

Sarcoptic Mange is an Emerging Threat to Biodiversity in the Qinling Mountains in China

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July 1, 2022

Abstract

Sarcoptic mange, a disease caused by the burrowing mite *Sarcoptes scabiei*, is globally endemic and an emerging threat to wildlife. Although many studies have shown that wildlife diseases play key roles in biodiversity conservation, knowledge about sarcoptic mange is still insufficient. In this study, we aim to improve the understanding of the impacts of sarcoptic mange on wildlife populations, the mechanisms involved in its ecoepidemiology, and the associated risks to public and ecosystem health by investigating mass death events in gorals and serows in the Qinling Mountains. We conducted interviews with practitioners and local people in the central Qinling Mountains. From the same locations, we collected 24 cutaneous samples from various animals and surveillance data from infrared cameras. Pathological, parasitological and microbiological examinations of the samples were performed. Mite-induced cutaneous lesions, mites and eggs were observed in samples from dead gorals and one dead serow, but not in other species. Molecular analysis confirmed the mites to be *S. scabiei* that originated from rabbits. The data obtained from the interviews and infrared cameras indicated that the death of wildlife was related to sarcoptic mange infection and that there had been a decrease in the goral population since the outbreak of the disease. We confirmed that sarcoptic mange was the major cause of the mass death events and may have spread from the western to eastern Qinling Mountains. Based on our findings, we propose several protection strategies to help preserve biodiversity in the Qinling Mountains.

Introduction

Wildlife diseases play major roles in biodiversity conservation and the effects of most diseases in wildlife species remain unclear (Astorga et al., 2018; Sebastiano et al., 2019). A relatively recent event in China is the mass deaths of gorals (*Naemorhedus goral*) and Chinese serows (*Capricornis milneedwardsii*), two rare and endangered animals listed in Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) appendix I, belong to order Artiodactyla, family Bovidae, and subfamily Caprinae and are widely distributed in the Qinling Mountains, and these events have been recorded many times in local routine patrols since 2012. Unfortunately, those events have not attracted enough attentions from administrators and scholars because they thought that this was a normal ecological regulatory mechanism. Most of the carcasses had extensive white and thickened skin lesions characterized by lichenification and alopecia, and the causes of death were unclear until 2017. In 2017, a similar death event occurred in gorals in the Qinling Mountains again, and we confirmed initially that the sarcoptic mange, which was pathologically diagnosed, was an important factor in this event (Wu et al., 2019).

Sarcoptic mange, which is caused by the burrowing mite *Sarcoptes scabiei* (*S. scabiei*), is globally endemic and is an emerging threat to wildlife (Escobar et al., 2022; Pence & Ueckermann, 2002). There have been reported disease outbreaks in many species, such as red fox (*Vulpes vulpes*), wild boar (*Sus scrofa*), Iberian ibex (*Capra sibirica*) and alpine chamois (*Rupicapra r. rupicapra*) in Europe; raccoon dogs (*Nyctereutes procyonoides*) and blue sheep (*Pseudois nayaur*) in Asia; cheetah (*Acinonyx jubatus*) in Africa; and wombats (*Vombatus ursinus*) in Australia, resulting in sharp declines in these wildlife populations in recent decades (Bianca et al., 2019; Dagleish et al., 2007; Gakuya et al., 2012; Haas et al., 2018; Iacopelli F et al., 2020; Old et al., 2018; Sugiura et al., 2018; Turchetto et al., 2014). According to these reports, herbivores seem to be more susceptible and have higher mortality rate than carnivores. Sarcoptic mange manifests as alopecia, hyperkeratosis, and bleeding crusts (mite-like lesions) on the skin of infected animals (Cardells et al., 2021). Recent sarcoptic mange outbreaks in wildlife appear to demonstrate ongoing geographic spread, increase in the diversity of hosts and increased virulence (Escobar et al., 2022). However, the impacts of the sarcoptic mange in wildlife populations, mechanisms involved in its eco-epidemiological dynamics, and risks to public and ecosystem health remain unclear (Astorga et al., 2018; Sosa et al., 2022).

Similarly, the situation in the Qinling Mountains is also urgent, as incoming impressionistic data suggests that sarcoptic mange may spread geographically and be transmitted among different species. The Qinling Mountains are the most important natural climatic, geographic and biological boundaries in China and have a high biodiversity (Huang et al., 2016). Many rare and endangered wild animals, such as the giant panda (*Ailuropoda melanoleuca*), takin (*Budorcas taxicolor*), golden monkey (*Rhinopithecus*), and crested ibis (*Nipponia nippon*), live within this ecosystem, and their populations have gradually recovered because of effective protection measures in of China in recent decades (Ma et al., 2018). Sarcoptic mange in the gorals and serows is very likely to bring risks to these sympatric rare animals.

