Novel Pathogens In Quails of the Trans-Pecos Ecoregion of Texas

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There are four species of quails who call the Lone Star State home. Three of these, Scaled Quail (*Callipepla squamata*), Gambel’s Quail (*C. gambelii*), and Montezuma Quail (*Cyrtonyx montezumae*), live within the Trans-Pecos ecoregion of Texas.

These charismatic species draw many bird watchers to the region every year. Quail are also considered economically important game birds throughout the country. For instance, hunters who pursue Northern Bobwhite Quail (*Colinus virginianus*) in Texas spent an average of $254 in 2011 and 2012 to bag a single bird and about $1.5 billion annually on hunting expenses.

Unfortunately, quail populations in Texas have waned over the past few decades. It is estimated that Northern Bobwhite Quail and Scaled Quail populations in Texas have declined 3-4 percent annually since the 1980s. Researchers have identified habitat loss and urban sprawl as the primary cause of this decline.

It has also been speculated that pathogens may negatively impact these quail populations. Pathogens are organisms or other agents that can cause disease. Helminths, protozoa, and bacteria are all examples of pathogens.
Helminths, or parasitic worms, are heavily studied and commonly recorded in wildlife species. On the other hand, the roles of single-celled microorganisms like protozoa and bacteria in wildlife are not well understood. Many pathogens are their respective hosts. The pathogens documented in Gambel’s and Montezuma quails of the Trans-Pecos. These findings, along with the decline of Texas’s quail populations, set precedence for investigating pathogen communities in Texas’ quails. Recently, several studies identified pathogens, primarily helminths, in Northern Bobwhite Quail of the Rolling Plains of Texas and southern Texas. Fewer studies have analyzed the pathogen communities in scaled, Gambel’s and Montezuma quail of the Trans-Pecos.

To address this knowledge gap, researchers at Borderlands Research Institute surveyed the region’s quails for pathogens. Desert quails were harvested from ranches across the Trans-Pecos from 2019 to 2020. Those quail were then necropsied and examined for pathogens.

To ensure pathogen identification accuracy, they were submitted to the Texas A&M University Veterinary Medicine Diagnostic Lab in College Station, Texas. This process provided valuable new information regarding pathogens in desert quails.

Our study documented eight pathogens that were novel within their respective hosts. The pathogens *Dispharynx* sp., *Sarcocystis* sp., and *Mycobacterium* sp. were recorded in Scaled Quail, *Oxyspirura petrowi* and *Aulonocephalus pennula* were recorded in Texas’s Gambel’s Quail, and *Subulura* sp., *Physaloptera* sp., and a cestode were found in Montezuma Quail for the first time. Though all of these findings are noteworthy, some may prove to be more crucial than others.

The proventriculus of a Scaled Quail was infected with *Dispharynx* sp. The infected individual experienced severe ulceration within the proventricular tissues.

This damage was comparable to that caused by *D. nasuta* in Blue Grouse and pen-reared bobwhites. Moreover, it has been shown that *D. nasuta* can cause increased mortality in Blue Grouse and pen-reared Northern Bobwhite Quail.

It is likely that *Dispharynx* sp. can negatively impact individual quail similar to our sample. However, due to their low prevalence it is unlikely that they are affecting wild Scaled Quail populations.

Within the muscular tissue of one Scaled Quail, we also recorded *Sarcocystis* sp., a protozoa that has not been documented in wild quail of the United States. This genus of protozoa parasite uses carnivores as definitive hosts.

*S. calchasi* has been reported in White-winged Doves (*Zenaida asiatica*) and Eurasian Collared-Doves (*Streptopelia decaocto*) from Texas. It was determined that these protozoa caused fatal encephalitis in the dove they infected.

Similarly, *S. calchasi* caused early-stage encephalitis in domestic pigeons (*Columba livia f. domestica*). In both cases, avian species were negatively impacted by *S. calchasi* infections. If the Sarcocystis sp. we documented is *S. calchasi*, Scaled Quail may be experiencing similar effects.

The liver and spleen of one Scaled Quail were infected with *Mycobacterium* sp., likely *M. avium-intracellulare* complex or *M. genavense*. This is the first documentation of a bacterial infection in a desert quail.

Both species of bacteria are capable of causing avian tuberculosis. *M. avium* caused death and lower egg production in pen-reared Ring-necked Pheasant (*Phasianus colchicus*).

The Scaled Quail that was infected with *M. sp.* was likely suffering from liver failure. This supports the idea that quail infected with *M. sp.* have a decreased chance of survival.

The pathogens documented in Gambel’s and Montezuma quails were less detrimental to the hosts. However, they are still significant due to the lack of knowledge surrounding pathogen communities of these species.

This study helped describe the pathogens that can be found in Trans-Pecos quails. Pathogens documented in this study, such as *Dispharynx* sp. and *Mycobacterium* sp., can negatively impact individual quail, while other helminths in desert quails may not be detrimental to their hosts.

This lends credence to the idea that more prevalent pathogens may be more prevalent because they have lesser effects on their hosts, and less prevalent pathogens may be less prevalent because they are more likely to negatively impact their hosts. However, more research is currently needed to determine the pathogens’ prevalence and pathogenicity documented here before such speculation can be substantiated.