



A systematic review of the microbial community in taiassuids: a One Health approach

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Abstract

Collared and white-lipped peccaries are sympatric and are distributed in most of South America and in the humid tropical forests of Mexico and Central America. Historically, these species have been used as a source of protein by traditional and/or indigenous human communities, but currently they have been used for legal consumption in different countries. Thus, there has been greater interaction between these wild species and domestic animals and humans, enabling microbial interactions between different niches. The present study presents a systematic review of the literature on the microbial community of collared peccaries and white-lipped peccaries distributed throughout the world, focusing on experimental studies related to the detection of microorganisms as well as the prevalence of the animal species and its characterization of the studied population, in situ or ex situ. Seventy-two studies were selected, mainly in South American countries, related to different species of microorganisms isolated or serologically detected (viruses, bacteria, fungi, and parasites), either as microbiota, pathogens or commensals, many of which are of zoonotic interest, such as *Leptospira*, *Toxoplasma*, *Brucella*, among others. Therefore, these wild mammals are characterized as sentinel agents of anthropic action and require the implementation of studies in relation to their contribution to the spread of microorganisms, being a potential source of amplification and transmission of pathogens.

Keywords *Dicotyles tajacu* · Microbiota · *Pecari tajacu* · *Tayassu pecari* · *Tayassu tajacu* · Zoonotic transmission

Introduction

In recent years, there have been increasing outbreaks of pathogens resulting from a spillover of infectious agents from wild animals to humans. An example is the COVID-19 pandemic

caused by SARS-CoV-2 and, more recently, the cases of monkeypox in human populations in different countries [1]. In this sense, understanding the microbiota-related microorganisms and the infectious agents with the capacity to compromise animal and human health is fundamental to implementing control measures and preventing disease spread.

Research has highlighted the correlation between the human microbiota and various illnesses that transcend the infectious-contagious point of view, such as cancer, allergies, autoimmune diseases, cardiovascular, metabolic and central nervous system dysfunctions [2, 3]. The advent of these scientific discoveries has contributed to increasing interest in the role of the normal microbiota of domestic and wild animals, as well as its relation with potential therapeutic and biotechnological applications [4]. However, the microbiota of wild animals can also be considered a natural reservoir for animal and human pathogens, whose mapping and knowledge of the species could elucidate the routes of their transmission and adaptation in these populations [5].

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In recent years, studies related to the normal microbiota of production and companion animals have increased. However, research on the microorganisms that cohabit in wild animals is still incipient. This research involves not only the characterization of microbial diversity, but also the evolution of species, the transmission of pathogens in the production chain, the interface of anthropogenic activity on the environment, zoonotic potential and antimicrobial resistance [6–8].

