

**Small ruminants' diseases and genetic disease resistance in
Africa: A review**

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Draft report on
Small ruminants' diseases and genetic disease resistance in
Africa: A review

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ACRONYMS

ADG	Average Daily Gain
AJOL	African Journal On Line
BCS	Body Condition Score
CCPP	Contagious Caprine Pleuropneumonia
EPW	Egg Per Worm
FAMACHA	FAffa MAlan CHArt,
FAO	Food and Agricultural Organization
FEC	Fecal Egg Count
ICARDA	International Centre for Agriculture in Dry Areas
IFN- γ	Interferon Gamma
ILRI	International Livestock Research Institute
GIN	Gastro Intestinal Nematodes
GIT	Gastro Intetestinal Tract
GWAS	Genome Wide Association Studies
LWT	Live Weight
OIE	Office International Des Epizootics
MHC	Major Histocompatibility Complex
MOT	Malignant Ovine Thleriosis
PCR	Polymerase Chain Reaction
PCV	Packed Cell Volume
QTL	Quantitative Trait Loci
PPR	Peste des Petits Ruminants
RVF	Rift Valley Fever
SEA	Small East African
SAMM	South African Mutton Merino
SNP	Single Nucleotide Polymorphism
TBD	Tick Borne Diseases

WAD	West African Dwarf
WB	Worm Burden
WGS	Whole Genome Sequence
WHO	World health Organization

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EXECUTIVE SUMMARY

This review was initiated by ICARDA to collect and summarize the available research evidences on small ruminant disease and their impact, diseases resistant traits among sheep and goat, and the extent of selective breeding for traits identified in Africa,. To this end, a guideline for literature selection and spread sheet template for data extraction was developed by the principal author. The guideline was a milestone to retrieve articles from online sources and assesse the standard of the manuscripts. Likewise, the template was meant to help identify specific qualitative and quantitative data and maintain uniformity in course of double entry data extraction. Both the guideline and the data extraction template were commented and enriched by subject matter experts in the review team before use. Once such platform was in place, the review proper commenced with electronic search for published articles from online sources written in English language. Google scholar and Yahoo search engines were used to retrieve manuscripts from scientific databases including Medline, Web of science, Sicinedirect, AJOL, and CabDirect. Altogether, over 660 published manuscripts were retrieved from 42 African countries. Five hundred eighty six of them were on parasitic and infectious diseases occurrence, their management and impact. The remaining 74 articles contained 89 studies on diseases resistance profile in small ruminants both within and between breeds. To be clear, this review may not be exhaustive; however, it is exploratory and indicative of the study status in the continent. Much of the reports retrieved were from east Africa mainly, Kenya, Ethiopia, Uganda, Sudan, and Tanzania followed by West African countries i.e. Nigeria, Togo, Burkina Faso, Ghana, Cameron and the Gambia. The next highest report was obtained from South Africa, Zimbabwe, Mozambique, Madagascar and few North African countries including Egypt, Tunisia, Morocco and Algeria. Reports from Central and south West Africa were very much limited. Quantitative and qualitative summary were made based on the nature of the data and the findings were eventually organized under four major headings. The first part is about the type and origin of retrived articles, second on the magnitude and distribution of diseases, followed by diseases impact and the last part is on genetic studies for diseases resistance traits in small ruminants and possibility for selective breeding.

Accordingly, over 15 parasitic diseases were reported from 37 countries. Categorically, the diseases reported belong to gastrointestinal nematodes (GINs), flukes, lung worms, haemoparasites, myiasis, tick infestation, mangemites and intestinal protozoans. In the nematode category, *Haemonchus contortus* was the most widely distributed GIT parasite and highly pathogenic agent reported from all the countries where the report came from. *Haemonchus contortus* along with other GINs were found responsible for serious health problems in small ruminants of the continent. The other important parasitic diseases documented were trypanosomosis followed by tick-borne diseases and skin diseases due to mangemites. In the infectious diseases category about 11 bacterial and viral diseases were reported; diseases like pest des petits ruminans (PPR), Contagious Caprine Pleuropneumonia (CCPP), Sheep and Goat pox, hemorrhagic septicemia, leptospirosis, Maedi-visina, rift valley fever, bluetongue, brucellosis and contagious-ecthyma were among important diseases noted. Nevertheless, PPR and CCPP were considered to be the leading cause of morbidity and mortality in small ruminants in the continent.

In terms of economic impact, the evidences available on financial losses associated with specific diseases were limited and where available they were given in local currencies. In fact, in countries like Zimbabwe, Nigeria and Ethiopia financial estimates in hard currency have been captured for few parasitic diseases. In this connection Zimbabwe lost 5.6 million dollars in 10 years' time due to coudieriosis alone in small ruminants. For Ethiopia, a loss of 250,000 tons of fresh meat has been documented from seven million helminth-infected sheep slaughtered annually. Likewise in Nigeria, liver fluke alone caused organ condemnation worth 77,900 dollar per annum. At a larger scale, small ruminant mortality up to 40% was estimated due to helminth in tropical Africa in the absence of treatment intervention. For CCPP the estimated mortality was 50 % in Tanzania and as high as 65% in Eritrea due to seasonal outbreaks. Likewise, for PPR mortality of 49 % in sheep and 64.4% in goats were reported in Nigeria. In Gabon, the case fatality of PPR was observed to reach as high as 98%. From this, one can easily speculate how much impact PPR alone inflicts as it is one of the preponderance viral diseases reported from east to western corner of the continent. Apart from specific diseases impact due to morbidity, mortality, reproductive inefficiency, or any other, the presence of these and other trans-boundary diseases like Rift Valley fever, sheep and goat pox have limited the export of live

animals and meat to markets in the west due to sanitary and phytosanitary restrictions. Condemnations of whole or part of carcasses and edible organs due to some of the disease causing agents residing in apparently healthy animals presented for slaughter have also been shown to incur huge financial losses to many abattoirs. Likewise, pathogens such as mange, ticks and other micro-predators inflict serious damage on the skin causing considerable financial loss to the leather industry. In this regard the available evidence in Ethiopia indicated a damage as high as 35% to sheep skin and 56% to goat skin every year. The other impact noted in this review is the presence of multiple drug resistance reported for antitripanocidal drugs, antihelmintics, antibiotics and occasionally to acaricides. Twelve countries have reported the presence of resistance to one or more drugs or chemicals used in animal health interventions. Pertinaciously, residue in the small ruminants product, nothing much could be retrieved.

The third chapter of this report is about studies on resistance of small ruminants to diseases and identifying the source of variation both within and between breeds that may be exploited for selective breeding. In this regard, of the 54 African countries studies on small ruminants' resistance to various diseases were obtained from only 12 countries. Much of these reports were again from eastern part of the continent followed by West and southern Africa. The studies employed various approach including, natural observation, clinical control trial and fully experimental approach. Despite the presence of several parasitic and infectious diseases in Africa, studies on selection for genetic resistance in small ruminants mainly focused on three diseases. These are gastro intestinal nematodes (mainly *H. contortus*), trypanosomosis and tick infestation along with few tick-borne diseases. In 73% of the studies, phenotypic traits such as, fecal egg count (FEC), packed cell volume (PCV), worm burden (WB), parasitemia, body condition score (BSC), degree of infestation, and immunological responses were used as proxy-indicator for resistance traits. In the remaining 27% of the studies, the approaches were quantitative genomics and techniques that include quantitative trait loci (QTL), Genome wide association studies (GWAS) and whole-genome sequencing. In both phenotypic and genomic approaches, the heritability reported for resistant traits were low to moderate level. This fact has been substantiated by polygenic nature of the diseases resistance traits in small ruminants.

Among the 19 pure sheep breeds and their crosses investigated in 61% of the studies, nine of them were reported to have resistance traits for one or the other type of diseases. Red Maasai sheep from Kenya, and Djallonke from West Africa were the two sheep breeds for which multiple reports were obtained about their resistance for both GIN and trypanosomosis. Sabi sheep from Zimbabwe was resistant for GIN as well. Namaqua Africaner from South Africa, queue fine de l'Quest and Barbarine from Tunisia were breeds reported to have resistance for ticks and some tick-borne diseases. The Ethiopian Horro and Sudanese Garag and watesh sheep breeds were noted for moderate resistance to fasciolosis and malignant ovine theileriosis, respectively. Pertinent to goat, the number of breeds compared was the same, however, evidence of resistant traits were reported in 6 of them. The small east African Goat from Kenya, Uganda and Tanzania, the West African dwarf goat in countries of West Africa, the Red Sokoto from Nigeria, Xhosa and Nuguni from South Africa and Mubende goat breeds from Uganda were noted to have resistance for GIN. For Trypanosomosis, the West African dwarf goats from Nigeria and Small east African goats from Kenya were reported to have resistance/tolerance profile over the comparison breeds. Xhosa goats were the only goat breed reported to have resistance for tick infestations. When resistance to diseases is compared within each breed in 35% of the studies, most of the resistant sheep and goat breeds reported were noted to have individual variations on resistance profile that can be exploited to develop nucleus elite flocks via selective breeding. The remaining 3 % of the studies compared the difference between species, i.e. Djallonke Sheep verses WAD Goats. The available evidence on diseases resistance traits selective breeding was limited to H. contortus in single farm from South Africa on Dhone Merino flock.

The last part of this report summarized conclusive remarks on the findings of each topic and suggested the way forward accordingly. The conclusion is that small ruminant production in Africa is constantly challenged by plethora of diseases affecting their welfare and seriously undermining the economic return expected from the sector due to mortality, reduced production and trade bans. This is further aggravated by poor management, inadequate focus on small ruminants as important driver of the rural economy and food security; consequently exposing the sector to huge financial losses. Therefore, the need for capacity building on animal health and genetic disease resistance traits research, the importance of strengthening small ruminants' disease survey and surveillance in all African countries, developing locally adapted strategy for

disease control, the need for expanding and strengthening research on genetic markers of diseases resistance traits among indigenous small ruminant breeds and integrating this functional traits in breeding programs and developing comprehensive breeding policy before any breeding intervention on indigenous small ruminant breeds and many other key areas were proposed for future intervention.

1. INTRODUCTION

The ever increasing number of global population demanded an equally dynamic livestock sector to meet the increasing demand of livestock products. Selective breeding in livestock, as a way out to address this issue, has brought about great genetic gains in milk and meat production (Shrestha and Fahmy, 2007; Gipson, 2019). The success of such breeding business has been linked to a number of factors including high accuracy of breeding value estimation, moderate to high heritability of production traits and the integral use of production records of many animals and their genetic relationships (Rauw *et al.*, 1998). Over the years, the utility of biometrics and advanced genomic techniques in breeding have enlightened the understanding of livestock breeding including small ruminant and transformed the sector enormously (Gipson, 2019). Thus, breeders of our time are at a better position to deal with genome mapping and functional genomics that help identifying quantitative trait loci (QTL) and specific genes affecting several nonfunctional traits in small ruminants and other livestock species (Marletta *et al.*, 2007; Gipson, 2019).

Despite such advance in genomics of production traits and improvement in various livestock species, innate disease resistance ability has been noted to decline with intensive selection (Rauw and Gomez-Raya, 2015). Technically, the phenomenon has been linked to the unfavorable genetic relationship between production and functional traits (reproductive performance, disease resistance and meat quality) (Oltenacu and Broom, 2010) leading to compromised animal robustness due to trade-offs between performance and fitness functions. The decline in robustness and poor welfare condition due to selection for high production had also been linked to lack of adequate nutritional resource for coping up (Rauw *et al.*, 1998). Consequent to such unfortunate experience, breeders have started incorporating functional traits in the routine breeding business since 1990 (Miglior *et al.*, 2005; Konig and May, 2018). Genetic improvement in functional traits including disease resistance and ability to resist environmental adverse conditions become element of selection and breeding (Miglior *et al.*, 2005; Barillet, 2007; Mrode *et al.*, 2018). Perhaps such approach could help in developing the future small ruminant's breeds that work

better for the developing world as they bash through infectious and vector-borne diseases pressure.

Diseases in general, and infectious and parasitic diseases in particular have been noted as one of the leading hurdles that have constrained the optimum utilization of small ruminant resource in Africa. Some of these diseases include, peste des petits ruminants (PPR), sheep and goat pox and contagious caprine pleuropneumonia (CCPP), which are highly infectious and contagious in nature (Jones *et al.*, 2016; Hamdi *et al.*, 2021; Ahaduzzaman, 2021). Vector-borne diseases such as trypanosomosis, Rift Valley Fever (RVF), blue tongue, as well as parasites (helminths and ectoparasites) are also among the constraints hindering the productivity of small ruminants (Kusiluka and Kambarage, 1996; Linthicum *et al.*, 2016; Gahn *et al.*, 2020; Kusiluka *et al.*, 1998, McDermott *et al.*, 2013). Other category of diseases with substantial impacts including brucellosis, Q-fever (coxiellosis), Maedi visna, contagious ecthyma (orf), leptospirosis, and pneumonia due to *Pasteurella multocida* and/or *Mannheimina hemolytica* cause serious problems in small ruminants productive and reproductive performance (Kusiluka and Kambarage, 1996).

Most diseases (e.g., PPR, CCPP, trypanosomosis, RVF, etc.) are characterized by very high morbidity and mortality and cause considerable economic losses. Diseases like RVF and brucellosis are zoonotic in nature and infect humans in addition to small ruminants (Dundon *et al.*, 2020; Ahaduzzaman, 2021; Linthicum *et al.*, 2016). Some of these infectious diseases (e.g., brucellosis, coxiellosis, leptospirosis) have characteristic impact on reproductive performance and resulting abortion, premature delivery, stillbirth and weak offspring leading to decrease in milk yield and kid crop (Kusiluka and Kambarage, 1996; McDermott *et al.*, 2013; Kardjadj *et al.*, 2016). Economic losses caused by the aforementioned and other diseases of sheep and goats raid at the core of vulnerable livelihoods as well as national and regional livestock production (Kosgey *et al.*, 2008). While both the direct and indirect impact of these diseases cause devastating cumulative annual economic losses to countries that experience the problems, the indirect effect is even more serious especially the trade ban due to the existence of these major transboundary diseases and other negative impacts on agriculture and other sectors (FAO, 2004). In market-oriented terms, the costs of disease are- estimated to range from 35% to 50% of the

turnover within the livestock sector in the developing world (Bishop, 2012). Probably, this marks disease as one of the leading hurdles in tropics that constrained both the actual and future potential of the livestock industry in limiting the use of improved breeds and their crosses (Kosegy, 2004). Albeit, research evidences regarding most of these diseases in small ruminants are not available, and good quality data that can be interpreted in strict epidemiological terms are rather scarce.

Technically animals get sick or die of disease. Consequently, drastic fall in production and/or loss of product quality is anticipated. To keep livelihood or the business alive, livestock keepers are forced to use a number of approaches to reduce such negative effect of diseases on livestock and their products. In this connection, the use of chemotherapy, vaccination, physical and chemical means for vector control and other biosecurity interventions are high on the list (FAO, 2007). Unfortunately, none of these have been found sufficient enough to prevent or control disease and its impact independently. Moreover, the growing uses of chemicals for therapy, chemoprophylaxis, growth promotion, and vector control, have gradually instigated the development of drug resistance and loss of efficacy. Hence the fight against diseases and or vectors is confronted with questionable future using the conventional approaches (Perry *et al* 2002; Kaplan *et al*, 2004; Van Boeckel *et al.*, 2015). Besides, the growing environmental concern and food safety issues are also alarming. Therefore, the delivery of standard animal health service thus far has been customized through combination of available means for the maximum possible effect.

In the third world, there is more concern in addition to the above factors, *i.e.* the question of affordability and accessibility of the conventional animal health services to poorer livestock keepers that heighten the case (Zvinorova *et al.*, 2016). For both political and economic reason in developing countries, the public sector handles the cases through subsidy and in some case full cost recovery for trans-boundary diseases like PPR and pox. However, as expenses are far too high and beyond the government capacity, the routine clinical services are left to the resource poor livestock keepers. Unfortunately, this opens up the door for a wide use of counterfeit veterinary products and keeps the available service far below the acceptable standard. These all factors accentuate disease and its management as a critical challenge of our time, and will remain

so, unless the scientific exploration pushes the boundaries of the existing knowledge beyond its current horizon. The livestock business therefore demands additional measures that somehow complement or supplement the gap stated and provide reflection to both environment and consumer concerns. Indeed, strategies based on multiple approaches have inherently proved resilience and relative stability (Bishop, 2012).

Albeit lack of sufficient information on genetic architecture of disease resistance traits (Kemper *et al.*, 2011), the effect of host genetic variation on disease resistance has now been recognized for many diseases, in all major domestic livestock species including small ruminants (Bishop and Morris, 2007; Jovanovic *et al.*, 2009). Many breeders and animal health experts believe that, the genetic approach has potential to supplement/complement the conventional approaches. Individuals vary in their susceptibility to disease and farmers and breeders can exploit this genetic variation to identify and use animals that are relatively resistant to diseases. There are a number of advantages in using resistant stock including increased production, improved animal welfare, and reduced environmental contamination by veterinary products (Hu *et al.*, 2020).

In this connection, Karrow *et al.* (2014) emphasized the importance of variation in phenotype and corresponding genotype, for enhanced genetic selection to establish helminth resistant breeds. The maintenance of genetic heterogeneity has also been documented as genetic advantages for thriving in a disease endemic area (Jovanović *et al.*, 2009). This underlines genetic diversity as fundamental resource to meet the growing need for resistant breed development through selective breeding (Springbett *et al.*, 2003). In fact, the rate of genetic gain for trait of interest in selective breeding is governed by the accuracy of the selection criteria, the intensity of selection, and the generation interval in addition to genetic variability within and between populations (FAO, 2007). Yet, the bottom line is the amount of genetic diversity; if such diverse genetic resources is not maintained or lost due to selection or any other intervention, potentially important traits of combating disease could be lost (Springbett *et al.*, 2003). According to Bishop (2012), the existence of extensive genetic variation in resistance, both within and between breeds has enabled selective breeding engagement. The breeding schemes were empirically initiated with the choice of appropriate breeds adapted to the local

environmental conditions, followed by phenotypic selection for resistance. This fact heightens the interest for indigenous breeds as a large repository of genetic diversity in developing world (Baker, 1995; Devendra, 2002). Therefore, it is worth paying attention to this matter when breeding policy is instituted to any of endogenous livestock breeds.

As it has already been stated above, classical breeding in production animals did not have much attention to functional traits (Egger-Danner *et al.*, 2015). Breeds developed in the long-term selection for production traits were observed to suffer serious physiological and immunological imbalances (Rauw and Gomez-Raya, 2015). The negative side effects of intensive selection for aforesaid traits raised concern on animal welfare, ethical aspects, and medical management that leveraged the main arguments supporting for paradigm shift of classical breeding strategy (Konig and May, 2018). The other worth mentioning driving force is the marginal position livestock keepers in developing world have in using such improved breeds. Therefore, it is high time to balance between the need for more production and the physiological and immunological integrity of the animal. In addition, the growing environmental concern and public safety should also be reflected with pragmatic approaches that include selective breeding for both functional and non-functional traits.

Africa being the second largest home for small ruminant population in the world (Miller and Lu 2019), it is logical and reasonable to join the global efforts in contributing the future small ruminants breeds that can address the environmental, consumer, and ethical concerns. Besides, the poor small ruminant keepers of the continent need to benefit from the resource they have and alleviate the ever-increasing demand for food of animal origin through appropriate small ruminants' selective breeding venture. In this connection, the diverse small ruminants' breed Africa has is a potential genetic pool for presumed breeding business (Devendra, 2002). In order to come up with pragmatic plan that can help tapping the genetic resource for intended purpose, there is a need for understanding the current context in terms of research finding and level of practical engagement in breeding for diseases resistant traits. Therefore, this review is initiated to assess the available research evidence on disease occurrence and impact as well as genomic studies for disease resistant traits in small ruminants in Africa.

Objectives

- Overview the occurrence and impact of common parasitic and infectious diseases of small ruminants in Africa;
- Summarize the existing research evidences on phenotypic/genotypic diseases resistance traits in small ruminants and highlight the scope of studies in Africa;
- Explore the within and between breed differences for disease resistance traits based on the available research evidences;
- Identify the indigenous sheep and goat breeds reported to have disease resistance traits based on the available research evidences in the continent;
- Consolidate the evidence on the extent of small ruminants' selective breeding activities that targets for disease resistance traits in Africa.

2. METHODOLOGY

2.1. Review protocol

This review was organized based on the data and information acquired from online sources. To this end, a guideline and spreadsheet template was developed for systematic literature selection and acquisition of data or information from selected articles. The first guideline was used to retrieve articles and select the manuscripts of interest based on the standards of the manuscript, while the second was meant to extract data or information objectively from the available sources. The guidelines were commented and enriched by experts prior to use. Therefore, there were common understanding on what type of database to use and how retrieved manuscripts were assessed for intended purpose. Once the manuscript of interest was selected to meet the review objectives, data or information capturing was managed using predesigned template (excel sheet) that has been commented and enriched by all parties, *i.e.* consultant team and experts from ICARDA. The report was organized topic by topic to reflect the review questions based on the depth and width of the data/information acquired.

2.2. Literature search and manuscript assessment

Articles from reputable sources, *i.e.* journals, reports from international organizations like FAO, OIE, and WHO or higher learning institutes and research centers were retrieved. The databases used were CAB direct, AJOL, Medline, Sciencedirect and Web of Science. To this end, key strings related to the topic in question were used. The major ones were “sheep, goat, small ruminants, diseases, parasites, infectious, resistance, susceptibility, breed, phenotype, genotype, genomics, QTL, genetic marker, SNP, Africa”. Once an article was found, the preliminary scanning was made based on the title and abstract to figure out its relevance to the review question. The specific topics used for preliminary assessment were the species of concern, geographic context, topicality, and availability of relevant information that complies with objectives stated. When an article passes the preliminary screening, further scanning was made for quality assessment. In this regard, the inclusion criteria focused on the objective clarity, study design, sample size involved, technical assays, result presentation and other relevant

methodological issues were checked in line with respective paper objective. The qualifying manuscripts were categorized in to two broad categories. The first category was on disease occurrence and impact, while the second was on diseases resistance traits and selective breeding. For the first category, due to large number of manuscripts and redundancy, a maximum of 15 reports per diseases per country were used based on topicality (most recent, diversity of attributed risk factors considered, mortality, morbidity, or any other impact of diseases in line with review objectives). However, in countries where there has been limited sources (less than 5 articles per diseases), all the qualified available articles were used to generate the data of interest. Pertinent to the second category, disease resistance trait and selective breeding, all qualified sources as per the inclusion criteria were used to generate required data.

2.3. Data extraction, management and synthesis

For disease occurrence and related matters, variables considered were, authors, year of publication, DOI number, link, country, specific location, type of small ruminants, type of study design (cross-sectional, case control, longitudinal) for analytical aspect, and (case report, case serious and survey) for descriptive evidence, type of diseases (infectious and parasitic), etiology, antimicrobial profile, mode of transmission, nature of pathology, prevalence, potential impact, breed susceptibility profile, if any were extracted. For diseases resistance or sensitivity profile additional data, that include, type of study design (experimental challenge, natural infection), type of selection and breeding technique (with in /between breeds), traits used (phenotypic/genotypic) type of phenotypic traits measured (FEC, PCV, Post mortem parasitic recovery (worm burden, fecundity and worm size), total plasma protein, pepsinogen level, WBC differential count, somatic cell count, liver enzymes, live weight, growth rate, clinical condition including lameness) were recorded. The other aspect noted were mechanism of resistance (Immunoglobulins and Immuno-regulators (MHC, IFN- γ , or any other chemokines) and degree of infestation for external parasites. On genomic bases (polygenic, monogenic), type of genomic techniques used (Genome Wide Association Study (GWAS), QTL mapping), genetic markers used (microsatellite, SNP), number and type of chromosome involved, and type of gene or genes involved. All the entire process of article search, manuscript selection and data extraction were made independently by two individuals. However, in time of ambiguity and article selection due

to redundancy, a third party from the consultancy team involved to assist the decision process based on the reference given above. In the course of literature selection, review articles were used to trace the original manuscript for secondary data and capturing conclusive statement and synthesis. Eventually, the data analysis or synthesis were made either quantitatively (descriptive summery) or qualitatively (content synthesis) depending on their nature.

