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Moniezia expansa and *Moniezia benedeni* a parasitosis in ruminants: an overview of their taxonomical aspects

Moniezia expansa y *Moniezia benedeni* una parasitosis en rumiantes: una visión general de sus aspectos vinculados a su taxonomía

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Resumen

Moniezia species are a group of parasites with worldwide distribution that cause intestinal diseases in ruminant species characterized by decreased animal production and, in some cases, host death. A systematic bibliographic review was carried out under a qualitative approach of narrative design and descriptive scope on an overview of the importance of *Moniezia expansa* and *Moniezia benedeni*, as well as some aspects related to their taxonomy, the two main species responsible for gastrointestinal infections in ruminants. The main databases including Scopus, Web of Science, Taylor & Francis, PubMed, Latindex, SciELO, Dialnet, among others, were consulted using the Boolean logical operator. Gastrointestinal parasites were found to be one of the main threats that limit the development and profitability of the livestock industry in tropical and subtropical areas. Among the causative agents of gastrointestinal diseases, monieziasis, caused by *Moniezia* spp. constitutes a pathology with a higher frequency of occurrence among different species of livestock. There are limitations in the identification of *M. expansa* and *M. benedeni* when only morphological characters are used, so molecular techniques have shown potential to overcome the identification problems of these and other species belonging to this genus. The contributions of molecular biology are useful not only for inferring the phylogenetic relationships among cestodes but also for identifying suitable molecular markers for future studies on diagnosis, population genetics, and molecular ecology in *Moniezia* species. However, a greater number of studies on genetic markers are required to accurately identify *Moniezia* species and serve as a basis for taxonomic research.

Abstract

Las especies de *Moniezia* son un grupo de parásitos con distribución mundial que causan enfermedades intestinales en especies rumiantes caracterizados por la disminución de la producción animal y, en algunos casos, la muerte del hospedero. Se hizo una revisión bibliográfica sistemática bajo un enfoque cualitativo de diseño narrativo y alcance descriptivo sobre una visión general de la importancia de *Moniezia expansa* y *Moniezia benedeni*, así como algunos aspectos vinculados a su taxonomía, las 2 principales especies responsables de infecciones gastrointestinales en rumiantes. Para la búsqueda fueron consultadas las principales bases de datos incluidas Scopus, Web of Science, Taylor & Francis, PubMed, Latindex, SciELO, Dialnet, entre otras, utilizando el operador lógico booleano. De acuerdo con la revisión, los parásitos gastrointestinales constituyen una de las principales amenazas que limitan el desarrollo y rentabilidad de la industria ganadera en zonas tropicales y subtropicales. Entre los agentes causales de enfermedades gastrointestinales, la monieziosis, causada por *Moniezia* spp., constituye una patología de mayor frecuencia de ocurrencia entre diferentes especies de ganado. Existen limitaciones en la identificación de *M. expansa* y *M. benedeni* cuando se usan solo caracteres morfológicos, por lo que las técnicas moleculares tienen su potencial para superar los problemas de identificación de estas y otras especies del género. Los aportes de la biología molecular resultan de utilidad no solo para inferir sobre las relaciones filogenéticas entre los cestodos, sino también para identificar marcadores moleculares para futuros estudios sobre diagnóstico,

genética de poblaciones y ecología molecular en especies de *Moniezia.* Sin embargo, se requiere un mayor número de estudios sobre marcadores genéticos para identificar con precisión las especies de *Moniezia* y ser base para investigaciones taxonómicas.

Introduction

Production animals generally harbor a series of parasites in the gastrointestinal (GI) tract, particularly helminths, causing clinical or subclinical parasitism, negatively affecting their health status, causing enormous economic losses to the livestock industry, and also affecting productive performance and reproductive of livestock[1]. Helminths are endoparasites classified into 2 main groups: nematodes (roundworms) and platyhelminths (flatworms), the latter are subdivided into trematodes (trematodes) and cestodes (tapeworms) that can exhibit complex life cycles involving one or more intermediate hosts that house juvenile stages and a definitive host where the sexually mature parasites are found[2].

The genus *Moniezia* belongs to the family Anoplocephalidae in the Order Cyclophyllidea, characterized by the absence of hooks and rostellum, its body consists of a small anterior scolex, neck, followed by a long chain strobile with a specific pattern for each species[3]. *Moniezia* species are included in cestodes and they show a worldwide distribution; causing intestinal diseases in ruminant species characterized by a decrease in animal production and, in some cases, death[4].

Since the description of the genus by Blanchard in 1891, 11 species were included, but later 6 species were added; however, regardless of the number of species recorded, *Moniezia benedeni* (Moniez, 1879) and *Moniezia expansa* (Rudolphi, 1810) remain the 2 most important species, with prevalence levels ranging from 1 to 21 % in various geographic regions or different seasons of the same regions[5].