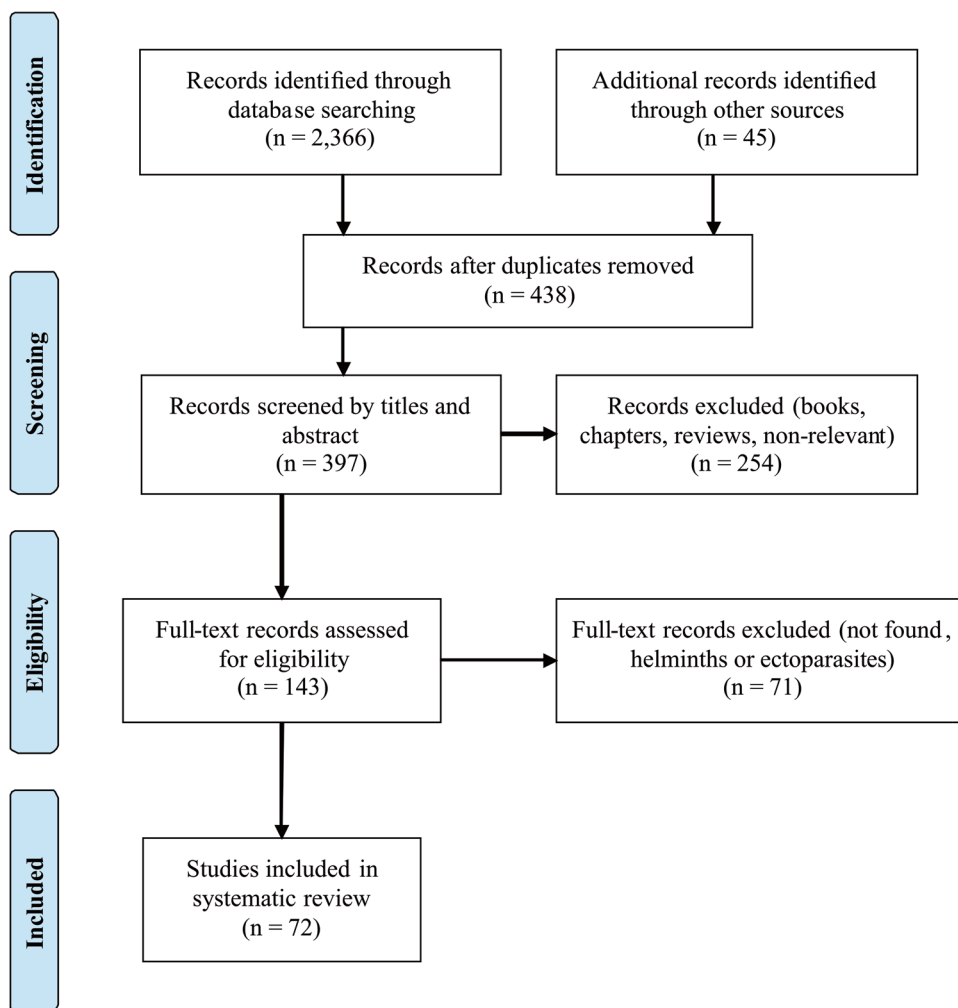
The world's wild mammal fauna comprises more than 6400 species, and Brazil is one of the countries with the highest biodiversity [9]. Many of these wild mammals have historically been used as a source of protein by traditional and/or indigenous human communities [10, 11]. In addition, motivated by exotic cuisine, world consumption of legalized bushmeat is increasing every year [12, 13], which enables greater interaction between the microbial communities of these animals and the production environment.

Among the wild animals with growing productive interest and frequent contact with domestic and human populations, the

Tayassuidae family stands out, represented mainly by the species *Pecari tajacu* (collared peccaries) and *Tayassu pecari* (white-lipped peccaries), which bear similarities to pigs, living in a great diversity of habitats, from humid tropical forest regions to semi-arid regions. Their distribution ranges from the southwestern states of the USA, large extent of Mexico and Central America, the entire Amazon basin and countries of South America, as far as the North-eastern and Southern regions of Brazil [14–19].

Therefore, considering the worldwide concern of the risk of emergence of new pathogens, with pandemic potential in wild animals, and provided that taiassuids have high economic potential, either as a source of protein or for the manufacture of several items with their skin [20, 21], the relevance in identifying normal or zoonotic microbiota is important. Allied to this fact there is a scarcity of information gathered on the microbial communities in taiassuids [22, 23]. Thus, the present study aimed to pool worldwide information on the microbial communities of *Pecari tajacu* and *Tayassu pecari*.

Fig. 1 PRISMA literature search flow diagram



Material and methods

This systematic review followed the guidelines proposed by the Preferred Reporting Items for Systematic Review and Meta-Analysis, PRISMA [24]. The files were consulted in the online databases (Medline, PubMed, Lilacs, Scielo, Web of Science, Virtual Health Library - VHL, Virtual Library on Veterinary Medicine and Zootechnics - BVS-VET, ScienceDirect, Scopus, Digital Library of Thesis and Dissertations - BDTD, JSTOR, Microsoft Academic and Google Scholar), in the time interval between January 1970 and December 2021. To increase the chances of selectable records, this interval considered only the complete years of the last five decades until the date of the last search, carried out in November 2022.

Documents written in English, Spanish, and Portuguese were collected from the following keywords and limits:

(Tayassuidae) OR (*Tayassu tajacu*) OR (*Pecari tajacu*) OR (*Dicotyles tajacu*) OR (*Tayassu pecari*) AND ((Microbiota) OR (Microbiome) OR (Microorganism) OR (Disease) OR (Host) OR (Carrier)). Due to the changes that occurred in the nomenclatures of these species in the last century, and due to a delay in its standardization, all known terms were used as search terms for records.