To better understand sarcoptic mange and aid biodiversity conservation, we conducted this research to attempt to reveal the relationship between the disease and the mass death events in gorals and serows. Based on the previous case research, we expanded the temporal, spatial and species' ranges in this study and collected data from interviews, pathological, parasitological and microbiological examinations of the skin samples and surveillance records from infrared cameras. This study is the first to illustrate the epidemic characteristics and threat of sarcoptic mange in wildlife populations in the Qinling Mountains.

Materials and methods

Study area

The study was carried out in the following areas of the Qinling Mountains (Shaaxi Province, China): Taibai County, Fopin County, Ningshan County, Zhashui County, the mountainous areas of Zhouzhi County, Huyi District, and Changan District (107°6' to 109°42'E, 33°11' to 34°11'N). The study area covered approximately 15,000 km² (Fig 1). Among these areas, Taibai, Fopin, Zhouzhi and Ningshan are within the range of Giant Panda National Park. In the study area, the main wild mammals include the giant panda, takin, golden monkey, goral, Chinese serow, forest musk deer (*Moschus berezovskii*), leopard (*Panthera pardus*), black bear (*Ursus thibetanus*), muntjac (*Muntiacus reevesi*), tufted deer (*Elaphodus cephalophus*) and wild boar (*Sus scrofa*). Of these, only the numbers of giant panda, takin and golden monkey populations are known, with approximately 350, 5000 and 4000 individuals, respectively (Zhou et al., 2017).

Interview surveys

Because there are no accurate records of wild animals that died of sarcoptic mange from 2013-2021, we had to acquire data via interviews. Data from 2012 were collected from the fourth giant panda survey of China but exclude Changan District and Zhashui County. The interviewees were mainly staff from the protection stations and farmers who often travelled to the mountains to collect herbs or Chinese chestnut. Whether an animal died of sarcoptic mange or not was confirmed by the presence of obvious, white and thick skin lesions, characterized by lichenification and alopecia (mite-induced lesions). The number of interviewees in each county/district and the questions are shown in S1. A total of 24 staff members from 14 protection stations and 53 farmers in 39 villages were interviewed.

Sampling and storage

From December 2017 to December 2021, the cutaneous samples from 10 gorals, 3 takins, 3 golden monkeys, 2 giant panda, 1 serow, and 5 wild boars were collected. All the animals except one panda, had died naturally, and the details of sampling are presented in table 1 and Figure 1. The samples were fixed with 4% neutral formalin and stored at 4 and -20 respectively. Cutaneous lesions on each dead animal were recorded and scored using a numerical scale according to the area and severity of lesions (Borchard et al., 2012). The severity of the gross lesions was assessed and assigned with a score of 0 to 3 scale based on the gross observation, corresponding to the lesion area on different parts of the body: 0 (no obvious lesions), 1 (25% area), 2 (25%~50% area), or 3 (50%~100% area).

Parasitological examination

Skin samples were collected by scraping with a surgical blade, stored at 4°C and cultured in culture dishes at 37°C for two hours. The scrapings and cultures from skin samples were smeared on microscope slides with cedar wood oil and observed using light microscopy. Morphological characteristics, including the total size; morphology of the idiosoma, gnathosoma and legs; presence and characteristics of spines on the dorsal surface; and position of the anal plate, and taxonomic assignments were recorded (Samuel et al., 2001).

Histopathological examination

The paraffin-fixed skin samples were sectioned and stained using hematoxylin-eosin for pathological examination. Histopathological anomalies, such as hyperplasia of the epidermis, hyperkeratosis, inflammatory infiltrates, or epidermal degeneration, were recorded and scored using a numerical scale. The gross and histological scores of the lesion samples from Changan and Ningshan were analyzed using the independent samples T test in SPSS 20.0 (IBM Corp., 2011) because the quantity of sample from other districts were too small to compare.

Molecular assays

Portions of cutaneous samples stored at -20°C were macerated in liquid nitrogen, and genomic DNA was extracted from each sample using a Universal Genomic DNA Extraction Kit (D2100, Solarbio, China) and subjected to PCR analysis. Fragments of *S. scabiei cytochrome oxidase 1 (cox-1)* (374 bp) and the second internal transcribed spacer gene (ITS2) (361 bp) were amplified (S2) (Fraser et al., 2018; Naz et al., 2020). The amplification products were sequenced by Sangon Biotech (Shanghai) Co., Ltd and identified by BLAST (NCBI).

