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Full Length Research Paper

Genetic diversity of *Mycobacterium bovis* in Jalisco, Mexico: Tracing back sources of infection

Sara González-Ruiz[1], Susana L. Sosa-Gallegos[2], Elba Rodríguez-Hernández[3], Susana Flores-Villalva[3], Sergio I. Román-Ponce[3], Isabel Bárcenas-Reyes[2], Germinal J. Cantó-Alarcón[2] and Feliciano Milián-Suazo[2*]

[1]Doctorado en Ciencias Biológicas, Facultad de Ciencias Naturales, UAQ, Mexico.
[2]Facultad de Ciencias Naturales, UAQ, Mexico.
[3]Centro Nacional de Investigación Disciplinaria en Fisiología Animal-INIFAP. km 1 Carretera a Colón. Ajuchitlán, Querétaro, Mexico.

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Bovine tuberculosis (bTB) is a disease of cattle that presents risk to public health, causing severe economic losses to the livestock industry and difficulty in eradication because of its complex epidemiology. The aim of this study was to identify relationships between *Mycobacterium bovis* strains from cattle in the State of Jalisco, and those of other States of México. Molecular fingerprints of 337 *M. bovis* isolates from Jalisco, and 1152 from other States of México were included in the study. Isolates were obtained from tubercles between 1997 and 2015. Evolutionary relationship was determined throughout spoligoforest (www.emi.unsw.edu.au/spoltools/). From 337 isolates from Jalisco, 59 spoligotypes were obtained, ten of them included 48% of all isolates in the state. Five spoligotypes were common to beef and dairy cattle. The molecular analysis showed eight clusters in a philogenetic three: one with three subclusters of nine isolates each, all from dairy cattle; four with two isolates, including dairy and beef cattle. All spoligotypes from Jalisco have been reported in other states, four of the most frequent ones: SB0673, SB0971, SB0669 and SB0140, were the same as in other states. The most frequent spoligotypes of *M. bovis* found in Jalisco were also the most frequent ones in other parts of Mexico. However, there is no evidence to conclude that Jalisco is the source of infection to other states since no information on movement and destination of cattle could be documented.

Key words: Tuberculosis, *Mycobacterium bovis*, spoligotyping, cattle, Jalisco, molecular epidemiology.

INTRODUCTION

Bovine tuberculosis (bTB) is an infectious disease caused by *Mycobacterium bovis,* a member of the *Mycobacterium tuberculosis* complex, which also includes *M. tuberculosis*, *M. cannettii*, *M. africanum*, *M. bovis*, *M. pinnipedii*, *M. caprae* and *M. microti.* Bacilli in this group are 99.9% genetically similar at the nucleotide level with identical 16S rRNA sequences (Boddinghaus et al., 1990; Sreevatsan et al., 1997) but with different host

*Corresponding author. E-mail: feliciano.milian@uaq.mx. Tel: 442 192 12 00. Ext: 5384.

preferences; *M. bovis* has the broadest host range, causing disease in a wide range of mammals, including humans (O'Reilly and Daborn, 1995; Blischak et al., 2015). The proportion of cases due to *M. bovis* in humans in the last two decades has been variable, ranging from 0.5 to 13% depending on the study population, and it is estimated that nearly 10 million people are affected by tuberculosis worldwide every year (Müller et al., 2013; Olea-Popelka et al., 2017; Perea-Razo et al., 2017). Transmission to humans occurs by inhalation of infectious droplets from infected cattle, and consumption of contaminated unpasteurized dairy products (de la Rua-Domenech et al., 2006).

bTB causes direct and indirect economic losses to the livestock industry, infected animals have poor production performance, die or are culled prematurely. Free trade of animals and animal products in affected areas is prohibited, especially for exportation (Bawinek and Taylor, 2014; El-Sayed et al., 2016).

Like many countries, Mexico has a national program for the control and eradication of tuberculosis (NOM-031-ZOO-1995). This program is based on tuberculin testing and culling of reactors; however, after about two decades, the success has been partial, prevalence in beef cattle has been reduced to low levels (<0.5%) in 85% of the national territory, but in dairy cattle prevalence remains in about 16% (Plan Estratégico de la Campaña Nacional de la Tuberculosis Bovina en México, 2008-2012; Milián-Suazo et al., 2016). Poor participation of dairy farmers in the program, who are not willing to eliminate reactors is one of the main reasons. Nevertheless, the elimination of bTB in Mexico is a high priority task.

Another reason that has hampered the complete success of the bTB program in Mexico, and in other developing countries is the lack of a good system to trace back sources of infection and the indiscriminate movement of animals. Fortunately, in the last ten years, the arrival of molecular techniques to genotype strains of *M. bovis* has enormously supported epidemiological studies focused on detecting areas of risk. Because of simplicity and the low levels of DNA required in the analysis, spoligotyping is one of the methods most frequently used for studying genetic relationship between strains, and the spatial and temporal distribution of *M. bovis* (Kamerbeek et al., 1997; Rodríguez-Campos et al., 2011).

Spoligotyping detects presence or absence of spacers of the Direct Repeat (DR) locus in the *M. bovis* genome (Supply et al., 2006). The DR region contains a large number of DR´s of 36 bp interspersed by spacers from 35 to 41 bp in length. These repeats are present in isolates of the *M. tuberculosis* complex only, and it has been shown that this region is variable (Kemmerbeek et al., 1997). Presence or absence of DR´s allows phylogenetic analysis to determine genetic relationship between individual or groups of strains (Acosta-Salinas et al., 2009; Jagielski et al., 2014).

Molecular genotyping suggests that isolates with similar fingerprints are epidemiologically related and differ from those epidemiologically unrelated (Maslow and Mulligan, 1993); however, the desirable characteristic for typing is related to its stability within the strain and its diversity within the species (Kemerbeek et al., 1997; Zhou et al., 2011; Kim et al., 2017). Strains with the same spoligotype are assumed to be individuals recently derived by clonal replication from a single ancestral cell; therefore, epidemiological related strains should have higher genetic similarity than those no related (Rodríguez-Campos et al., 2011; Milián et al., 2016). Furthermore, spoligotyping has been used successfully in epidemiological studies in many countries (Gibson et al., 2004; Parra et al., 2005; Duarte et al., 2010; Rodríguez et al., 2010; Skuce et al., 2010; Ruettger et al., 2012; Mwakapuja et al., 2013).

Bacilli of the *M. tuberculosis* complex are clonal, exchange of DNA between individual does not exist. Therefore, it is widely accepted that spoligotypes provide enough information to estimate recent evolution events to perform phylogenetic analysis for epidemiological purposes (Supply et al., 2006), and together with MIRU-VNTR has been recognized as the new gold standard for molecular epidemiological investigations of TB (Jagielski et al., 2014). Currently, there are many reports about the spatial and temporal distribution of *M. bovis* in different geographic areas around the world; however, no information on the role of specific geographic areas in the dissemination of bTB is available.

Therefore, the objective of this study was to use spoligotyping patterns to better understand the population structure of *M. bovis* in cattle in Jalisco, and to evaluate the role of this state as a source on infection for other regions in Mexico.