After a full analysis of all documents, as well as other sources that have not been observed in the database search, such as references lists, to identify any record that was not observed in the database search, the eligibility/inclusion criteria adopted were experimental studies related to the isolation or serology of species that make up the microbial community of collared peccaries and white-lipped peccaries, whether as microbiota, pathogens or commensals. The studies that did not meet these criteria were classified as non-relevant and excluded from the systematic review, as well as

Table 1 Main characteristics of studies related to the microbiota of taiassuids included in the systematic review

Reference	Locality	Taiassuid	Anatomical site	Microorganisms
[25]	Port of Spain, Trinidad, Trinidad and Tobago	Collared peccaries	Semen	<i>Salmonella</i> sp.
[26]	Port of Spain, Trinidad, Trinidad and Tobago	Collared and white-lipped peccaries	Feces	<i>Escherichia coli</i>
[27]	Barranquilla, Atlántico, Colombia	Collared peccaries	Nasal mucosa	<i>Escherichia coli</i>
[28]	Palmas, Tocantins, Brazil	Collared peccaries	Feces	<i>Staphylococcus</i> sp., <i>Salmonella</i> sp., <i>Pseudomonas</i> sp.
[29]	Belem, Pará, Brazil	Collared peccaries	Duodenum and feces	<i>Escherichia coli</i> , <i>Citrobacter</i> sp., <i>Enterobacter</i> sp., <i>Proteus</i> sp., <i>Providencia</i> sp., <i>Edwardsiella</i> sp. (only in the duodenum), <i>Klebsiella</i> sp. and <i>Shigella</i> sp. (only in feces).
[30]	Goiás, Brazil	Collared and white-lipped peccaries	Rectum	<i>Escherichia coli</i>
[31]	Teresina, Piauí, Brazil	Collared peccaries	Rectum	<i>Citrobacter freundii</i> , <i>Citrobacter koseri</i> , <i>Klebsiella oxytoca</i> , <i>Enterobacter aerogenes</i> , <i>Enterobacter cloacae</i> , <i>Serratia marcescens</i> , <i>Salmonella</i> sp., <i>Shigella</i> sp. <i>Escherichia coli</i> , <i>Yersinia enterocolitica</i> and <i>Pantoea agglomerans</i> .
[32]	Belem, Pará, Brazil	Collared peccaries	Semen	<i>Streptococcus</i> sp., <i>Staphylococcus</i> sp., <i>Micrococcus</i> sp., <i>Corynebacterium</i> sp., <i>Enterococcus</i> sp.
[33]	Mossoro, Rio Grande do Norte, Brazil	Collared peccaries	Foreskin mucosa and semen	<i>Corynebacterium</i> sp., <i>Staphylococcus</i> sp., <i>Bacillus</i> sp. and <i>Dermabacter</i> sp. (both); <i>Microbacterium</i> sp. and <i>Rhodococcus</i> sp. (only in the mucosa); <i>Arcanobacterium</i> sp. (only in the semen).

multiple publications, books, chapters, microbial community not found and review articles.

Three independent reviewers determined article eligibility and assessed repertoire variation, according to animal species involved, microorganisms isolated, anatomical site, geographical location, and type of preservation, in situ or ex situ. It should be noted that the following were considered as ex situ: the studies conducted in zoos, commercial breeding farms, and conservation centers.

Results and discussion

A total of 2411 publications were found in the databases, including articles, theses, dissertations, monographs, books, and event records. These, in turn, were included in the bibliography management software Mendeley®, which removed the duplicates. After applying the eligibility criteria, a reduced number of studies that evaluated the microbial community of taiassuids were assessed (Fig. 1).