The sequences of *cox 1* and ITS2 were aligned and analyzed using MegAlign (7.1). Phylogenetic trees were constructed based on the *cox 1* gene with MEGA-7 software (7.0) using the neighbor-joining method (Peltier et al., 2017a).

Surveillance of the goral population during an outbreak of sarcoptic mange

We acquired the surveillance data from 5 infrared cameras that were installed in an approximately 4-km long valley where the gorals were abundant in a reserve in Zhashui County (Fig. 1). These infrared cameras recorded images from January to December in 2018, 2019 and 2020, for a total of approximately 300 days each year. We used the change in the takin population as a reference because it was relatively stable. Additionally, the numbers of serow photos were too small to be analyzed in 2018, 2019 and 2021.

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image1.wmf available at <https://authorea.com/users/492622/articles/575273-sarcoptic-mange-is-an-emerging-threat-to-biodiversity-in-the-qinling-mountains-in-china>

We used the numbers of captured photos of goral and takin per 10 days (P10) as the assessment index:

where T_i is the total number of photos of each animal every year, and D is the number of days the infrared cameras were working.

The changes in goral and takin numbers in 2018, 2019 and 2020 were analyzed using ANOVA in SPSS 20.0.

Results

Numbers and distributions of dead animals with mite-induced cutaneous lesions

According to the interviews and data from the fourth giant panda survey of China, the dead animals with mite-induced cutaneous lesions included gorals, serows, takins and wild boars. Among these, gorals and serows were the main animals affected, and there were clear visual records (S3A and B). Dead takins and wild boars with cutaneous lesions were observed rarely, and there were no visual records available. Therefore, we mainly analyzed the numbers of gorals and serows from 2012-2021. The detailed data are shown in table 2, but only the data from the giant panda survey had corresponding Global Positioning System (GPS) information (Zhu et al., 2021). The mean centres of dead gorals and serows in Taibai, Foping, Zhouzhi and Ningshan in 2012 are shown in Figure 1 (Turchetto et al., 2014).

According to the interviews, the animals with cutaneous lesions mainly died on the banks of rivers from November to early April, and the unusual increase in the number of goral deaths began in 2008; therefore, the number of goral and serow carcasses in 2012 reported in the fourth giant panda survey should cover 2008 to 2012. Table 2 and Figure 2A show that increased numbers of deaths due to sarcoptic mange usually persisted for 2-3 years in the goral and serow populations. Among the animals that died from sarcoptic mange in Taibai, Fopin, and Zhouzhi, gorals and serows were the most common from 2012-2014. The number of dead gorals in Huyi was the lowest, which may be related to the distribution of animals. Goral deaths in Ningshan had two peaks in 2012-2014 and 2016-2017 (Fig. 2A). The first goral death event occurred west of the G5 freeway, and the second goral death event occurred in the eastern area of Ningshan, which is near the boundary of Changan District. The peaks in deaths among gorals in Changan District and Zhashui occurred in 2017-2020 and 2019-2020, respectively. Therefore, sarcoptic mange was transmitted among gorals and serows in the Qinling Mountains from west to east. Sarcoptic mange continued to be observed in gorals and serows after the death events.

Additionally, two interviewees from Foping District said that their dogs presented similar moderate cutaneous lesions and that these dogs were free-roaming and often went into the mountains.

Pathological and parasitological examinations of samples from dead animals

All of the dead gorals and 1 dead serow had obvious mite-induced cutaneous lesions, characterized by bleeding crusts, hyperkeratosis, cutaneous chapping and alopecia, on all four legs and the head and trunk (Fig. 3). The gross records of cutaneous lesions from the dead animals are shown in table 3. Sarcoptic mange mainly occurred on all four legs and the head, especially on the lips and joints (Fig. 3). This would severely impact eating and walking in these animals (S4).

Histopathologically, mites in the epidermal layer were observed in all goral and serow samples but not in samples from the other animals in this study (Fig. 4A, Band C). Typical histopathological lesions were characterized by hyperkeratosis, hyperplasia and papillomatosis in the epidermal layer; squamous epithelium degeneration; and inflammatory cell infiltration (Fig. 4A, Band C). The capillaries were dilated and congested in dermis (Fig. 4A). In the alopecic area, tissue with extensive exfoliated hyperkeratosis covered the epidermis, and all the epidermis and dermis tissues exhibited necrosis and extensive neutrophil infiltration (Fig. 4B). The histopathological scores are presented in table 3. The number of cutaneous lesions between gorals from Changan and Ningshan was not significantly different ($p = 0.21; 0.05$). Dead takins, giant pandas, golden monkeys and wild boars had no cutaneous lesions on gross or histological examination in this study.