MATERIALS AND METHODS

Isolates data

Data from a total of 337 *M. bovis* isolates from cattle in the State of Jalisco, and 1,152 from other states in Mexico between 1997 and 2015 were included in the study. Isolates were obtained directly from bTB suspicious tissue collected from carcasses in slaughterhouses, and cultured in Stonebrink and Lowenstein-Jensen with pyruvate. Briefly, tissue samples were first decontaminated with 1:1000 solution of sodium hypochlorite and then macerated and decontaminated with a 10% solution of hydrochloric acid. DNA for spoligotyping was obtained by the CTAB-chloroform method, according to de Almeida et al. (2013). Briefly, a total of 500 µL of suspended colonies in TE 1X buffer was transferred into lysozyme (10 mg/ml) and incubated at 37°C for 1 h. Then, proteinase K and sodium dodecyl sulfate 10% were added, and the suspension was incubated at 65°C for 30 min. Subsequently, a solution consisting of a mixture of NaCl and CTAB (NaCl 5 M and CTAB 10%) was added, and the suspension was incubated for 30 min at 65°C. DNA was then extracted with chloroform/isoamyl alcohol (24:1). The supernatant was transferred to a new tube and isopropanol was added. The suspension was

Table 1. The most frequent *M. bovis* spoligotypes in Jalisco and other States of Mexico, by breed.

State	Breed	Spoligotype (SB)										Other	Total
		0673	0971	0669	0140	0145	0121	0663	0269	1116	0119		
Jalisco	Dairy	35	14	30	15	18	10	10	8	7	9	163	319
	Beef	0	0	0	1	0	0	2	0	0	0	2	5
	Unknown	2	0	0	0	0	0	0	1	2	1	7	13
	Total	37	14	30	16	18	10	12	9	9	10	172	337
Other States	Dairy	148	60	67	75	66	70	27	21	13	11	284	842
	Beef	8	19	13	4	0	0	7	5	10	1	24	91
	Unknown	22	33	13	14	10	4	4	7	10	3	99	219
	Total	178	112	93	93	76	74	38	33	33	15	407	1152
Grand total		215	126	123	109	94	84	50	42	42	25	579	1489

kept at -20°C for 2 h and centrifuged for 15 min at 14,000 g. The pellet was washed with 500 µL of 70% ethanol and centrifuged for 5 min at 14,000 g, and 50 µL of TE buffer was added.

Spoligotyping

Spoligotyping was performed according to Kamerbeek et al. (1997). The DR region was amplified using the primers DRa (GGTTTTGGGTCTGACGAC, 5_ biotinylated) and DRb (CCGAGAGGGGACGGAAAC). The amplified product was hybridized to a nylon membrane to which 37 spacer sequences from *M. tuberculosis* H37Rv and 6 spacer sequences from *M. bovis* BCG were covalently bound (Isogen Bioscience BV, Maarssen, The Netherlands). For the detection of hybridizing DNA, chemiluminescent ECL detection system (Amersham Biosciences; Piscataway, NJ) was used, followed by exposure to X-ray film (Kodak) for 45 min. Spoligotypes were named according to the website *M. bovis* spoligotype database (www.mbovis.org).

Phylogenetic analysis

Spoligotyping data were converted to binary character data (absent=0 and present=1) for the 43 probe hybridization positions. Genetic relationship between spoligotypes was determined by using the algorithm MIRU-VNTRplus available in www.miru-vntrplus.org. Evolutionary relationship was determined throughout spoligoforest in the spolTools webpage (www.emi.unsw.edu.au/spoltools/) for all spoligotypes clustering at least three isolates. Spoligoforest provides an evolutionary genetic tree showing the most probable relationship of all the spolgotypes in the data set (Reyes et al., 2008). This algorithm uses a model that considers mutations by irreversible deletions of spacers and assigns probabilities to the lengths of these deletions. The number of isolates in the cluster determines the size of each node in the tree. Edges between nodes reflect evolutionary relationships between spoligotypes with arrowheads pointing to descendants. Spoligotypes from Jalisco were matched to spoligotypes from other States of Mexico to determine the level of dissemination of *M. bovis* in the country.

RESULTS

Out of 337 isolates from Jalisco, a total of 59 spoligotypes were obtained, ten: SB0673, SB0971, SB0669, SB0140, SB0145, SB0121, SB0663, SB0269, SB1116, and SB0119 included 48% of all isolates from Jalisco; grouping between nine and 37 isolates. Ten spoligotypes grouped between two and three isolates, and 39 were orphans. When comparing spoligotypes from Jalisco with those from other states, it was found that the most frequent spoligotypes in Jalisco were also the most frequent ones in other States of Mexico. Five spoligotypes from Jalisco were common to beef and dairy cattle, suggesting related strains between these two breeds (Table 1).

Out of the 1,152 isolates from states other than Jalisco, a total of 159 spoligotypes were obtained, which included 56% of all isolates in the data set, 98 were orphans. The ten most frequent spoligotypes in Jalisco were also the ten most frequent ones in other parts of Mexico; two hundred and sixty-six were not found in the *www.mbovis.org* data set. From all the isolates in the data set, 1,161 came from dairy, and 96 from beef cattle; the rest had not information for this variable (Table 1).

Figure 1, shows the phylogenetic tree of spoligotypes from Jalisco, containing groups of at least three isolates each. Eight clusters were formed in this tree: one with three subclusters with nine isolates each, all from dairy cattle. Four with two isolates, including dairy and beef cattle, and three with one subcluster; one including an isolate from beef cattle. Isolates from other states matching spoligotypes from Jalisco are described in Table 2. All spoligotypes from Jalisco have been reported in other States, four of the most frequent spoligotypes in Jalisco: SB0673, SB0971, SB0669 and SB0140, were also the most frequent ones in other states. Some spoligotypes are common to dairy and beef cattle, suggesting related strains of bTB between these two breeds.

Figure 2 shows the spoligoforest hierarchical layout of isolates from Jalisco, where the continuity of lines indicates the weight of the hypothetical evolutionary

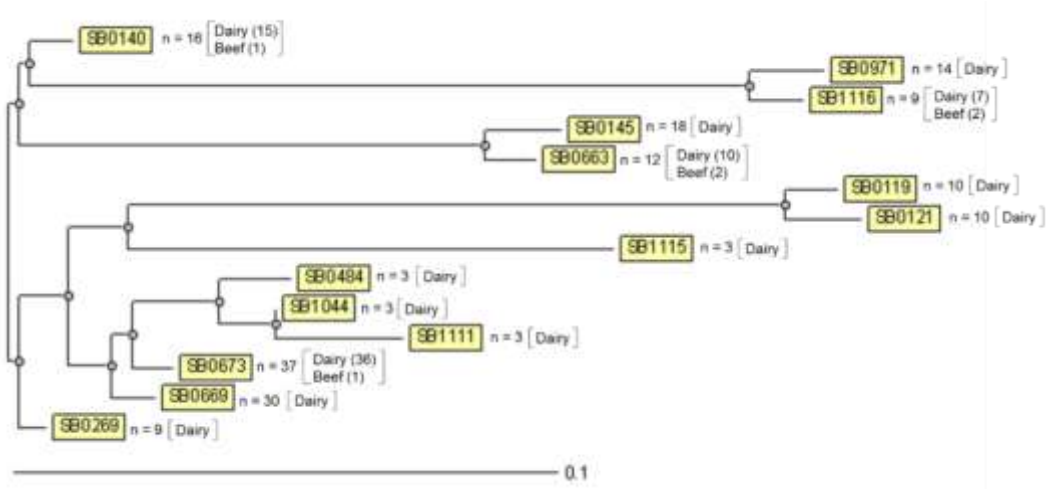

Figure 1. Phylogenetic tree of *M. bovis* isolates obtained from cattle in the State of Jalisco. Number in brackets indicates the number of isolates per breed.

relationship between spoligotypes; continuous line indicates stronger relationship. The spoligoforest shows two trees with connected components. The biggest tree, the one with the largest number of branches, is rooted by strain SB0140, suggesting this as the oldest strain in the tree.