3. RESULTS AND DISCUSSIONS

3.1. Characteristics and distribution of identified research reports

In this review, about 660 published manuscripts were retrieved from online sources. Out of 54 African countries, data on one or the other aspect were obtained from 42 countries. The number of reports on parasitic diseases was 350 from 35 countries followed by 236 reports on infectious diseases from 37 countries and the remaining 74 articles were on genetic studies obtained from 12 countries. Due to content redundancy, 252 (72 %) articles on parasitic diseases, and the entire qualified articles on infectious diseases and genetic studies were used for this report. The reports were all published in reputable journals in a period from 1970 to 2021. Much of the information on diseases and its impact were primary data from observational studies, including cross-sectional, case control and longitudinal studies. Some of the manuscripts used were secondary data from outbreak reports, abattoir studies, and other industrial repositories. The genetic studies were largely clinical control trials, followed by natural observation and some fully experimental studies (Table 1).

Accordingly, for parasitic diseases most of the studies originated from Eastern and Western Africa followed by Southern and countries of Northern Africa. Sources for infectious diseases and genetic studies follow the same pattern for eastern part of the continent, however, variability noted regarding other regions (Figure 1).

Table 1. Types of studies and their approaches summarized in small ruminants diseases and resistance in Africa

Types of studies	Number
Cross-sectional field surveys	284
Cross-sectional abattoir study	81
Longitudinal studies	52
Clinical Control trials	34
Experimental studies	28
Outbreak reports	11
Drug efficacy study and residue	32
Disease impact assessment	21
Reviews	19

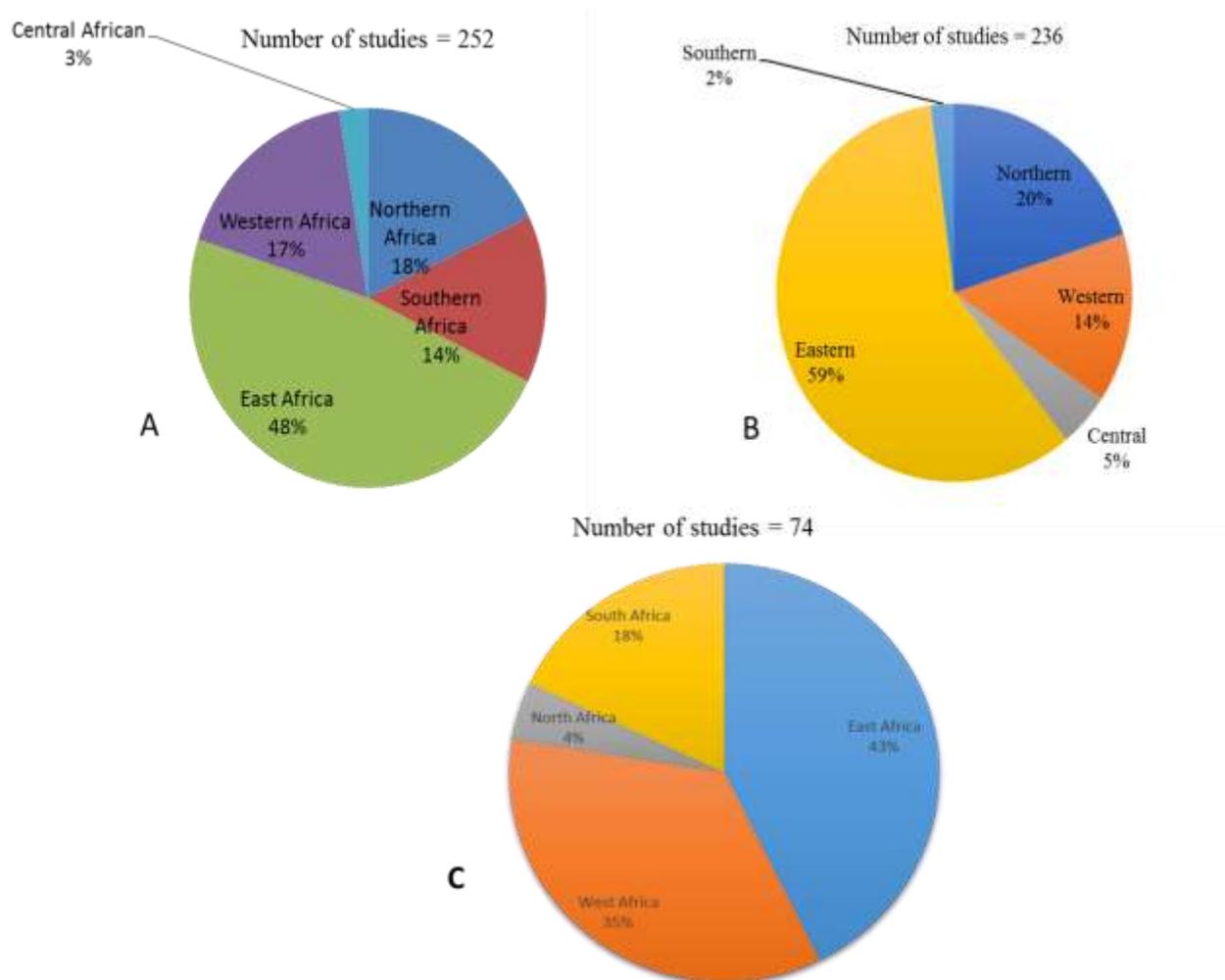


Figure 1. Distribution and proportion of research reports retrieved on parasitic diseases (A), infectious diseases (B) and genetic studies (C) of small ruminants in Africa

3.2. Diseases reported, and pattern of occurrence in Africa

3.2.1. Parasitic diseases

Parasitism is of prime importance in many countries and still a serious threat to the livestock industry in Africa. Parasites of small ruminants fall under three main groups, namely, helminthes, protozoa and arthropods. The output of literature search in this study on works related to parasites affecting small ruminants in Africa revealed that 61%, 20% and 19% of them focused on helminthes, protozoa including vector-borne diseases and others such as arthropods. Gastrointestinal helminth infections are recognized as a major constraint to livestock production

throughout the tropics and elsewhere. Other helminth parasites such as lungworms also play a significant role in causing ill thrift (Asmare *et al.*, 2018) and mortality in severe case. Similarly, protozoan parasites such as trypanosomes and piroplasms (*Babesia*, *Theileria*, etc) constitute among the debilitating and often fatal parasitic problems (Osaer *et al.*, 1999, Ng'ayo *et al.*, 2005). Arthropods such as ticks, mange mites and myiasis agents also cause loss of productivity and degrade hide and skin quality in ruminant hosts (Yasine *et al.*, 2015; Kumsa *et al.*, 2012; Kebede, 2013).

However, it should be noted that the prevalence and intensity of infections may vary significantly from place to place and among geographic regions of the continent. A meta-analysis by Asmare *et al* (2016b) on gastrointestinal infections in Ethiopia has brought to light the varying occurrence of different species of nematodes with pooled prevalence estimate in the random effect model of 75.8%. Absence of or very scant data on trematode and cestodes infections in Southern and Central African countries may suggest that these parasites are not as important in these regions as in other parts of Africa (Table 2).

Table 2. Summary of prevalence of parasitic infections reported in Africa (1970-2021). The lowest and the highest prevalence values were taken from all studies.

Region	Animal species	Helminth prevalence (%)			Protozoa + tick borne diseases	References
		Nematode	Trematode	Cestode		
Northern Africa	sheep	10-37	2-35	0.7-20	1.5-95	Akkari <i>et al.</i> , 2013; Ben Said <i>et al.</i> , 2015; , Elsify <i>et al.</i> , 2015; Haridy <i>et al.</i> , 1999; Hammami <i>et al.</i> , 2007; Khalafalla <i>et al.</i> , 2011; Mazyad & El-Nemr, 2002; Mazyad & Khalaf, 20002; Ouchene-Khalifi <i>et al.</i> , 2018; Pandey <i>et al.</i> , 1986; Saidi <i>et al.</i> , 2020; Sultan <i>et al.</i> , 2016; Tashani <i>et al.</i> , 2002
	goat	25-96	2.5-68	1.4-12	7.3-69	
Southern Africa	sheep	65-76	1.2.	1.9	13-85	Jansen <i>et al.</i> , 2020; Tsotetsi <i>et al.</i> , 2012; Chhabra & Pandey, 1992; Goma <i>et al.</i> , 2007; Mbatlana <i>et al.</i> , 2002; Matsepe <i>et al.</i> , 2021; Tagwireyi <i>et al.</i> , 2019
	goat	31-54	0.9	1-4.2	5-100	
Eastern Africa	sheep	40-92	6.6-43	1-68	0.8-93	Asmare <i>et al.</i> , 2018; Kumssa <i>et al.</i> , 2006; Ng'ang'a <i>et al.</i> , 2004; Bekele <i>et al.</i> , 1992; Mungube <i>et al.</i> , 2006; Bedada <i>et al.</i> , 2017 ; Terefe <i>et al.</i> , 2019; Sissay <i>et al.</i> , 2007; Kusiluka <i>et al.</i> , 1996; Sinshaw <i>et al.</i> , 2006
	goat	42-83	5.2-38	0-65	0.1-91	
Western Africa	sheep	43-94	12-39	58	1.4-70	Nwosu <i>et al.</i> , 2007; Karshima <i>et al.</i> , 2020; Owusu <i>et al.</i> , 2016; Odeniran <i>et al.</i> , 2021; Isah, 2019; Bell-Saky <i>et al.</i> , 2003; Tonouhewa <i>et al.</i> , 2019; Daniel <i>et al.</i> , 1994
	goat	56-67	2-35	53	5-53	

Central Africa	sheep	96	23-27	No ref.	19-62	Mbuh <i>et al.</i> , 2008; Takang <i>et al.</i> , 2019; Jean-Richard <i>et al.</i> , 2014; Awa <i>et al.</i> , 1997; Maganga <i>et al.</i> , 2020
	goat	86	12	No ref.	7.8-65	

3.2.1.1. Helminthosis

Gastrointestinal nematode infections continue to represent a major constraint on animal productivity throughout the world. The major diseases caused by helminthes in Africa which covered close to 2/3 of the 350 publications reviewed include: haemonchosis and other gastrointestinal nematode infections, lungworm infections, fasciolosis, hydatidosis and other cestode infections. Multiparasitism is a common phenomenon in sheep and goats (Zinsstag *et al.*, 1998; Asmare *et al.*, 2016b; Zouyed *et al.*, 2018; Khalafalla *et al.*, 2011) and hence, animals often harbor more than one type of parasites. Studies on helminthiasis caused by the gastrointestinal tract nematodes take the lion share (Haile *et al.*, 2018; Mhomga *et al.*, 2012; Gatongi *et al.*, 1998) of which reports on haemonchosis predominate (Figure 2) throughout Africa. Other helminth infections include fasciolosis among trematodes (Odeniran *et al.*, 2021; Eguale *et al.*, 2009; Haridy *et al.*, 1999) and hydatidosis and coenurosis among cestode (Ohiolei *et al.*, 2020; Miran *et al.*, 2015; Gebremariam *et al.*, 2014; Bart *et al.*, 2004) parasites of small ruminants. The few studies on lungworms come from East and North African nations (Asmare *et al.*, 2018; Regassa *et al.*, 2010; Berrag and Cabaret, 1996).

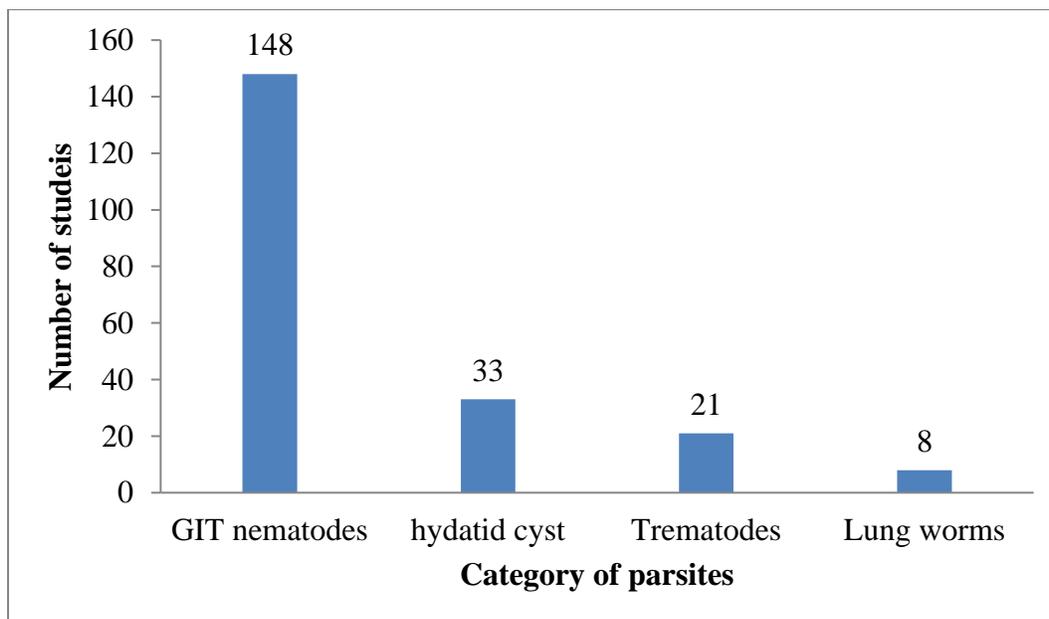


Figure 2. Summary of studies focusing on different groups of helminthes of small ruminants in Africa

3.2.1.2. Protozoan infections

Among the 105 studies retrieved on protozoan parasites of sheep and goats, the common protozoan diseases reported are trypanosomosis (35% of the studies), tick borne protozoan diseases (38% of the studies) and other studies constituting 27% of the reports. While most of them are evenly distributed throughout Africa (Table 2), reports on trypanosomosis come specifically from East, West and Central African countries. *Trypanosoma Congolese*, *T. viva* and *T. brucei brucei* are the most commonly reported species. Although the impact of the disease is known to be considerable (Wanyangu and Bain, 1994) different breeds of sheep and goats have been shown to vary in their susceptibility to the infection (Geerts *et al.*, 2009; Faye *et al.*, 2002; Goossens *et al.*, 1999; Bengaly *et al.*, 1993; Griffin and Allonby 1979) suggesting that there is a potential to include parasite resistance traits into sheep and goat breeding programs.

Anaplasmosis, Theileriosis, Eirlichiosis and Babesiosis are the dominantly reported tick borne diseases of small ruminants (Elsify *et al.*, 2015; Teshale *et al.*, 2016; Ringo *et al.*, 2018) whereas other protozoan infections such as intestinal coccidiosis, Cryptosporidiosis and Toxoplasmosis are in the list of frequently reported protozoan parasites (Kusiluka *et al.*, 1996; Gebremedhin *et al.*, 2014; Rouatbi *et al.*, 2019; Baroudi *et al.*, 2018) throughout Africa.

3.2.1.3. Arthropod infestation

The importance of arthropod parasites is explained by the fact that they cause ill health and degrade skin quality due to their bite (ticks, mites, lice, etc.) and their effect as myiasis agents (such as presence of larvae of *Oestrus ovis* fly in the nasal cavity). More importantly, it is explained by their role as vectors of several parasitic, bacterial and viral diseases. Among the 32 studies identified, 47% are from Eastern African countries. Asmare *et al* (2016a) reported a pooled prevalence estimate of 4.4% prevalence of mange mites in Ethiopia based on 18 cross-sectional studies carried out between 2003 and 2015. Similarly, Mulugeta *et al* (2010) in Ethiopia reported that up to 55% of sheep and 58% of goats were infested with ectoparasites including *Melophagus ovinus*, different species of ticks, *Damalinia ovis*, *Linognatus africanus* and *Ctenocephalides felis*. In Benin, prevalence of scabies in sheep and goats was reported to be 28.3% (Salifou *et al.*, 2013) while *Oestrus ovis* infestation was 35% in sheep and 19% in goats (Attindehou *et al.*, 2012). Ticks are also one of the most important ectoparasites encountered on sheep and goats (Asmare *et al.*, 2014). Elati *et al* (2018) in Tanzania registered 10.4% prevalence of ticks in sheep. Studies on ticks sometimes accompanied investigations on tick borne diseases

where highly pathogenic *Rickettsia*, *Theileria* and *Babesia* organisms were detected (Springer *et al.*, 2020). Parallel to the finding of several species of ticks, a pooled prevalence of babesiosis (3.7% in goats) and anaplasmosis (3.9% in sheep) was reported in a systemic review by Asmare *et al* (2017) on major vectors and vector-borne diseases in small ruminants in Ethiopia. In this review, molecular evidence on the presence of theileriosis in sheep (93%) and goats (1.9%) was recorded in Ethiopia.

3.2.2. Infectious diseases

This part of the review is organized based on the data acquired from 236 articles published in a period from 1974 to 2021. Data on bacterial diseases was generated from 44.9% (106 articles) and the remaining 55.1% (130) articles were used to generate data on viral diseases. The regional distribution of these studies on infectious diseases is given in the figure below (Figure 3).

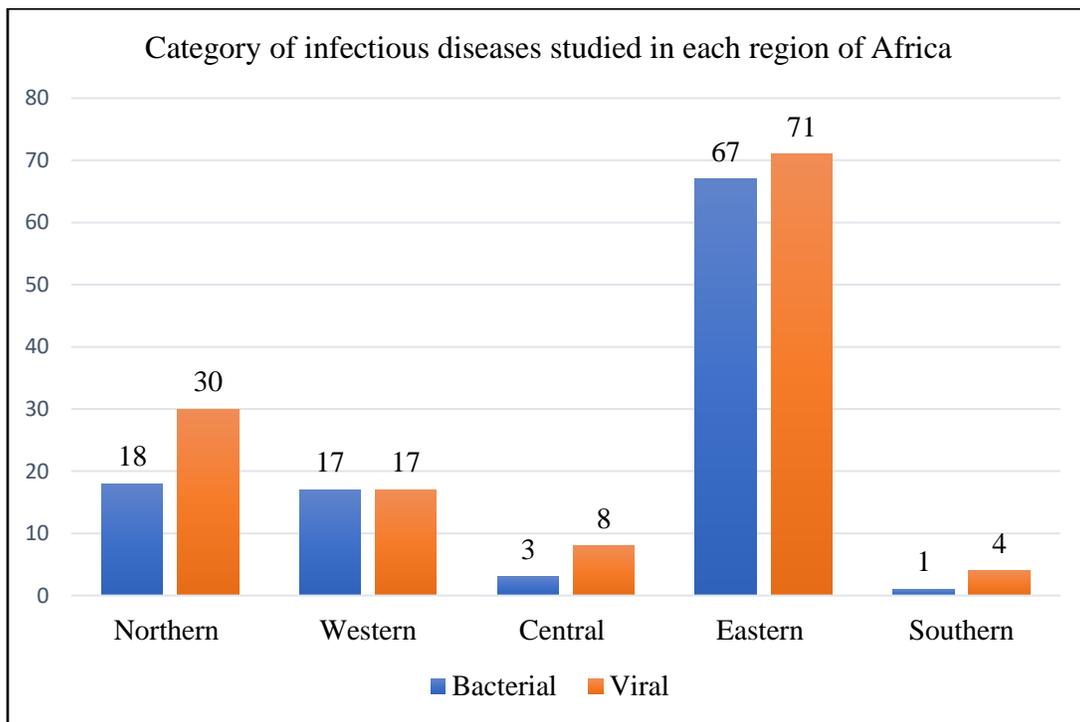


Figure 3. Category of infectious diseases of sheep and goats studied in each region of Africa (n=236)

Much of these studies (185 or 78.4%) involving infectious diseases affecting sheep and goats in Africa were carried out in a period from 2011-2020, while few were made earlier. As it is depicted on the figure above, the largest number of reports on bacterial and viral diseases was

obtained from east African countries. Among the 11 infectious diseases reported, relatively larger number of studies was captured on brucellosis, PPR, contagious caprine pleuropneumonia, rift valley fever, Q-fever and Maedi visna.

3.2.2.1. Bacterial diseases

Among the five bacterial diseases for which published evidences were retrieved, brucellosis (52 articles) was leading followed by contagious caprine pleuropneumonia with 29 articles (CCPP) (Figure 4).

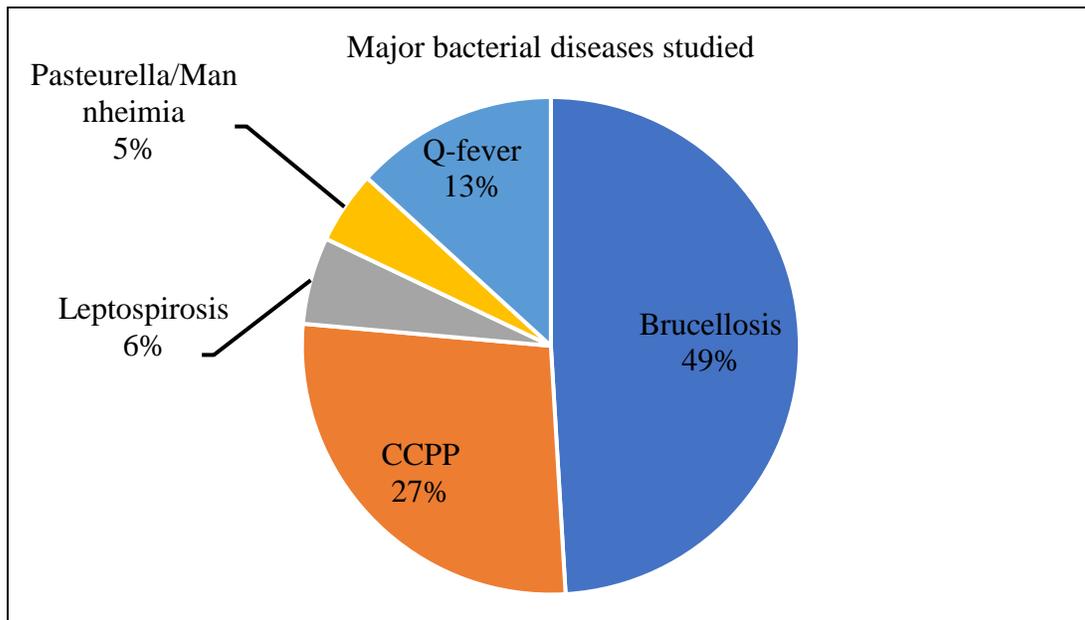


Figure 4. Major bacterial diseases of small ruminants studied in Africa from 1996-20 (n=106)

Brucellosis

Representative evidence on small ruminant brucellosis was retrieved from 18 African countries. The largest number of published evidence on brucellosis was obtained from Ethiopia followed by Egypt, Kenya, Nigeria, Uganda, Morocco, Tanzania and Libya reporting at least two. Most of these studies were serological, and used RBPT (43) as screening test with additional ELISA, CFT as confirmatory test. There were also studies reported based on ELISA alone (8) or with qPCR or Card test. In sheep, the highest prevalence was 24.0% reported from Libya followed by 20.7% from Egypt (Ahmed *et al.*, 2010; El Sherbini *et al.*, 2007), while the lowest results (i.e., lower than 1%) were recorded in 12 reports from 8 countries including Chad, Cote de Ivoire, Ethiopia, Morocco, Nigeria, Somaliland, Tanzania and Zambia. Likewise, studies in goats reveal

prevalence report as high as 33.4% in Libya (Ahmed *et al.*, 2010; Al-Griw *et al.*, 2017) and the lowest (*i.e.*, lower than 1%) results were reported in 12 studies from 9 countries (*i.e.*, Chad, Cote de Ivoire, Ethiopia, The Gambia, Morocco, Niger, Nigeria, Tanzania and Zambia) (Table 3). As these studies were conducted on different context, variability due to population type and methodological approach is anticipated in addition to the natural dynamics of the diseases itself. The critical gap is that sufficient evidence on circulating biotypes is lacking since studies on pathogen isolation and characterization are very scant. Yet, the evidence accrued is informative enough on the possible occurrence and likely distribution pattern of the diseases in the continent.

Table 3. Overview of Brucellosis reports in small ruminants from different African countries.