Parasitologically, mites and eggs were observed in only cutaneous scrapings and cultures from all dead gorals and serows under the microscope. Mites from both gorals and serows presented a globular idiosoma with triangular spikes on the dorsal surface, a wide gnathosoma, short and thick posterior legs and a terminal anus, consistent with *S. scabiei* morphology (Fig. 4D)

Molecular identification and phylogenetic tree construction

A total of 22 sequences, including 11 sequences of *cox 1* and 11 sequences of ITS2, were obtained from 10 gorals and 1 serow. All samples were confirmed to be *S. scabiei* through BLAST searching (NCBI). All the sequences of *cox 1* and ITS2 were submitted to GenBank (GenBank accession numbers: *cox 1*: ON428480-ON428489 and ON514171; ITS2: ON426154-ON426163 and ON514602).

The alignment results showed that 11 *cox 1* sequences and 11 ITS2 sequences of *S. scabiei* collected from gorals and serows in different areas had 98.6% to 100% and 99.1% to 100% identity, respectively (Fig. 5A and B). The phylogenetic tree of *cox 1* showed that the 11 sequences were within the clade of *S. scabiei* that originated from rabbits in China (Fig. 5C).

Assessment of the impact of sarcoptic mange on the goral population

In this study, changes in the takin population are used as the reference. Because of the impact of coronavirus disease 2019 (COVID-19), staff did not place the infrared camera in 2020. Therefore, only infrared camera (SG-880V, Bestguarder, China) data from 2018, 2019 and 2021 were analyzed. The results showed that the number of gorals decreased rapidly in 2021 and was significantly lower than those in 2018 and 2019 ($p < 0.05$) (Fig. 2B). There was no significant change in the number of takins in 2018, 2019 or 2020. This shows that sarcoptic mange led to the mass death of gorals, consistent with the results of the survey.

Discussion

In our study, we further confirmed that sarcoptic mange is the reason that caused the mass death events in gorals and serows in the past years and is still being transmitted in the gorals and serows in the Qinling Mountains based on expand surveys and sampling. Our results showed that mites from samples of all the dead gorals and serows were *S. scabiei* according to both morphological and PCR analyses of the *cox 1* and ITS2 genes (Fraser et al., 2018; Pence & Ueckermann, 2002). According to previous reports, scabies can cause serious cutaneous lesions, characterized by alopecia, marked lichenification and thick crusting on the legs, head and trunk of blue sheep, ibex, chamois and hare (Cardells et al., 2021; Dagleish et al., 2007; Oleaga et al., 2019; Sarasa et al., 2011). These lesion characteristics have also been observed in foxes and wombats with sarcoptic mange in pictures from infrared cameras or online (Arenas et al., 2002; Borchard et al., 2012; Scott D. M. et al., 2020); therefore, we can confirm that sarcoptic mange has been spreading among gorals and serows since at least 2012, as the same cutaneous lesions were recorded in photos and described by people. In these photos, severe cutaneous lichenification on the joints and lips obviously impacts the activity of animals, and infected animals may have difficulty walking on hillsides (S4). This may be an important factor, as the majority of the dead gorals and serows were found at low altitudes and on mild slopes in our previous study (Zhu et al., 2021).

We could not accurately map the accurate path of transmission of scabies without the GPS coordinates of all the dead gorals and serows in each year. In the Alpine chamois population, the spatial spread of sarcoptic mange presented an “oil spot”-like pattern, with an average annual spread of approximately 4.64+3.12 km/year (Rossi et al., 2007; Turchetto et al., 2014). In our study, gross observation indicated that sarcoptic mange was spreading in the Qinling Mountains from west to east. Moreover, the distance between mean center of dead animal’s GPS coordinates in Ningshan in 2012 and the main place of dead animals in Zhashui was about 70 km in 2019-2020, consistent with this spreading speed. Additionally, these results refute our previous hypothesis that climate change or excessive population densities caused sarcoptic mange outbreaks in goral and serow populations throughout the Qinling Mountains. On larger spatial and temporal scales, we noted that sarcoptic mange in goral and serow populations in the Minshan Mountains has persisted since 1996 (Cheng et al., 2018; Yang et al., 1997). The Micang Mountains are situated between the Qinling Mountains and Minshan Mountains, and there are no reports of sarcoptic mange in wildlife in the Micang Mountains. Additionally, the survey by our institute conducted in the western Qinling Mountains in Gansu Province showed similar patterns of goral and serow deaths, and pictures were captured by an infrared camera (S2C). Therefore, we need additional evidences to reveal the relationship of sarcoptic mange in wildlife located between the Minshan Mountains and Qinling Mountains.