A total of 141 isolates descended from SB0140, in four clearly defined clusters with 9 to 37 isolates each. The hypothetical evolutionary relationship between spoligotypes SB0140 and SB0673, the spoligotype with the largest cluster in the data set is strong, suggesting a small number of changes in the DR region sequence. Spoligotype SB0669, the second largest cluster, has a strong relationship with spoligotype SB0673 but is not directly connected to spoligotype SB0140, suggesting a new evolutionary route.

Spoligotypes SB0145, SB0269 and SB0971 all directly descended from SB0140. SB0145 and SB0971 have their own evolution route since other spoligotypes are derived from them (SB0663 and SB1116, respectively). From the second tree, rooted by spoligotype SB0121, only one lineage is formed, giving origin to strain SB0119.

Figure 3 shows the spoligoforest hierarchical layout of isolates from states apart from Jalisco in Mexico. Like the Jalisco´s spoligotypes, the other States spoligoforest shows two separated trees, originating also from SB0121 and SB0140. The only big difference between the two spoligoforests is the presence of spoligotype SB0971 with a large number of isolates in a separated branch, suggesting a new genetic line. As before, spoligotype SB0140 seems to be the older spoligotype in the country.

DISCUSSION

Spoligotypes SB0673 and SB0669 were the most frequent spoligotypes in Jalisco. These spoligotypes SB0971 and SB0669 were also the most frequent ones in the rest of the country; however, this fact does not necessarily mean that Jalisco is the source of infection since no epidemiological evidence connecting strains from different sources in Mexico could be obtained. It is known that Jalisco is an important source of dairy replacements to other regions in Mexico under especial circumstances; however, this could not be confirmed due to the lack of information on movement of cattle. It is known from personal communication that Jalisco acted as a source of dairy heifers for other regions in the years 2003 to 2006, when Mexico closed the border to the importation of cattle from the United States (US) and Canada because of the bovine spongiform disease outbreak; the US and Canada are the main sources of replacements for dairy in Mexico. It was not known, however, what the distribution of *M. bovis* strains in the country was before that event, for comparison.

Beef and dairy cattle are maintained under different conditions in Mexico. Dairy cattle are raised in close intensive settings with a large number of cattle per square meter; in some regions it is possible to observe 10,000 cattle in a single unit operation. On the contrary, beef cattle are raised in open extensive areas with a low number of cattle per hectare. Because of this, the prevalence of bTB in dairy cattle is higher ≈16% (range 0 to 40%) than in beef cattle ≈0.5% (range 0 to 1%) (Plan Estratégico de la Campaña Nacional de la Tuberculosis Bovina en México, 2008-2012). Therefore, infected dairy populations are a risk to bTB-free or bTB-low prevalence areas of beef cattle. Fourteen of the isolates from beef cattle had spoligotypes SB0673 or SB0669, two of the most frequent spoligotypes in dairy cattle, suggesting transmission between breeds. From the epidemiological point of view, this is relevant because transmission from

Table 2. Frequency and relationship of *M. bovis* isolates from Jalisco and other States of Mexico by breed.

Spoligotypes from Jalisco	Number of isolates	State (number of isolates by State for States other than Jalisco)		Unknown
		Dairy	Beef	
SB0673	182	Ags (9), BC (3), Chih (6), Coah (16), EdoMex (17), Gto (9), Hgo (17), Qro (66), Sin (2), SLP (1), Ver (1), Zac (1).	Chih (1), Dgo (1), Gto (2,), Zac (4).	Ags (7), Coah (2), Col (1), Gro (1), Mich (1), Mor (7), Qro (7).
SB0971	109	Ags (6), BC (1), Chis (1), EdoMex (10), Gto (8), Hgo (8), Mich (1), Qro (22), SLP (1), Ver (1).	Gto (1), Mich (1), Qro (15), Son (1), Ver (1).	Ags (8), EdoMex (7), Gto (3), Gro (1), Mor (1), Nay (2), Qro (7), SLP (2),
SB0669	173	Ags (11), BC (1), Coah (10), Col (1), Dgo (3), EdoMex (18), Gro (2), Gto (5), Hgo (9), Qro (4), SLP (2), Tlax (1).	Gto (2), Mich (1), Nay (8) y Zac (2).	Gro (2), BL (1), Pueb (4), SLP (3), Son (1), Zac (1).
SB0140	90	Ags (10), Chih (8), Coah (2), Edo Mex (5), Gto (3), Hgo (9), Mich (3), Qro (33), Zac (2).	Gto (1), Mich (1), Zac (2).	Ags (6), EdoMex (2), Gto (2), Mor (1).
SB0145	74	Ags (4), BC (14), EdoMex (16), Gto (4), Hgo (5), Qro (20), Ver (2), Zac (1).	--	Ags (2), Nay (1), Qro (2), Sin (2), Ver (1),
SB0121	74	Ags (1), BC (1), Chih (29), Coah (2), EdoMex (3), Hgo (20), Qro (14).	--	Mich (3), Nay (1).
SB0663	37	Ags (5), BC (10), Chih (1), Dgo (1), Edo Mex (3), Gto (2), Qro (4), Zac (1).	Mor (1), Nay (4), Son (1) y Ver (1).	Sin (1), Son (1), Ver (1).
SB1116	33	Ags (5), Col (1), Dgo (1), Edo Mex (2), Mich (1), Qro (2), Zac (1).	Gro (1), Nay (1), Ver (8).	Pue (2), SLP (3), Sin (1), Tamps (2),Ver (2).
SB0269	33	Ags (5), Coah (1), Dgo (1), Edo Mex (2), Gro (1), Hgo (3), Qro (2), Ver (6).	Camp (3), Gto (1), Sin (1).	Col (1), Nay (1), Pue (2), SLP (3).
SB0119	14	Chih (4), Coah (2), Dgo (1), Hgo (3),y NL (1).	Gto (1).	Col (1), Sin (1).
SB0484	10	Edo Mex (3), Gto (1), Hgo (3) Qro (1), SLP (2).	--	--
SB1044	9	Edo Mex (3), Hgo (2), Qro (2).	--	Qro (1), Zac (1).
SB1115	1	Ags (1)	--	--
SB1111	1	Edo Mex (1)	--	--

dairy to beef cattle might jeopardize the goals of the national program to eradicate bTB, and the exportation of calves, an important source of currency for Mexican farmers. In this study, it is not known however if beef animals found infected are from cattle for beef operations or from dairy operations, where sometimes, beef bulls are used for breeding cows with reproductive problems, and beef calves are kept for fattening in the same farm.

Even though clustering of isolates occurred, the diversity of spoligotypes is wide. This agrees with previous reports (Cobos-Marín et al., 2005; Santillán-flores et al., 2006; Reyes et al., 2008; Pérez-Guerrero et al., 2008; Bobadilla-del Valle et al., 2015; Sandoval-Azuara et al., 2017), where in spite of studying samples from different and specific regions of Mexico, the diversity of strains has been evident, suggesting an intense and continuous exchange of animals, and new genetic lines emerging as a consequence of the high prevalence of bTB in dairy cattle.