Country	Prevalence range (%)		Diagnostic tests	Other impacts	References
	Sheep	Goats			
Cameroon	8.04	1.1	RBPT, iELISA		Kamga <i>et al.</i> 2020
Chad	0	0	RBPT		Schelling <i>et al.</i> 2003
Côte d'Ivoire	0	0	RBPT, iELISA		Kanoute <i>et al.</i> 2017
Egypt	12.2 - 20.7	11.1 - 11.3	RBPT, iELISA; CFT; qPCR, SAT		El Sherbini <i>et al.</i> 2007; Abdelbaset <i>et al.</i> 2018; Wareth <i>et al.</i> 2015; Hegazy <i>et al.</i> 2011; Selim <i>et al.</i> 2019
Eritrea	1.4	3.8	RBPT, CFT		Omer <i>et al.</i> 2000
Ethiopia	0 - 6.7	0 - 14.4	RBPT, CFT, cELISA, iELISA	abortion reports from 6.5 to 12.4%	Ashenafi <i>et al.</i> 2007; Bekele <i>et al.</i> 2011; Edao <i>et al.</i> 2020; Ibrahim <i>et al.</i> 2021; Megersa <i>et al.</i> 2011; Asmare <i>et al.</i> 2013; Sintayehu <i>et al.</i> 2015; Teklue <i>et al.</i> , 2013; Molla & Delil, 2015; Teshale <i>et al.</i> , 2006; Mohamed & Eyob, 2019; Tegegn <i>et al.</i> 2016; Amenu <i>et al.</i> , 2010; Wubishet <i>et al.</i> , 2018; Kelkay <i>et al.</i> , 2017; Tesfaye <i>et al.</i> , 2020; Tsegay <i>et al.</i> , 2015; Megersa <i>et al.</i> 2012
The Gambia	3.69	0	RBPT, ELISA		Germeraad <i>et al.</i> , 2016
Ghana	3.3	10	RBPT		Jarikre <i>et al.</i> , 2015
Kenya	0 - 7.3	2.9-10.7	qPCR, iELISA, cELISA		Wainaina <i>et al.</i> 2020; Osoro <i>et al.</i> 2015; Kairu-Wanyoike <i>et al.</i> 2019
Libya	9.2-24	31-33.4	RBPT, iELISA		Al-Griw <i>et al.</i> , 2017; Ahmed <i>et al.</i> , 2010
Mali	4.6	3.1	RBPT, cELISA		Traore <i>et al.</i> , 2021
Morocco	0.2-13.4	0 - 13.2	RBPT; mRBPT		Azami <i>et al.</i> 2018; Benkirane <i>et al.</i> 2015
Niger	3.6	0.7	iELISA		Boukary <i>et al.</i> 2013
Nigeria	0 - 14.5	0.86 - 19.6	RBPT; SAT; cELISA		Brisibe <i>et al.</i> 1996; Aworh <i>et al.</i> 2017; Olufemi <i>et al.</i> 2018; Dogo <i>et al.</i> , 2016; Cadmus <i>et al.</i> , 2006; Bertu <i>et al.</i> , 2010; Agada <i>et al.</i> , 2018
Somaliland	0.5		RBPT		Hassan <i>et al.</i> , 2020
Tanzania		0 - 1.6	RBPT, cELISA		Assenga <i>et al.</i> 2015a; Shirima <i>et al.</i> 2016
Uganda	2.6	8.8 - 10	RBPT, Card test		Miller <i>et al.</i> 2015; Lolli <i>et al.</i> 2016; Kabagambe <i>et al.</i> 2001
Zambia	0	0	RBPT, cELISA		Muma <i>et al.</i> 2006

Contagious caprine pleuropneumonia (CCPP)

Next to brucellosis, CCPP was the second most frequently studied bacterial disease in Africa among the studies published the last two decades. Except one from Egypt, almost all reports on goats came from east African countries with sixteen from Ethiopia followed by Tanzania (five), Kenya (three) and one each from Eritrea, Mauritius, Somalia and Uganda. This suggests the importance of this disease in small ruminants of Eastern Africa. In sheep, only six studies (those from Egypt, Ethiopia, and Tanzania) reported results of antibody detection where the highest prevalence (52.1%) was detected using c-ELISA in 2007 in Tanzania. However, the prevalence had dropped to 35.5% in a study conducted for a second time in the same study population to determine a seroconversion to CCPP in 2009 (Mbyuzia *et al.*, 2014). In fact, the lowest prevalence of the diseases (4.2%) was also detected some years later in the same country (Chota *et al.*, 2019) which may imply control efforts are yielding their fruits. Three studies conducted in different sites of Tigray and Borana areas of Ethiopia using CFT or c-ELISA had recorded the prevalence in the range of 7.14-18.25% in sheep (Gelagay *et al.*, 2007; Hadush *et al.*, 2009; Teshome *et al.*, 2019), while the study from Egypt reported 5% using histopathology and molecular detection methods (Abd-Elrahman *et al.*, 2020).

In goats, a total of nineteen studies out of 29 reported results and revealed prevalence records greater than 10%. Despite an exceptionally high seroprevalence record of 87% reported in goats (Molla & Delil, 2015) from Dassenech district of South Omo Zone (Ethiopia), much of the reports were generally in the range of 13.2% to 48.3% in five African countries (i.e., Egypt, Ethiopia, Kenya, Tanzania and Uganda). In Ethiopia, prevalence records that range from 31.2% to 48.3 % were reported in different parts of the country in a period between 2009 and 2019 (Gizaw *et al.*, 2009; Hadush *et al.*, 2009, Sherif *et al.*, 2012; Teshome *et al.*, 2019). A prevalence as high as 47.2% in Kenya (Kipronoh *et al.* 2016) and 32.5% in Egypt (Abd-Elrahman *et al.* 2020) were also reported. On the other hand, prevalence that range from 0% to 8.5% were also reported in goats from the above three countries where the lowest (0%) was from Kenya (Wesonga *et al.* 2004) while the rest from Ethiopia (Abrhaley *et al.*, 2019; Yousuf *et al.* 2012) and Tanzania (Swai *et al.* 2013; Chota *et al.* 2019). There are also studies from Eritrea, Ethiopia, Kenya, Mauritius and Tanzania attempted to describe the impact in terms of morbidity and mortality associated with disease outbreaks. In the studies selected, various serological,

histopathological and molecular techniques were used as screening and/or confirmatory tests. More details can be found in table 4 below.

Table 4. CCPP reports in small ruminants from different African countries.

Country	Prevalence range (%)		Diagnostic tests	Other impacts	References
	Sheep	Goats			
Egypt	5	32.5	Molecular;	8% and 30% case fatality	Abd-Elrahman <i>et al.</i> 2020
Eritrea	NA	NA	histopathology LAT; CFT	90% morbidity;	Houshaymi <i>et al.</i> 2002
Ethiopia	7.14 - 8.25	4.92 - 87	CFT; cELISA	65% mortality	Eshetu <i>et al.</i> 2007; Mekuria & Asmare, 2010; Teshome <i>et al.</i> 2019; Mekuria <i>et al.</i> 2008; Gelagay <i>et al.</i> 2007; Hadush <i>et al.</i> 2009; Molla & Delil, 2015; Bekele <i>et al.</i> , 2011; Sharew <i>et al.</i> , 2005; Regassa <i>et al.</i> , 2010; Shiferaw <i>et al.</i> , 2006; Aklilu <i>et al.</i> 2015; Ahrhaley <i>et al.</i> , 2019; Gizaw <i>et al.</i> 2009; Yousuf <i>et al.</i> 2012; Sherif <i>et al.</i> 2012;
Kenya	NA	0 – 47.2	qPCR, cELISA		Renault <i>et al.</i> 2019; Wesonga <i>et al.</i> 2004; Kipronoh <i>et al.</i> 2016
Mauritius	NA	NA	LAT, immunoblotting	death of 300 goats linked to import from Kenya	Srivastava <i>et al.</i> , 2010
Somalia	NA	49	Capri-LAT		Abdi <i>et al.</i> 2020
Tanzania	4.2- 52.1	3.3- 36.7	Clinical;	Morbidity ≤ 90	Swai <i>et al.</i> 2013; Kusiluka <i>et al.</i> 2000; Msami <i>et al.</i> 2001; Chota <i>et al.</i> 2019;
			Pathological; cELISA	mortality ≤ 50%	Mbyuzia <i>et al.</i> 2014
Uganda		20.8	cELISA		Atim <i>et al.</i> , 2016

Coxiellosis (Q-fever)

Coxiellosis (Q-fever) was a third frequently reported disease caused by bacteria in small ruminants. The disease was reported from nine countries (Algeria, Chad, Egypt, Ethiopia, Gambia, Ghana, Kenya, Nigeria and Sudan). All the studies indicated results in both sheep and goats simultaneously except the study from Sudan whose result was in goats alone. Except the study from Nigeria (Elelu *et al.*, 2020) reporting lowest prevalence results of 3.85% in sheep and 3.16% in goats; all the remaining reports revealed prevalence exceeding 10% in both species. The highest prevalence records in sheep were detected from Egypt; 56.0% (Abbass *et al.*, 2020), followed by Ethiopia; 28.9% (Ibrahim *et al.*, 2021) and Ghana, 28.4% (Johnson *et al.*, 2019), while the remaining reports showed results in the range from 11% in Chad (Schelling *et al.*,

2003) to 25.68% in Egypt (Abushahba *et al.*, 2017). In goats, prevalence records were as high as 48.8% in Ethiopia (Ibrahim *et al.*, 2021; Tesfaye *et al.*, 2020) and 45.7% in Egypt (Abbass *et al.*, 2020) (Table 5).

Table 5. Q-fever (Coxiellosis) reports in small ruminants from different African countries.

Country	Prevalence range (%)		Diagnostic tests	References
	Sheep	Goats		
Algeria	14.1 (small ruminants)		iELISA, qPCR	Khaled <i>et al.</i> 2016
Chad	11	13	iELISA	Schelling <i>et al.</i> 2003
Egypt	22.7-56	12.5-45.7	iELISA, qPCR	Abushahba <i>et al.</i> 2017; Selim <i>et al.</i> 2018; Abbass <i>et al.</i> 2020
Ethiopia	18.31-28.9	35.49-48.8	iELISA	Ibrahim <i>et al.</i> 2021; Tesfaye <i>et al.</i> 2020
The Gambia	24.2	18.5-24.9	iELISA	Klaasen <i>et al.</i> 2014; Bok <i>et al.</i> 2017
Ghana	28.4	10.0	iELISA	Johnson <i>et al.</i> 2019
Kenya	12.2-13	18-26	iELISA	Larson <i>et al.</i> 2018; Muema <i>et al.</i> 2017
Nigeria	3.85	3.16	iELISA	Elelu <i>et al.</i> 2020
Sudan		24.22	iELISA	Hussien <i>et al.</i> 2012

Leptospirosis

As reports show, the available data on leptospirosis seem to be sporadic and dependable evidences were limited only to five countries, namely Egypt, Morocco, Sudan, Senegal and Tanzania. The study from Morocco (Benkirane *et al.*, 2014) detected the organism in 5 samples of sheep out of 20 where the highest prevalence was 18%. A study from Senegal also recorded 7% (Roqueplo *et al.*, 2019) while it was 2% in Sudan (Shigidi, 1974) and below in Tanzania (Allan *et al.*, 201) in sheep. In goats, a prevalence of 34.6% was reported using microscopic agglutination test from Senegal (Roqueplo *et al.*, 2019) and 30.8% from Sudan (Shigidi, 1974). Likewise, Benkirane *et al.*, (2014) reported 20% reactors among 30 serum samples tested in Morocco. In Tanzania, a prevalence of 8.47% among 248 goats were reported using modified agglutination test (Assenga *et al.*, 2015b). On the contrary, no positive result could be retrieved on 25 sheep samples (blood, serum and tissue) from Egypt despite the use of culture, microscopic agglutination test (MAT), and/or PCR (Felt *et al.*, 2011).

Pasteurellosis

Regarding Pasteurellosis /hemorrhagic septicemia / due to *Mannheimia hemolytica* and/or *Pasteurella* infections in sheep and goats in Africa, all the available studies were from different parts of Ethiopia (Assefa and Kelkay, 2018; Berhe *et al.*, 2017; Legesse *et al.*, 2018; Marru *et al.*, 2013; Molla and Delil, 2015). An indirect hemagglutination based study on 192 sheep and 192 goats in Tigray, northern Ethiopia reported a potential clustering of multiple serotypes within

individual animals (Berhe *et al.*, 2017). In this work, about eight serotypes were identified. Over 90% of the infected animals had at least four or more serotypes. In sheep, *Mannheimia hemolytica* serotypes were detected in 97.4% of the animals and *Pasteurella multocida* serotypes in 69.8% while in goats the proportion for the aforesaid serotypes were 98.4% and 64.1%, respectively. A similar higher prevalence (86%) in sheep was recorded in a study in Dassenech district of South Omo Zone using Indirect hemagglutination (Molla and Delil, 2015). Another study in goats in Tigray had also reported *Mannheimia hemolytica* in 28.2% and *Pasteurella multocida* in 16.9% of the sampled animals (Assefa and Kelkay, 2018). Moreover, a bacteriological study in sheep in Haromaya (eastern Ethiopia) detected *Mannheimia hemolytica* in 87.5% and *Pasteurella multocida* in 12.5% of the samples (Marru *et al.*, 2013). Additionally, a case study in sheep using molecular characterization in central Ethiopia isolated *Mannheimia hemolytica* in 34.21% of the samples (Legesse *et al.*, 2018); strongly suggesting the role of pasteurellosis as major health constraint to small ruminant production in Ethiopia.

3.2.2.2. Viral Diseases

Altogether, about 130 articles published in a period from 1974 to 2021 were retrieved on viral diseases affecting small ruminants in Africa. Like earlier reports, much of these studies (71 or 54.6%) were from east Africa. PPR, Rift valley fever, blue tongue, Maedi visna, sheep and goat pox, and contagious ecthyma (orf) were the most frequently reported diseases (Figure 5).

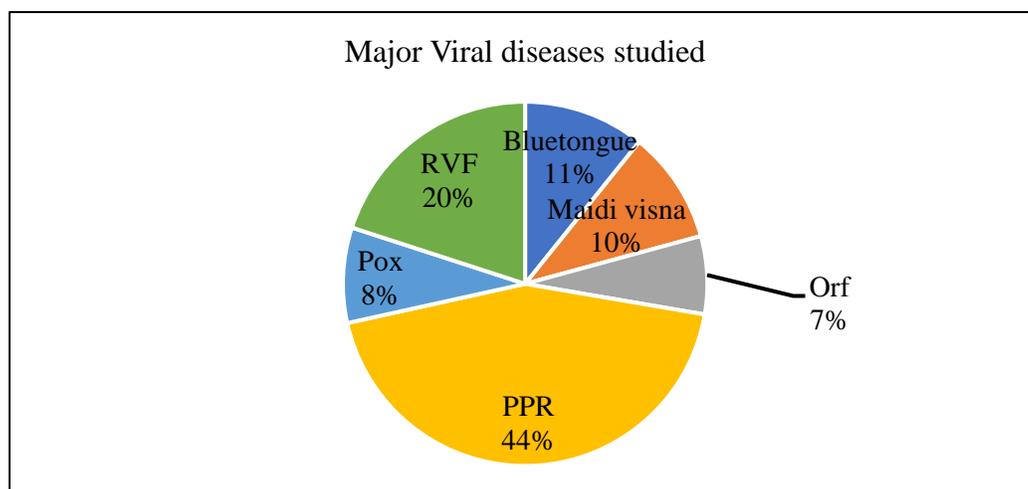


Figure 5. Major viral diseases of small ruminants studied in Africa from 1976-2021(n=130)

Peste des petits ruminants (PPR)

PPR is the most abundant viral disease of sheep and goats in Africa. Most of these reports came from four east African countries namely; Ethiopia (13), Sudan (8), Tanzania (7), Kenya (5) and Uganda (3) followed by North African country *i.e* Egypt (4) and then Nigeria (6) from west Africa (Table 6). The remaining eleven articles were reports from Algeria, Burundi, Chad, Djibouti, Eritrea, Gabon, Libya, Niger, Rwanda, Sierra Leone, and Tunisia one each. The screening tests used in these studies were c-ELISA and RT-PCR. Reported prevalence records vary between different studies as well as country to country. Among east African countries, the reported prevalence ranges from 6.98% to 50.85% in sheep and 4.53 to 71.4% in goats in Ethiopia. The disease is noted to be one of the most widely distributed diseases in the country; being reported from northern, western, central, eastern and southern parts (Gari *et al.* 2017; Gelana *et al.*, 2020; Molla and Delil 2015; Faris *et al.*, 2012; Megersa *et al.* 2011; Alemu *et al.*, 2019). In Kenya, the prevalence was 32% in sheep and 14.28 to 40% in goats (Kihu *et al.*, 2015a; Omani *et al.*, 2019). For Tanzania, the highest prevalence report in sheep was 49.5% (Swai *et al.*, 2009) and 66.7% in goats (Kgotlele *et al.*, 2014) while the lowest was 22.1% (Kivaria *et al.*, 2013) in both hosts. While it was 17.4% in sheep and 13.6% in goats in Rwanda (Shyaka *et al.*, 2021), the prevalence was 37.5% for Burundi (Niyokwishimira *et al.*, 2019) and in the range of 9.4% to 70.47% for Uganda reported collectively in small ruminants (Ruhweza *et al.*, 2010; Nkamwesiga *et al.*, 2019).

Likewise, reports confirm PPR as an important disease in Sudan with very high prevalence that range from 43.5% (Salih *et al.*, 2014) to 84.5% (Osman *et al.*, 2018) in sheep while 43.5% (Saeed *et al.*, 2018) to 66.1% (Osman *et al.*, 2018) in goats. Moreover, three reports of high prevalence *i.e.*, 71.7% (Mahmoud *et al.*, 2017), 66.7% (Abd El-Rahim *et al.* 2010) and 48.5% (Elhaig *et al.* 2018) obtained from Egypt as well. From North African countries, PPR was reported at 44.3% in sheep and 59.2% in goats (Almeshay *et al.*, 2017) in Libya while 20% in sheep and 34.7% in goats (Kardjadj *et al.*, 2015) in Algeria. In central Africa, the report was 56.2% in sheep and 48.9% in goats in Chad (Mahamat *et al.*, 2018) while it is 75% in sheep in Gabon (Maganga *et al.* 2013). In west African countries, reports from Nigeria and Niger show that the lowest prevalence in sheep was 13% (Woma *et al.*, 2011) and the highest 42% (Farougou *et al.*, 2013) while it is in the range of 47.9 to 51.52% in goats (Farougou *et al.*, 2013; Luka *et al.*, 2011).

Table 6 . PPR in sheep and goats reported from different African countries.

Country	Prevalence range (%)		Diagnostic tests	Other impacts	References
	Sheep	Goats			
Algeria	20	34.7	cELISA		Kardjadj <i>et al.</i> 2015
Burundi	37.5 (small ruminants)				Niyokwishimira <i>et al.</i> 2019
Chad	56.2	48.9	cELISA		Mahamat <i>et al.</i> 2018
Djibouti	2.66	6.83	cELISA		Moumin <i>et al.</i> 2018
Egypt	48.5-71.7	45-92	VI, RT-PCR; cELISA	54.2% morbidity	Elhaig <i>et al.</i> 2018; Soltan & Abd-Eldaim, 2014; Mahmoud <i>et al.</i> 2017; Abd El-Rahim <i>et al.</i> , 2010
Eritrea	3	29	RT-PCR		Oshiek <i>et al.</i> 2018
Ethiopia	6.98-50.85	4.53-71.4	cELISA; RT-PCR	Mortality 7.4-8.7; Morbidity 16.4-39.7	Alemu <i>et al.</i> 2019; Gelana <i>et al.</i> 2019; T Jones <i>et al.</i> 2020; Waret-Szkuta <i>et al.</i> 2008; Megersa <i>et al.</i> 2011; Mebrahtu <i>et al.</i> 2018; Gari <i>et al.</i> 2017; Fentie <i>et al.</i> , 2018; Faris <i>et al.</i> , 2012; Delil <i>et al.</i> , 2012; Afera <i>et al.</i> , 2014; Abraham <i>et al.</i> 2005; Molla & Delil, 2015
The Gabon	75		RT PCR	CFR. 98.9 & 18.2% respectively	Maganga <i>et al.</i> 2013
Kenya	32.0	14.28-40.0	cELISA		Kihu <i>et al.</i> 2015a; Kihu <i>et al.</i> 2015b; Omani <i>et al.</i> 2019; Gitao <i>et al.</i> 2014; Dundon <i>et al.</i> 2017
Libya	44.3	59.2	cELISA		Almeshay <i>et al.</i> , 2017
Niger	42	47.9	cELISA		Farougou <i>et al.</i> , 2013
Nigeria	13	49-51.52	cELISA, RT-PCR	Mortality; sheep (49%); goats (64.4)	Emkipe and Akpavie, 2011; Adedeji <i>et al.</i> 2019; Luka <i>et al.</i> 2011; Woma <i>et al.</i> 2015; Opasina & Putt, 1985; Bello <i>et al.</i> , 2018
Rwanda	17.4	13.6	cELISA		Shyaka <i>et al.</i> 2021
Sierra Leone			Reports	48% case fatality	Sundufu <i>et al.</i> 2015
Sudan	43.7-84.5	43.3-66.1	cELISA;		Salih <i>et al.</i> 2014; Saeed <i>et al.</i> 2010; Osman <i>et al.</i> , 2018; Saeed <i>et al.</i> 2018; Ishag <i>et al.</i> 2015; Intisar <i>et al.</i> , 2017; Haroun <i>et al.</i> 2002; Abdalla <i>et al.</i> , 2012
Tanzania	22.1-49.5	22.1-66.7	iELISA cELISA, RT-PCR		Jones <i>et al.</i> 2020; Kgotlele <i>et al.</i> 2014; Swai <i>et al.</i> 2009; Torsson <i>et al.</i> 2017; Kivaria <i>et al.</i> 2013; Mbyuzi <i>et al.</i> 2014; Kgotlele <i>et al.</i> 2015
Tunisia	5.7	11.8	cELISA		Ayari-Fakhfakh <i>et al.</i> , 2011
Uganda	NA	57.6-70.47			Mulindwa <i>et al.</i> 2011; Nkamwesiga <i>et al.</i> 2019; Ruhweza, <i>et al.</i> , 2010

Rift valley fever

There were about 26 reports selected on Rift valley fever in a period from 2008 to 2020 from 17 countries. The distribution of the studies shows that eight articles equally shared between

Tanzania and Kenya while Mozambique and Uganda reported two articles each. The remaining 12 countries (in the western, central, southern, eastern and northern Africa) reported one each (Table 7). An investigation of the 2006/07 outbreaks in different locations in Tanzania revealed the highest prevalence of 50% in sheep and 39% in goats using RVF-specific inhibition enzyme-linked immunosorbent assay (I-ELISA) but this result had changed to only 5.9% in sheep and 18.4% in goats when tested by RT-PCR method (Chengula *et al.* 2014). This is a reminder for African researchers to develop diagnostic capacities towards a reliable data generation. The lowest reports came from a study conducted in Egypt on 438 sheep and 26 goats in which it was 0.46% in sheep but no goats were detected positive by using cELISA (Mroz *et al.* 2017).

Table 7. Rift Valley Fever in sheep and goats reported from different African countries.

Country	Prevalence range (%)		Diagnostic tests	References
	Sheep	Goats		
Burkina Faso	7.0;	4.0	cELISA	Boussini <i>et al.</i> 2014
Cameroon	4.6	2.3	cELISA	Poueme <i>et al.</i> 2019
Central African Rep	12.9	5.0	cELISA	Nakoune <i>et al.</i> 2016
Chad	10.8	8.8	cELISA	Abakar <i>et al.</i> 2014
Comoros	39.0	33.5	cELISA	Roger <i>et al.</i> 2009
D.R. Congo	7.3	5.6	cELISA, RT-PCR	Tshilenge <i>et al.</i> 2019
Egypt	0.46	0.0	cELISA, VNT	Mroz <i>et al.</i> 2017
Ethiopia	7.4	6.3	c ELISA	Ibrahim <i>et al.</i> ,2021
Gabon	8.4	4.7	iELISA; RT-PCR	Maganga <i>et al.</i> 2017
Kenya	10.14-32.2	6.77-25.8	cELISA, RT-PCR	Bird <i>et al.</i> 2008; Nanyingi <i>et al.</i> 2016; Rich and Wanyoike, 2010; Orinde <i>et al.</i> 2012
Madagascar	24.7 (small ruminants)		cELISA	Jeanmaire <i>et al.</i> 2011
Mauritania	39.0 (small ruminants)		cELISA; RT-PCR	Jäckel <i>et al.</i> 2012
Mozambique	9.2- 44.2	11.6-25.1	VNT, cELISA	Fafetine <i>et al.</i> 2013; Blomström <i>et al.</i> 2016
Nigeria		2.3	cELISA; RT-PCR	Opayele <i>et al.</i> 2019
Somalia				Peyre <i>et al.</i> 2015
Somaliland	2	5	cELISA	Soumare <i>et al.</i> 2007
South Africa	28.0	9.3	iELISA	Ngoshe <i>et al.</i> 2020
Tanzania	11.37-50	4.7-39	cELISA, RT-PCR; iELISA	Sindato <i>et al.</i> 2015; Kifaro <i>et al.</i> 2014; Sumaye <i>et al.</i> 2013; Chengula <i>et al.</i> 2014
Uganda	4.0-6.8	3.6-7.0	cELISA, RT-PCR; iELISA	Nyakarahuka <i>et al.</i> 2018; Budasha <i>et al.</i> 2018

Bluetongue

Bluetongue was reported from eleven countries with Egypt, Ethiopia and Tunisia providing each two reports while the rest eight countries (Algeria, Kenya, Libya, Madagascar, Senegal, Sudan, Tanzania and Zambia) providing one from each in the period from 1974 to 2020 (Table 8). In sheep, except two studies i.e., from Senegal (Gahn *et al.*, 2020) and Zambia (Chambaro *et al.*,

2020) that did not detect either antibody to the virus or the viral genome in the samples, other nine studies from seven countries had reported high prevalence of the infection. Hence, the prevalence records in sheep were in the range of 14% in Algeria (Madani *et al.*, 2011) to 69.01% in Ethiopia (Gizaw *et al.*, 2016). Likewise, ten studies from eight countries had reported records of detection of blue tongue in goats with the prevalence in the range of 7.2% (Chambaro *et al.*, 2020) in Zambia to 60.53% (Gizaw *et al.*, 2016) in Ethiopia. However a study in Senegal (Gahn *et al.*, 2020) did not detect the virus in goats. On the other hand, there was an exceptional report from Madagascar where a national level study conducted in 2008 on 998 small ruminants has documented prevalence as high as 83.7% (Andriamandimby *et al.*, 2015). Competitive ELISA and RT-PCR were the techniques used in most studies as tools for detection of the virus but IFAT and AGID were also considered in few studies.