In all records, the dead animals were mainly found in the winter and early spring. Sarcoptic mange in

red deer and ibex showed similar seasonal patterns, with peaks in early spring (Iacopelli F et al., 2020). According to researches, *S. scabiei* mites are transmitted by direct or indirect contact (Arlian & Morgan, 2017). Off their hosts, *S. scabiei* mites are able to survive for 24-36 h at 21degC and 40-80% relative humidity, allowing transmission to a new host, and lower temperatures and higher humidity values can prolong their survival (Heukelbach & Feldmeier, 2006; Niedringhaus, Brown, & Ternent et al., 2019). Additionally, the average survival time of an infected ibex is 121±71 days (Alasaad et al., 2013). Therefore, we hypothesize that dead and weak wild animals infected with scabies are important sources of infection for healthy animals in winter and early spring, and subsequently, the newly infected animals maintain the transmission cycle of sarcoptic mange. In this way, sarcoptic mange is continually spread, and the distribution expands among gorals and serows in the Qinling Mountains.

The pathogenic characteristics of sarcoptic mange are mainly related to the invasion and lifecycle of the mites. Once a mite has identified a suitable location on the skin, it rapidly penetrates into the epidermis and burrows approximately parallel to the corneal layer at a rate of 0.5-5 mm per day; the saliva, feces and eggs produced by the mite cause acute pruritus in the host (Hengge et al., 2006; Heukelbach & Feldmeier, 2006). Accordingly, hyperplasia of the epidermis, hyperkeratosis, hyperplasia of the sebaceous glands and inflammatory infiltrates have frequently been observed in the red deer, chamois, roe deer (*Capreolus capreolus*), red fox, vicuna, lynx and so on (Oleaga et al., 2012; Oleaga et al., 2019). In our samples, most of the pathological changes were similar; however, there was no hyperplasia of the sebaceous glands, and only moderate inflammatory infiltrates were observed. Whether the absence of hyperplasia of the sebaceous glands and only a moderate inflammatory infiltrates indicates milder lesions is unclear. The results of the gross and histopathology examinations showed that the whole skin area of the dead animals was severely damaged. This suggests that the skin of the animal lost the ability to maintain body temperature. This is also an important factor in the death of infected animals that died in winter and early spring. Additionally, breaks in the epidermis allow the development of pathogenic bacterial infection (Abdel-Saeed, 2020; Romani et al., 2015). In humans, crusting is a rare manifestation of scabies, caused by the uncontrolled proliferation of mites in the skin as a result of an insufficient immune response by the host (Karthikeyan, 2009). However, crusting has often been observed in wildlife in our research and in other reports. This suggests that the dead animals experienced a long period of infection and that the immune response failed at the end of life. Therefore, improving animal immunity and administering anti-infection therapies are important measures during the treatment of wild animals with severe scabies.

Although the genus *Sarcoptes* has only one species, genetic diversity among *S. scabiei* from different hosts and areas has been proven (Gomez-Puerta et al., 2022; Soglia et al., 2007). The ITS2 region and *cox 1* gene are widely used in the molecular diagnosis of sarcoptic mange, and ITS2 sequencing is more suitable for phylogenetic studies of astigmatid mites than the characterization of different species based on geographical distribution (Alasaad et al., 2009; Oleaga et al., 2012). However, the *cox 1* gene is also suitable for the phylogenetic analysis of *S. scabiei* (Gomez-Puerta et al., 2022; Lastuti et al., 2019; Peltier et al., 2017b). *S. scabiei* is distributed among three genetically distinct clades; human-origin *S. scabiei* from Panama and Australia comprise 2 distinct clades, respectively, and rabbit-origin *S. scabiei* from China comprise 1 distinct clade, all of which have been reported in previous reports (Andriantsoanirina et al., 2015; Peltier et al., 2017b). In contrast to results from black bears and other wildlife in Japan, the 11 mite sequences in the current study belonged to the rabbit-origin clade based on phylogenetic analysis and are evolutionarily similar to mites from rabbits in China (Patrice et al., 2015; Peltier et al., 2017a). Members of the rabbit-origin clade have the largest number of hosts and widest distribution among mites in the three clades (Andriantsoanirina et al., 2015). This indicates that these mites have the capacity to infect multiple hosts and that the primary infection source among wildlife may be domestic rabbits. More in-depth research is needed to prove this hypothesis.

Sarcoptic mange can cause decreases in wildlife populations and is a substantial threat to global biodiversity (Rossi et al., 2007). Since the outbreaks of sarcoptic mange in the study regions, local residents have noticed a decrease in the number of gorals. However, the effects of sarcoptic mange on gorals have not been assessed. Thus, we analyzed data from an infrared camera installed in a channel where gorals were relatively

abundant before and after the outbreak of sarcoptic mange. The results clearly showed that the number of photos of gorals significantly decreased during the outbreak. This area is also a takin reserve, and the takin population remained relatively stable. Because the numbers of photos of serows were small in 2018 and 2019, changes in the serow population were difficult to assess. Nevertheless, similar to previous reports on other wildlife species, the goral's population suffered a substantial decline owing to sarcoptic mange. The takin population has not yet been affected.