Table 2 Serological studies used in the surveillance of pathogens in taiassuids

Pathogen	Reference	Locality	
Bacterial	<i>Leptospira</i> sp.	[34]	Belem, Pará, Brazil
		[35]	Loreto and Ucayali, Peru
		[36]	Teodoro Sampaio, São Paulo, Brazil
		[37]	Iquitos, Loreto, Peru
		[38]	Mandaguaçu and Guarapuava, Paraná, Brazil
		[39]	Southern Pantanal, Mato Grosso do Sul, Brazil
		[40]	Peruvian Amazon, Madre de Dios, Peru
		[41]	Ilha Solteira, São Paulo, Brazil
		[42]	Ilha Solteira, São Paulo, Brazil
		[43]	Uacaxtún, Guatemala
		[44]	Locations of Colombia
		[45]	Brazilian cerrado, Minas Gerais, Goiás and Bahia, Brazil
		[46]	Paraíba, Rio Grande do Norte and Piauí, Brazil
		[47]	Southern Pantanal, Mato Grosso do Sul, Brazil
		[34]	Belem, Pará, Brazil
		[36]	Teodoro Sampaio, São Paulo, Brazil
		[40]	Peruvian Amazon, Madre de Dios, Peru
[43]	Uacaxtún, Guatemala		
Protozoan	<i>Borrelia bergdorferi</i>	[48]	Trans-Pecos region, TX, USA
	<i>Yersinia pestis</i>	[48]	Trans-Pecos region, TX, USA
	<i>Mycoplasma</i> sp.	[49]	Belem, Pará, Brazil
	<i>Toxoplasma gondii</i>	[50]	Petit-Saul, Sinnamary, French Guiana
		[40]	Peruvian Amazon, Madre de Dios, Peru
		[51]	Mexico City, Mexico
		[52]	Yavarí-Mirín River, Peruvian Amazon, Peru
		[53]	Cordoba, Spain
		[54]	Foz do Iguaçu and Curitiba, Paraná, Brazil
		[55]	Peruvian Amazon, Madre de Dios, Peru
[56]	Rio de Janeiro, Rio de Janeiro, Brazil		
<i>Trypanosoma</i> sp.	[57]	Rio Negro region, southern Pantanal, Brazil	
[42]	Ilha Solteira, São Paulo, Brazil		
<i>Leishmania</i> sp.	[42]	Ilha Solteira, São Paulo, Brazil	
<i>Neospora caninum</i>	[55]	Peruvian Amazon, Madre de Dios, Peru	
Viral	Bluetongue virus (BTV)	[58]	Rosana, São Paulo, Brazil
		[59]	Peruvian Amazon, Madre de Dios, Peru
	Hepatitis E virus (HEV)	[60]	Piriápolis, Maldonado Department, and Parque Lecocq, Montevideo Department, Uruguay
		[44]	Locations of Colombia
	Classical swine fever virus (CSFV)	[44]	Locations of Colombia
	Porcine circovirus (PCV-2)	[44]	Locations of Colombia
	Vesicular stomatitis virus (VSV)	[44]	Locations of Colombia
	Yellow fever virus (YFV)	[61]	Petit-Saul, Sinnamary, French Guiana
	Bovine viral diarrhea (BVDV-1)	[45]	Brazilian cerrado, Minas Gerais, Goiás and Bahia, Brazil
	Influenza A virus	[62]	São Paulo and Goiás, Brazil

Given the criteria, the search resulted in a total of 72 eligible files, of which nine analyzed the microbiota (Table 1), 29 were related to serological tests for pathogen detection (Table 2), 10 to pathogen isolation in taiassuids (Table 3), and 28 as carriers of a particular micro-organism. Four records [36, 38, 43, 47] have described more than one of these microbial population types in the same work. The prevalence of the species analyzed as well as the type of population conservation is presented in Fig. 2.

Historically, scientific nomenclatures involving the taiassuids are controversial, undergoing quite a bit of change in recent centuries. Names such as *Tayassu tajacu*, *Pecari tajacu*, and *Dicotyles tajacu* are found in the literature referring to the same species, with a common name known as collared peccaries. Even though it is proposed to use the names *Dicotyles tajacu* (Linnaeus, 1758) for collared peccaries and *Tayassu pecari* (Link, 1795) for white-lipped peccaries, based on Palmer's model of species designation [73], a criterion already adopted by different mastozoological societies, the International Union for Conservation of Nature and Natural Resources – IUCN, maintains the nomenclature *Pecari tajacu* in the Red List of threatened species. However, it already recognizes the need for

further studies to clarify the varieties that occur in these species, to better classify them [14, 18, 74–76].

The geographical distribution of the animals used in the assessed studies (Fig. 3) corroborated with the area of occurrence already described for these species, except for 5.5% (4/72), where European countries were mentioned. However, all four papers related to animals conserved ex situ in zoos, failing to describe their origin [53, 77–79].

More than half of the registrations (52.8%, 38/72) were in Brazilian territory, mainly in the North, Central-West, and Southeast regions [32, 72, 80]. Figures 4 and 5 detail the geographic distribution in Brazilian states in terms of published records referring to serological studies and the presence of commensal microorganisms in taiassuids.