Table 8. Bluetongue in sheep and goats reported from different African countries.

Country	Prevalence range (%)		Diagnostic tests	References
	Sheep	Goats		
Algeria	14	21	cELISA	Madani <i>et al.</i> , 2011
Egypt	17.5-45	14.7-37	AGPT; cELISA	Mahmoud <i>et al.</i> , 2014; Mahmoud <i>et al.</i> , 2017
Ethiopia	23.2-69.01	40.9-60.53	cELISA	Abera <i>et al.</i> , 2018; Gizaw <i>et al.</i> , 2016
Kenya		34	IFAT	Davies and Walker, 1974
Libya		50.3	cELISA	Mahmoud <i>et al.</i> , 2018
Madagascar	83.7 (small ruminants)		cELISA	Andriamandimby <i>et al.</i> , 2015
Senegal	0	0	cELISA	Gahn <i>et al.</i> , 2020
Sudan	28	11.2	AGID	Eisa <i>et al.</i> , 1979
Tanzania	28.6 (small ruminants)		qRT-PCR	Jones <i>et al.</i> , 2020
Tunisia	0; 37	0; 0	qRT-PCR	Sghaier <i>et al.</i> , 2017; Lorusso <i>et al.</i> , 2018
Zambia	0	7.2	qRT-PCR	Chambaro <i>et al.</i> , 2020

Sheep and goat pox

Pox disease was reported from five countries (Algeria, Ethiopia, Kenya, Morocco and Nigeria) providing eleven publications. Even though, the anecdotal evidences portray that pox is common and wide spread in sheep and goats, the available published reports are scanty. A cross sectional study conducted in Ethiopia using virus neutralization test confirmed detection of infection in 17% sheep and 14% goats (Fentie *et al.*, 2017). In Morocco, a test conducted in 2018 on 10 goats using VNT and qPCR had detected positive results in all animals examined (Hamdi *et al.*, 2021). A questioner-based survey carried out in Algeria demonstrated that 21 out of 150 flocks visited, were positive for sheep pox and goat pox (SPGP) with an overall flock prevalence of 14%

suggesting that SPGP is endemic in the country (Kardjadj, 2017). A study conducted to characterize the infection of pox virus in sheep and goats in pastoral areas of Kenya following outbreaks revealed an enzootic situation where up to 82 % of animals showed specific antibody to the virus (Davies, 1976) but the report did not show which species had suffered the most. Moreover, Limon *et al.* (2020) had also reported a 20% morbidity and case fatality rate of up to 40% in sheep and goats due to pox diseases in a questionnaire study conducted in Nigeria.

Maedi visna

Like pox diseases of sheep and goats, studies made on Maedi visna were also limited. Only thirteen published reports on maedi visna were available of which ten from Ethiopia, two from Morocco and the other one from Algeria. Studies used ELISA and AGID as diagnostic tools. Except the study from Algeria involving 1313 goats tested using indirect ELISA in which a prevalence of 29.7% detected (Idres *et al.*, 2019) and one from Ethiopia with prevalence of 17.11% in goats (Mekibib *et al.*, 2019), all the rest had detected the infection in sheep alone. In Morocco, reports were ranging from 2.8% (Mahin *et al.* 1984) to 24.8% (Bouljihad and Leipold, 1994) in AGID based studies. The prevalence in Ethiopia was between 3.24% (Yizengaw *et al.*, 2020) to 61.25% (Garedew *et al.*, 2010). Moreover, high prevalence reports were available from different parts of Ethiopia that include a study involving microscopic examination of pneumonic lungs from 35 sheep detected lesions well-matched with maedi-visna in 25.7% of the samples (Woldemeskel and Tibbo, 2010). And more, a study on 1788 sheep sera from North Shewa, Arsi, Bale, North Omo and Gurage zones tested by using ELISA revealed the presence of antibodies against the virus in 24.2% (433) of the animals sampled (Mekonnen *et al.*, 2010). An outbreak investigation of respiratory disease complex (RDC) carried out in 3641 Menz and Awassi x Menz cross sheep in Central Ethiopia using clinical, serological, microbiological, post-mortem and histopathological examinations, showed the prevalence to be as high as 17% (Tibbo *et al.*, 2001).

Contagious Ecthyma (Orf)

Contagious ecthyma (Orf) is one of the diseases with only few reports in this data extraction. Of the nine reports obtained from four countries (Ethiopia, Gabon, Nigeria, Sudan), prevalence records were reported in only three of the studies in both sheep and goats. In Ethiopia,

prevalence records of 15.5% in sheep and 8.5% in goats (Tedla *et al.*, 2018); 7.18% in goats (Wondmnew *et al.*, 2018) as well as 1.1% in sheep were reported from different study sites. Likewise, the presence of two virus isolates and reports of 3% morbidity was recorded in Ethiopia (Gelaye *et al.*, 2016). Moreover, a case study confirmed detection of the virus in 6 goats out of 8 in Gabon (Maganga *et al.* 2016). Furthermore, a case fatality rate of 2.8% in sheep and 1.3% in goats were recorded in Sudan (Khalafalla *et al.*, 2020). In Nigeria, an outbreak had affected 30 lambs and 12 goats (Obi and Gibbs, 1978) while a 100% mortality in West African Dwarf breed of goats was also reported (Adedeji *et al.*, 2018).

3.3. Overview of small ruminant disease impacts in Africa

3.3.1. Economic loss

Epidemic and endemic diseases such as peste des petits ruminants (PPR), Rift valley Fever (RVF) and theileriosis threaten the small ruminant production sector by direct effects through high degree of morbidity and mortality, control or eradication program costs and restrictions to trade in livestock and livestock products (FAO, 2002). Zoonotic diseases such as RVF, brucellosis, hydatid disease do affect human health as well. Endemic diseases such as parasitic diseases like trypanosomosis and helminthosis have impacts on livestock keepers and consumers because of productivity losses, control costs and indirect losses.

Despite their socio-economic importance in the livelihood of most rural families of Africa, , small ruminants received little emphasis in studies elucidating the impacts of diseases on health and productivity of these animals, and the few studies available are often overshadowed by the extensive works in cattle. Moreover, efforts to estimate direct and indirect losses from parasitic diseases are undermined by often chronic nature of the problem which is frequently complicated by concurrent infections caused due to other infectious agents; altogether limiting the number of reports retrieved regarding estimation of impacts of parasitic, bacterial and viral infections in this group of livestock. Among the 26 published manuscripts qualifying for this criterion, 12 focused on parasitic infections; majority being gastrointestinal parasitism, 9 on bacterial diseases (mainly brucellosis and contagious caprine pleuropneumonia (CCPP)) and 12 on viral diseases (Peste des petits ruminants (PPR), sheep and goat pox, and rift valley fever).

Parasitic diseases economic impact in Africa

The true costs of disease are complex; depending on direct, indirect and intangible costs, which vary according to assumptions made about who is affected by the disease and the disease control measures (Perry and Grace, 2009). The scale of the problem caused by parasites in small ruminants is normally estimated from losses associated to cost of treatment, mortality, reduced weight gain and production, reduced market value of the animals, reduced quality of animal products and byproducts and condemnation of edible organs such as the liver (Odenirana *et al.*, 2021; Wanyangu and Bain, 1994; Akerejola *et al.*, 1979). In the tropics, gastro-intestinal nematodes in ruminants are often considered as major constraints to optimal productive performance. Under certain circumstances, helminth infestations can result in high mortalities, but more often their effects are on morbidity. According to a review by Wanyangu and Bain (1994) on the impact of helminth infection on small ruminant production in tropical Africa, mortality rates may exceed 40% in the absence of an effective intervention.

A review by Biffa *et al.* (2006) clearly demonstrated the heavy economic losses to African farmers due to parasitic diseases affecting small ruminants. This review highlighted that in sub-Saharan Africa alone; endoparasites cause losses of US\$ 81.8 million annually due to mortality and over US\$ 43.2 million due to reduced productivity. In Ethiopia, a loss of 250,000 tons of fresh meat has been recorded from seven million helminth-infected sheep slaughtered annually of which US\$ 1.2 million alone could be attributed to reduced weight gain of grazing sheep, in the absence of anthelmintic treatment. In the analysis of causes of sheep mortality from 1982 to 1986 at the DebreBerhan sheep breeding station, coenurosis was one of the predominant causes of mortality in both adult and young sheep, with proportional mortality of 5-16.2%. A 15-year retrospective study in Kenya by Kagira and Kanyaria (2001) has also revealed the role of parasitic diseases in causing mortalities in small ruminants. Among sheep deaths due to diseases, 32 % was by parasitic diseases. The major cause of mortality was helminthosis followed by heart water.

Productivity losses through reduced feed intake and decreased feed utilization efficiency are often the largest economic losses arising from helminth parasitism. *Haemonchus contortus*, a blood-feeding abomasal worm, is responsible for most losses from small ruminant nematode parasitism. Lung worm infections (Verminous pneumonia) caused by nematode parasites such as

Dictyocaulus filaria and metastrongylids may also cause significant health problems and associated production losses especially in young animals. Fasciolosis caused by trematode species, *Fasciola hepatica* and *F. gigantica*, is a disease commonly found in sheep and goats and affects mainly the liver and the gall bladder (Charlier *et al.*, 2020; Tibbo *et al.*, 2008; Ngategize *et al.*, 1993; Akerejola *et al.*, 1979). While the importance of helminthiasis is understood, few works translate the biological influence of parasitism into economic terms.

A review by Jackson *et al* (2009) has shown that subclinical nematode infestations in sheep alone can cost the UK sheep industry up to GBP 84 million and huge financial losses have also been estimated in many studies in Africa (Odenirana *et al.*, 2021; Ngategize *et al.*, 1993). An old estimate in Nigeria (Akerejola *et al.*, 1979) reported annual losses due to helminths may account for 60 million Naira while the cost of preventive/curative anthelmintic treatment was estimated at 16 million Naira/year. The same study has shown annual loss of 9 million Naira due to liver fluke infection alone (Table 9). In a similar situation, Odenirana *et al.* (2021) assessed losses arising from small ruminant fasciolosis using pooled prevalence obtained from literature and field epidemiological data. They estimated a total loss of US\$ 77,940,024/annum of which US\$ 55,671,620 was ascribed to mortality and US\$ 552,448 was due to liver condemnation. Direct losses were estimated at US\$ 60,132,318 and indirect losses at US\$ 17,807,706. This estimate was based on only 2.1% pooled prevalence of fasciolosis in Nigeria. Therefore, one can easily appreciate how much loss could be expected if the prevalence was much higher as it is the case in some countries. According to a review by Mehmood *et al* (2017), among African countries, maximum average prevalence of fasciolosis reported in sheep was 40.2% in Ethiopia, 35% in Tunisia, 23% in Chad. The same review reported average highest fasciolosis prevalence in goats to be 68.4% in Tunisia, 12% in Chad and 9.60% in Ethiopia. Ngategize *et al.* (1993) reported total loss per year of 48.4 million Ethiopian Birr due to fasciolosis of which 46.5% was due to mortality, 48.8% due to productivity losses and 4.7% due to Liver condemnation. In Nigeria, about 11% of the flock value is estimated to be lost each year due to helminthiasis (Akerejola *et al.*, 1979).

In a similar situation to helminth parasitism, diseases caused by protozoan parasites also pose serious impediment to small ruminant production in Africa. More importantly, the blood parasites, Trypanosomes cause a debilitating and commonly fatal disease occurring mainly in

sub-Saharan Africa. Much of information available regarding socioeconomic impacts of African animal Trypanosomosis come from cattle studies and data on small ruminants is scant. The few available studies have demonstrated that *Trypanosoma congolense*, *T. vivax* and *T. brucei* are the most important species causing economic losses due to mortality, reduced weight gain and reproductive failures such as abortion (Masiga *et al.*, 2002; Edeghere *et al.*, 1992) in sheep and goats. A study in Nigeria on the impacts of animal trypanosomosis in small ruminants has also revealed 16.7% abortions among pregnant animals, 100% death of infected animals and 33.3% neonatal deaths (Edeghere *et al.*, 1992). A similar study in Kenya on financial implications of rearing sheep and goats under natural trypanosomosis challenge at Galana Ranch, has estimated losses due to mortality, reduced weight gain and cost of treatment to be 471 and 275 Ksh/year per sheep and goat, respectively (Irungu *et al.*, 2002). In a similar manner, investigation on growth and mortality of sheep and goats under high tsetse challenge documented 25-63% mortality among infected animals (Masiga *et al.*, 2002), altogether suggesting the huge economic impact of animal trypanosomosis in small ruminant production.

Other vector-borne/tick-borne diseases such as Caudriosis (heart-water) caused by *Ehrlichia ruminantium*, Babesiosis (red urine) caused by *Babesia ovis*/*B. motasi* and malignant ovine/caprine Theileriosis caused by species such as *Theileria lestoquardi* also posse significant economic burden in endemic areas (Mureithi and Mukiria, 2015). Enormous financial losses are expected from tick borne diseases such as heart water caused by *Ehrlichia ruminantium* (Mukhebi *et al.*, 1999) and ectoparasitism degrading quality of sheep and goat skins and causing rejections at tanneries (Kebede, 2013, Sertse and Wossene, 2007). According to Sertse and Wossene (2007), prevalence of cockle (marks of skin lesion) was closely linked to infestation with *Melophagus ovinus* (sheep ked) and *Damalinia ovis* (Lice) in sheep and sarcoptic mange in goats. A follow-up study of randomly selected pickled sheep skins and wet blue goat skins by the same authors revealed that 71% of the former and 42% of the later had cockle lesions. Deterioration of processed skin grade was found proportional to the appearance of cockle consequently causing an estimated annual loss (in 2002/2003) of 1.6 million USD for pickled sheep and 0.6 million USD for wet blue goat skins in two tanneries located in Northern Ethiopia alone.

Table 9. Summary of the impacts of small ruminants' parasitic infections in Africa

Parasitic diseases	Country of study	Impact	Reference
GI helminthiasis	Ethiopia	Anthelmintic treated sheep performed significantly better than their non-treated contemporaries with marginal profit of Eth. Birr 28 vs. 8 Birr	Tibbo <i>et al.</i> , 2008
GI helminthiasis	Nigeria	Overall annual losses: 60 million Naira <ul style="list-style-type: none"> • Cost of treatment: 16 million Naira/year • Loss due to liver fluke: 9 million Naira 	Akerejola <i>et al.</i> , 1979
GI helminthiasis	Botswana	Correlation coefficients were strongly negative: -0.95 for FECs and live weight	Nsoso <i>et al.</i> , 2001
Fasciolosis	Nigeria	A total of US\$ 77,940,024 / annum economic losses <ul style="list-style-type: none"> • Losses due to mortality US\$ 55,671,620, • Losses due to liver condemnation US\$ 552,448 	Odenirana <i>et al.</i> , 2021
Fasciolosis	Ethiopia	Total loss per Year: 48.4 million Ethiopian Birr of which <ul style="list-style-type: none"> • 46.5% due to mortality • 48.8% due to productivity losses • 4.7% due to Liver condemnation 	Ngategize <i>et al.</i> , 1993
Fasciolosis	Ethiopia	More than 12% of livers are infected and about 4000 USD lost due to condemnation in a single Municipal abattoir	Abunna <i>et al.</i> , 2010
Trypanosomosis	Nigeria	The infection resulted in 16.7% abortion, 100% death and 33.3% neonatal deaths	Edeghere <i>et al.</i> , 1992
Trypanosomosis	Kenya	losses (mortality, reduced weight gain, cost of treatment): 471 and 275 Ksh/year in sheep and goats respectively	Irungu <i>et al.</i> , 2002
Trypanosomosis	Kenya	Reduced live weight, 25-63% mortality	Masiga <i>et al.</i> , 2002
Heartwater	Zimbabwe	Annual national losses amount to Z\$ 61.3 million (US\$ 5.6 million) over 10 yr. <ul style="list-style-type: none"> • Acaricide cost (76%), • Milk loss (18%) • Treatment cost (5%) 	Mukhebi <i>et al.</i> , 1999
Ectoparasites	Ethiopia	<ul style="list-style-type: none"> • six tanneries have rejected 2,037,745 pieces of skins (loss of USD 6.3 million in a year) • Ectoparasitic skin diseases were responsible for 35% of sheep skin and 56% of goat skin rejections. 	Kebede, 2013
Ectoparasites	Ethiopia	<ul style="list-style-type: none"> • The annual economic losses in 2002/2003 due to in two tanneries was estimated to be 1.6 million USD for pickled sheep and 0.6 million USD for wet blue goat skins 	Sertse and Wossene, 2007

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- Deterioration of processed skin grade was found proportional to the appearance of cockle
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Appart from the detrimental role of parasites on animal health, productivity and hence their cumulative economic impact, some parasites such as cestode infections specifically caused by metacestodes of *Taenia multiceps* (Coenurosis caused by *Coenurus cerebralis*) and *Ecchinococcus granulosus* (hydatidosis caused by hydatid cyst) are of major concern in some parts of Africa and elsewhere not only because of their impact on animal health and production but also due to their zoonotic nature (Asmare *et al.*, 2016c). Similarly, Toxoplasmosis and Cryptosporidiosis among the protozoan parasites infecting small ruminants (Robertson *et al.*, 2020) have significant zoonosis potential (Baroudi *et al.*, 2018; Gebremedhin *et al.*, 2014) and these animals may serve as reservoirs of infection for humans (Ng'ayo *et al.*, 2005).

Altogether, parasitic diseases of small ruminants pose significant economic, social and public health challenges. Reduction in productivity due to mortality and other health problems means a persistent challenge to food production, household livelihood and food security of the countries affected. Minimizing such impacts hence means installing and implementing sustained and effective preventive and control strategies customized to the regional distribution of the most important groups of parasites. It should also be noted that there is only a fragmented understanding of the true costs of helminth parasitism. This must be solved if future control strategies are to be economically sensible and well integrated into the different farming systems including the pastoral settings of Africa.

Economic Impacts of infectious diseases in Africa

Most infectious diseases of small ruminants endemic in Africa are a major burden to the economy of most countries and create a huge impact on the livelihood of the society. Indeed, brucellosis is a well-known disease causing direct socio-economic impact in livestock-keeping populations who depend on animal production for food security and cash income. Studies in Ethiopia (Edao *et al.*, 2020; Megersa *et al.*, 2011) suggest that *Brucella* seropositivity was significantly associated to abortion and reduced number of young animals produced by breeding females (Megersa *et al.*, 2011). Brisibe *et al.* (1996) reported the zoonotic and economic implications accruing from small ruminant brucellosis in Nigeria. Moreover, the records of

brucellosis and its association with abortion in small ruminants were also reported from Côte d’Ivoire (Kanouté *et al.*, 2017) and Morocco (Benkirane *et al.*, 2015). Unlike brucellosis, CCPP is characterized by high morbidity and mortality that often occurs in outbreak forms. In this connection, outbreaks characterized by a very high morbidity that go as high as 90% and 65% mortality in goats were recorded from Eritrea (Houshaymi *et al.*, 2002) as well as Tanzania (Kusiluka *et al.*, 2000) and costed an annual loss of 1,712.66 Euros per standard flock of 100 heads of animals to Kenya (Renault *et al.* 2019).

PPR represents a major threat to small ruminants in Africa and hence records of low to high morbidity and mortalities were reported from different countries including Egypt (Elhaig *et al.*, 2018), Ethiopia (Alemu *et al.*, 2019), Gabon (Maganga *et al.*, 2013), and Nigeria (Adedeji *et al.*, 2019). Similarly, losses due to PPR for Kenya were also estimated at US\$ 19.1 million (Kihu *et al.*, 2015b). The impacts of RVF outbreaks had also caused huge losses to countries especially in East Africa. In Kenya, a loss of around US\$10 million was reported due to food insecurity, loss of income and capital as a result of RVF (Rich and Wanyoike, 2010). Furthermore, the impact of RVF on Kenyan public health during the 2006-2007 outbreaks as described by estimating the burden of the disease in DALYs and cost of treatment was estimated at US\$120 for every human case reported and the total estimated cost of US\$82,000 for the outbreak (Orinde *et al.*, 2012). Likewise, an embargo on the importation of live animals from east Africa following the 1997 RVF outbreak, had resulted in a loss of over US\$300 million to Somalia (Peyre *et al.*, 2015). Details on the impact of infectious diseases of small ruminants are provided in Table 10 below.

Table 10. Summary of the economic impacts of infectious diseases in small ruminants in Africa

Infectious disease	Country	Impact	Reference
Brucellosis	Ethiopia	Seropositivity associated with abortion in goats with history of abortion being 6.5%; and 12.4%	Edao <i>et al.</i> , 2020;
		Reduced number of young animals produced by breeding seropositive females	Megersa <i>et al.</i> , 2011 Megersa <i>et al.</i> , 2011
	Nigeria	estimated annual loss in excess of US\$ 3.2 million at 3.3% prevalence in sheep and 4.5% in goats	Brisibe <i>et al.</i> , 1996

	Morocco	history of abortion being 10.74% in sheep and 10.83% in goats associated with seropositivity	Benkirane <i>et al.</i> , 2015
	Côte d'Ivoire	history of herd-level abortions during the last birthing season were 79.5% (31/39) in sheep and 77.3% (17/22) in goat herds	Kanouté <i>et al.</i> , 2017
CCPP	Egypt	case fatality of 8% in sheep and 30% in goats	Abd-Elrahman <i>et al.</i> , 2020
	Eritrea	very high morbidity as high as 90% & 65% mortality in goats	Houshaymi <i>et al.</i> , 2002
	Tanzania	high morbidity up to 90% & mortality of 50%	Kusiluka <i>et al.</i> , 2000
	Kenya	annual economic losses estimated at €1,712.66 (Euros) for a standard flock of 100 heads	Renault <i>et al.</i> 2019
PPR	Egypt	morbidity of 54.2% & mortality of 8.5%	Elhaig <i>et al.</i> , 2018
	Ethiopia	16.4-39.7% morbidity & 7.4-8.7% mortality in small ruminants	Alemu <i>et al.</i> , 2019
	Nigeria	mortality of 49% in sheep & 64.4% in goats	Adedeji <i>et al.</i> , 2019
	Gabon	case fatality of 98.9% in outbreaks	Maganga <i>et al.</i> , 2013
	Kenya	Losses due to mortality of small stock valued at US\$ 16.8 million and loss due to lost milk and weight at US\$ 2.3 million	Kihu <i>et al.</i> , 2015a
RVF	Kenya	<ul style="list-style-type: none"> ✓ US \$10 million due to food insecurity and loss of income and capital linked to outbreaks ✓ burden of human disease in DALYs and cost of treatment due to RVF was estimated at US\$120 per human case with total estimated cost of US\$82,000 for 2006/07 outbreak 	Rich and Wanyoike, 2010 Orinde <i>et al.</i> , 2012
	Somalia	loss of over US\$300 million due to livestock export ban following 1997 RVF outbreak	Peyre <i>et al.</i> , 2015
Pox disease	Uganda	24.1% abortion prevalence in sheep & 18.8% in goats	Budasha <i>et al.</i> , 2018
	Nigeria	case fatality of 34 % in sheep and 33% in goats; a median of US\$1.96 (0.19-27.5) per herd per day cost of antibiotic treatments; and overall losses at farm level range from US\$9.6 to 6,340.	Limon <i>et al.</i> , 2020
		Forced selling of sheep and goats at lower costs (58 and 57% less) than would have been sold if it was healthy because of the disease	Limon <i>et al.</i> , 2020
Unspecific	Tanzania	direct losses as a proportion of household income due to deaths and abortions account for a loss of 10.2% and 0.5% in sheep and 15.2% and 2.1% in goats	Ahmed <i>et al.</i> , 2019

3.3.2. Drug resistance

Antibiotic resistance in small ruminants in Africa

Therapeutic remedies, including antimicrobials, have greatly reduced the burden of disease in animals and contributed to improved quality of life and food production. However, the use of antimicrobials in animal production is a worldwide concern in the presence of rising resistance levels of commensal, pathogenic and zoonotic bacteria (Mathew *et al.*, 2020; Mouiche *et al.*, 2019). In a study conducted in Haramaya district of Ethiopia, *Pasteurella multocida* and

Mannheimia haemolytica were isolated from samples of lung and nasal cavities collected from sheep brought to abattoir and clinic and the isolates had exhibited uniformity in their sensitivity to majority of the antibacterial agents. Although Chloramphenicol (100%) was the most effective drug followed by Sulfamethoxazole (89.1%) and Tetracycline (84.4%), both species were completely resistant to Gentamycin and Vancomycin (Marru *et al.*, 2013).