Our primary concern is the cross-species transmission of *S. scabiei* in this study. As mentioned above, this scabies species belongs to the genetic rabbit-origin clade and impose a potential risk of multi-host infection(Andriantsoanirina et al., 2015; Fraser et al., 2016). This is concerning because many rare and endangered wildlife species live in the Qinling Mountains. However, there is still debate concerning host specificity in *S. scabiei* (De et al., 2020; Old et al., 2018; Samuel et al., 2001).Whether scabies can cause mass deaths among giant panda, takin, leopard, and gold monkey populations is an important issue. In the Alps, sarcoptic mange has caused mass death events among chamois, and mass death events have been sporadically reported in other sympatric wild ruminants(Rossi et al., 2007). Efficient transmission of scabies from *Capra pyrenaica* to the sympatric Sardinian moufflon (*Ovis musimon*), a red deer, has been observed in northern Spain since the appearance of scabies in *Rupicapra r. pyrenaica* (Fernandez-Moran et al., 1997). Interestingly, prey-to-predator scabies transmission among wild animals has been proven(Francis et al., 2011). According to these reports, host susceptibility, host traits and adaptation strategies of scabies play key roles in cross-species transmission(Browne et al., 2022; Niedringhaus, Brown, & Sweeley et al., 2019).

In our study, although there was no evidence of sarcoptic mange in wild animals other than gorals and serows, the risk of sarcoptic mange spillover from gorals and serows into other animal populations remains in the Qinling Mountains. This risk is due to the following: 1. Other wild animals are susceptible to scabies. Reports of scabies in other animals in the same order are common(Escobar et al., 2022). Although there are no reports of sarcoptic mange in the giant panda, psoroptic acariasis is common in the captive giant panda(Wang et al., 2018). 2. These animals share similar environments with gorals and serows (S5). In our collected samples, the location of G9 was near to that of M2. Notably, giant pandas eating dead takin and other animals have been reported in the news. This means that giant pandas and leopards may contract scabies by eating dead gorals. 3. The high population density of takins and golden monkeys may promote the spread of scabies(Devenish-Nelson et al., 2014). Therefore, we think that the main wild mammal populations in the Qinling Mountains are at high risk of sarcoptic mange outbreaks.

Based on our results, we propose the following protective measures. 1. *Carry out specific monitoring* . Especially in winter and early spring, locating and burying carcasses with scabies are very important measures for interrupting the transmission of sarcoptic mange in wildlife in a timely manner. 2. *Actively treat infected animals*. The application of sarcoptic mange therapies is easier in animals with mild infections, and fluralaner and ivermectin are very effective for the treatment of this disease in wildlife(Rowe et al., 2019; Wilkinson et al., 2021). Consequently, recovered animals will be resistant to scabies recurrence(Alasaad et al., 2013). Therefore, locating and treating infected animals as soon as possible is beneficial. These cured animals may play an important role in the recovery of populations. Regarding treatment of free-range wildlife, the greatest challenge is locating and capturing sick animals. Herein, we propose a feasible noncontact therapeutic regimen according to the characteristics of sarcoptic mange and routine activities of sick animals. A bionic injection device containing drugs can be installed on a tree on the sides of rivers. When sick animals scratch the infected area on the tree to relieve itching, the drugs are injected into the subcutaneous tissue. 3. *Strengthen monitoring of the giant panda, takin, golden monkey and other animals*. Locating dead animals and collecting samples as soon as possible could help identify sarcoptic mange spillover, which needs further study, and this could guide the establishment of more effective protection strategies to prevent outbreaks in time. 4. *Eliminate the risk of transmission of scabies among wild animals, domestic animals and humans*. Mange is an ideal disease for One Health research because it can infect domestic and wild animals as well as humans, and the environment can play a role in transmission(Astorga et al., 2018). In our survey, farmed swine and goats were frequently in close proximity to free-ranging animals in the Qinling Mountains. This is an important route of transmission for zoonotic diseases. Therefore, this contact should be limited to a

specific area; this could also prevent other diseases from being transmitted among the domestic and wild animals and humans.

In conclusion, this report is the first to reveal the prevalence and pathogenic characteristics of sarcoptic mange in wild animal populations in the Qinling Mountains, analyze the risk factors for transmission and propose protection strategies. This information can guide the design of future management and control strategies and contribute to the preservation of biodiversity in the Qinling Mountains.