M. expansa is commonly located in the small intestine of cattle, sheep, goats, deer, among others, however, frequently mature animals do not generally present clinical symptoms, while young animals are more susceptible and develop soft feces, which then become diarrheal accompanied by mucus, segments of the parasite and can suffer intestinal obstruction, intestinal torsion and even intestinal rupture[6]. *M. benedeni* primarily a livestock parasite, like *M. expansa,* occur more frequently in animals less than 6 to 8 months old, while older animals tend to be less susceptible; after 2 years, they rarely have more than one or a few worms[7].

This article presents a review on the importance of *M. expansa* and *M. benedeni* as gastrointestinal parasites (GIP) in ruminants, and also presents a discussion on the taxonomic problems in both species with the contributions that molecular biology has had to elucidate the identification confusions of both species.

Materials and methods

The present article was based on a systematic bibliographic review on the current information on *M. expansa* and *M. benedeni* in GI infections in ruminants,

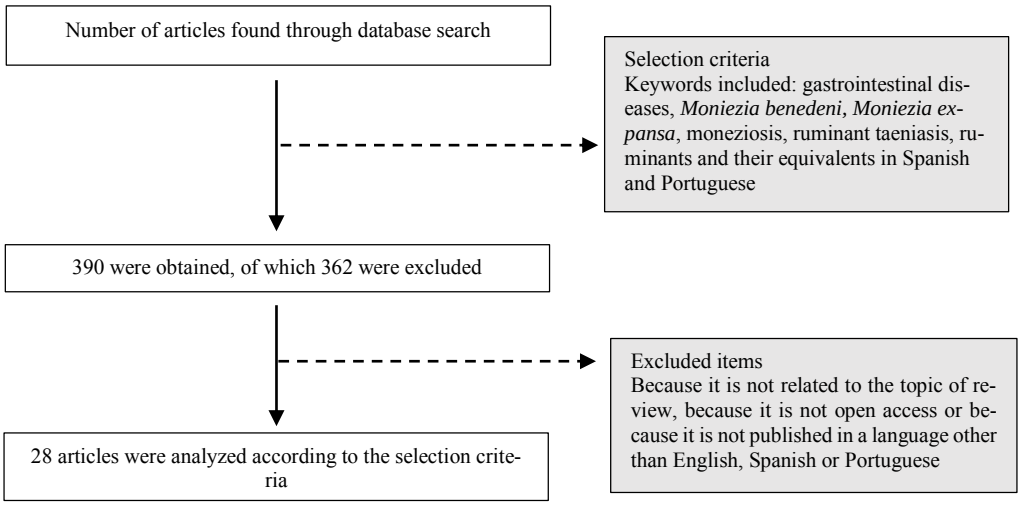
it was approached under a qualitative approach of narrative design and descriptive scope[8]. According to Cesário et al.[9], the bibliographic review is a type of research based on already constructed material, such as monographs or articles published in scientific journals.

For the search, the main scientific databases were consulted, including Scopus, Web of Science, Taylor & Francis, PubMed, Latindex, SciELO, Dialnet, among others, using the Boolean logical operator "AND" and "OR". The criteria for selecting the articles to be analyzed included those publications that contain the following key words in Spanish: GI diseases, *M. benedeni*, *M. expansa*, moneziosis, taeniasis of ruminants, ruminants with their equivalents in Spanish and Portuguese. In the first search, 390 articles were obtained, of which 27 articles were selected, which were analyzed for the review. For this selection, only open access articles were taken into account, related to topics related to the species *M. expansa* and *M. benedeni,* written in English, Portuguese or Spanish.

In addition, a restriction was made in the search for scientific articles to the last 5 years in order to carry out the analysis of the most up-to-date information on the current status of *M. expansa* and *M. benedeni* in GI infections in ruminants.

Finally, the review followed the inclusion, selection, identification and review criteria Figure 1.

Figure 1 Flowchart for the selection of articles included in the review



Development

GI diseases in ruminants. In general, livestock can be affected by different types of parasites that include species of nematodes, trematodes, cestodes and coccidia. Zooparasitic helminths lodge in their digestive tract, are usually associated with subclinical infections and can occasionally cause direct mortality in affected animals[10]. In tropical and subtropical areas, GIP are one of the main threats that limit the development and profitability of the livestock industry[11].

These types of GIP cause a significant impact on the health of production animals, causing a reduction in the rate of growth, reproduction, milk/meat production and, ultimately, death, causing considerable economic losses[12]. According to Charlier et al.[13], the decrease in productivity is due to the fact that helminths cause alterations in metabolic functions, resulting in a low level of utilization and assimilation of food and consequently results in delayed growth, weight gain, malnutrition, decreased appetite, loss of body weight, emaciation, and increased susceptibility to other pathogens.