The spoligoforest demonstrates all possible relations of spoligotypes under the assumption of spoligotype mutation, with genetic instability ranging from 10 to 20 years (Brosch et al., 2002; Gutiérrez et al., 2005; Smith et al., 2006). In the data set, the largest root of the tree was spoligotype SB0140. Spoligotype SB0140 has infected cattle, deer, badgers and people in

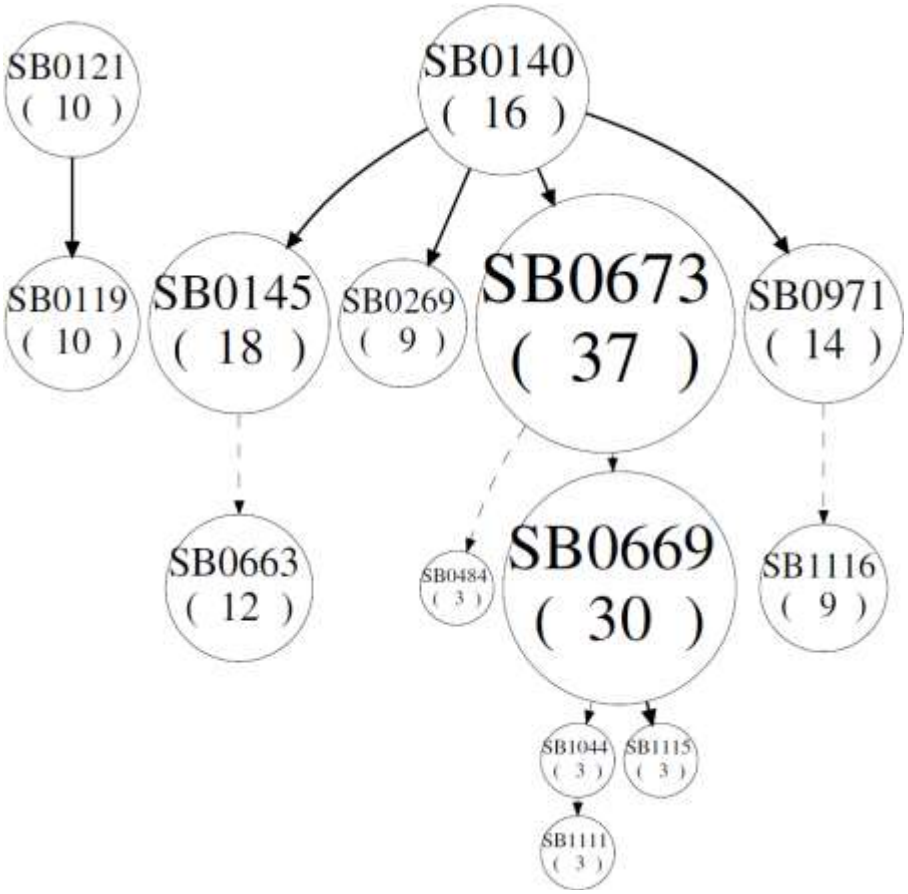

Figure 2. Spoligoforest of *M. bovis* spoligotypes obtained from cattle in Jalisco, Mexico. Nodes are labeled with the SB identifier as indicated in *mbovis.org*; numbers in parenthesis indicate cluster size. Lines between nodes reflect hypothetical evolutionary relationships among spoligotypes with arrows denoting descendence. Continuous lines indicate stronger relationship.
Source: http://spoltools.emi.unsw.edu.au/

Ireland (de la Rua-Domenech et al., 2006; McLernon et al., 2010), and cattle in the United Kingdom (de la Rua-Domenech et al., 2006; McLernon et al., 2010). It has also been reported as the most frequent spoligotype in pigs (Barandiaran et al., 2011), cattle and cats in Argentina (Zumárraga et al., 2009), and humans in the United States (Rodwell et al., 2008) and Mexico (Bobadilla-del Valle et al., 2015).

Spoligotype SB0140 has been studied profoundly in the United Kingdom (Smith et al., 2003). It was concluded that the frequency of strains with SB0140 in that country cannot be explained by random drift without selection. It has been concluded that some genotypes increase in number in a specific region in a “clonal expansion” by selection of favorable mutations when some cells find new host species or new geographical regions. In Mexico, it is believed that both situations are possible at least for the most frequent spoligotypes: selection of favorable mutations due to the high prevalence of *M. bovis* in the population and ecological opportunity by the indiscriminate movement of animals between regions.

Clusters with similar or highly similar *M. bovis* spoligotypes are considered the result or recent transmission, and that the orphans arise from migration or reactivation of acquired infections (Luciani et al., 2008). However, other factors may be involved in that clustering, that is, sampling and the mutation rate of the molecular marker used in fingerprinting (Tanaka and Francis, 2005). In the current study, both clustering and a high frequency of orphan spoligotypes occur. Clustering might well be a consequence of the conditions in which dairy cattle are maintained, in high density populations and orphans, the result of the indiscriminate movement of animals between regions or the high prevalence of the disease, which gives rise to new genetic lineages.

Something that is clear from the current study is that molecular information itself is not enough to explain the epidemiology of a disease. In the present study, no data on movement of animals from Jalisco could be obtained in spite of intensive search of data, and this is clearly a

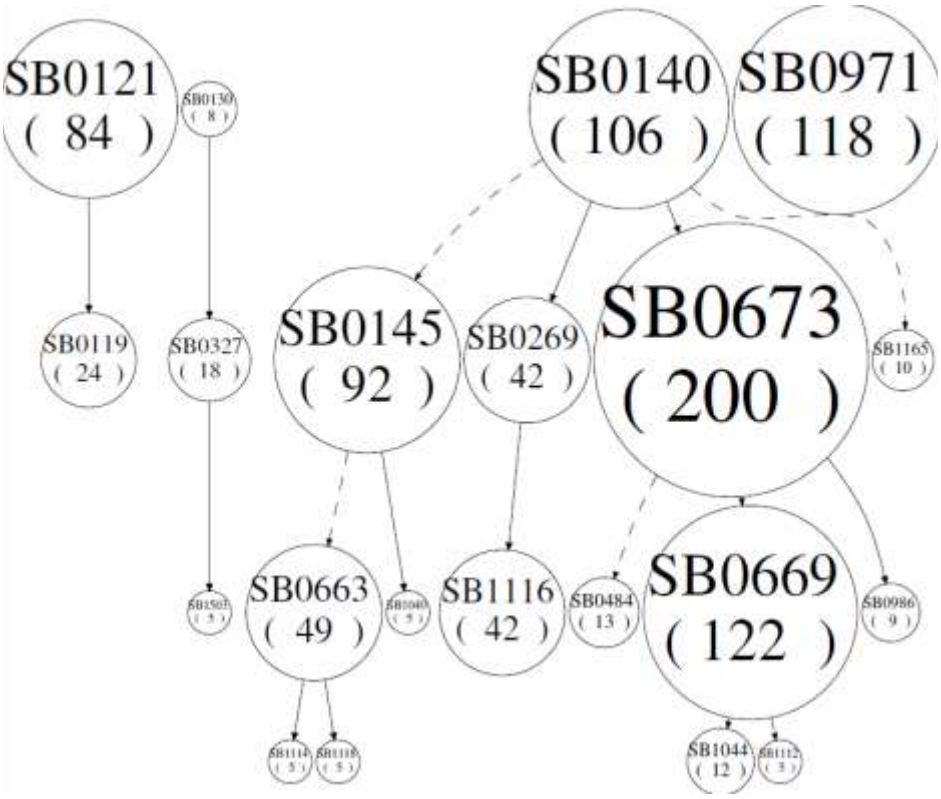

Figure 3. Spoligoforest of *M. bovis* spoligotypes obtained from States other than Jalisco in Mexico. Nodes are labeled with the SB identifier as indicated in *mbovis.org*; numbers in parenthesis indicate cluster size. Lines between nodes reflect hypothetical evolutionary relationships among spoligotypes with arrows denoting descendence. Continuous lines indicate stronger relationship.
Source: http://spoltools.emi.unsw.edu.au/

weakness of this study. This suggests that more knowledge on epidemiological methodologies, especially databases maintenance by bodies responsible for animal health care in Mexico, is required.