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Figure legends:

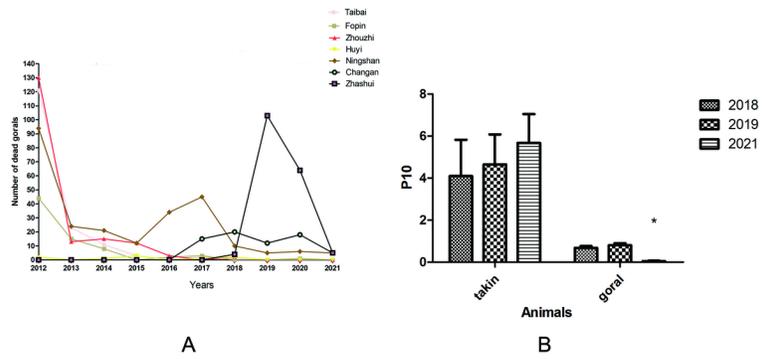
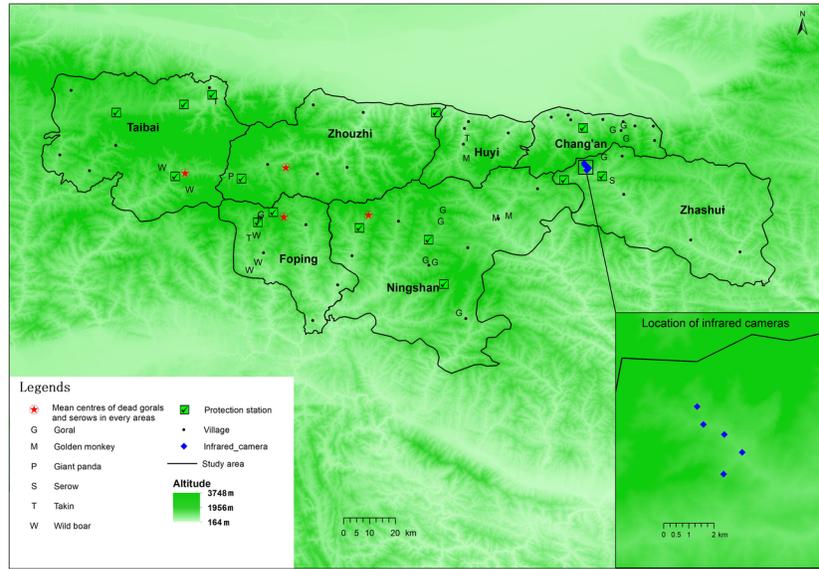
Figure 1. Location of the study area, which partially covered an area of the National Giant Panda Park. The spatial distributions of villages and protection stations where people were interviewed, the sampling locations, and mean centers of dead gorals and serows in Taibai, Foping, Zhouzhi and Ningshan in 2012 are also shown. The locations of the infrared cameras are shown in the lower right corner. Maps were created by ArcGIS 10.8.

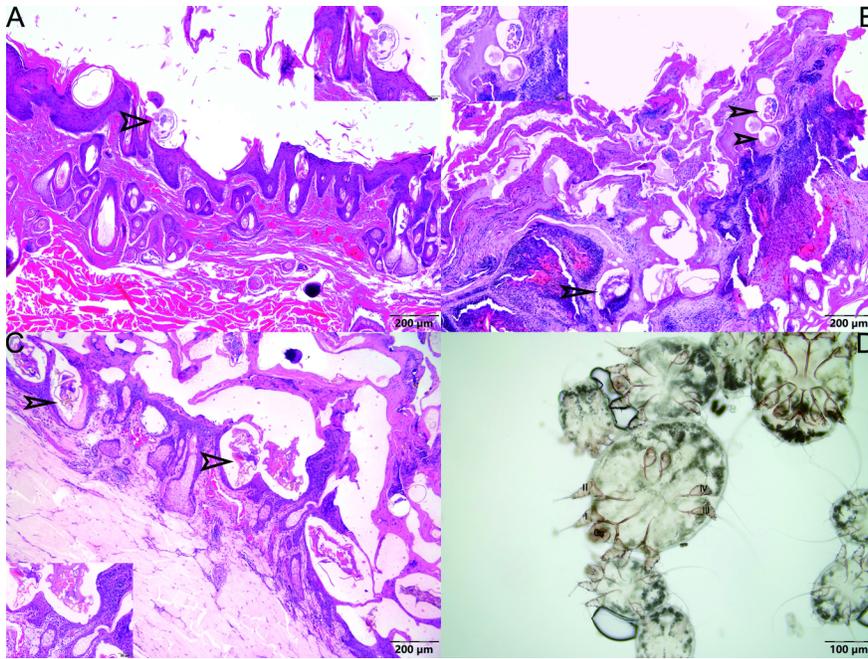
Figure 2. A. Annual changes in the numbers of dead gorals in each county/district from 2012 to 2021. There were two death events among gorals in Ningshan County in 2012-2014 and 2016-2017. B. The P10 change in takins and gorals in the same area in 2018, 2019 and 2021. The number of gorals decreased rapidly in 2021 and was significantly lower than those in 2018 and 2019 (*: $p < 0.05$). There was no significant change in the number of takins in 2018, 2019 or 2020.