Studies on the microbiota of peccaries are scarce and focused on the evaluation of reproductive functions and the intestinal microbiome (Table 1). Only one study evaluated the resistance of pathogenic bacteria colonizing the respiratory tract of peccaries in zoos in Barranquilla, Colombia [27], demonstrating the need to extend the investigation of the other anatomical sites and species of taiassuids.

Interestingly, the methodologies applied to identify microbial species in wild pigs were limited exclusively to

Table 3 Records of pathogens in infectious processes in peccaries

Reference	Locality	Microorganism	Diagnostic technique	Description
[63]	Mossoro, Rio Grande do Norte, Brazil	<i>Bacillus</i> sp.	Ear secretion culture	Bilateral otitis in a collared peccary
[64]	Ilhéus, Bahia, Brazil	<i>Clostridium perfringens</i>	Histopathology, culture, and polymerase chain reaction	Collared and white-lipped peccaries with lethargy and inappetence followed by sudden death.
[65]	Tucson, AZ, USA	<i>Clostridium perfringens</i> e <i>Salmonella</i> spp.	Necropsy, histopathology, and culture of various organs	Death of 105 collared peccaries, first case of salmonellosis outbreak reported
[66]	Rio Grande do Sul, Brazil	<i>Mycobacterium bovis</i>	Necropsy, histopathology, culture, and polymerase chain reaction	Collared peccary dead in captivity
[67]	Brazos County, TX, USA	<i>Coccidioides immitis</i>	Histopathology of various organs	A single case of disseminated coccidioidomycosis and three cases of primary respiratory coccidioidomycosis in a herd of collared peccaries
[68]	Albany, NY, USA	<i>Cryptococcus neoformans</i>	Necropsy, histopathology of various organs and serology	Collared peccaries died after showing signs of paralysis.
[69]	Pinal County, AZ, USA	<i>Alternaria</i> sp.	Histopathology and culture of pus within the rostrum	Collared peccary with severe fungal dermatitis and cellulitis.
[70]	Arizona, USA	Canine distemper virus (CDV)	Pathologic and Microscopic examinations	Three collared peccaries that became moribund with signs of encephalitis.
[71]	Arizona, USA	Canine distemper virus (CDV)	Serology	Outbreak in collared peccaries with signs of encephalitis.
[72]	Rio de Janeiro, Brazil	Betacoronavírus Ptajacu-CoV	Polymerase chain reaction in anal wash	Collared peccaries with prostration, apathy and dehydration, followed by death.