Furthermore, a review report on antimicrobial use and resistance in food producing animals and the environment from African perspective revealed that the percentage of farms using antimicrobials in animal production ranged from 77.6% in Nigeria to 100% in Tanzania, Cameroon, Zambia, Ghana and Egypt. The most antibiotics used in these farms were tetracycline, aminoglycoside and penicillin groups. The percentage of multi drug resistant isolates ranged from 20% in Nigeria to 100% in South Africa, Zimbabwe and Tunisia. In the environment, percentage of multi drug resistant isolates ranged from 33.3% in South Africa to 100% in Algeria. None of the countries documented national antimicrobial use and resistance surveillance system in animals (Kimera *et al.*, 2020). A similar review on antibiotic resistance in food animals in Africa revealed that most studies were mainly conducted in Nigeria, with *Escherichia coli*, Salmonella species and Campylobacter species being the main bacteria. As a result, the pooled estimates showed high level of antibiotic resistance (86%) and multidrug resistance (73%) suggesting that antibiotic resistance is substantively prevalent and poses a serious threat for food safety and security in Africa (Founou *et al.*, 2018).

In Uganda, a nation-wide annual agricultural survey of data on antimicrobial use in livestock based on key questions administered by the Uganda Bureau of Statistics (UBOS) in collaboration with the Food and Agriculture Organization of the United Nations (FAO) gathered data from 6 thousand agricultural households. Hence, the findings show that AMU is considerable among livestock keeping households (35%), who use antibiotics not only for curative treatment (~58%) but also for disease prevention (~44%) and growth promotion (~5%) (Mikecz *et al.*, 2020).

In Cameroon, a study carried out from 2014 to 2019 to evaluate the consumption trends of antimicrobials for veterinary use in food-producing animals revealed that 217.67 tons of antimicrobials (by weight of active substance) were imported during the 6-year period, with an average of 36.28 ± 10.11 tons per year. Tetracyclines (31.71%), sulfonamides (23.84%), quinolones (11.11%) and β -lactams (10.17%) were the most commonly imported classes of

antimicrobials. With regard to the importance of veterinary antimicrobials to human medicine, critically important antimicrobial (34.3%), reserve (4.6%) and watch (25.5%) groups as classified by the WHO Access, Watch, and Reserve (AWaRe) categorization were recorded. Overall, a mean of 5.24 ± 1.40 mg/PCU (population correction unit) was used in all food-producing animals during the 6-year period. However, the mean quantity of antimicrobials adjusted by animal biomass was highest in poultry (213.32 ± 50.26 mg/kg), followed by pigs (63.04 ± 18.87 mg/kg), cattle (4.11 ± 2.20 mg/kg), sheep (0.83 ± 0.43 mg/kg) and goats (0.47 ± 0.24 mg/kg) (Mouiche *et al.*, 2020).

This situation is suggestive of the intensive usage of antimicrobials in the management of animal diseases which may cause selection for resistance among microorganisms. Transmission of resistant bacteria from the wild and domestic food animals to humans may occur via the food chain, environment, or direct interaction with animals and this may lead to the emergence of infections that are challenging to manage. It is now estimated that antimicrobial resistance (AMR) among bacteria or viruses causes 700,000 deaths annually hence posing a significant public health challenge across the world. The resistant clones of bacteria have gained a global distribution with over 90% being resistant to commonly used antibiotics such as co-trimoxazole, penicillin, ampicillin, and gentamicin among others. Most human diseases originate from animals with 61% being zoonotic. Bacteria from animals are among the predominant causes of diseases in the food chain (Iramiot *et al.*, 2020). In conclusion, strict surveillance systems of antimicrobial consumption are vital to optimize control strategies and monitoring importation data of veterinary antimicrobial products could be useful for sub-Saharan African countries to quantify consumption and estimate trends for antimicrobial usage effectively (Mouiche *et al.*, 2020).

Anthelmintic, trypanosidal and acaricide resistance

The extensive use of anthelmintics for the control of helminth infections on grazing livestock over many years has significantly lowered their efficacy and often led to the development of resistance in many countries of Africa (Wakayo and Dewo, 2015; Sissay *et al.*, 2006; van Wyk *et al.* 1997; Waruiru, 1997). Since the first suspicion of resistance to phenothiazine in 1960s, the phenomenon of anthelmintic resistance has shown a constant development (Kaplan, 2004; Jackson and Coop, 2000). The increasing occurrence of helminth populations resistant to the

limited classes of anthelmintic we have threatened the sustainability and efficiency of small ruminant production and the livelihood of the resource poor farmers of Africa (Table 11). Waruiru (1997) reported multiple resistances of *H. contortus* to albendazole, levamisole and ivermectin. Highly prolific species of worms such as *H. contortus* have a higher risk of developing diverse resistance-alleles due to spontaneous mutations than the less prolific *T. colubriformis* (Silvestre & Humbert, 2002). Van Wyk *et al* (1999) from South Africa reported that 16% of the strains of *H. contortus* were < 60% susceptible to three of the four anthelmintics tested, and 8% of the strains were < 40% susceptible to all four of the anthelmintics. In a similar manner, a study in Zambia has shown resistance to albendazole in five of six farms tested (Gabrie *et al.*, 2001). Most of the studies have used the fecal egg count reduction tests and the most common worm detected by fecal culture following detection of resistance was *H. contortus*. Generally, anthelmintic resistance is becoming a continental problem, and *Haemonchus*, a highly prolific and successful parasite is frequently mentioned to resist almost all available anthelmintic compounds. A review by Mpahlele *et al* (2019) has shown this parasite had developed resistance to almost all classes in South Africa, to fenbendazole, albendazole, oxfendazole, levamisole and rafoxanide in Zimbabwe, to ivermectin and albendazole in Zambia and to ivermectin and fenbendazole in Kenya. The situation has now reached a stage where the efficiency of this mode of chemical control is dramatically challenged (Torres-Acosta and Hoste 2008), calling for an urgent and efficient alternative or complementary mode of helminth control.

Trypanosomosis is one of the major vector borne diseases of cattle and small ruminants. There is no effective vaccine against the disease and in the absence of environmentally friendly and sustainable vector control strategy control of trypanosomosis continues to rely principally on chemotherapy and chemoprophylaxis. Although it is cheaper and easier to kill the parasite than the fly vectors, some of the trypanocides, however, display varying degrees of toxicity and their effectiveness has dangerously declined with the emergence of more and more drug resistant trypanosome strains (Wilkinson and Kelly, 2009). Trypanocidal drug resistance is a commonplace in many countries of Sub-saharan Africa. Even though many of the reports on large animals originate from studies on cattle, it is believed that similar strains of parasites circulate among species of ruminants and hence drug failures may also be common in sheep and goats. Resistance to Diminazene aceturate and isometamidium chloride is common in cattle in West and Eastern parts of Africa (Degneh *et al*, 2019; Anene *et al.*, 2001). Among the few

reports in small ruminants are Vitouley *et al* (2012) and Ogbaje *et al* (2015) who confirmed occurrence of resistance by *T. vivax* and *T. congolense*.

For external parasites, different classes of acaricides have been in use for decades in Africa and elsewhere in the world. These include: organophosphates such as coumaphos and diazinon, synthetic pyrethroids such as permethrin and deltamethrin, amidines such as amitraz and macrocyclic lactones such as ivermectin and moxidectin (De Meneghi *et al.*, 2016). Tick surveys and acaricide resistance studies are more abundant for cattle than for small ruminants (Jobre *et al.*, 2001; Vudriko *et al.*, 2016). However, as reviewed in Mkwanzazi *et al.* (2021), small ruminants are alternative hosts for several tick species when the appropriate host is unavailable allowing the ticks to complete their life cycle. A review by De Meneghi *et al.* (2016) and a study by Horak *et al* (2009) have also shown that cattle and small ruminants share some genera and species of ticks in common. Hence, any resistance report for cattle ticks may also apply to ticks infesting small ruminants. In Africa, more precisely in Southern and Eastern Africa, one-host ticks (*R. microplus* and *Rhipicephalus decoloratus*) have become resistant to the majority of acaricides within pyrethroid and organophosphate classes (De Meneghi *et al.*, 2016). Similarly, acaricide-resistance in ticks has been detected in Uganda (Vudriko *et al.*, 2016) and Ethiopia (Jobre *et al.*, 2001). Ticks were collected from cattle, sheep and goat in different parts of Uganda. Acaricide failure was reported for 98.0 % of the ticks belonged to the genus *Rhipicephalus* with some species coming from small ruminants and multi-acaricide resistance was also common (Vudriko *et al.*, 2016).

Table 11. Summary of anthelmintic and trypanocidal drug resistance in small ruminants in Africa

Model parasite	Country	Animal host	References
<i>Trypanosoma vivax</i>	Algeria	Sheep	Vitouley <i>et al.</i> , 2012
<i>T. vivax</i> , <i>T. congolense</i>	Nigeria	Sheep	Ogbaje <i>et al.</i> , 2015
GI nematodes	Burkina Faso	Goat	Bentounsi <i>et al.</i> , 2006
<i>H. contortus</i>	Egypt	Sheep	Aboelhadid <i>et al.</i> , 2020
GI nematodes	Ethiopia	Goat	Kumsa and Abebe, 2009, Kumsa <i>et al.</i> , 2010
GI nematodes	Ethiopia	Sheep	Bahiru <i>et al.</i> , 2017
<i>H. contortus</i> , <i>T. colubriformis</i>	Ethiopia	Sheep, Goat	Sissay <i>et al.</i> , 2006
<i>H. contortus</i> , <i>T. colubriformis</i>	Kenya	Sheep	Maingi, 1991; Maingi <i>et al.</i> , 1998; Waruiru <i>et al.</i> , 1997
GI nematodes	Kenya	Sheep, Goat	Wanyangu <i>et al.</i> , 1996; Mwamachi <i>et al.</i> , 1995

<i>H. contortus</i>	Kenya	Goat	Mungube <i>et al.</i> , 2015; Waruiru <i>et al.</i> , 1998
<i>H. contortus</i>	South Africa	Sheep	Mphahlele <i>et al.</i> , 2021; van Wyk <i>et al.</i> , 1997; Louw and Reinecke, 1993
<i>H. contortus</i>	South Africa	Sheep, Goat	Tsotetsi <i>et al.</i> , 2013; van Wyk <i>et al.</i> , 1999
<i>H. contortus</i>	Sudan	Goat	Mohammedsalih <i>et al.</i> , 2019; Mohammedsalih <i>et al.</i> , 2020
GI nematodes	Tanzania	Sheep	Bjørn <i>et al.</i> , 1990
GI nematodes	Tanzania	Sheep, Goat	Keyyu <i>et al.</i> , 2002; Sailen <i>et al.</i> , 2017
GI nematodes	Uganda	Goat	Nabukenya <i>et al.</i> , 2014; Byaruhanga <i>et al.</i> , 2013; Nsereko <i>et al.</i> , 2013
GI nematodes	Zambia	Sheep	Gabrie <i>et al.</i> , 2001
<i>H. contortus</i>	Zimbabwe	Sheep	Boersema and Pandey, 1997
Ticks	Uganda	Sheep, goat	Vudriko <i>et al.</i> , 2016

3.3.3. Residues in foods of animal origin

Antibiotic residues

Veterinary drugs used in food producing animals have been useful to sustain animal food production (Chandra *et al.*, 2014) and thus approximately 80% of all food producing animals receive medication for part or most of their lives currently (Lee *et al.*, 2001). The most commonly used antimicrobials in food producing animals are the β -lactams, tetracyclines, aminoglycosides, lincosamides, macrolides, pleuromutilins, and sulfonamides (Lee *et al.*, 2001). Following administration, such treatments leave residues in the tissues of animals and the foods derived from them (Wassenar, 2005). The presence of antimicrobial residues in foods of animal origin, combined with failure to comply with the instructions for their use (dosage and withdrawal period) or poor livestock production practices, can have serious consequences for consumer health (Chou *et al.*, 2011; Tunipssed and Andersen, 2008).

The resultant risks of pharmaceutical residues reaching edible products and the potential health hazards associated with their consumption have become a public safety issue (Teale, 2002). It is now recognized that these drugs may exert effects other than those for which they are administered, including toxic effects, transfer of antibiotic resistant bacteria to humans, immunopathological effects, carcinogenicity (e.g., sulphamethazine, oxytetracycline, and furazolidone), mutagenicity, nephropathy (e.g., gentamicin), hepatotoxicity, reproductive

disorders, bone marrow toxicity (e.g., chloramphenicol), and allergy (e.g., penicillin) (Nisha, 2008; Azzouz *et al.*, 2011).

In most developing countries, antimicrobials like tetracycline, erythromycin, streptomycin, and penicillin are used in animals indiscriminately for the prevention and treatment of bacterial infections (Kabir *et al.*, 2004). However, failure to respect waiting periods (Fagbamila *et al.*, 2010) leads to high exposure to antimicrobial residues (Aning *et al.*, 2007).

In Africa, studies on the presence of antimicrobial residues in foods of animal origin are very limited. Evidences show that antibiotics are being used inappropriately in livestock production and reports of occurrence of antimicrobial residues in poultry, beef and milk products are available from Algeria, Ethiopia, Cote de Ivoire, Ghana, Kenya, Mali, Morocco, Nigeria, Senegal, Tanzania, and Uganda (Addisalem and Bayleyegn, 2012; Bonfoh *et al.*, 2003; Brown *et al.*, 2020; Basulira *et al.*, 2019; Desalegne *et al.*, 2014; Kang'ethe *et al.*, 2005; Kurwijila *et al.*, 2006; Mensah *et al.*, 2014). However, studies involving samples from small ruminant products are available only in a very few occasions. In Ghana, the prevalence of antimicrobial residues is 29.3% for kid goat meat, and 24% for lamb (Donkor *et al.*, 2011). In Nigeria, samples collected from muscles, liver and kidney of 40 slaughtered goats analyzed by using the four-plate agar diffusion method revealed that 10 (25%) were positive for antimicrobial residues. The residues occurred more and equally in kidney and liver than in the muscle. The result of this study clearly suggests that the rampant use of antimicrobial drugs in slaughter animals coupled with non-adherence to withdrawal periods is grossly practiced in Nigeria (Ezenduka and Ugwumba, 2012) and other African countries as well.

Antihelmintics trypanocidal and acaricide residue

Since the invasion of parasites causes substantial economic losses, antiparasitic drugs are frequently used in veterinary medicine. The use of such drugs in farm animals may be associated with the presence of their residues in varying concentrations in tissues and milk posing health risks to consumers and undermining the significance of their use to boost productivity.

While there are evidences on antibiotic residues in animal products arising from veterinary drug use (Treiber and Beranek-Knauer, 2021), very little study has been done on other veterinary drugs such as anthelmintics, trypanocides, coccidiostates, and acaricides. When such study exists, they come from countries outside Africa and the results were often inconclusive. For example, Jedziniak *et al.* (2015) have analyzed samples of sheep and goat dairy products in Poland and reported that none of the samples were found above the acceptable limit, CC α (1-10 $\mu\text{g}/\text{kg}$) except one which was suspected. In goats, Isometamidium was not detectable in milk following administration of therapeutic doses while no drug was detectable in the liver, kidney and spleen tissues from treated goats 6 weeks after drug administration (Kinabo and McKellar, 1990) in Tanzania. On the other hand, a review by Lumaret *et al.* (2012) has clearly demonstrate that regarding environmental impacts many macrocyclic lactones are substances of high concern particularly with larval instars of invertebrates in the dung.

3.4. Research evidence on small ruminant disease resistance traits in Africa

3.4.1. Historical overview of disease resistance study in small ruminants in Africa

Of all 54 countries of the continent, studies on disease resistance traits in small ruminants were retrieved only from 12 countries. The earliest retrieved report was obtained from Kenya. Griffin and Allonby (1979) compared trypanotolerance profile of indigenous sheep and goat breeds with exotic once. The phenotypic parameters used after experimental infection with *T. congolense* were parasitemia, mortality rates, packed cell volume (PCV), fever and weight loss. Accordingly, they found out that indigenous breeds performed better compared to exotic once. Latter more and more studies came from Kenya, Tanzania and Nigeria and The Gambia (Preston and Allonby, 1979; Mutayoba *et al.*, 1985; Whitelaw *et al.*, 1985, Adah *et al.*, 1993; Shavulimo *et al.*, 1985; Osaer *et al.*, 1994). Much of these studies were on trypanosomosis and haemonchosis and the assessments were made based on phenotypic traits with few exceptions such as the work in Kenya by Marshall *et al.*, (2012) who reported on quantitative trait loci for resistance to *Haemonchus contortus* in Red Masai and Dorper sheep. In recent years however, it seems that tick and tick borne diseases are getting attention (Mohamed and Hassan, 2007; Gopalraj *et al.*, 2013, Cloete *et al.*, 2013; Cloete *et al.*, 2016a; Elati *et al.*, 2018; Khamassi Khbou *et al.*, 2021). Despite, the four-decade history, the investigation has not moved much and the majority of the

study reports are still from Eastern and Western regions (Figure 2-C) of the continent. No study could be identified from countries in central Africa, while only few studies were accessed online from Northern and southern African regions (Elati *et al.*, 2018; Marume *et al.*, 2011). In the specified regions, Kenya, Nigeria, The Gambia and Ethiopia contributed vastly to these studies (Table 12).

Table 12. Available reports on disease resistance of small ruminants in Africa (1979-2021)

Region	Country	Disease(s)	Host	Reference
Eastern	Ethiopia	GIN, Fasciolosis, Haemonchosis	Sheep	Baker <i>et al.</i> , 1998b; Rege <i>et al.</i> , 2002; Haile <i>et al.</i> , 2002; Eguale <i>et al.</i> , 2009; Getachew <i>et al.</i> , 2015
		GIN	Goats	Haile <i>et al.</i> , 2017
	Kenya	GIN, Haemonchosis, Trypanosomosis, Fasciolosis	Sheep	Griffin and Allonby, 1979; Preston and Allonby, 1979; Mugambi <i>et al.</i> , 1996; Mugambi <i>et al.</i> , 1997; Wanyangu <i>et al.</i> , 1997; Baker <i>et al.</i> , 1998b; Baker <i>et al.</i> , 1999; Waweru <i>et al.</i> , 1999; Baker <i>et al.</i> , 2003; Baker <i>et al.</i> , 2004; Mugambi <i>et al.</i> , 2005a; Mugambi <i>et al.</i> , 2005b; Silva <i>et al.</i> , 2011; Marshall <i>et al.</i> , 2012; Benavides <i>et al.</i> , 2015
		GIN, Haemonchosis, Trypanosomosis	Goats	Griffin and Allonby, 1979; McGuire <i>et al.</i> , 1985; Whitelaw <i>et al.</i> , 1985; Shavulimo <i>et al.</i> , 1988; Mutayoba <i>et al.</i> , 1989; Baker <i>et al.</i> , 1998a; Baker <i>et al.</i> , 1998b; Baker <i>et al.</i> , 2001
	Sudan	MOT	Sheep	El Imam <i>et al.</i> , 2015
	Tanzania	GIN, Trypanosomosis	Goats	Mutayoba <i>et al.</i> , 1989; Agillah <i>et al.</i> , 2002
	Uganda	Haemonchosis, Trypanosomosis	Goats	Katunguka-Rwakishaya <i>et al.</i> , 1997; Onzima <i>et al.</i> , 2017
Western	Burkina Faso	Haemonchosis, GIN	Sheep	Traore <i>et al.</i> , 2017; Soudre <i>et al.</i> , 2018; Alvarez <i>et al.</i> , 2018; Álvarez <i>et al.</i> , 2019; Bengaly <i>et al.</i> , 1993
	Ghana	GIN	Sheep	Yaro <i>et al.</i> , 2019
	Nigeria	GIN, Haemonchosis, Trypanosomosis	Sheep	Chiezey and Oyedipe, 2009; Idika <i>et al.</i> , 2012a; Idika <i>et al.</i> , 2012b, Idika <i>et al.</i> , 2012c
			Goats	Adah <i>et al.</i> , 1993; Fakae <i>et al.</i> , 1999; Chiejina <i>et al.</i> , 2002; Fakae <i>et al.</i> , 2004; Chiejina <i>et al.</i> , 2005; Behnke <i>et al.</i> , 2006; Makun <i>et al.</i> , 2008; Chiejina <i>et al.</i> , 2009; Chiejina <i>et al.</i> , 2010; Behnke <i>et al.</i> , 2011; Makun <i>et al.</i> , 2020
	The Gambia	GIN, Haemonchosis, Trypanosomosis	Sheep	Osaer <i>et al.</i> , 1994; Goossens <i>et al.</i> , 1997; Goossens <i>et al.</i> , 1998; Goossens <i>et al.</i> , 1999
Trypanosomosis		Goats	Osaer <i>et al.</i> , 1994; Goossens <i>et al.</i> , 1998; Faye <i>et al.</i> , 2002; Dhollander <i>et al.</i> , 2005	

Region	Country	Disease(s)	Host	Reference
	Togo	Trypanosomosis	Sheep	Dayo <i>et al.</i> , 2020
Northern	Tunisia	GIN, Ticks, TBD*	Sheep	Elati <i>et al.</i> , 2018; Ahbara <i>et al.</i> , 2021; Khamassi Khbou <i>et al.</i> , 2021
Southern	South Africa	Haemonchosis, Ticks	Goats	Marume <i>et al.</i> , 2011; Gopalraj <i>et al.</i> , 2013,
			Sheep	Cloete <i>et al.</i> , 2013; Cloete <i>et al.</i> , 2016a; Mpetile <i>et al.</i> , 2015; Mpetile <i>et al.</i> , 2017; Dlamini <i>et al.</i> , 2019 (**Snyman <i>et al.</i> , 2019); Matebesi-Ranthimo <i>et al.</i> , 2014; Nieuwoudt <i>et al.</i> , 2002; Riley and van Wyk, 2009; Cloete <i>et al.</i> , 2016b; Snyman <i>et al.</i> , 2018; Snyman and Fisher, 2019;
	Zimbabwe	GIN (predominantly Haemonchosis)	Sheep	Matika <i>et al.</i> , 2003

GIN, gastrointestinal nematodes; *MOT*, malignant ovine thleriosis TBD*, Tick-borne diseases (theleriosis, babesiosis); **Snyman *et al.*, 2019 contained a duplicate with Dlamini *et al.*, 2019;

3.4.2. Overview of methodological approaches in diseases resistance studies

Earliest pilot studies used experimental infections to identify resistant breeds (Griffin and Allonby, 1979). Since then, both experimental and cross-sectional and longitudinal observational studies were conducted to study within breed and between breed resistance or susceptibility to diseases (Table 13, Table 14). Experimental studies used in identifying resistance to GINs and fasciolosis include: single infection with determined dose of the parasites (Waweru *et al.*, 1999; Eguale *et al.*, 2009; Marume *et al.*, 2011; Getachew *et al.*, 2015; Onzima *et al.*, 2017; Soudre *et al.*, 2018), trickle infection using a particular dose repeated over a period of time (Chiezey and Oyedipe, 2009; Makun *et al.*, 2008) trickle infection with escalating dose of the infective stages of the parasites (Idika *et al.*, 2012a; 2012b; 2012c), trickle superimposed infections and those trickle infections separated by anthelmintic abbreviations (Chiejina *et al.*, 2002; Fakae *et al.*, 2004; Haile *et al.*, 2004; Chiejina *et al.*, 2010). The studies also included mixed trypanosomosis and haemonchosis/GIN infections to determine the impact of the interaction that exist between the parasites (Goossens *et al.*, 1997; Chiejina *et al.*, 2009; Behnke *et al.*, 2011). Trypanotolerance studies were generally conducted using experimental exposure to trypanosomes either through parenteral injection with a given dose of trypanosomes or by allowing infected tsetse flies to feed on experimental animals (Adah *et al.*, 1993; Osaer *et al.*, 1994; Faye *et al.*, 2002).