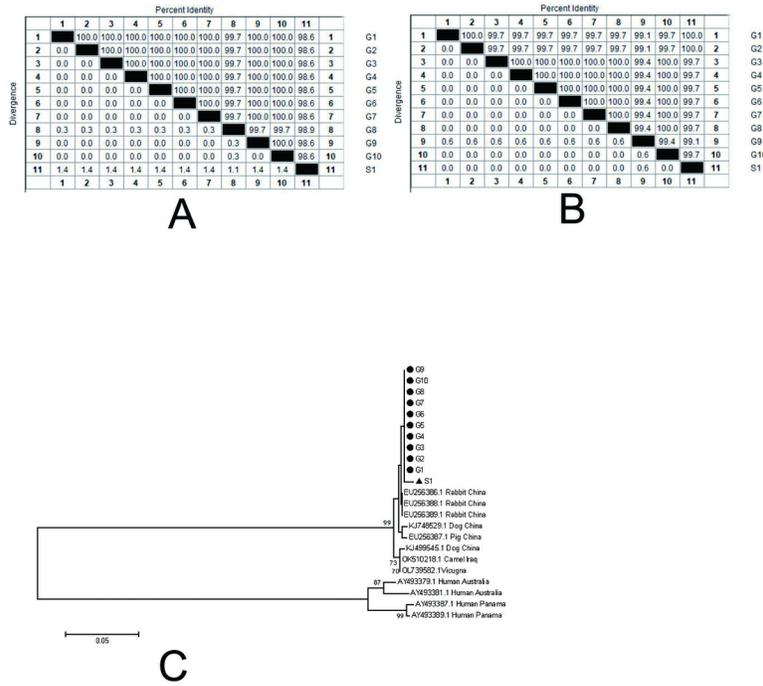
Figure 3. Gross cutaneous lesions for gorals and serows infected with *Sarcoptes scabiei*. A. Goral G2 that died on the side of the river and had no obvious alopecia; bloody crusts and cutaneous chapping were observed on the neck and elbow joints (on the upper corner of left). B. Goral G9, with severe alopecia and crusting on the trunk and neck. C. Goral G10, with severe alopecia and crusting on the skin of the neck and scapula. The photo of a carcass is in the upper right corner. D. A photo of serow S1 before its death. Severe crusting and alopecia were visible on the skin of the head, face, trunk and limbs.

Figure 4. Histopathological changes in cutaneous lesions and the morphology of mites. A. Sample from goral G2. Mild hyperkeratosis and hyperplasia of the stratum spinosum were present in the epidermis. The capillaries in the dermis were dilated. Mites were located in the epidermis (on the upper corner of right). B. Sample from G9. The entire skin area was necrotic. Mass necrotic neutrophils and numerous mites were visible in the area (in the upper left corner). C. Sample from S1. The epidermis showed papillomatosis, moderate hyperplasia and necrosis, the presence of inflammatory infiltrates, and severe hyperkeratosis. Numerous mites were present in the epidermis (in the lower left corner). Edema was observed in the dermis. D. Morphology of the mites. A large number of approximately 0.4-mm long mites with a globular idiosoma and wide ganthosoma, short and thick posterior legs and a terminal anus. Gn: gnathosoma; I, II, III and IV, legs. A, B and C stained using hematoxylin and eosin. Images were captured with an Olympus CX 43 microscope and EPview Ver 1.2. (www.olympus-sis.com).

Figure 5. Alignment of the nucleotide sequences of the *cox 1* gene and ITS2 region of *S. scabiei*. A. Alignment of *cox 1*. Eleven *cox 1* sequences shared 98.6% to 100% identity with mites from gorals and serow in different areas. B Alignment of ITS2. Eleven ITS2 sequences shared 99.1% to 100% identity with mites from gorals and serows in different areas. C. Phylogenetic tree based on the nucleotide sequences of *cox 1*. The phylogenetic tree shows that 11 sequences fell within the clade including *S. scabiei* from rabbits in China. The tree was constructed with MEGA 7.0 using the neighbor-joining method.







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