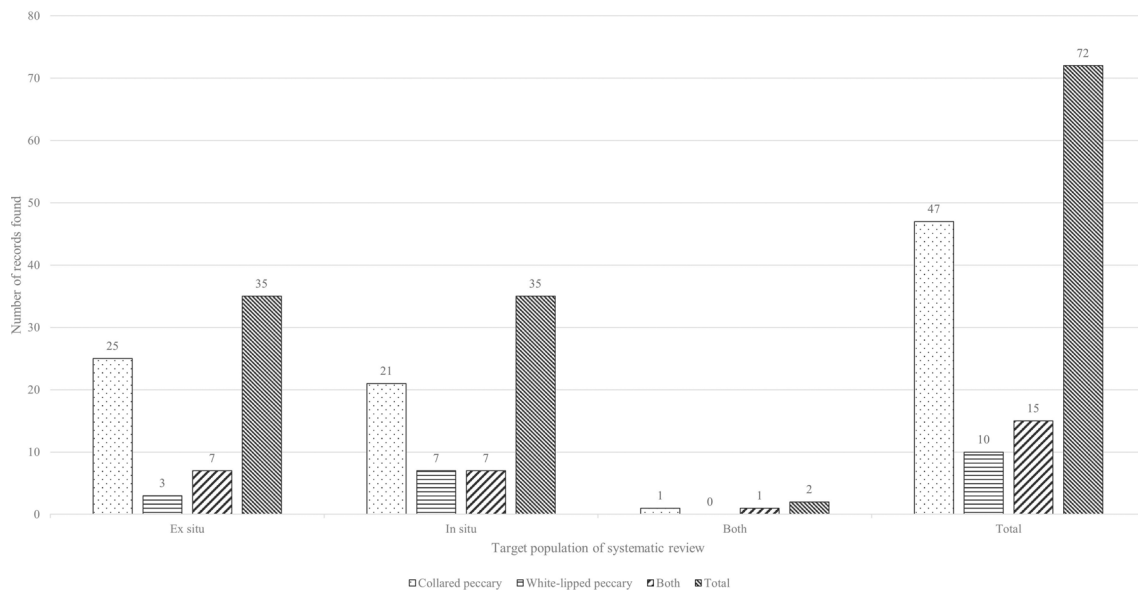


Fig. 2 Occurrence of peccary species and population type in the records found

phenotypic tests. The very isolation of *Shigella* sp. and *Yersinia* sp. in some of the selected papers did not use genotypic proof, weakening the consistency of these studies due to the possibility of environmental contaminants interfering with the results of fecal samples [29, 31]. Until then, these bacterial species had not been isolated in these animals; therefore, the use of phenotypic tests alone is not enough to differentiate them from other bacteria. It is also known that many microorganisms are difficult to be grown in the laboratory, increasing false-negative results for the detection of these pathogens [7].

Due to the difficulty in cultivating microorganisms in the laboratory, some studies have used immunodiagnostic techniques (Serum agglutination, Haemagglutination, Agar gel immuno-diffusion and ELISA) as an alternative to complement the epidemiological studies. As these techniques are based on the detection of the present circulating antibodies, even after the infection has been cured, they have proved to be efficient for the characterization of active infections with clinical or subclinical manifestations. In addition, they are advantageous when used on free-living wild animals, as