Even though parasitic diseases represent an important challenge in livestock farms worldwide, knowledge about the epidemiology of GIP is still limited, mainly in low-income countries[10]. Therefore, it is necessary to investigate the morbidity of diseases caused by GIP, both in production and domestic animals, to establish strategies that ensure welfare and management.

Moniezia species and their impact on livestock farming worldwide. Causative agents of the disease known as monieziasis, characterized by the ability to produce a gastrointestinal disorder in ruminants, which is generally considered to have mild pathogenicity, especially in adult cattle, the effects on calves and lambs can cause significant economic losses[3].

Moniezia spp., infections have become a major concern in the livestock industry, although the damage caused by cestodes is generally minor compared to the damage caused by gastrointestinal nematodes, the former has shown that they are capable of causing significant economic losses. worldwide in some types of livestock such as buffaloes and sheep[14].

Moniezia have been described, however, given that identification at the species level has been based on the use of morphological characters, its taxonomy is currently quite controversial and there are authors who recognize up to 17 species[3,15]. On the other hand, there is only information on genetic sequencing for the 3 main species; *M. expansa*, *M. benedeni* and *M. monardi*[16]. In that sense, morphologically, the differentiation between *M. expansa* and *M. benedeni* is based on the shape of the interproglottid glands, which have a rosette pattern in *M. expansa*, while in *M. benedeni* it has a short and continuous linear pattern[3]. However, this characteristic is difficult to observe in some specimens, making them not morphologically distinguishable[5], which is why other biochemical and molecular techniques have been developed for the differentiation of these 2 species. Additionally, in Australia the existence of cryptic species in *M. benedeni* has been pointed out through multilocus enzyme electrophoresis[15,17], which highlights the need to investigate genetic variation between geographical populations for the establishment of an accurate identification, as well as for re-evaluation of conventional taxonomy.

M. benedeni and *M. expansa*. *Moniezia* spp., infections are included among those that affect the small intestine in sheep and goats, although it also includes a wide range of definitive hosts, including cattle and other wild ruminants, with *M. expansa* being the most important species due to its high frequency of occurrence in sheep and goats compared to other ruminants[4].

Moniezia species have an indirect biological cycle, in which 2 host species are required, including ruminants as definitive or final host, where occurs sexual reproduction and the eggs produced pass from the intestine of the ruminant into the gravid proglottids and are expulsed through the feces to the soil where they penetrate the oribatid mites that become intermediate hosts (where asexual reproduction occurs)[18].

M. benedeni are widely distributed parasites and are

commonly associated with wild and domestic ruminants, although they are generally considered to be of low pathogenicity, because the host does not present specific or serious symptoms, however, a decrease in the growth rate has been observed. in infected animals, therefore, with a reduced value at the time of sale[19]. In one study, the prevalence of *M. benedeni* in European bison from 3 months to 26 years of age in a primeval forest in Białowieża, infection was reported to be 42.3 %, with infection intensity ranging from 2 to 25 tapeworms (average 5.8 specimens), being higher in calves (50 %) than in adult bison (33.3 %)[20]. According to the authors, the high prevalence of this parasitosis in European bison could be due to poor condition or weak immunity of infected animals.

Although it is uncommon, coinfections of *M. benedeni* and *M. expansa* have been verified. In this sense, in Romania Iacob et al.[21] reported that Carpathian goat kids (aged 6 to 8 months) with acute digestive syndrome presented infection with both species, 56.1 % corresponded to *M. expansa*, 43.9 % *M. benedeni*, with a mean infection intensity of 7.5 *M. expansa* per animal, compared to 4.5 *M. benedeni* per animal. Infection with both species caused severe pathological lesions in the small intestine such as occlusion, intestinal obstruction, total intestinal villous atrophy and ulcerations.

Therefore, research has indicated that even when the pathogenicity is low, it is necessary to apply control, such as the use of praziquantel at doses of 3.75 and 5.0 mg kg^{-1}, which can be effective for the complete deworming of sheep and goats, respectively, but there is no information on the optimal dose for the control of *M. benedeni* in cattle[19]. In Bolivia, praziquantel was applied in combination with albendazole resulting in 100 % efficacy and even a high level of control was observed with the use of albendazole. On the other hand, the use of Fenbendazole caused a 60 and 75 % reduction in infections with *M. expansa* and *M. benedeni*, while albendazole also achieved a 75 and 95 % reduction in oviposition in *M. expansa* and *M. benedeni*, respectively, although the authors do not specify the administered dose of Fenbendazole and albendazole[22].