Conclusions

The most frequent spoligotypes of *M. bovis* found in Jalisco are also the most frequent ones in other parts of Mexico. However, there is no evidence to conclude that Jalisco is the source of infection since no information on movement and destination of animals could be documented. It is believed that similarity of spoligotypes around the country is in fact due to the indiscriminate movement of animals. The long history of bTB in Mexican herds, which favors the increase and dissemination of new and existing *M. bovis* strains in the population could be another reason.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Prevalence of bovine of schistosomosis in and around Nekemte, East Wollega zone, Western Ethiopia

Abriham Kebede[1]* Jiregna Dugassa[1], Geremew Haile[1] and Berhanu Wakjira[2]

[1]School of Veterinary Medicine, College of Medical and Health Science, Wollega University, P. O. Box, 395, Nekemte, Ethiopia.
[2]School of Veterinary Medicine, College of Agriculture and Veterinary Medicine, Jimma University, Ethiopia.

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A cross-sectional study was conducted from March 2016 to May 2016 at Guto Gida District, Nekemte, Ethiopia to determine the prevalence of bovine schistosomosis. Simple random sampling method was used to select the study animals and sedimentation technique was applied for finding *Schistosoma* eggs from fresh fecal samples. Out of 384 fecal samples examined, 22 were found positive indicating an overall prevalence of 5.7% schistosomosis in the study area. The prevalence of bovine schistosomosis was higher in Jirenga kebele (9.1%) than Gaarii kebele (4.6%) and Dalo kebele (3.7%). However, no statistically significant difference in the prevalence of bovine schistosomiasis in relation to origin was found. Similarly, there was no statistically significant difference observed between both sexes (P>0.05). The prevalence in body condition category was reported relatively higher in poor body condition (8.4%) and lower in good body condition (3.8%). However, no statistically significant differences appreciated among the three body condition categories (P>0.05). The finding indicated that, schistosomosis should be taken into consideration as one of the major limiting factor to livestock productivity at Guto Gida District. The control measures against schistosomosis must be designed to target either the parasite or the snail intermediate host.

Key words: Bovine, *Guto Gida,* prevalence, schistosomiasis

INTRODUCTION

Schistosomosis is an infection which occurs due to trematodes of genus *schistosoma.* The disease, characterized by its chronic nature, affects the productivity and production performances and predisposes animals to other diseases in the World (Mc-Cauley et al., 2000), and it is endemic in the tropical and subtropical countries of Africa, Asia and Southern Europe (Lawerence, 2001).

Epidemiological studies on bovine schistosomosis are suggestive of the endemicity of the infection particularly in areas with large permanent water bodies and marshy pasture areas. In Ethiopia, the optimum range for distribution of *S. mansoni* has been reported as 1500 to 2000 m above sea level (masl) (Gashaw, 2010). *Schistosoma* bovis has a localized distribution found commonly in Northern, Eastern, South Western and

*Corresponding author. E-mail: abrahamkebede2016@gmail.com Tel: +251-917-095-077.

central parts of Ethiopia (Fekade et al., 2002); It is affecting all ages of animals and mainly prevalent in cattle kept around lakes and rivers (Dwight et al., 2003; Pitchford, 2006).

Schistosomosis is transmitted by using snails as an intermediate host; the immature infective form penetrates the skin of the host and may also infect cattle by ingestion through drinking water (Allen et al., 2002; Lindbergh et al*.,* 2006). Animals affected by the disease show different clinical signs such as diarrhea, sometimes blood stained and containing mucus, and also anorexia, thirst and emaciation is the sign shown by animals with disease (Gutierrez, 2004).

Diagnosis of the disease is primarily based on the history of schistomosis in the area and the identification of snail habitats with history of access to natural water bodies (Bedarkar et al*.*, 2000; Pawar et al*.,* 2016). Postmortem examination, hematological tests and examination of feces for *schistosoma* eggs are also useful. The clinical signs alone will not be sufficient to arrive at definitive diagnosis but, it should be used to indicate the necessity of feces examination, which reveals the eggs of parasites mixed with blood and mucous (Thrusfied, 2005).

For treating the disease, older drugs include antimonial preparation, tartar emetic, antimosan and stibophen, and niridirozole and trichlorphon. The praziquantel, which is a drug of choice for treatment of human schistosomosis is also effective in ruminant at 15-29 mg/kg, peros (Gracia and Bruckner, 2007).

The effective control of the disease is to prevent contact between the animals and the parasite by fencing of infected waters and supplying clean water and also by the destruction of intermediate host or snails (Hansen and Perry, 2004). Even though, schistosomiasis is an economically important disease of livestock leading to huge economical losses, due to morbidity and mortality and thereby contributing to productivity loss, there is no considerable work done on the prevalence of the disease in and around Nekemte.

Therefore, the objective of this study was to determine the prevalence of Schistosomiasis in cattle in Nekemte area.

MATERIALS AND METHODS

Study area

The study was conducted from March to May, 2016 in Guto Gida district, Nekemte town, East Wollega Zone of Oromia Regional State, Ethiopia. The district is about 331 km from Addis Ababa to the West. The area has average temperature of 20°C and mean annual rainfall of 21500 mm. The altitude of the area ranges from 1300 – 3140 m a. s. l. According to the Nekemte District Agricultural Office, livestock population of cattle in head is 85,584, sheep 14,702, Goat 11,861, Equine 98,674, chicken 94,276 and mixed crop and livestock farming system is the mode of agriculture in the district in which cattle and sheep operate as major livestock, highly important for livelihood of the local population (NWAROD, 2016).

Study population

The study population was cattle with different age groups, body condition and sex. The age of animal was determined based on dentition (Pope, 2008) and the body condition of the animals was classified into three groups:- poor, medium and good based on visibility of skeleton by inspectional examination (Debont et al., 2005).

Study design

A cross sectional study was used to determine the prevalence of bovine schistosomosis and its risk factors at Nekemte area from March to May, 2016.

Sampling and sample size determination

From area of Nekemte town the Kebeles (Jirenga, Gaari and Dalo) were selected by purposive sampling based on animal population of the Kebeles and consideration of the representativeness.

The desired sample size was determined by using the formula given by Thrushfield (2004); also, with 95% confidence level and 5% desired absolute precision, and since there was research conducted in this area, 50% expected prevalence was taken.

$$N = \frac{1.96 * P\,exp\,(1 - Exp)}{d^2}$$

where
n = required sample size
$p_{exp=}$ prevalence
d^2 = Desired absolute precision.

$$N = \frac{1.96 * 0.5(1 - 0.5)}{(0.05)}$$

=384

Accordingly, animals were selected randomly to estimate the prevalence of the infection in the study area.

Study method and sample collection

Coproscopic examination

The fresh fecal sample was collected directly from rectum of randomly selected animals and preserved in 10% formalin in universal bottle to prevent hatching of miracidia. Then eggs were examined by fecal sedimentation techniques and observed under microscope in the laboratory (Ash and Orihel, 2004).

Data management and analysis

The data was entered into MS excel Database, coded, thence analyzed using SPSS 20.0 version statistical software program. The prevalence was calculated by dividing number of positive animals by total number of animals tested. Pearson's chi square (x^2) was used to evaluate the association between the prevalence the disease with related risk factors. P value < 0.05 was considered as significant in the analysis.

RESULTS

Overall prevalence

Among 384 cattle examined using coproscopical

Table 1. Prevalence of bovine schistosomosis based on PAs or kebeles.

PAs or Kebeles	No. examined	No. infected	Prevalence (%)	X^2	P value
Garii	129	6	4.6		
Jirenga	120	11	9.1	0.928	0.055
Dalo	135	5	3.1		
Total	**384**	**22**	**5.7**		

Table 2. Prevalence of bovine schistosomosis based on sex.