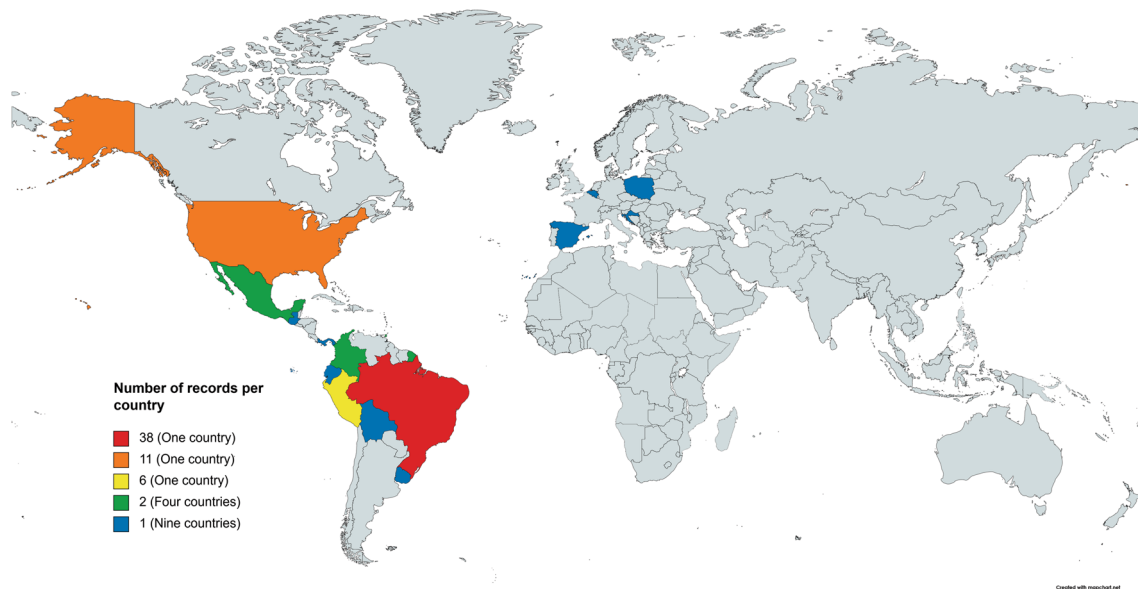


Fig. 3 Geographic distribution of records used in the study

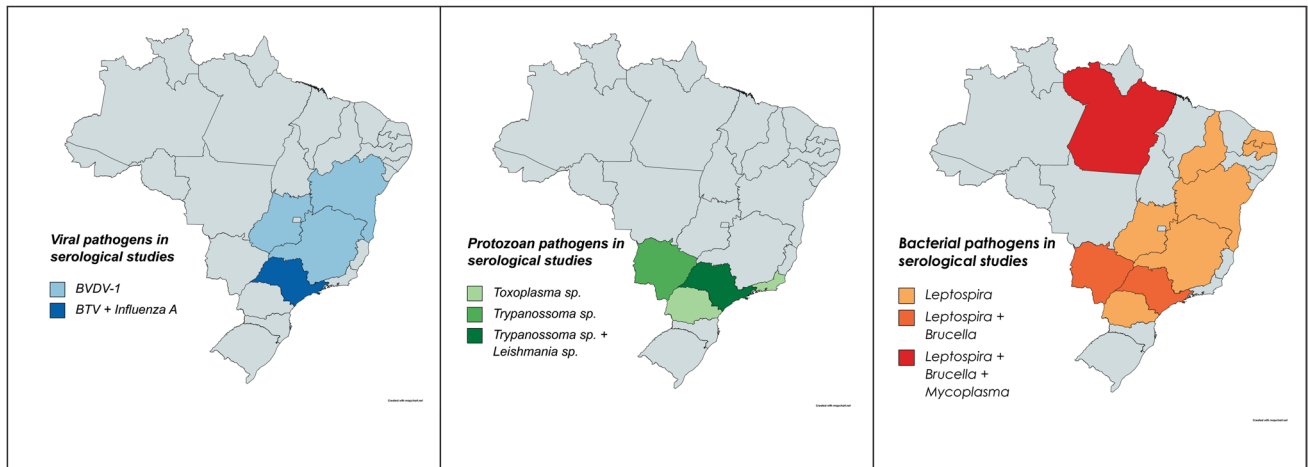


Fig. 4 Geographic distribution in Brazilian states regarding published records referring to serological studies

the positive result of these tests will not be confused by the interference of vaccine antibodies [81, 82].

Among the infections investigated in the selected studies, anti-*Leptospira* antibody research stands out, with 13 records found; of anti-*Brucella* antibody, with five records; and anti-*Toxoplasma* antibody, with eight (Table 2). The infection with *Leptospira*, *Brucella*, and *Toxoplasma* causes zoonotic diseases and the wild animals studied here are considered potential reservoirs and disseminators of these microorganisms into the domestic environment when the environments of these feral pigs interface with production animals [40, 54]. It was possible to identify different species of pathogenic *Leptospira*, for example *L. interrogans*, *L. santarosai*, and *L. nogushi*, and opportunistic, such as *L. liceraciae*, as well as several serotypes (Icterohaemorrhagiae, Iquitos, Butembo, and Autumnalis) [34, 36, 37].

As for viral pathogens, it was possible to verify the detection of viruses of interest for production animals, such as domestic and wild ruminants, among other mammals. Historically, bluetongue virus, classical swine fever virus, and porcine circovirus have been reported frequently in animals of the *Suidae* family and more recently in the *Tayassuidae* family. On the other hand, the bovine viral diarrhoea virus was first reported in white-lipped peccaries in 2020, in animals from a commercial farm in the Brazilian cerrado region. Because these are wild animal species that are widely reproduced ex situ in different American territories, and potential reservoirs of pathogens that can affect the health of other animals (domestic or wild) and even humans, monitoring studies on the health aspect of these herds become important, in order not to compromise national animal health programs [44, 45, 58, 59].