The taxonomic problem in some species within the genus Moniezia. The taxonomy of this genus has been based mainly on morphological characters, making the status of the species uncertain. Taxonomic confusion could be derived from the fact that the description of the species has been based on a limited number of morphological characteristics that are often convergent, which generates controversy about the taxonomy of the genus[3,16]. In this sense, there have been confusions and errors in the identification of the 2 main species of *Moniezia*, *M. expansa* and *M. benedeni*, which have been differentiated based on the shape of their interproglottid glands and eggs[3,16]. *M. expansa* has a short continuous linear pattern of interproglottid glands, while *M. benedeni* has a row of small circular patterns on the interproglottid glands. Regarding the eggs, these have a triangular shape in *M. expansa* and a tetragonal shape in *M. benedeni*[23]. However, there are problems in identification when specimens lack interproglottid glands or when the eggs have an altered shape[3,16]. Additionally, the morphological recognition of these species is also based on features related to the scolex, neck and strobile and the presence of transparent anterior, posterior, mature and gravid segments[15].

Furthermore, Chilton et al.[14] pointed out, through the use of multilocus enzyme electrophoresis techniques, the existence of cryptic species in *M. benedeni*, which highlights the limitations of identifying *Mon-*

iezia species solely based on morphological characters. On the other hand, the use of molecular techniques to elucidate the DNA sequence (ITS1 and 5.8S) have been used to distinguish these 2 species[16,25]. According to Chilton et al.[24], a greater number of genetic markers must be developed to accurately identify *Moniezia* species and serve as a basis for taxonomic investigations.

Also, ribosomal ITS2 is considered a very useful marker for establishing relationships between helminth species[26]. Yan et al.[5] amplified and sequenced the 18S rDNA regions of *M. benedeni* and *M. expansa* for precise species identification, obtaining that the lengths and GC contents of the sequenced regions were 2476-2487 bp and 51.9-52.1 % for *M. benedeni* and 2473 bp and 51.9-52.0 % for *M. expansa*, respectively, in addition the alignment and comparison of the 18S sequences in both species revealed a homology of 92.5 to 93.3 %. Finally, the results suggest no matches in the 18S regions of *M. benedeni* and *M. expansa* with other species using the BLAST search, suggesting that the 18S sequences are appropriate markers for the design of distinctive primers for the 2 species of *Moniezia*.

Similarly, Gao et al.[27] characterized, for the first time, the complete mitochondrial genome of *M. sichuanensis* and noted that the total length of the circular genome was 13652 bp, which consisted of 12 protein-coding genes (PCGs), 22 transfer RNA genes, and 2 ribosomal RNA genes, which are typical of *Moniezia* mitochondrial genomes.

Additionally, an increasing number of complete mitochondrial (*mt*) genome sequences provides the opportunity to optimize the selection of molecular markers for studies in ecology, evolutionary biology, and population genetics[23]. Complete *mt* genomes provide individual markers with different levels of sequence variation, as well as combined mtDNA molecular markers for intra-and interspecies studies[27].

In conclusion, phylogenetic analysis using the concatenated amino acid sequences suggests that *M. benedeni* and *M. expansa* represent close but distinct taxa and, furthermore, the data support the view of the existence of cryptic species in *M. benedeni* and *M. expansa*. According to Guo[23] the complete *mt* genomes of these 2 species will be useful not only to infer phylogenetic relationships between cestodes, but also to identify suitable molecular markers for future studies on diagnosis, population genetics and molecular ecology in Moniezia species.

Conclusion

Among GIP species, *Moniezia* species, causal agents of the disease known as monieziasis, occur most frequently in cattle, sheep and goats, being characterized by the presence of a gastrointestinal disorder in the host and, although they generally produce symptoms with mild pathogenicity, especially in adult cattle, the effects on calves and lambs can cause significant economic losses.

The taxonomy of the genus *Moniezia* has been based mainly on morphological characters, making the status of the species uncertain, and consequently the exact number of species in the genus is not known. Concomitantly, errors have been made in the identification of the 2 main species of *Moniezia*, *M. expansa* and *M. benedeni*, which have been differentiated based on the shape of their interproglottid glands and eggs. Therefore, the use of molecular techniques has served as a basis to distinguish these two species; however, it is necessary to obtain a greater number of genetic markers to accurately identify *Moniezia* species and serve as a basis for taxonomic research. Fi-

nally, the correct identification of parasite species associated with production animals is a crucial step in establishing management strategies for infections in livestock, so the present review presents relevant information that contributes to the elucidation of the taxonomic problems among *Moniezia* species.

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Conflicts of interest

There is no conflict of interest in this investigation.

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Ethical considerations

The authors declare that the writing of the article was developed carefully using previous studies in the literature and acknowledge them through the respective authors and sources cited.

Authors' contribution to the article

María Génesis Almeida-Caicedo, *Roberto Ismael Almeida Secaira*, *Oscar Patricio Nuñez Torres* and *Bryon Enrique Borja Caicedo*, contributed with the conception and design of the study, search for information, discussion of results, drafting of the manuscript, approval of the final version of the manuscript.

Research limitations

The authors point out that there were no limitations in the present research work.

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