Sex	No. examined	No. infected	Prevalence (%)	X^2	P value
Male	187	13	6.9	1.009	0.382
Female	197	9	4.5		
Total	**384**	**22**	**5.7**		

Table 3. Prevalence of bovine schistosomosis based on body condition**.**

Body condition	No. examined	No. infected	Prevalence (%)	X^2	P value
Poor	119	10	8.4		
Medium	135	7	5.1	0.503	0.073
Good	130	5	3.8		
Total	**384**	**22**	**5.7**		

examination, 5.7% (22/384) were found to be positive for bovine schistosomosis or infected.

Prevalence based on origin

According to the present study, the prevalence of bovine schistosomosis was higher in Jirenga kebele (9.1%) than Gaarii kebele (4.6%) and Dalo kebele (3.7%). However, there was no statistically significant difference on the prevalence of bovine schistosomosis based on three PAs (p>0.05) as indicated in Table 1.

Prevalence based on sex

The study indicated that, the prevalence of bovine schistosomosis in male and female was 6.9% and 4.5%, respectively. Although the prevalence was relatively higher in female as indicated in Table 2 the difference was not statistically significant (P>0.05).

Prevalence based on body condition

Prevalence of bovine schistosomosis on poor body condition animals was 8.4% and medium body condition (5.1%). However, animals with good body condition showed prevalence of 3.8%. As described in Table 3, significant difference (P > 0.05) was not observed among body condition of the study animals for the occurrence of schistosomosis.

Prevalence based on age

According to the age of animal, the prevalence of schistosomosis varied. Low prevalence was observed in young (4.9%), and highest prevalence was observed in adult (6.2%). However, there was no significant difference (P > 0.05) among age groups (Table 4).

DISCUSSION

The overall prevalence of bovine schistosomosis infection of the study area was found to be 5.7%. When this result is compared with the prevalence of other authors in the country it is much lower than the finding of Mersha et al. (2012) which was 13.7% in Fogera. Similarly, 22.06% was reported in and around Bahir Dar (Solomon, 2008) and 27.13% in Dembia (Alemseged, 2010). The difference in prevalence may be due to the variation in the study seasons, sample size, humidity, management and climate change between various agro ecologies. The present study is nearly similar with that of Mihret and

Table 4. Prevalence of bovine schistosomosis based on of animal age.

Age	No. examined	No. infected	Prevalence (%)	X^2	P value
Young	161	8	4.9	0.297	0.661
Adult	223	14	6.2		
Total	**384**	**22**	**5.7%**		

Samuel (2015) (7.6%) in and around Debre Tabor town, South Gondar Zone of Amhara region, Northwestern Ethiopia, which can be due to similar management in the areas.

The relatively greater prevalence of the disease was in Jiregna and Gaarii PAs maybe due to swampiest and moisture nature of most of the grazing areas in these PAs. Similarly, many authors also reported that water lodged and poorly drained areas with acidic soils are often endemic for schistosomosis (Almaz, 2007). Mihret and Samuel (2015) also reported that there was difference of bovine schistosomosis prevalence based on origin but there was no significant difference between origin and the infection.

The higher prevalence of bovine schistosomosis was in adult animals in this study and agrees with the work of (Alemseged, 2010) who reported a prevalence of 17.6% in young animals and 30.10% in adults in Dembia district, disagreeing with the work of Taylor et al*.* (2007) who reported highest prevalence in young animals.

The variation in the prevalence was found in male (6.9%) and in female (4.5%) revealing no statistically significant (P>0.05) difference. This variation is similar with previous study which was 29.61% in male and 19.54% in female (Solomon, 2008), in and around Bahir Dar and 30.70% in male and 23.30% in female (Alemseged, 2010) in Dembia district. The study disagrees with the study conducted by Mihret and Samuel (2015) and found higher prevalence in female (33.1%), and lowers in male (27.1). The results indicated that both sexes have the same risk to acquire disease. This is because of equal exposure to the risk factors since there were no restrictions on movement for grazing and contact with the parasite and animals in terms of sex.

This exacerbates the multiplication of *Schistosoma* and increases the epidemiology of the disease. It was also reported that the increased contact time with *Schistosoma* infested habitat increases the rate and endemicity of schistosomosis.

Schistosoma infection rate in relation with body condition score in the present study varied in cattle. Animals with poor body condition score were more affected than other groups of animals. Similarly, Merawe et al*.* (2014) affirmed that the infection rate increase with animals which have poor body condition score. This could be due to the acquired immunity status of poor body condition and weak animals becoming more suppressed and susceptible possibly due to malnutrition and other parasite infection. Thus, infected animals may require long period of time to respond against *Schistosoma* infection. This gives suitable time for establishment and fecundity of the parasite in animals. This finding also coincides with the work of Belayneh and Tadesse (2014) that accounted the prevalence of *Schistosoma* as more common in animals with poor body score animals than medium and good body condition.

CONCLUSION AND RECOMMENDATION

According to the present study, the overall prevalence of bovine Schistosomosis was found to be 5.7% in and around Nekemte. The study also revealed that the prevalence of schistosomosis is high in Jirenga and followed by Gari peasant associations. The prevalence of the disease is also closely linked with environmental factors that are suitable for the development and multiplication of snail which is intermediate hosts and the parasite. Therefore, depending on the result of the study, the following recommendations are forwarded:

(i) There should be initiation and awareness creation on the prevention and control of snails.
(ii) Further epidemiological investigations should be conducted to assess the *Schistoma* infection and its associated risk factors.
(iii) There should be regular deworming and veterinary service in the study area.
(iv) Grazing management should be involved to avoid grazing around marshy area in which snail population is high.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Status of mange infestation in indigenous sheep and goats and their control practices in Wag-Himra zone, Ethiopia

Adane Agegnehu, Basaznew Bogale*, Shimelis Tesfaye and Shimelis Dagnachew

College of Veterinary Medicine and Animal Sciences, University of Gondar, Gondar, P. O. Box 196 Ethiopia.

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A cross sectional study was conducted from December 2016 to April 2017 to estimate the status of mange infestation in indigenous sheep and goats and identify the major species of mites and potential risk factors in selected districts with different agro-ecological zones of Wag-Himra zone. In addition, a questionnaire survey was conducted to assess the awareness and control practices of livestock owners on mange mite's infestation. From a total of 384 small ruminants (120 sheep and 264 goats), 105 (27.33%) were positive for mange mites infestation on skin scraping examination. *Sarcoptes scabiei* was the only mange mites species identified with a prevalence of 33.3% (n=40) in sheep and 24.6% (n=65) in goats. Host factors such as species, sex, age and body condition were not found as a risk factor of *S. scabiei* infestation in the current study. However, there was a statistical significant (P<0.031) difference in prevalence of *S. scabiei* infestation in small ruminants between the three agro-ecological zones. The pathological lesions (crusts formation and loss of hair) caused by *S. scabiei* were observed on the face, head, ear and tail regions. The result of the questionnaire survey indicated that mange was considered as an important disease by small ruminant holders. From the interviewed livestock owners, 86.27% respondents explained that they use modern acaricides for the treatment of mange. The results of this study indicates that the agro-ecology had effect on the prevalence of *S. scabiei* in sheep and goats in the study area.

Key words: Cross sectional, ectoparasites infestation, small ruminants.