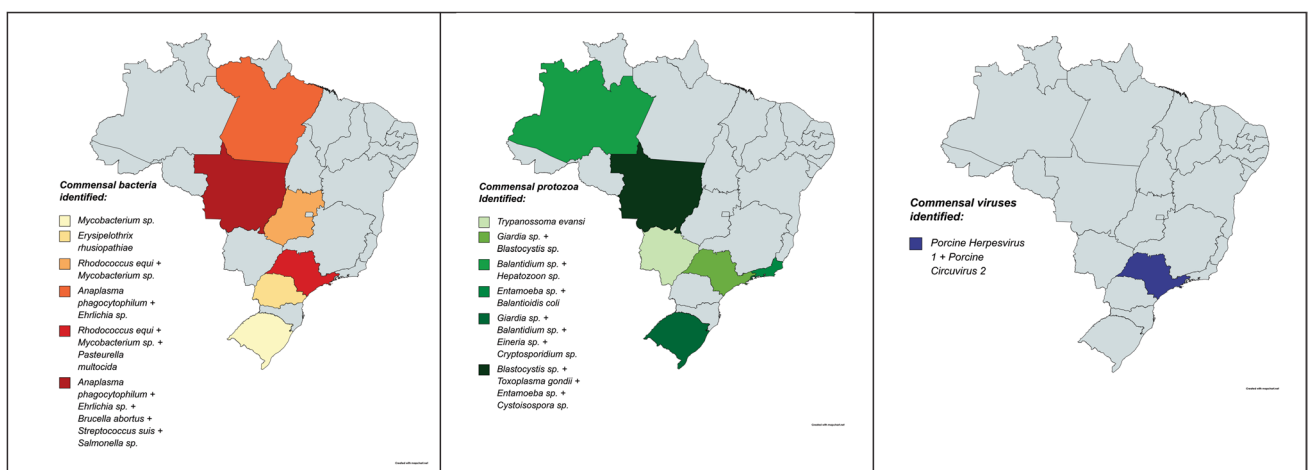


Fig. 5 Geographic distribution in the Brazilian states of published records regarding the presence of commensal microorganisms

For this systematic review, pathogenic microorganisms were considered as those reported as an infectious process in the animal, causing their death or not. Diagnosis for these infections involved everything from serological assays, microbiological culture, histopathological analysis of tissues, and polymerase chain reaction (PCR). The presence of pathogens of bacterial, fungal, and viral origin was observed, and reported in isolated cases or even in outbreaks within a taiassuid community (Table 3).

Of the 10 records included in this questionnaire, clinical symptoms ranged from mild symptoms ($n=2$), such as bilateral otitis and fungal dermatitis, up to more severe symptoms ($n=8$), involving the neurological, respiratory, and/or gastrointestinal systems. The deaths or euthanasia of these animals was also reported in eight of these files. These data emphasize how important it is to investigate the microbial community in these animals, both for the healthcare promotion for individuals and the population, in addition to the role that they play as sentinels of diseases of interest in production and zoonotic risk, such as tuberculosis, for example [36, 83].

However, there are still records of the presence of microorganisms without causing the disease in the animal, as a commensal or when the animal is a carrier. The diagnostics used for the detection of these commensal agents ranged from classical techniques, such as coprological examinations and direct microscopy of feces and blood, up to molecular, like PCR.

The main bacterial species identified in the taiassuids were as follows: *Rhodococcus equi* [83], *Mycobacterium* sp. [83, 84], *Anaplasma phagocytophilum* and *Ehrlichia* sp. [85], *Listeria monocytogenes* [77], *Mycoplasma hyopneumoniae* and *Pasteurella multocida* [86], *Erysipelothrix rhusiopathiae* [38], *Brucella abortus* and *Streptococcus suis* [87], *Salmonella* sp. [87, 88], and Shiga-toxin producing *Escherichia coli* [88].

As for protozoa, there were records of different species associated with peccaries, such as the following: *Giardia* sp. [36, 78, 89, 90], *Balantidium* sp. [89, 91–93], *Hepatozoon* sp. [94], *Blastocystis* sp. [79, 80, 95], *Toxoplasma gondii* [96], *Entodinia caudatum* and *Dasytricha* sp. [97], *Eimeria chaparralensis*, *E. dicotylensis* and *E. pecari* [89, 98–100], *Trypanosoma evansi* [47, 101], *Cryptosporidium* sp. [89, 90], *Babesia* sp. [43], *Entamoeba* sp. [80, 90, 102], *Balantioides coli* [102], *Endolimax nana* [90], *Isospora* sp. [99], and *Cystoisospora* sp. [80]. Also, porcine herpesvirus 1 and porcine circovirus 2 viruses have also been diagnosed in these conditions [86].

Although studies on the microbial community in taiassuids are still scarce, it should be noted that the diversity of the microbial groups described reveals the ecological role of these mammals as potential reservoirs and/or transmitters of zoonotic microbial species or with epidemic potential in

domestic animals. Closer relations between man and wild animals, especially when taiassuids are reared as a potential expanding protein source for marketing as exotic meat and/or its skin for the manufacture of several items, make the knowledge of these microorganisms that pose a risk to humans and animal health necessary [20, 103].

Conclusion

In this work, a qualitative evaluation of studies on the microbiota described in taiassuids was carried out, demonstrating the presence of various species of commensal and/or pathogenic microorganisms. Several of these are shared between these animals and humans, indicating the role of peccaries as sentinels of ecosystem health and thus revealing anthropogenic action.

Data availability The data analyzed during the current study was available from the corresponding author on reasonable request.

Declarations

Ethics approval and consent to participate None required.

Competing interests The authors declare no competing interests.

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