Type of Diseases

Despite the presence of large number of diseases with devastating impacts on small ruminant production in the continent, studies that investigate resistance profile focused on three diseases by and large (Figure 6). These are GINs (as general mixed infections both under natural or experimental conditions), haemonchosis and trypanosomosis. The other disease category for which few information is available include tick infestation, babesiosis, theileriosis and fasciolosis (Table 12). No studies were available online regarding genetic resistance to some of the commonly occurring infectious viral and bacterial diseases. This implies the search for resistance breeds was limited only to parasitic diseases affecting the GI system, trypanosomosis and tick and tick-borne diseases. Therefore, there is a need for further studies on important infectious diseases like trans-boundary disease with huge morbidity, mortality and small

ruminant trade impact especially in situations where effective vaccines are lacking for most and the use of antibiotics is discouraged for various reasons.

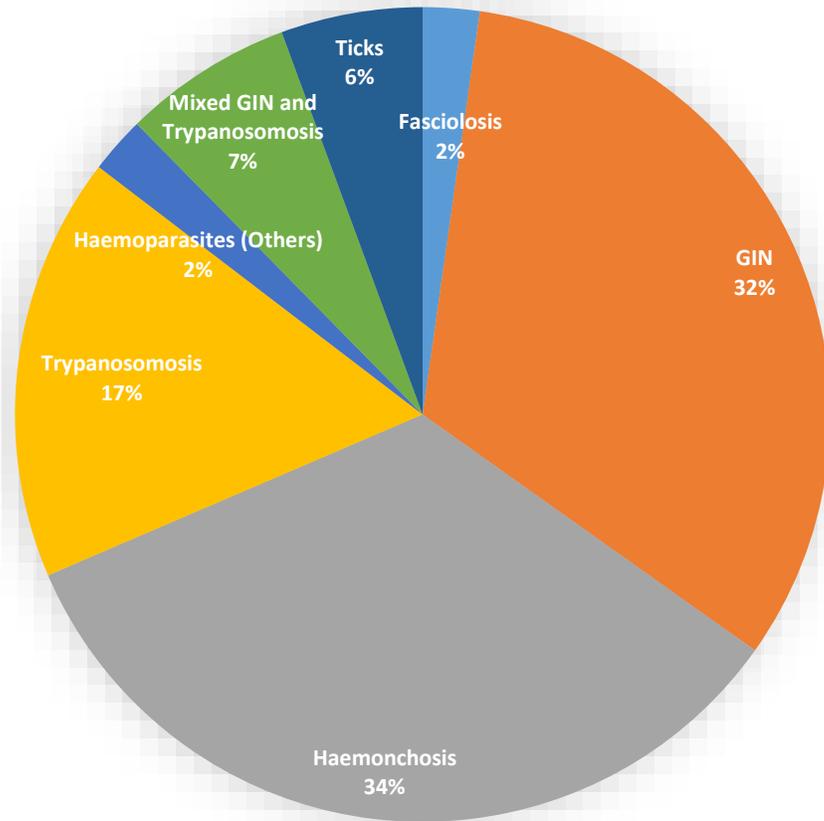


Figure 6. Proportion of diseases covered in studies of disease resistance in small ruminants in Africa

3.4.3. Phenotypic studies

3.4.3.1. Disease resistance in sheep breeds

Genetic manipulation of sheep by selective breeding offers a means to reduce the current reliance on chemotherapy for the control of gastro-intestinal nematodes. Experiences from South America and Europe show that it is possible to select sheep for resistance to helminth parasites. For example, St. Croix lambs shed significantly fewer eggs and harbor 99% fewer worms in the abomasum than the age-matched Dorset lambs during both natural and experimental infections

(Gamble and Zajac, 1992). Locally-adapted breeds such as Santa Ines sheep of Brazil have significantly reduced worm burdens and fewer nodular lesions under natural infections than Suffolk and Ile de France lambs on the same pasture (Amarante *et al.*, 2004). In Europe, resistance against *H. contortus* is shown to develop in Merino-land sheep than in Rhon sheep (Gauly *et al.*, 2002). Similarly, resistance/tolerance to liver flukes (Hansen *et al.*, 1999) in sheep and other parasitic infections such as tick borne diseases and trypanosomosis in cattle have been demonstrated in many parts of the world (Glass *et al.*, 2005; Mattioli *et al.*, 1995). Disease resistance studies in small ruminants in Africa started in the late 1970s and since then a number of sheep and goat breeds were identified. These include the small east African (SEA) goat and Red Maasai sheep in East Africa for haemonchosis (Griffin and Allonby, 1979; Baker *et al.*, 1998a, b; Mugambi *et al.*, 2005a, b), and The Djallonke and West African dwarf (WAD) goat in West Africa for haemonchosis and trypanotolerance (Osaer *et al.*, 1994; Soudre *et al.*, 2018). The details of resistance to various diseases will be discussed in the next sub-sections.

Resistance to nematodes (mixed, single infections) in sheep breeds of Africa

Disease resistance studies in Africa predominantly focus on resistance of breeds to gastrointestinal parasites acquired either through natural or artificial infections. The studies focus on mixed infection with multiple parasites as they occur under natural infection or artificial infection with some important parasites such as *H. contortus* and *Fasciola* spp. (Waweru *et al.*, 1999; Eguale *et al.*, 2009; Marume *et al.*, 2011; Getachew *et al.*, 2015; Onzima *et al.*, 2017).

Despite huge sheep population (FAOSTAT, 2021) and large number of indigenous and imported breeds of sheep in Africa (Iniguez, 2005; Gizaw *et al.*, 2007; Gizaw *et al.*, 2008; Molotsi *et al.*, 2020), studies on disease resistance of sheep breeds covered only few breeds in relatively small number of countries. Findings of the studies showed that there exist sheep breeds that were exceptionally resistant to GINs as a whole and haemonchosis and fasciolosis in particular. Red Maasai in Eastern Africa and the Djallonke sheep in western Africa were the most commonly studied breeds in this regard. The two breeds were identified as being resistant to nematode parasites by multiple studies. On the other hand, sheep breeds like Menz, Horro, Washera, Dorper and blackhead Persian/Somali sheep were reported to have relatively low resistance profile to gastrointestinal nematode parasites (Table 13).

Table 13. Phenotypic between breed variations in resistance of sheep to diseases in Africa

Disease	Breeds	Phenotypic markers	Resistant breed(s)	Study design and dose	Country	Reference
GIN	Red Maasai, Dorper, lambs	PCV, LWT, parasitaemia, Mortality, WBC, RBC, MCV, MCHC, antibodies	Red Maasai	Observational, natural infection	Kenya	Baker <i>et al.</i> , 1998b
GIN	Dorper, Red Maasai and Dorper x Red Massai crosses* ewes	LWT, PCV, FEC	Red Maasai	Observational, natural infection	Kenya	Baker <i>et al.</i> , 1999;
GIN	Dorper, Red Maasai and Dorper x Red Massai crosses, lambs	FEC, PCV	Red Maasai	Observational, natural infection	Kenya	Baker <i>et al.</i> , 2003
GIN	Red Maasai, Dorper, ewes#	LWT, PCV, FEC	Red Maasai	Observational, natural infection	Kenya	Baker <i>et al.</i> , 2004
GIN	Dorper, Dorper Backcross, Red Massai backcross, Red Massai	LWT, PCV, FEC, Mortality	Red Maasai, Red Massai backcross	Experimental, artificial infection	Kenya	Mugambi <i>et al.</i> , 2005a
Haemonchosis	Red Maasai, Dorper	FEC, PCV, Eosinophilia	Red Maasai	Both observational, experimental (5000 L ₃)	Kenya	Wanyangu <i>et al.</i> , 1997
Haemonchosis	Blackhead Persian, Corriedale, Dorper, Hampshire, Merino, Red Maasai	FEC, WB	Red Maasai	Experimental, natural infection	Kenya	Preston and Allonby, 1979
Haemonchosis	Merino, Red Maasai	FEC, WB	Red Maasai	Experimental, natural infection	Kenya	Preston and Allonby, 1979
Haemonchosis	Dorper, Red Maasai, in 4-5 month lambs	Mortality, FEC, PCV, Eosinophils, total serum	Red Maasai	Experimental, trickle infection	Kenya	Mugambi <i>et al.</i> 1996

Disease	Breeds	Phenotypic markers	Resistant breed(s)	Study design and dose	Country	Reference
		protein				
Haemonchosis	Red Massai, Blackhead Somali, Dorper, Romney Marsh	FEC, PCV, mortality	Red Maasai	Experimental, natural infection	Kenya	Mugambi <i>et al.</i> , 1997
Haemonchosis	Red Massai, Blackhead Somali, Dorper	Mortality, FEC, PCV	Red Maasai	Experimental, 10000 L ₃ orally	Kenya	Mugambi <i>et al.</i> , 1997
Haemonchosis	Dorper, Dorper Backcross, Red Massai backcross, Red Massai	LWT, PCV, FEC, Mortality	Dorper backcrosses	Experimental, trickle weekly infection	Kenya	Mugambi <i>et al.</i> , 2005b
Trypanosomosis	Merino, Blackhead persian, Red Maasai	PCV, parasitaemia, LWT, Mortality	Red Maasai	Experimental, 1*10 ⁴ Tc, iv	Kenya	Griffin and Allonby, 1979
Fasciolosis (F. gigantica)	Red Maasai, Dorper	FEC, PCV, WB, eosinophils	Red Maasai (relative)	Experimental, oral, 400 metacercariae	Kenya	Waweru <i>et al.</i> , 1999
GIN	Menz, Horro	FEC, PCV, LWT, Mortality	None*	Observational, natural infection	Ethiopia	Baker <i>et al.</i> , 1998b
GIN	Menz, Horro	FEC, PCV	None*	Observational, natural infection	Ethiopia	Rege <i>et al.</i> , 2002
GIN	Menz, Horro	FEC, PCV, LWT, WB	None*	Experimental, mixed trickle infection	Ethiopia	Haile <i>et al.</i> , 2004
Haemonchosis	Menz, Washera	FEC, PCV	None*	Experimental, 5000 L ₃	Ethiopia	Getachew <i>et al.</i> , 2015
Fasciolosis (F. hepatica)	Menz, Horro, Arsi	FEC, PCV, WB, LWT, liver WT, Eosinophils, Mortality	Horro (relative)	Experimental, oral, 300 metacercariae	Ethiopia	Eguale <i>et al.</i> , 2009
Malignant ovine	Garag, Watesh,	Morbidity, PCV, RBC &	Garag and Watesh	Experimental, natural	Sudan	El Imam <i>et al.</i> , 2015

Disease	Breeds	Phenotypic markers	Resistant breed(s)	Study design and dose	Country	Reference
theileriosis	Desert	WBC count,	(relative)	infection		
Haemonchosis	Djallonké, Sahelian	FEC, PCV, FAMACHA, mortality, LWT	Djallonké (based on mortality and live weight)	Experimental, 5000 L ₃	Burkina Faso	Soudre <i>et al.</i> , 2018
GIN and Trypanosomosis	Djallonké, Djallonké X Sahelian sheep	Parasitemia, PPP, antibody response	Djallonké	Experimental, natural infection for GIN and 1*10 ⁵ Tc, iv	The Gambia	Goossens <i>et al.</i> , 1999
Trypanosomosis	Vogan, Djallonke	PCV	Djallonké*	Observational, natural infection	Togo	Dayo <i>et al.</i> , 2020
Trypanosomosis	Djallonké, Sahelian Fulani sheep	Survival	Low mortality in Djallonké	Experimental	Burkina Faso	Bengaly <i>et al.</i> , 1993
Typanosomosis	Djallonké sheep and WAD goats	Weight gain, Parasitemia, PCV, survival rate	Both species are trypanotolerant		The Gambia	Osaer <i>et al.</i> , 1994
Tick infestation	Barbarine, Queue Fine de l'Ouest	Prevalence, tick counts	Barbarine	Observational, natural infestation	Tunisia	Elati <i>et al.</i> , 2018
Tick infestation	Barbarine, Queue Fine de l'Ouest	Prevalence, tick counts	Queue Fine de l'Ouest	Observational, natural infestation	Tunisia	Khamassi Khbou <i>et al.</i> , 2021
Tick infestation	Namaqua Africaner, Dorper, South African meat merino	Tick counts	Namaqua Africaner	Observational, natural infestation	South Africa	Cloete <i>et al.</i> , 2013; Cloete <i>et al.</i> , 2016a
Piroplasms	Barbarine, Queue Fine de l'Ouest	Prevalence, PCR	Queue Fine de l'Ouest	Observational, natural, PCR based	Tunisia	Khammisi Khamassi Khbou <i>et al.</i> , 2021
GIN	Sabi, Dorper	FEC, PCV	Sabi	Observational, natural infection	Zimbabwe	Matika <i>et al.</i> , 2003

BCS, body condition score; *FEC*, fecal egg count; *GIN*, gastrointestinal nematodes; *iv*, intravenous; *L3*, third stage larvae; *LWT*, live weight; *MCHC*, mean corpuscular hemoglobin concentration; *MCV*, mean corpuscular volume; *SEA*, Small East African goat; *Tc*, *T. congolense*; *Tb*, *T. brucei*; *WAD*, West African dwarf goat; *WB*, worm burden sc, subcutaneous

**Red Maasai X Dorper crosses are mid-way between the pure breeds; #there was a genotype by environment interaction (Red Maasai was better at humid costal zones, while no difference in the dry highlands of Kenya, i.e. Dorper are more productive on highlands as they are heavier than the red Maasai.*

**Menz sheep are better adapted to the experimental station where they are native however, GINs are not major problems of sheep to exert any selection pressure. In all experimental and natural infections at Debre Birhan, Menz sheep are more adapted than Horro and Washera.*

♦Depends on the location in Togo, Djallonke sheep in plateau region had significantly higher PCV than both the Djallonke and Vogan sheep in the maritime region.

The majority of small ruminant breeds in Africa are considered as ‘poorly productive’ and hence efforts at improving their productivity depend on transgression of exotic blood through cross breeding. Small ruminants in Africa are largely kept by small holder farmers in the mixed-crop livestock systems or by pastoralists in the low input/output harsh arid and semi-arid environments as indigenous breeds with little artificial selection for economically important traits. Therefore, the pressure exerted by the endemic diseases in their natural environment has resulted in a wide range of response phenotypes to the diseases to which they are exposed.

Studies to verify the presence of within breed variations for resistance to infection with nematode parasites were conducted by partitioning the study population into various groups based on FEC (measure of resistance) and PCV (measure of resilience). Strong responders (resistant phenotypes) therefore are characterized by low FEC or worm burden and higher PCV. The susceptible phenotypes have higher FEC and lower PCV. Accordingly, several studies confirmed the existence of wide within breed individual variations for resistance to GIN where majority of the study subjects harbor few or no parasites as determined by low fecal egg count or worm burden while others on the other cohorts harbor large number of worms and excrete large number of eggs per gram of feces on pasture (Table 14). Some animals were found intermediate between the two extremes. In some resistant breeds, the resistant phenotype is demonstrated by the majority of animals in the breed considered (Chiejina *et al.*, 2002; Fakae *et al.*, 2004; Behnke *et al.*, 2006). The individual variations in resistance to GINs may be exploited for selection of breeding animals within breed so that better performing animals based on phenotypic and genotypic markers are selected as the next breeding stock (Figure 7)

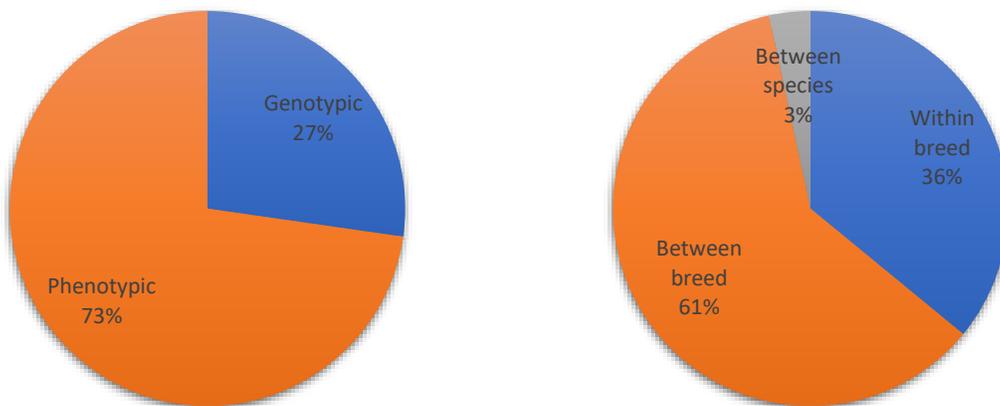


Figure 7. Types of resistance and sources of variations studied in small ruminants in Africa

Table 14. Phenotypic within breed variations in resistance of sheep breeds to diseases in Africa (1979-2021).

Disease	Within breed cohorts compared	Resistant cohorts	Study design	Country	Reference
Haemonchosis	trickle infections of L ₃ which totaled G1 = 35,000 (i.e. 5000L ₃ *7 day), G2 = 14,000 (2000L ₃ *7days) and G3 =2800 (400L ₃ *7 days) <i>Yansaka rams</i>	Survivors of the infection from all cohorts were resistant, as susceptible animals died early in the experiment	Experimental, trickle infection	Nigeria	Chiezey and Oyedipe, 2009
GIN	Low FEC, Intermediate FEC and High FEC cohorts based on EPG following escalating trickle infection of <i>WAD</i> ^ϕ <i>sheep</i>	Low FEC group	Experimental, escalating trickle infection	Nigeria	Idika et al., 2012a
GIN	H. contortus: Low Wb, High Wb; T. colubriformis: Low Wb, High Wb phenotypes of <i>WAD sheep</i>	Low Wb phenotype	Experimental, escalating, mixed trickle infection	Nigeria	Idika et al., 2012b
GIN	Strong, intermediate and weak responders based on EPG following escalating, trickle mixed H. contortus and T. colubriformis infection on <i>WAD sheep</i>	Strong responders	Experimental, escalating, mixed trickle infection	Nigeria	Idika et al., 2012c
GIN	<i>Djallonke sheep</i> were dewormed and returned to infected pasture; FEC was measured on D28 and D35	No difference in FEC, some sheep, however, had no detectable level of infection (FEC=0) (i.e. 40% male and 30% female lambs)	Observational, natural infection	Burkina Faso	Traore et al., 2017

EPG, egg per gram of feces; *FEC*, fecal egg count, *WAD*, West African Dwarf; *Wb*, worm burden; ^ϕ*WAD sheep* is another name for *Djallonk*

Resistance to *Fasciola* spp.

Despite the widespread prevalence of small ruminant fasciolosis in many countries of Africa (Odeniran *et al.*, 2021; Jules *et al.*, 2020; Isah, 2019; Adediran *et al.*, 2014; Mungube *et al.*, 2006; Haridy *et al.*, 1999) and its presumed economic impact (Abunna *et al.*, 2010; Nigategize *et al.*, 1993), the authors retrieved only two reports which have attempted to evaluate the resistance or resilience of African sheep breeds against *Fasciola* infections. Eguale *et al.* (2009) in their comparison between Arsi, Horro and Menz sheep of Ethiopia have indicated that Horro breed has performed better on the basis of fecal egg count, packed cell volume and weight gain than the other two. Similarly, the Red Maasai sheep in Kenya (Waweru *et al.*, 1999) was found to be relatively resistant to *F. gigantica* experimental infection.

Resistance to ticks

Resistance to ticks is expressed in terms of differences in the degree of tick infestation, tick abundance and intensity of tick infestation under natural pasture conditions. In few such studies that were available online, researchers in Tunisia compared the same two indigenous breeds of sheep (Barbarine, Queue Fine de l'Ouest) and reached at contradictory results as to which breed was resistant to tick infestation (Elati *et al.*, 2018; Khamassi Khbou *et al.*, 2021). The most recent study by Khamassi Khbou *et al.* (2021), who found Queue Fine de l'Ouest to be the resistant breed, argues that the earlier study that found Barbarine breed to be resistant, was conducted in large intensive farms in just one location in Tunisia and therefore, the finding could not be conclusive of the breeds in their natural environment and management systems across the country.

Two related studies in South Africa showed that breed difference affected the count of ticks in different body sites as well as the overall tick burden. Accordingly, the indigenous fat-tailed Namaqua Afrikaner (NA) sheep breed had the lowest tick count in all the different body areas compared to Dorper and South African Mutton Merino (SAMM), both of which are commercial breeds. The studies also showed that udder health (expressed on a score of 1-5 scale, where score 1 describes fully healthy udder and score 5 describes damaged udder and teats that may warrant culling) in ewes was genetically related to tick counts and both were heritable traits (Cloete *et al.*, 2013; Cloete *et al.*, 2016a). The udder health score was the lowest in NA. Udder health

deterioration worsened from NA to Dorper and from Dorper to SAMM with overall differences ranging from 47% in Dorper to 112% in SAMM compared to NA (Cloete *et al.*, 2016a).

Resistance to tick-borne haemoparasites

Tick-borne haemoparasites are recognized as part of the diseases that cause serious losses in livestock in Africa. Studies on breed resistance to diseases such as babesiosis and theileriosis are scanty. During the literature search for the current review, only few studies were accessed online. One such study from Sudan investigated the susceptibility of three sheep breeds in Sudan to malignant ovine theileriosis. The findings revealed that Garag and Watesh breeds were relatively less susceptible with morbidities of 43.8% and 53.3% respectively, than the Desert breed that suffered 92.9% morbidity when all ecotypes were experimentally exposed to sheep kept in a known infected sheep farm where both the parasite (*Theileria lestoquardi*) and its vector tick (*Hyalomma anatolicum*) were endemic (El Imam *et al.*, 2015). The other accessible study compared resistance of two common sheep breeds in Tunisia to piroplasms. Accordingly, out of 151 Queue Fine de l'Ouest (QFO) ewes tested for DNA of the parasites with PCR that targets a common sequence ARNr18S to both *Babesia* and *Theileria* genera using catch-all primers, no single animal was infected with the piroplasms. On the other hand, all 21 sheep that tested positive for the DNA of piroplasms (n=21/288) were from Barbarine sheep sampled from the same regions as that of the QFO (Khamassi Khbou *et al.*, 2021). However, whether this was the result of genetic resistance of the breed to the piroplasms or the result of resistance of the breed to vector ticks (as described earlier) or any other factors is a matter for further investigation.

Trypanotolerance

Early pilot study conducted on trypanotolerance of sheep breeds to trypanosomes was conducted by Griffin and Allonby (1979). The study demonstrated that the indigenous sheep breed, Red Maasai, demonstrated resilience against trypanosomes by having no mortality, short period of parasitaemia and continued weight gain up until week 17 following experimental infection as opposed to Merino sheep that suffered heavy weight loss and death in half of the experimental animals during fourth week of infection. Blackhead Persian sheep demonstrated better resilience than the Merino but lower than the Red Maasai.

In other trypanotolerance studies in west Africa, researchers at the International Trypanotolerance Center in The Gambia compared the relative resilience to trypanosomiasis between local indigenous goat and sheep breeds that were considered to be trypanotolerant. In these studies, the investigators based on phenotypic traits concluded that both WAD goats and Djallonke sheep in the Gambia are trypanotolerant even though the WAD goats appear to suffer relatively more than the Djallonke sheep (Osaer *et al.*, 1994; Goossens *et al.*, 1998). On the other Osaer *et al* (1999) from the same center reported that Djallonke sheep kept under high and moderate trypanosomiasis challenge did not show similar level of performance as the one described above. They exhibited significantly reduced PCV, depressed weight gain, longer parturition period and significant lamb mortality rate suggesting different factors (such as nutrition) may influence trypanotolerance under natural and experimental conditions. One other possible explanation could be, transgression of genes from susceptible sheep breeds into those that were supposed to be resistant might have resulted in loss of trypanotolerance. This was especially demonstrated in the Djallonke sheep in Togo, where the breed in the Plateau region was shown to be more trypanotolerant than those in the Maritime region that were in direct contact with the trypanosusceptible Vogan breed (Dayo *et al.*, 2020).