INTRODUCTION

Goats and sheep represent important sources of protein in the world, supplying a good percentage of the daily meat and milk products in urban and rural areas. Small ruminants are important contributors to the economy of Ethiopia (CSA, 2013). They are also important contributors to food production; providing 25% of meat and 14% of milk for domestic consumption (Metaferia et al., 2011). In addition, manure from these animals is very important as source of organic fertilizer from any farming populations in the country. Reports have indicated that

*Corresponding author. E-mail: basaznew2008@yahoo.com. Tel: 251918020923.

skin utilization is estimated to be 75% for goat and 97% sheep skin, with expected off-take rate of 33 and 35% for sheep and goat, respectively (Tadesse and Mebrahitu, 2010; Zeryehun and Tadesse, 2012). However, raw skin production from sheep and goats in Ethiopia has faced serious challenges as a result of skin diseases caused by external parasites (Bisrat, 2013). Ectoparasites such as mites, ticks, lice and fleas affect large numbers of sheep and goats in Ethiopia causing a wide range of health problems including mechanical tissue damage, and predispose to myiasis and dermatophilosis. Infestations increase susceptibility to other diseases and create sites for secondary invasion by pathogenic organisms and reduced productivity (Mersha et al., 2010). They have the ability to parasitize wide range of hosts (Sumbria et al., 2016). Though mites are active in keratin layer and causes direct damage to skin, also cause indirect economic loss by decreasing/ceasing reproduction and production performance (Soulsby, 1982).

Mange has been reported as one of the most prevalent and widely distributed skin disease in Ethiopia by degrading skin quality (Yacob, 2013). In Amhara Region mange has been the great threat for the production of small ruminants (Demissie et al., 2000). Despite national and regional efforts and emphasis given to the control programs against parasitic skin diseases, reports have shown that the problem seems to be still alarming (Seid et al., 2014; Yacob, 2014; Bedada et al., 2015).

This study was conducted to isolate and identify mange species and estimate their prevalence and assess their control practices by small ruminant owners in different agro-climatic conditions in the study area.

MATERIALS AND METHODS

Description of study area

This study was carried out in three selected districts (Gazgibla, Sekota and Ziquala) of Wag-Himra administrative zone, Amhara Regional State from November 2016 to April 2017. The districts represent three agro-ecological conditions; highland, midland and lowland, respectively. WagHimra zone is located between 12°C 23' and 13°C 16' north longitudes and 38°C 44' and 39°C 21' east latitudes, in the eastern part of the country. The annual rainfall, which is erratic in distribution, varies between 350 and 650 mm (CSA, 2013).

Study animals

The animals were indigenous breeds of sheep and goats kept in small flocks and managed under extensive farming system in different agro-climates. The sampled sheep and goats were stratified by sex, age and body condition. Animals aged up to one year were classified as young stock while those above two years were categorized as adults (Gatenby, 1991; Steele, 1996).

Study design and sample size determination

A cross-sectional study design was used. Semi-structured questionnaires were used to gather information on the level of awareness of sheep and goat owners about mange and its control practices. Purposive sampling techniques were used to select study districts based on their agro-ecology. In each study site, the farmers were randomly selected from a list prepared from the previous extension activities by the veterinary office. The sample size for the study was determined as described by Thrusfield (2005). Descriptive statistics (percentage, frequency distribution and correlation analysis) were used to determine the prevalence and associated risk factors.

Sample collection and examination

Skin scrapings were collected only from sheep and goats suspected for having clinical sign of mange encountered during field visits. Both superficial and deep skin scrapings were made to diagnose both burrowing and non-burrowing mites.

This was made by clipping the hair around affected areas with scissors, scraping the edges of the lesion with the scalpel blades until capillary blood was evident. The samples were collected in sterile plastic bottles containing 70% alcohol and taken to the parasitology laboratory of College of Veterinary Medicine and Animal Sciences, University of Gondar for proceeding diagnosis. Multiple sites were scrapped to increase the likelihood of mange mites' detection. The scraped material was then treated with 10% KOH solution in the test tubes and centrifuged at 1500 rpm for 5 min (Gupta and Singla 2012). The supernatant was discarded and the sediment was examined under a compound microscope using X10 and X40 magnification. Morpho-anatomical diagnosis keys provided by Soulsby (1982) and Pangui (1994) were used to identify the scabies agents.

Questionnaire survey

Semi-structured questionnaire format were prepared and used to collect information about the general attitude of the individual sheep and goat owners and to assess preventive and control practices against mange and evaluate risk factors on the occurrence of the disease. A total of 153 sheep and goat owners were selected. The information was collected by interviewing randomly selectedsheep and goats owners. The important points included in questionnaire survey were purpose of keeping animals, species of animals (sheep, goats) affected by mange, affected age group (young, adults), seasonality of the disease (wet, dry), effect of the disease on live animals and skin sale and control practices (modern, traditional).

Statistical analysis

Raw data was carefully recorded and stored in Microsoft Excel database system used for data management. Data were analysed using the SPSS for windows, version17.0.Descriptive statistics, percentages and 95% confidence intervals were used to summarize the proportion of infested and non-infested animals. The effects of different environmental and host risk factors were analyzed by using logistic regression and Chi-square test. Statistical significance was set at $p \leq 0.05$.

RESULTS

Questionnaire survey

The result of the questionnaire survey indicated that all

Table 1. Questionnaire survey results.

Focal point	Frequency (n)	Response (%)
Purpose of farming		
For income generation	128	83.66
For home meat and milk consumption	25	16.33
Affected species		
Goat	130	84.9
Sheep	23	15.03
Age group of animals affected		
Adult	123	80.39
Young	30	19.6
Seasonality of mange mites		
Dry season	131	85.62
Wet season	22	14.37
Effects of mange on sale		
Live animal	109	71.2
Skin	44	28.75
External parasite causing skin disease		
Mange mites	136	88.88
Lice	17	11.11
Way of treatment		
Modern	132	86.27
Traditional	21	13.72
Participation of farmers in the control practice		
Yes	149	97.38
No	4	2.61

respondents (153, 100%), practice keeping sheep and goats in the study area. The farmers in those study area keep their animals with the objectives of income generation (85.66%) and home meat and milk consumption (16.33%).

From interviewed respondents, 71.2% replied that mange mite infection had great enforcements to sale their live animals and skins. Concerning the treatment of mange mites, 86.27% of the respondents indicated that mange is more commonly treated using modern acaricides while 13.72% use traditional treatments (ethno-medicines) as well (Table 1).

In addition, 88.8% respondents explained that among external parasites, mange mites and lice infestation are the dominant ones that cause skin diseases and goats are highly affected (84.9%) than sheep's (15.03) by mange mites. Concerning the age groups, 80.39% of the respondents replied that adults are more affected than young animals. In relation to seasonal variation of mange occurrence, 85.62% of the respondents agreed that the infestation is highly aggravated during the dry or after the rainy season, whereas 14.3% of the respondents replied that mange is a problem during the wet season (Table 1).

Species and characteristics of lesion of mange

In the present study, the only isolated mange mite species affecting both sheep and goats was *S. scabiei*. In sheep and goats, *S. scabiei*a affected only the non-woolly areas of the body and lesions were observed mostly around the head, face and ear areas and nodule formation was the characteristics of lesions (Figure 1, A, B, C). The lesions were characterized by loss of hair,

Figure 1. Sheep (A) and Goat (B, C) infested with sarcoptic mange.

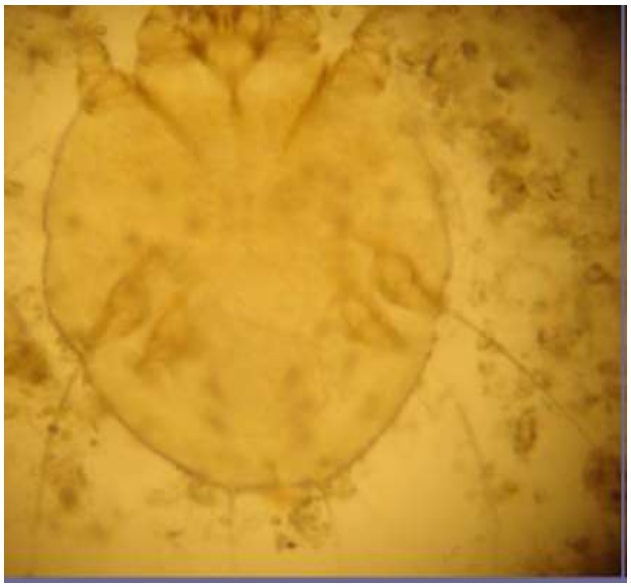

Figure 2. Ventral view of *Sarcoptes* mites.

ragged wool and crust formations and cracking and wrinkling of the skin.

