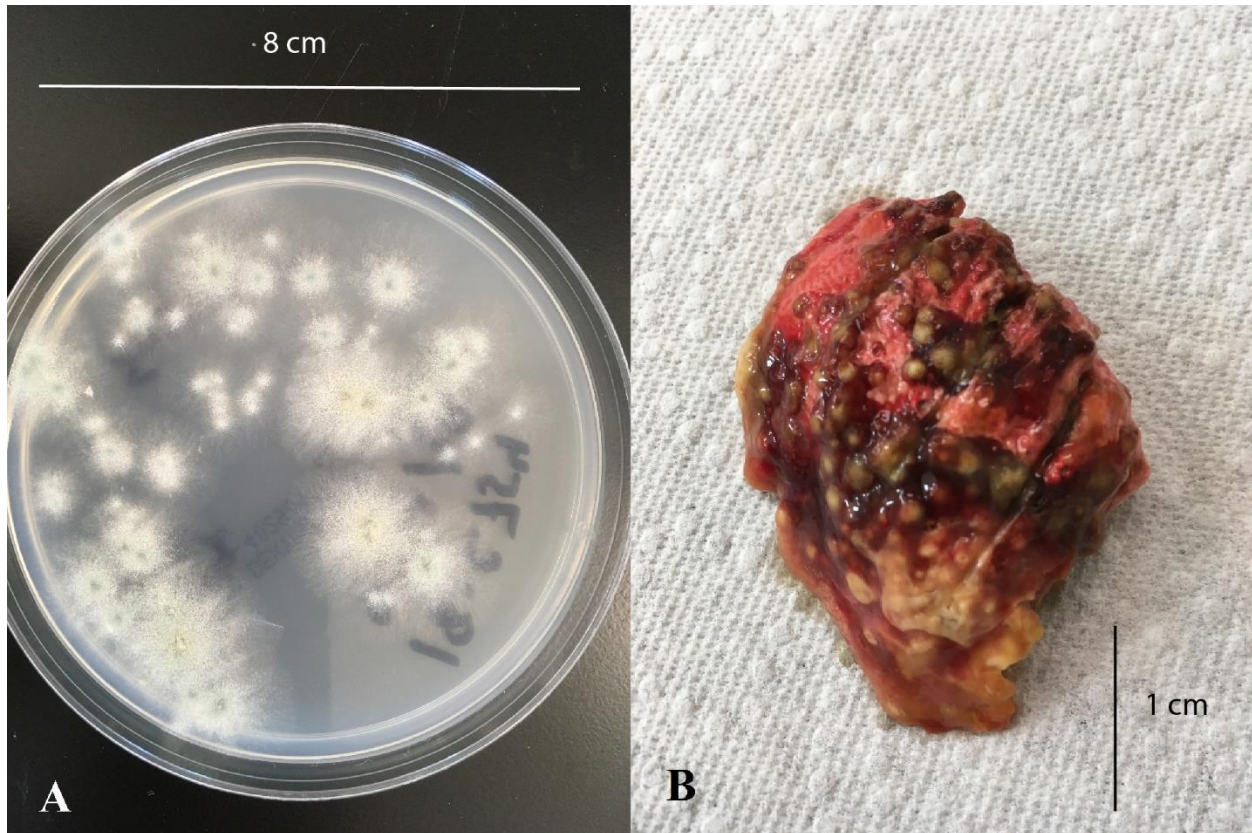


Figure 1: *Aspergillus spp.* culture (A) taken from a 2018 sample of the lung (B) infected female greater sage-grouse (*Centrocercus urophasianus*; sage-grouse) which was an individual translocated in 2017 into the study area as part of an effort to augment the residing sage-grouse population, Sheeprock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