This showed that classification of sheep into the various breeds using only phenotypic traits may undermine the usefulness of such studies as susceptibility to a particular disease might be associated with loss of resistance due to crossbreeding with other susceptible breeds in the region. In fact, genetic improvement programs based on crossbreeding without first understanding the merit of each indigenous breed under the conditions the breed evolved, would only result in the loss or erosion of important functional traits. In this regard, Baker *et al.*, (1998b), demonstrated that the Red Maasai performed two to three folds better than the improved Dorper breed under humid coastal regions of Kenya; therefore, under such circumstances crossbreeding would have no merit to the sheep herders.

3.4.3.2. Disease resistance in goat breeds

Resistance to gastrointestinal nematodes

Similar with the studies in sheep breeds, there were variations in goat breeds in Africa in their ability to respond to endemic diseases. Two goat breeds predominate the study of goat resistance

to different parasites and diseases in Africa. The Small East African goat and the West African Dwarf goat are recognized as breeds with some degree of resistance to mixed GIN and haemonchosis (Table 15). Goats that evolved under higher parasite burden such as the SEA and WAD goats in humid zones develop more resistance than other indigenous goat breeds of arid regions of Africa. Concerning SEA goat there were contradicting findings that suggest they may not be any different from other breeds of indigenous goats (Shavulimo *et al.*, 1988). A study in Uganda found that the local Mubende breed was more resistant to haemonchosis compared to SEA and Kigezi breeds. Other GIN resistant goat breeds from Africa include Xhosa and Nguni from South Africa, and Red Sokoto from Nigeria (Marume *et al.*, 2011; Makun *et al.*, 2008).

Variation between breeds of goats were also observed for different diseases. Small East African goats were identified to be resistant to GINs in most of the studies reported (Table 15). However, they were either not different from other goat breeds in their susceptibility to trypanosomosis (Whitelaw *et al.*, 1985) or only less susceptible compared to other breeds in Uganda (Katunguka-Rwakashaya *et al.*, 1997). Similarly, the Red Sokoto in Nigeria was more resistant to GINs compared to the Sahelian breed, but, susceptible to trypanosomosis compared to WAD goats. Therefore, comparative advantages for the utilization of these breeds need to be further studied in the context of the natural environment under which they evolved. For example, in the humid trypanosomosis and haemonchosis endemic regions of West Africa, the WAD goat appears to be the most advantageous breed to keep regardless of its dwarf stature (Chiejina *et al.*, 2009; Behnke *et al.*, 2011). In this environment, the WAD goats were 68% more productive than their larger counterparts in the presence of parasite challenge (ILCA, 1979). Moreover, they decrease the need for chemotherapy and therefore, the selection pressure on the parasites that might select for drug resistant phenotypes. With regards to GINs, resistant goat breeds shed lower number of parasite eggs on pasture, reducing pasture contamination and thereby re-infection (Saddiqi *et al.*, 2011).

Table 15. Phenotypic between breed variations in resistance of goats to diseases in Africa from 1979-2021

Disease	Breeds	Resistant breed(s)	Study design and dose	Country	Reference	
GIN	SEA, Galla	LWT, FEC, PCV	SEA	Observational, natural infection	Kenya	Baker et al., 1998a, 1998b, Baker <i>et al.</i> , 2001
Haemonchosis	SEA, Galla	LWT, FEC, PCV	None	Experimental, oral, 500L ₃ /kg	Kenya	Shavulimo <i>et al.</i> , 1988
Haemonchosis	Sahelian, Red Sokoto	LWT, FEC, PCV	Red Sokoto	Experimental, ascending trickle oral infection, 75 L ₃ /Kg, 100 L ₃ /Kg	Nigeria	Makun <i>et al.</i> , 2008
Trypanosomosis	WAD, Red Sokoto	Parasitaemia, PCV, LWT, Mortality	WAD	Experimental, 1*10 ⁵ Tc	Nigeria	Adah <i>et al.</i> , 1993
Haemonchosis	Xhosa, Nguni, Xhosa-Boer cross and Boer goats	LWT, BCS, PCV, FEC, Eosinophils	Xhosa and Nguni; Xhosa>Nguni	Experimental, oral, 7200 L ₃	South Africa	Marume <i>et al.</i> , 2011
Tick infestation	Nguni, Saanen, Saanen X Nguni crosses	Count, immunologic response on successive infestations	Nguni	Experimental, Adult ticks directly applied to shaved back skin infestations were measured	South Africa	Gopalraj <i>et al.</i> , 2013
Trypanosomosis	Saanen, Saanen X Galla, Galla, SEA	PCV, parasitaemia, LWT, Mortality	SEA	Experimental, 1*10 ⁵ Tc (iv)	Kenya	Griffin and Allonby, 1979
Trypanosomosis	SEA, Galla	Parasitaemia, PCV, MCV, MCHC, Mortality	None	Experimental, 1*10 ⁵ Tc (sc)	Kenya	Whitelaw <i>et al.</i> , 1985
Trypanosomosis	SEA, Galla, SEA X Galla, SEA X Nubian, SEA X Toggenburg	>>	None	Experimental, (Allowing infected tsetse to feed)	Kenya	Whitelaw <i>et al.</i> , 1985

Disease	Breeds	Resistant breed(s)	Study design and dose	Country	Reference	
Trypanosomosis	Toggenburg, Nubian, Alpine, Saanen	Parasitaemia, PCV, LWT, Mortality	None	Experimental, 1*10 ⁴ Tc and later 1*10 ⁴ Tb per Kg of LWT (iv), imported goats	Kenya	McGuire <i>et al.</i> , 1985
GIN	Boran, Bati, Shinille	FEC, PCV, LWT, BCS	inconclusive	Observational, natural infection	Ethiopia	Haile <i>et al.</i> , 2018
Trypanosomosis	Kigezi, Mubende, SEA	PCV, parasitaemia, LWT, Mortality	SEA*	Experimental, 1*10 ⁵ Tc (iv)		Katunguka-Rwakishaya <i>et al.</i> , 1997
Haemonchosis	Kigezi, Mubende, SEA	FEC, PCV, LWT, WB	Mubende	Experimental, oral, 18000 L ₃	Uganda	Onzima <i>et al.</i> , 2017

*least susceptible; BCS, body condition score; FEC, fecal egg count; GIN, gastrointestinal nematodes; iv, intravenous; L₃, third stage larvae; LWT, live weight; MCHC, mean corpuscular hemoglobin concentration; MCV, mean corpuscular volume; SEA, Small East African goat; Tc, *T. congolense*; Tb, *T. brucei*; WAD, West African dwarf goat; WB, worm burden sc, subcutaneous

Within breed individual variations that may be exploited for improvement of the indigenous goats are common among the goat breeds of Africa. This was shown by the presence of various phenotypes of WAD goats and different phenotypic ecotypes of the SEA goats with different degrees of resistance to GIN infections including haemonchosis. As for studies in sheep breeds, WAD goats were segregated into different FEC and Wb groups and phenotypic markers were measured either under natural infection (Behnke *et al.*, 2006) or following artificial challenge (Fakae *et al.*, 2004). The findings showed that there are resistant individuals and strains or ecotypes of goats within the breed (Table 16).

Table 16. Phenotypic within breed variations in resistance of goats to diseases in Africa (1979-2021).

Disease	Within breed cohorts compared	Resistant cohorts	Study design	Country	Reference
GIN	WAD goats: Strong responders, Intermediate responders, weak responders	Strong responders	Observational, Live goats, FEC	Nigeria	Behnke <i>et al.</i> , 2006
GIN	WAD goats: Strong responders, Intermediate	Strong responders	Observational, slaughtered goats, Wb	Nigeria	Behnke <i>et al.</i> , 2006

	responders, weak responders based on FEC & Wb				
GIN	Strains of SEA: Ujiji, Newala, Gogo,	Gogo	Experimental, 2000 larvae/ml two times fortnightly	Tanzania	Agillah <i>et al.</i> , 2002
Haemonchosis	WAD goats: High FEC/Wb, Low FEC/Wb phenotypes	Low FEC/Wb phenotypes, however, >80% goats had <5% of the challenge dose	Experimental, trickle escalating infection with anthelmintic abbreviation and re-infection	Nigeria	Fakae <i>et al.</i> , 2004
Haemonchosis	WAD goat: High FEC, Low FEC phenotypes	Both phenotypes maintained good resistance	Experimental, trickle escalating infection with anthelmintic abbreviation	Nigeria	Chiejina <i>et al.</i> , 2010
Haemonchosis	WAD goats: Experiment 1 = 5000 L ₃ ; experiment 2 = 2000 L ₃ primary + 2000 L ₃ challenge	Resistant genotypes exist among the WAD goat population; 63% of the inoculum established but 77% of established worms were expelled by week 5	Experimental, following exposure to 5000 L ₃ ,	Nigeria	Fakae <i>et al.</i> , 1999
Trypanosomosis	SEA goat strains: Lambwe, Arusha, Morogoro, Imbo	Morogoro (better), however, all suffered from morbidity and mortality	Experimental, 2.4*10 ⁵ Tc inoculated (iv)	Tanzania and Kenya	Mutayoba <i>et al.</i> , 1989
GIN infection, Trypanosomosis	WAD goats	Majority of WAD maintained good BCS and PCV	Observational, natural exposure	Nigeria	Behnke <i>et al.</i> , 2011
Haemonchosis, Trypanosomosis	WAD goats: good responders (low FEC), poor responders (high FEC)	No significant difference between the two for FEC; Low FEC > high FEC phenotypes for PCV and Wb in Tb infected groups	Experimental, escalating trickle infection (total L ₃ =9500 Hc); followed by 5*10 ⁷ Tb	Nigeria	Chiejina <i>et al.</i> , 2005
Haemonchosis, Trypanosomosis	WAD ecotypes: Humid zone, savannah zone	Both phenotypes are resistant to haemonchosis and are trypanotolerant	Experimental, 5*10 ⁶ Tb inoculation (sc) followed by 6000 L ₃ orally	Nigeria	Chiejina <i>et al.</i> , 2009

BCS, body condition score; FEC, fecal egg count; GIN, gastrointestinal nematode; Hc, H. contortus; Wb, worm burden; iv, intravenous; L₃, third stage larva; PCV, packed cell volume; sc, subcutaneous; SEA, small East African; Tb, T. brucei; Tc, T. congolense; WAD, West African Dwarf

Resistance to ticks

Resistance of goat breeds to tick is rarely studied, only one study from South Africa was available online during literature search for this review. In this study by Gopalraj *et al.* (2013), unfed adult *Rhipicephalus appendiculatus* ticks were glued in a linen bag onto a shaved back of indigenous South African breed (Nguni), Saanen and Nguni X Saanen crosses. Ticks were allowed to feed till engorgement where they are collected and followed by another batch of unfed ticks for a total of three batches. Gamma globulin levels, engorged female tick mass and number of ticks completing the blood meal were evaluated. The result revealed that the level of gamma globulin levels increased significantly for all the three breeds indicating strong acquired immune response against successive exposure to ticks. However, the increases in gamma globulin levels were significantly higher in Nguni. Considering all the three parameters measured, Nguni breed had the strongest immune response to tick infestation followed by the Saanen X Nguni crosses and Saanen.

Trypanotolerance

Griffin and Allonby (1979) observed SEA goats to be resistant among other breeds of goats which included the exotic Saanen, Galla and Saanen X Galla crosses. Latter, Whitelaw *et al.* (1985) conducted two experimental studies where goats were inoculated subcutaneously with the same dose as those used by Griffin and Allonby, and another one where goats were exposed to infected tsetse flies. Their findings suggest that there was no difference in trypanotolerance between all breeds of goats in the experiment including SEA X Galla, SEA X Nubian and SEA X Toggenburg crosses in addition to SEA and Galla breeds (Table 15). The difference between the two might be explained by the difference in the pathogenicity of the strains of *T. congolense* used or the previous experience of goats used in the experiments with trypanosomes. Indeed, the prior history of goats used in the Griffin and Allonby (1979) experiment was not described. A similar inconsistency can be observed in studies performed on Wad goats in West Africa. Although Osaer *et al.* (1994) and Goossens *et al.* (1998) in their experimental studies suggested that the WAD goats from West Africa are trypanotolerant based on phenotypic parameters, other more recent reports show that this may not be the case. Investigators in the same center in the Gambia did not find the WAD goats and their F1 crosses with Saanen to be trypanotolerant. These studies showed that both breeds were equally susceptible to *T. congolense* under

experimental infections (Faye *et al.*, 2002; Dhollander *et al.*, 2005). One essential difference between the two groups of studies was that the later studies used a ten-fold infectious (10^4 vs 10^5) dose of *T. congolense* as those used in the previous studies. The other plausible explanation could be the presence of different ecotypes of goats within the breeds with varying degrees of trypanotolerance as demonstrated by Agillah *et al.* (2002) where some ecotypes of the SEA goats were more resistant than others.

Within breed variation in trypanotolerance was observed in various breeds of goats in Africa. It was demonstrated in studies conducted on WAD goats that transgression of genes from trypano-susceptible goats such as the Sahelian into the WAD has considerably reduced the trypanotolerance of the breed in WAD populations in The Gambia (Dhollander *et al.*, 2005). Therefore, studies conducted in such regions based on phenotype of the goats alone might result in erroneous conclusions.

3.4.4. Genotypic studies

3.4.4.1. Heritability of disease resistance traits in small ruminants in Africa

Heritability of resistance traits were studied in few breeds of sheep and goats and their progenies. Overall, the heritability of indirect measures of resistance, *i.e.* FEC, and measures of resilience, PCV, to GINs appears to be small (Table 17). Implying that genetic gains would be small and any improvement in resistance to GINs requires long time and many generations of selection. The traits were better inherited in the less resistant (in Dorper sired lambs (0.35 ± 0.16) than in Red Maasai (0.06 ± 0.07)) or less adapted (0.23 ± 0.09 in Horro compared to 0.09 ± 0.05 in Menz sired lambs) sheep breeds (Baker *et al.*, 1998b; Rege *et al.*, 2002; Baker *et al.*, 2003). Recently, however Dlamini *et al* (2019) in their genomic study reported a bit different finding to the earlier reports where the majority (88%) of animals in resistant genetic cluster (principal component analysis cluster) were the progeny of sires selected from resistant line and consequently concluded the possibility of using helminth resistant sires for development of the traits in question in selective breeding program. In fact, as per Snyman and fisher (2019), the heritability of proxy indicators, *i.e.* FEC, FAMACHA and body condition scores in the entire observation were moderate. On the other hand, the sheep breeds in Ethiopian were considered sensitive to

nematode parasites, but the proxy traits considered showed the heritability noted in the summary below.

Table 17. Heritability (h^2a) of GIN resistance in sheep and goat breeds in Africa

Country	Breed (s)	Age	Heritability (h^2a) of traits		Remark	Reference
			LFEC	PCV		
Kenya	Red Maasai, Dorper, sires and their crosses (sheep)	At 3-months	0.01±0.04 (NS)	NS		Baker <i>et al.</i> , 1998b
		At 6-month	0.09±0.03*	0.11±0.05*		
		At 8-month	0.18±0.08	NA	h^2a for LFEC is higher in Dorper sired lambs (0.35±0.16) than in Red Maasai sired ones (0.06±0.07)	
Ethiopia	Menz, Horro, sires and their crosses (sheep)	At 3-month	0.14±0.05*	NA	Better adapted Menz lambs had lower h^2a than Horro (0.09±0.05 Vs 0.23±0.09)	
		At 1 year	0.01±0.02	NA		
Kenya	Galla, SEA goat, sires and their crosses	At 5-month	0.10±0.06	0.11±0.07		
Kenya	Galla, SEA goat, sires and their crosses	At 4·5 and 8 month	0·13±0·07	0.18±0.08		Baker <i>et al.</i> , 2001
Ethiopia	Menz, Horro	At 1-month	NA	0.18±0.04	Horro lambs had higher numerical h^2a at weaning than Menz (0.21±0.08 vs 0.09 ±0.04)*	Rege <i>et al.</i> , 2002
		At 2-month	0.15±0.04*	0.09±0.03*		
		At 3-month	0.13±0.04*	0.07±0.03*		
		At 12-month	0.01±0.02	0.10±0.04*		
Kenya	Red Maasai, Dorper and Red Maasai × Dorper crossbred	At 6 and 8 months	0·12±0·05 (sire model)	0·14±0·05 (animal model)	h^2a for four repeated measures (6, 8, 10, 12) for LFEC, Dorper sired lambs had significantly higher h^2a than Red	Baker <i>et al.</i> , 2003
		6, 8, 10 and 12 months	0·10±0·03 (sire model)	0·11±0·04 (animal model)		

	lambs				Maasai (0.150±0.05 Vs 0.00±0.02) in animal model and (0.19±0.07 Vs 0.01 ±0.02) in sire model	
Burkina Faso	Djallonke sheep ^φ	2, 3 and 4 months	0.063±0.037 to 0.173±0.076	0.073±0.045 to 0.133±0.084	to	Álvarez <i>et al.</i> , 2018
South Africa	Merino	9-12 months	0.10 ± 0.04	NA		Mpetile <i>et al.</i> , 2015
South Africa	Merino	NA	0.07 ± 0.05 in autumn, 0.13 ± 0.05 in winter and 0.19 ± 0.05 in spring	NA		Mpetile <i>et al.</i> , 2017
South Africa	Merino		0.18 ± 0.033	NA		Cloete <i>et al.</i> , 2007
South Africa	Merino	13-16 months	0.16	NA		Matebesi-Ranthimo <i>et al.</i> , 2014
South Africa	Merino		0.24 ± 0.02	0.14 ± 0.02		Nieuwoudt <i>et al.</i> , 2002
South Africa	Merino lambs	4-10 months	0.22 ± 0.06	0.25 ± 0.06		Riley and Van Wyk, 2009
South Africa	Merino	weaners, hogget	0.12±0.04 to 0.14±0.05	NA		Cloete <i>et al.</i> , 2016b
South Africa	SA Dohne Merino	lambs	0.22 ± 0.06	NA		Snyman <i>et al.</i> , 2018
South Africa	SA Dohne Merino	lambs	0.26 ± 0.05			Synman and Fisher, 2019

*significant at stated age; *not significant; ^φ artificial pedigree estimation of heritability using relationship matrix obtained from an artificial pedigree constructed using the program MOLCOAN and between-individuals Ritland's (1996) coancestry matrix, LFEC: Log transformed fecal egg count, PCV: Packed cell volume

Heritability of log transformed FEC and PCV reported from genotypic studies in South African Merino sheep breed lines selected for various production traits are mostly moderate. The

heritabilities were affected by season of the year (Mpetile *et al.*, 2017), locality (Cloete *et al.*, 2016b), degree of parasite challenge, weather FEC values from sheep drenched with anthelmintics during the study were excluded from analysis or included with some penalty ((Riley and Van Wyk, 2019) and mathematical transformations used in analysis (Matebesi-Ranthimo *et al.*, 2014). Generally, genetic gains for resistance to GINs, especially *H. contortus*, in these breeding lines may be achieved relatively faster.

In fact, in South African Dohne Merino stud farm at Wauldby, where rampant resistance to at least five families of anthelmintic constrained sheep production, project aimed at selecting for resistance to *H. contortus* without affecting reproductive performance and production traits commenced in 2011. Based on FEC, FAMACHA score and BCS, the most resistant ewes were mated with the most resistant rams in a single sire mating (1 ram with 40 ewes). In the consecutive generations, only lambs that required no anthelmintic drenching were used as replacements. Over the years, the number of lambs that required anthelmintic drenches reduced successively. During 2011 lambing season only 33 % of ewe and 45% of ram lambs required no drenching. However, lambs born during 2016, became more resistant to haemonchosis so that no anthelmintic drenching was required for 77 and 82% of ram and ewe lambs, respectively. Moreover, the most resistant sire mated to resistant ewes, produced only 53% lambs that required no drenching in 2011, this figure improved to 77% in 2014 and 97% in 2016 (Snyman and Fisher, 2018) supporting the possibility of achieving good result in relatively shorter period when heritability is reasonably high.

With regards to heritability of tick counts, a study by Cloete *et al.* (2016a) indicated that counts from different parts of the body were heritable and repeatable in different sheep breeds. Heritability of different body area tick counts in three sheep breeds of South Africa (NA, Dorper, SAMM) range from 0.07 ± 0.06 for perineum-breech-tail tick count (PBTTC) to 0.53 ± 0.04 for udder-pelvic limb tick count (UPLTC). Heritability for head-thoracic limb tick count (HTLTC), total tick count (TTC) and udder health score were 0.26 ± 0.04 , 0.44 ± 0.06 , and 0.61 ± 0.03 , respectively. The genetic correlation between the HTLTC and UPLTC was 0.58 and that between UPLTC and udder health score was 0.47 indicating that ewes with high tick counts were more likely to have damaged udder and teats (Cloete *et al.*, 2016a). No other study in Africa reported heritability of tick counts.

3.4.4.2. *QTL-based disease resistance using microsatellite markers in small ruminants in Africa*

In this regard, only few studies conducted using microsatellites were available. Studies by Silva *et al.* (2011) and Marshall *et al.* (2012) were both conducted on the same population of Red Maasai and Dorper backcrosses under natural infection or artificial in house exposure to mixed *H. contortus* and *T. colubriformis* infections, respectively. In both studies, 172 microsatellite loci covering 25 autosomes (total map distance of 1560.7 cM) were performed for average FEC (AVFEC), average PCV (AVPCV), PCV at start of the exposures (PCVST), packed cell volume decline (PCVD) and average live weight (AVLW). These studies clearly demonstrated that the measured phenotypic traits were under the control of multiple quantitative trait loci distributed over large number of chromosomes implying that resistance to GINs is polygenic. The fact that different QTL mapping models (Fixed in one breed Vs segregating between both breeds, (Marshall *et al.*, 2012) and identification of some significant QTLs following certain mathematical transformations (Box-Cox transformation, Benavides *et al.*, 2015) that otherwise would have been missed, indicate that there are opportunities for identification of other QTLs and associated genes that contribute to resistance towards GINs. Almost all studies, using multiple microsatellites markers and GWAS, identified novel regions involved in GIN resistance that were not previously described (Table 18).

The other remarkable findings in studied involving the same group of Red Maasai and Dorper double backcrosses that were first exposed to natural pasture challenge (Mugambi *et al.*, 2005a) followed by in house artificial exposure to mixed *H. contortus* and *T. colubriformis* infections (Mugambi *et al.*, 2005b), revealed different results when QTL mapping associated with the above mentioned phenotypic traits using microsatellites were conducted. The studies by Silva *et al.* (2011) identified significant QTLs on chromosomes 1, 3, 5, 6, 8, 9, 13, 14, 15, 16 and 17 that were not identified on chromosomes of the same sheep when artificially infected (Marshall *et al.*, 2012). Instead, the latter study identified significant QTLs on chromosomes 2, 4, 10, 12 and 25 that were not identified in the previous study. Both studies identified significant QTLs on chromosomes 18, 22, 23 and 26. In fact, phenotypic studies of the same sheep population led to inconsistent results. Exposure of the double backcrosses to natural pasture infection clearly demonstrated the superior GIN resistance of backcrosses with higher Red Maasai blood (i.e. $\frac{3}{4}$

Red Maasai) (Mugambi *et al.*, 2005a). The results, however, were not the same when the same group of sheep were later exposed to indoor experimental challenge where $\frac{3}{4}$ Red Maasai showed an unusual susceptibility to mixed infection compared to the $\frac{3}{4}$ Dorper backcrosses (Mugambi *et al.*, 2005b). In these studies, Red Maasai and Red Maasai backcrosses responded differently to artificial and natural parasite challenges. Therefore, the differences identified by the two microsatellite based QTL mapping studies might be the reflection of these differences.