Prevalence of *S. scabiei*

Out of 384 animals (120 sheep and 264 goats) examined, 105 (27. 33%) were found to be infested with *S. scabiei* (Figure 2). Of these, 65 (24.60%) were goats and 40 (33.33%) were sheep. The difference in the prevalence between the two host species was not statistically significant (X^2=3.1519, p=0.076 (Table 2).

In this study, both male and female sheep and goats were infested with *Sarcoptes* mange with an overall prevalence of female and male sheep as 32.55 and 35.29%, respectively while the prevalence in female and male goats was 22.39 and 30.55%, respectively without a statistical difference in prevalence between sex categories in both host species (Table 2).

The overall prevalence of *S.* scabiei in young and adult sheep was 34.28 and 32.94%, respectively (Table 3). The overall prevalence of *Sarcoptes* mite in young and adult goats was 30.43 and 22.5%, respectively. However, there was no statistically significant deference (p>0.05) between the prevalence of age groups in both host species (Table 2).

An overall prevalence of 32.5 and 33.75% *Sarcoptes* mites infestation in sheep and 28.8% and 22.15% in goats was recorded in animals with good and poor body conditions, respectively without any statistical significant difference (p > 0.05) (Table 2).

The prevalence of *S. scabiei* in highland, midland and

Table 2. Prevalence of *Sarcoptes* spp. in sheep and goat based on different risk factors.

Risk factor	Number examined	Prevalence (%)	95%CI	x^2(P-value)
Species				
Sheep	120	40(33.3)	0.24-0.41	
Goat	264	65(24.6)	0.19-0.29	3.1519(0.076)
Female	278	71(25.5)	0.20-0.30	
Male	106	34(32.0)	0.23-0.40	1.6501(0.199)
Age				
Adult	280	72(25.7)	0.20-0.30	
Young	104	33(31.7)	0.22-0.40	1.3817(0.240)
Body condition				
Poor	247	64(25.9)		0.20-0.31
Good	137	41(29.9)	0.22-0.37	0.7154(0.398)
Agro-ecology				
Lowland	130	26(20)		0.13-0.26
Midland	172	46(26.7)	0.20-0.33	
Highland	82	33(40.2)	0.29-0.50	10.4280(0.005)
Overall	384	105(27.33)		

Table 3. Prevalence of *Sarcoptes* spp. in sheep and goats in the three agro-ecological zones.

Goat			Sheep			x^2(p-value)
Lowland	**Midland**	**Highland**	**Lowland**	**Midland**	**Highland**	
n=111	n=121	n=32	n=19	n=51	n=50	
Sarcoptes	22(19.8)	32(26.4)	11(34.4)	4(21.0)	22(44)	10.4288(0.005)

lowland was 44.0, 27.4 and 21.0% in sheep and 34.3, 26.4 and 19.8% in goats, respectively. The prevalence of *Sarcoptes* spp. in highland, midland and lowland was 44.0, 27.4 and 21.5 % in sheep and 34.3, 26.4 and 19.8 % in goats, respectively. The overall prevalence of *S. scabiei* infestation significantly varied (X^2=10.4288, P=0.005) among the three agroecological zones/ districts (Table 2).

Factors affecting the prevalence of *S. scabiei*

Univariable logistic regression analysis indicated that, agro-ecological variations were the only factors that showed a significant (p<0.031) association in the prevalence of *S. scabiei* infestation between the study populations. A significant association (p<0.031) between *S. scabie* infestation and agro-ecology was observed in which sheep and goats reared in highland areas were1.46 times at risk for sarcoptic mange than those reared in midland and sheep and goats reared in midland were 0.547 times less likely to be affected than those reared in lowland.

DISCUSSION

In the present study, the only isolated mange mite species affecting both sheep and goats was *S. scabiei* with an overall prevalence of 27.33%. This species was also identified in different agro-ecological areas in Ethiopia (Mulugeta et al., 2010; Fekadu et al., 2013). This value was higher than the prevalence reported by Sertse and Wossene (2007) in Amhara Regional State, and by Beyecha et al. (2014) in central Oromia. The possible explanation for these differences in prevalence among different works could be variations in environmental and host factors, study seasons, control practices and management systems.

In this study, sex was not associated with prevalence of

S. scabiei which was in agreement with the work of Sheferaw et al. (2010) and Enquebaher and Etsay (2010). However, the prevalence was slightly higher in male than female goats in this study. This may be due to frequent contact of male goats at the time of mating and fighting.

The higher prevalence was observed in young animals than adult ones in the present study. This result agreed with the findings of Kasaye and Kebede (2010) and Shiferaw et al. (2010) who reported higher prevalence of *S. scabiei* in young animals than the old age group. It might be related to the degree of movement and frequent contacts of young animals with other flocks. Furthermore, age was reported to have no significant effect on the prevalence of mange mites (Yacob et al., 2008). Mange mite infestation is described to be independent of age and sex (Soulsby, 1982). Therefore, sex and age of the host animals are not contributing factors for the differences in the prevalence of mange in the study area.

In the current study, the highest level of prevalence was observed in animals with good body condition compared to the prevalence in poor body condition. This result disagreed with the findings of Sretse and Wossene (2007a) who reported that poor body conditioned goats were 4.3 times at risk for sarcoptic mange than good body conditioned goats with the explanation that poorly nourished animals appear to be less competent in getting rid of infestation as compared to that of well-managed animals (Sertse and Wossene, 2007).

In the present study, the highest prevalence of *S. scabiei* in goats was observed in highland (40.24%) area than midland (24.74) and lowland (20%) area. This finding disagreed with previous reports of Beyecha et al. (2014). This might be associated with difference in animal population which causes favorable condition for the transmission of mites between animals (Sertse and Wossene, 2007). Therefore, incidence of mange mite is higher in wet, cold areas which are optimum for reproduction, multiplication and mite development favoring its infestation (Olubumni et al., 1995*).*

Agro-ecological variations was a factor that yielded significant ($p<0.0.31$) association to the prevalence of *S. scabiei* infestation among the study population. Goats found in highland areas were 1.46 times at risk of acquiring *S. scabiei* infestation than midland areas. This finding disagreed with those reports by Pangui (1994). The high prevalence of the *S. scabiei* in the highland may be associated with the ideal micro climate environment in these areas which favors the breeding and multiplication of mange mite eggs to their developmental stages (Pangui, 1994).

The result of the questionnaire survey indicated that all respondents (100%) keep sheep and goats in the study area. The farmers in those study area keep their animals with the objectives of income generation and home meat and milk consumption (85.66%). The majority of interviewed respondents (71.2%) replied that mange mite infestation had great enforcements to sale their live sheep and goats and skins.

From the present study, it is possible to conclude that *Sarcoptesscabiei* is prevalent in sheep and goats in the study area which underlines the need of effective control measures.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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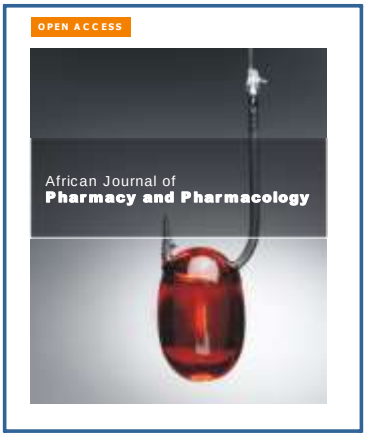

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