3.4.4.3. Genome-wide association studies (GWAS), whole-genome sequencing and their results so far in small ruminants in Africa

Only few sheep breeds were analyzed for resistance to GIN using single nucleotide polymorphism (SNP) based genome wide association studies (Benavides *et al.*, 2015; Álvarez *et al.*, 2019; Ahbara *et al.*, 2021). The first three studies in Table 18 (Silva *et al.*, 2011; Marshall *et al.*, 2012; Benavides *et al.*, 2015), were conducted on the same cohorts of double backcrosses of Red Maasai and Dorper breeds used in previous phenotypic studies by Mugambi *et al.* (2005a) and Mugambi *et al.* (2005b). The sheep were developed in coastal area of Kenya for developing a record that was used as a pedigree in the QTL studies. The other breed studied was the Djallonke from Burkina Faso (Alvarez *et al.*, 2019). In this study, the investigators overcame the need for pedigree by first generating artificial pedigree using computer programs (Alvarez *et al.*, 2018). The study from Tunisia did not describe the breeds considered (Ahbara *et al.*, 2021).

The studies identified several genomic regions and tentative genes associated with resistance to GINs. These genes include those involved in mucin production, cytokine signaling, haemostasis, innate immunity, intestinal wound healing and expulsion of worms from the gastrointestinal tract (Table 18). The current trend appears that every new study identifies several new genomic regions associated with phenotypic markers of resistance or resilience to GIN parasites. There are also several QTLs identified in the non-annotated regions of *Ovis aries* genome suggesting the involvement of multiple genes spanning several chromosomes. This implies that finding combinations genetic markers that maybe used in screen individual animal resistant to GINs is challenging and necessitate further research. It also implies that genetic gains for resistance to GINs is not simple and require combinations of a panel of QTLs.

Inconsistencies observed in identifying QTLs associated with disease resistance between the different studies may suggest differences in the methods of analysis used, sensitivity of the analytical methods, characteristics of the study population (i.e., differences in breed, age, sex, physiological conditions), number of animals used in the studies, climatic conditions, nature of exposure to the disease agents (natural vs artificial infections), farming systems and the disease agents involved (Zvinorova *et al.*, 2016). Nevertheless, the application of whole-genome sequencing (WGS) could solve these challenges and help in identifying selection signatures for disease resistance genes and markers that may be used in the future for breed characterization and selective breeding activities. Indeed, a single study conducted on the Djallonke and Sahelian sheep breeds in Ghana demonstrated the usefulness of the technique in identifying genes associated with disease resistance. In a study by Yaro *et al.* (2019), WGS identified 33 genes associated with resistance to resistance. Among these genes 25 were associated with resistance to *H. contortus* (some of them also are involved in other GINs) and eight were identified to be involved in trypanotolerance based on their orthologues in trypanotolerant cattle.

The resolution of WGS could be demonstrated by its ability in identifying genes involved in multiple disease resistance in a single study as opposed to other genome based studies such as SNP based GWAS studies described previously. Whole-genome sequencing enables comparison among breeds much easier and faster. For example, of the 25 genes reported to be associated with resistance to haemonchosis and GINs identified in Yaro *et al.* (2019) and similar genes identified in other studies in various sheep breeds around the world, only four (*MHCII-DRB1* (Schwaiger *et al.*, 1995), *PIK3CD* (Periasamy *et al.*, 2014), *MUC15* (Benavides *et al.* 2016), *IL17RB* (Zhengyu *et al.*, 2016) were shared between the Djallonke and the Sahelian breeds. Others genes (*LRP8*, *ATP2B1*, *LAMC1*, *SOX9*, *UBE2N* (Benavides *et al.*, 2015), *DENND2D*, *CHI3L2*, *CHIA*, *RELN*, *NSUN2*, *HRH1* (McRae *et al.*, 2014), *IFNG* (Coltman *et al.*, 2001), *IL20RA* (Periasamy *et al.*, 2014), *ABCB9*, *SUGT1*, *PAK4*, *FCER2* (Yang *et al.*, 2015), *AREG*, *KIT*, *IL17RB*, *CXCL12* and *CXCR6* (Zhengyu *et al.*, 2016) were only co-located in the reduced heterozygosity regions found in the genome of Djallonke sheep.

Similarly, of the eight candidate genes for trypanotolerance reported based on orthologues in trypanotolerant cattle genomes (*CTSS*, *ARHGAP15*, *INHBA*, *SCAMP1*, *TICAM1*, *STX7*, *RAB35*, *CD19*) that co-localized with regions of reduced heterozygosity (RORH) in Djallonke, only two

(*SCAMP1*, *TICAM1*) were identified in the Sahelian. This confirms the phenotypic resistance observed for the Djallonke breed over the Sahelian breed in West Africa (Dayo *et al.*, 2020). However, the Sahelian sheep might have also undergone some degree of natural selection for trypanotolerance (Yaro *et al.*, 2019). Among eight genes identified for trypanotolerance, five of the genes (*STX7*, *SCAMP1*, *RAB35*, *CD19*, *CTSS*) co-localize with RORH identified in N'Dama cattle (O’Gorman *et al.*, 2009).

None of the microsatellite markers and SNP marker based GWAS studies in Africa were able to identify significant QTLs close to interferon gamma gene (*INFG*) on chromosome 3 or major histocompatibility complex (MHC) genes on chromosome 20 in the Djallonke and Sahelian sheep breeds before the WGS study by Yaro *et al.* (2019). This calls for the use of high density genomic methods for characterization of genetic resistance for diseases. The genes were identified in different previous GIN resistant studies in sheep (Coltman *et al.*, 2001; Miller and Horohov, 2006; Bolormaa *et al.*, 2010; Alba-Hurtado and Munoz- Guzmán, 2012).

Table 18. Genomic regions associated with GIN resistance in sheep in Africa.

Sheep Breed	Phenotypic markers	Study method	No. autosomes covered	Autosomes with significant QTLs	Genes involved	Remark	Reference
Double backcross of Red Maasai and Dorper sheep, both sexes, 6-8 months, under natural infection <i>H. contortus</i> and <i>T. colubriformis</i>	AVFEC, AVPCV, PCVST, PCVD, AVLWT	Microsatellite, 172 microsatellite (total map distance of 1560.7 cM)	25	1, 3*, 5, 6*, 8, 9, 13, 14*, 15, 16, 17, 18, 22*, 23, 26	Specific genes were not mentioned, however, genes associated with QTL on Chr 3, 6, 14 and 22 influence variations in immune response to GINs	overlapping QTL for AVFEC, AVPCV, PCVD on Chr. 22	Silva <i>et al.</i> , 2011
Double backcross of Red Maasai and Dorper sheep, both sexes, 6-8 months, under artificial infection with	LWT, ADG, PCVD, FEC, WC_total, WC_adult, WC_imm, AVFWL, EPW	172 microsatellite loci (total map distance of 1560.7 cM)	25	2, 4, 10, 12, 18, 22, 23, 25, 26	chemokine (C-X-C motif) receptor 4 gene (at 214–222 cM of chromosome 2) and the mannan-binding lectin serine peptidase 2 gene (at 57-63 cM of chromosome 12)	Chr. 26 contained QTL for all the nine phenotypic markers	Marshall <i>et al.</i> , 2012

mixed							
Double backcross of Red Maasai and Dorper sheep, both sexes, 6-8 months, representing the most resistant 10% and the most susceptible 10% and few F1 sires and pure grandparents for mixed H. contortus and T. colubriformis infection	AVFEC, AVPCV, AVLWT	GWAS, Illumina OvineSNP50 BeadChip	25	1, 2, 3, 5, 6, 7, 11, 12, 15, 17, 26	genes in mucus biosynthesis (GALNT4 and MUC15), cytokine signaling (SOCS2, UBE2N, EPS15, TLR10, KIT, LAMC1, and PDGFRA), and haemostasis (ATP2B1 and LRP8)	OAR2 (15 Mbp), OAR11 (58 Mbp), and OAR15 (54 Mbp) novel regions identified	Benavides <i>et al.</i> , 2015
184 DNA samples (64 males and 120 females) from both the Mangodara (166) and the Dédougou (18) localities in Burkina Faso (Djallonke sheep)	FEC, PCV, FAMACHA	GWAS, Illumina OvineSNP50 BeadChip	14	1, 2, 3, 6, 7, 8, 12, 13, 15, 17, 18, 19, 22, 23	five genes (TRIB3, CDK4, CSNK2A1, MARK1, and SPATA5) involved in immunity-related and cell-proliferation processes	22 novel genomic areas of putative areas were identified	Álvarez <i>et al.</i> , 2019
Tunisian autochthonous sheep, infected Vs non-infected cohorts of slaughtered sheep from eight commercial abattoirs	FEC	GWAS, Illumina Ovine 600 K SNP BeadChip	24	1, 3, 6, 8, 11, 12, 13, 14, 17, 18, 21	Genes enhancing innate immune defense (SLC22A4, SLC22A5, IL-4, IL-13), intestinal wound healing/repair (IL-4, VIL1, CXCR1, CXCR2) and GIN expulsion (IL-4, IL-13).		Ahbara <i>et al.</i> , 2021
Djallonke and Sahelian (Ghana)	None	Whole-genome sequencing	WGS	WGS	Genes associated with haemonchosis or GINs immune response and chemotaxis: <i>MHCII-DRB1</i> , <i>IL20RA</i> , <i>IL17RB</i> , <i>FCER2</i> , <i>HRH1</i> , response to pain and		Yaro <i>et al.</i> , 2019

					tissue homeostasis (<i>RELN</i> , <i>SOX9</i>), and protein coding, binding, methylation and phosphorylation (<i>ATP2B1</i> , <i>SOX9</i> , <i>MUC15</i> , <i>UBE2N</i> , <i>LRP8</i> , <i>RELN</i> , <i>NSUN2</i> , <i>LAMC1</i> , <i>ABCB9</i> , <i>PIK3CD</i> , <i>SUGTI</i> , <i>PAK4</i>). Other functions of the identified candidate genes include calcium binding and transport (<i>LRP8</i> , <i>LAMC1</i>) and carbohydrate metabolism (<i>CHI3L2</i> , <i>CHIA</i>); Trypanotolerance candidate genes: <i>CTSS</i> , <i>ARHGAP15</i> , <i>INHBA</i> , <i>SCAMP1</i> , <i>TICAM1</i> , <i>STX7</i> , <i>RAB35</i> , <i>CD19</i>	
South African Dohne Merino from Wauldby and Grootfontein	FEC, BCS, FAMACHA	GWAS, Illumina OvineSNP50 BeadChip	26	1, 2, 3, 4, 6, 7, 9, 10	No gene is identified	Dlamini <i>et al.</i> , 2019

*Chromosomes with highly significant QTLs for AVFEC. ADG, average daily gain; AVFEC, average FEC; AVFWL, average female worm length; AVPCV, average PCV; AVLWT, average live weight; cM, centiMorgan; EPW, egg per worm; GWAS, genome-wide association study; PCVST, PCV at start of experiment; PCVD, PCV decline; WGS, whole-genome sequencing

Microarray studies that compare gene expression patterns between susceptible and resistance breeds or between the most susceptible and the most resistant individuals within breed are powerful tools that help in studying the variation in genes expressed in the cohorts compared. The genes expressed in such circumstances are used to discern the genetic mechanisms and metabolic pathways that may be involved in the development of resistance to diseases (MacKinnon *et al.*, 2009). Such studies are not available in small ruminants of Africa.

3.4.5. Breeding for diseases resistance traits (within and between breeds)

In Africa, breeding programs in general for sheep and goats are much less frequently seen as a priority than programs for cattle (FAO, 2007). In those countries like Kenya, Ethiopia, Mali, Nigeria, where the effort has been going on for years, the focus has mainly remained on production traits through cross breeding (Ahuya *et al.*, 2009; Ojango *et al.*, 2010; Mohamed *et al.*, 2012; Gizaw *et al.*, 2013). The essence of this approach is technically meant to exploit the robustness of local breeds in face of harsh environmental challenge for exotic blood, while ripping the trait of interest for production reasonably in the resulting cross. In fact, disease is one of the element accounted for under the umbrella of “adaptability traits” in the harsh tropical environment, but disease resistant traits on their own has not been singled out as primary goal of the breeding except the report from south Africa (Dlamina *et al.*, 2019). According to this report, the farm (Wauldby) on to which genomic study was conducted had implemented selection for *H. contortus* resistance among South African Dohne Merino sheep. In the course of this particular selective breeding venture that lasted from 2011 to 2017, a feasible success was achieved with moderate heritability using resistant sire. On the other hand, there has also been selective breeding for establishment of nucleus elites and comparative studies among different indigenous sheep or goat breeds in some African countries, like Tunisia, and south Africa, that can withstand the prevailing environmental challenge and produce better in the ecological context (FAO, 2007; Mrode *et al.*, 2018). For some of these local breeds considered, in selective breeding, between breed comparison and or cross breeding, at least phenotypic evidence for diseases resistance traits were available (Behenke *et al.*, 2003; Fakaie *et al.*, 1999; Onzima, *et al.*, 2017). Nevertheless, to author’s knowledge no written evidence other than Wauldby farm could be retrieved from online sources for any of these disease resistant traits introgressed or selectively fixed in small ruminants breeding business reported in Africa.

4. CONCLUSIONS

Parasitic and infectious diseases

The livestock sector in developing countries is evolving in response to rapidly increasing demand for livestock products. However, small ruminant production in the African continent is seriously constrained by diseases of economic and public health significance. The chapters on parasitic and infectious diseases have attempted to summarize study findings in small ruminant production in Africa.

- Most of the studies on small ruminant diseases originated primarily from Eastern, Northern and Western Africa which seems to be in line with the huge small ruminant population and their significant contribution to the rural economy in these parts of the continent.
- The prevalence and intensity of infections vary significantly from place to place and among geographic regions of the continent;
- The assessments of the prevalence of these diseases in small ruminants and the reported findings varied due to the influence of the various local epidemiological characteristics as well as several important methodological gaps or tools utilized to diagnose the diseases.
- The output of literature search in this study on works related to parasites affecting small ruminants in Africa revealed that 61%, 20% and 19% of them focused on helminthes, protozoa including vector-borne diseases and arthropods (ectoparasites), respectively;
- Gastrointestinal helminth infections dominated by haemonchosis, protozoan infections such as trypanosomosis, babesiosis and theileriosis are recognized as major constraints to livestock production in Africa;
- Arthropods such as ticks, in addition to the damage they directly cause to the animal and its products, are responsible for the transmission of deadly animal and human diseases in many areas of the continent;
- This study has also shown that vector borne protozoan infections such as trypanosomosis, theileriosis and babesiosis are constraining sheep and goat production in different parts of Africa;

- Infectious diseases of small ruminants caused by bacteria and virus are common and highly prevalent in eastern part of Africa on regional basis compared to other parts of the continent.
- Research activities in livestock in Africa has shown a huge priority to cattle diseases for long, and hence the limited data retrieved regarding small ruminant diseases is a proof that these group of animals took very little attention even though they had significant contributions to the resource poor societies in most countries.
- Diseases including peste des petitis ruminants (PPR), contagious caprine pleuropneumonia (CCPP), Pox diseases, brucellosis, Q-fever (coxiellosis), rift valley fever (RVF) and blue tongue were reported to be most important to pose a serious challenge to the economy of the countries and the livelihood of the society in the region.
- The presence of antimicrobial, anthelmintic and acaricide resistance report in a number of countries could be due to lack of rational use or availability of counterfeit products in the market.
- While studies on the prevalence of ectoparasites is abundant for small ruminants, attempts to elucidate acaricide resistance on parasites such as ticks collected from small ruminants is virtually non-existent. Similarly, very little was said on the environmental impacts of these potentially toxic compounds.
- Despite the occurrence of highly contagious and transboundary diseases there is paucity of information on their economic impact and when present, they are fragmented and do not often take into account the transboundary nature of some of the pandemic diseases;
- It should also be noted that there is only fragmented understanding of the true costs of helminth parasitism; a complex task depending on direct, indirect and intangible costs, which may vary according to assumptions made about who is affected by the disease and the appropriateness of the study methodology and diagnostic tools employed;
- The economic burden due to diseases in small ruminants is complex and variable but often estimated from losses associated to mortality, cost of treatment, reduced weight gain and production, reduced quality of animal products and by-products and condemnation of edible organs as well as forced slaughtering or selling affected animals at low prices due to diseases. Additionally, quantitative evidence on the opportunistic cost of small ruminant diseases is hardly available.

- Reduction in productivity due to mortality and other health problems means a persistent challenge to food production, household livelihood and food security of the countries affected;
- From the estimates, with few parasite species, of losses arising from infections, it can be concluded that the cost of parasitic diseases is immense and treatment and control efforts have proven to have a positive impact in many aspects;
- However, chemotherapeutic approaches have been shown to face a growing emergence of drug resistance, Veterinary products used to treat and control various groups of parasites have been in African markets since long time. But, no study has attempted to monitor their residues and in food of animal origin and their impacts on animal and human health;
- The diagnostic techniques utilized were mostly serological tests and the use of more advanced methods for conclusive remark is limited in most situations.
- The presence of outbreak-based mortality and morbidity reports is the likely evidence for lack of strategic control intervention in animal health delivery.
- The preponderance of infectious diseases and lack of effective regulatory system for rational use of drugs might have contributed for emergence of drug resistance and presence of antimicrobial residues in foods of animal origin.
- External parasites and infectious diseases like pox demands special attention in order to minimize the loss attributed to skin damage.

Genetic studies

- Resistance of small ruminants to disease is studied only in 12 out of 54 countries in Africa. Most of the studies were obtained from East and West Africa, followed by South Africa and finally North Africa. No studies were available from many of countries in central Africa.
- Africa has huge small ruminant population following only, Asia. However, only few sheep and goat breeds were investigated regarding resistance to diseases.
- Despite the presence of large number of infectious, parasitic and metabolic diseases affecting small ruminants in Africa, studies on resistance of breeds to diseases were few

in number. Gastrointestinal nematode parasites infections including haemonchosis were the most commonly studied diseases. Trypanosomosis alone or in combination with haemonchosis were the second commonly reported disease. Few studies were available on tick infestation, fasciolosis and tick-borne diseases.

- All of the studies classified breeds based on phenotypes; and resistance to diseases was measured based on phenotypic markers such as FEC (InFEC, LFEC, AVFEC etc) as a proxy for resistance and PCV (AVPCV) as a measure of resilience.
- The studies identified that Red Maasai sheep and small East African goat in East Africa and Djallonke sheep and the West African dwarf goat breeds in West Africa are resistant to GINs. The latter two are also trypanotolerant. Djallonke sheep being more trypanotolerant than the WAD goats. Other small ruminant breeds identified as resistant to haemonchosis include Red Sokoto goats from Nigeria and Mubende goats of Uganda.
- Trypanotolerance and GIN resistance of Djallonke sheep and WAD goats appear to be on the decreasing trend in some of the West African countries because introgression of genes from susceptible breeds as a result of crossbreeding.
- Within breed individual variations that may be exploited for selection of more resistant phenotypes exist in indigenous sheep and goat breeds in most of the diseases studied.
- South African indigenous Namaqua Afrikaner sheep, QFO sheep of Tunisia and Xhosa and Nguni goats of South Africa demonstrated resistance to tick infestation.
- QFO sheep were reported to be resistant to piroplasms, however, whether the resistance was due to actual resistance to the piroplasms or resistance to the vector ticks was not clearly illustrated.
- Resistance to GINs and tick infestation of different body parts are heritable. Heritability of FEC and PCV as indirect measures of disease resistance and resilience appears to be low in indigenous African breeds by large. However, heritability of tick infestation counts on different body regions in South African sheep breeds was moderate.
- There are only few microsatellites based QTL mapping and SNP based GWAS studies available for sheep in Africa. The studies demonstrated that the QTLs are distributed over large number of autosomes clearly demonstrating that resistance to nematode parasites is polygenic and therefore panels of genetic markers are required to identify resistance strains or to follow genetic gains in selective breeding.

- Whole-genome sequencing of Djallonke and Sahelian sheep demonstrated the application of the technique in identifying genes involved in multiple diseases at the same time. The WGS in Djallonke identified several genes including INFG and MHC genes that were not detected in the same sheep breed using GWAS based on Illumina OvineSNP50 BeadChip.
- Genes involved in mucin production, cytokine signaling, haemostasis, innate and acquired immune responses and chemotaxis, intestinal wound healing and expulsion of worms from the gastrointestinal tract, response to pain and tissue homeostasis, protein coding, binding, methylation and phosphorylation were among those associated with GIN resistance.
- Gene expression studies on resistance to diseases in Africa are not available.
- No single QTL mapping or GWAS studies are available for disease resistance in goat breeds in Africa.
- The only available selective breeding program for disease resistant traits in small ruminants is obtained from Wauldby South African Dhone Merino flock. Encouraging results are already reported on selective breeding for resistance to *H. contortus*.

5. THE WAY FORWARD

Parasitic and infectious diseases

Given the diversity and the huge number of small ruminant populations in the African continent, their adaptation to limited feed resources and harsh environmental conditions, and their well appreciated socio-economic values both at household and national levels, there is a hope that this segment of livestock is amenable to improvement if a comprehensive breeding and management strategy is adopted.

- Attempts to improve understanding of small ruminant disease patterns and impacts and to design an effective control strategy, should follow a one-health approach, integrate local and regional efforts and pool resources for common and sustainable development goals;
- There is only a fragmented understanding of the true costs of diseases in small ruminant production. This must be solved if future control strategies are to be economically sensible and well integrated into the different farming systems including the pastoral settings of Africa;
- If a reliable data is to be obtained to aid decision making for future control and prevention programs, conventional techniques must be complemented or replaced by modern approaches and diagnostic tools allowing an in-depth investigation;
- Management of drug resistance should be a priority by exploring all possible alternatives and complementary approaches such as ways of prolonging the life of existing drugs and exploitation of the local genetic potential;
- As acaricide resistance is now a commonplace in cattle, development of this situation has to get equal attention in small ruminants;
- Concerns of the public on veterinary drug residues in food of animal origin and the environment should be given due attention, if Africa has to not only safeguard the health of its population but also to stay in global livestock and livestock products trade;
- Expansion of improved veterinary services at both national and regional levels with trained personnel, adequate laboratory facility accessible to most areas and other important resources made available;

- Assess reliable sensitive and specific diagnostic tests and standardize for improved detections of the pathogens involved in causing the diseases in small ruminants.
- Integrated regional approach with research, policy development, harmonization of diagnostics and implementation of controls since most diseases are highly contagious and transboundary transmitted and require regional cooperation in particular involvement of AU-IBAR initiative to harmonize control strategies for export purposes.
- Due to the presence of large number of infectious and parasitic diseases in Africa, the disease prevention or control strategy should follow an integrated approach on multiple diseases accounting biological, geographical, and logistical matters.
- Adequate funding and financial support are highly required to conduct research, promote veterinary service capacity, standardize diagnostics, develop, harmonize and implement strategies, regional collaboration, and provide other services wherever necessary.

Genetic studies

Studies for resistance of small ruminants to various diseases in Africa covered only few countries and relatively small number of breeds.

- Therefore, further studies covering large small ruminant populations and wider geographic regions should be designed and conducted to identify other genetic resources available in Africa. Such studies should identify more sheep and goat breeds resistant to various diseases based on their natural distribution and evolutionary history.
- Once such breeds are recognized the breeds should get appropriate attention for their genetic resources be conserved and developed in selective breeding program for establishment of nucleus elit with in the breed.
- The other important point that need attention in the future research is the low heritability of proxy traits for resistance to parasitic diseases, *i.e.* FEC and PCV. This finding clearly impacts the genetic gain from selective breeding on top of other challenges. The fact that no major QTLs based on microsatellites are available, *i.e.*, resistance to GINs is polygenic and appears to differ between different breeds of sheep and the same group of sheep reared under different exposure to the parasites so far, there is a need for further

fine tuning of the techniques to identify panels of QTLs necessary to identify the resistance in a particular breed(s) under the given production system.

- There is also a need to apply other genomic tools such as high density SNP based GWAS studies and microarray gene expression studies to identify differences between the resistant and susceptible breeds of small ruminants so that genes and metabolic pathways involved in the development of resistance are identified. Furthermore, whole-genome sequencing helps in identifying the source of genetic variations between the two populations compared at SNP level.
- The other pressing issue is the introgression of genes from susceptible small ruminant breeds that is currently affecting the resistance to diseases identified in various African small ruminant populations. Therefore, responsible breeding policy need to be instituted to avoid indiscriminate crossbreeding and countries should strive to conserve their genetic resources.
- To this end, whole-genome sequencing and gene annotations help in characterizing the small ruminant breeds with regards to their genetic status (pure bred vs introgression of genes), production potentials, disease resistance and tolerance to other stresses and environmental factors. These technologies generally require establishment of specialized laboratories which may hinder their utilization in resource constrained countries in Africa. However, countries may pool their resources together and such facilities may be established in strategic locations so that they serve regional countries in their effort to identify valuable genetic resources and help in their utilization and conservation.

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