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**NETWORK ANALYSIS AND MAPPING OF SMALL RUMINANT TRADE
MOVEMENTS IN SOMALI REGION AND BORENA ZONE, ETHIOPIA:
IMPLICATION FOR POTENTIAL SPREAD OF PESTE DES PETITS RUMINANTS
VIRUS**



MVSc THESIS

**ADDIS ABABA UNIVERSITY, COLLEGE OF VETERINARY MEDICINE AND
AGRICULTURE, DEPARTMENT OF VETERINARY CLINICAL STUDIES**

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**JUNE, 2024
BISHOFTU, ETHIOPIA**

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VIRUS**



**A Thesis submitted to College of Veterinary Medicine and Agriculture of Addis Ababa
University in partial fulfillment of the requirements for the degree of Master of Veterinary
Science in Veterinary Epidemiology**

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**June, 2024
Bishoftu, Ethiopia**

Addis Ababa University
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Department of Clinical Studies

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IN SOMALI REGION AND BORENA ZONE, ETHIOPIA: IMPLICATION FOR POTENTIAL
SPREAD OF PESTE DES PETITS RUMINANTS VIRUS

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First, I declare that this thesis is my *bonafide* work and that all sources of material used for this thesis have been duly acknowledged. This thesis has been submitted in partial fulfilment of the requirements for an advanced (MVSc) degree at Addis Ababa University, College of Veterinary Medicine and Agriculture and is deposited at the University/College library to be made available to borrowers under rules of the Library. I solemnly declare that this thesis is not submitted to any other institution anywhere for the award of any academic degree, diploma or certificate.

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LIST OF ABBREVIATIONS

CC	Clustering coefficient
FAO	Food and Agricultural Organization
FMD	Foot and mouth disease
GCES	Global Control and Eradication Strategy
GDP	Gross Domestic Product
GIS	Geographic Information System
GPS	Global Positioning System
GSCC	Giant strongly connected components
GWCC	Giant weakly connected components
HIV	Human immunodeficiency virus
MoA	Ministry of Agriculture
OBI	Outbreak investigation
OIE	Office International des Epizooties
PDS	Participatory disease surveillance
PL	Path length
PPR	Peste des petits ruminant
PPRV	Peste des petits ruminant virus
SARS	Severe Acute Respiratory Syndrome
SNA	Social network analysis
TADs	Transboundary animal diseases

ABSTRACT

Livestock movement through trade is central driving factor for the spread of trans-boundary animal diseases (TADs) including Peste des petits ruminant virus (PPRV) since pathogens can spread long distance via movement of infected animal. Hence, understanding animal trade network structure is fundamental step for surveillance and to implement effective animal disease control measures. This study aims to characterize small ruminant trade network patterns in the Borena Zone and Somali region by using social network analysis (SNA) approach. Additionally, the study seeks to assess the potential role of trade network structure in the risk of PPRV diffusion and control. Small ruminant market movement data including source, destination and volume of exchange was recorded from January to December, 2023 in selected eight markets in Borena Zone and Somali region. A total of 365,261 individual animals (sheep and goats) were traded through 64 identified markets and 20 non-market premises including abattoirs and cross-border destinations. The whole small ruminant trade network was sparsely connected (Density = 2.4%), and showed small-world network topology, with high clustering coefficient (CC= 0.73), and short path length and diameter (PL = 2.21, diameter =5). Degree-distribution of markets in network was right skewed and disassortatively mixed (assortativity = -0.517). Centrality-based percolation analysis showed remarkably faster reduction in connected components size than random removal of markets. Analysis of threshold parameter showed average epidemic threshold ($q = 0.392$) and Basic Reproduction Number ($R_0 = 2.75$), with maximum risk at August ($q = 0.199$, $R_0 = 5$). This study highlighted that; the whole small ruminant trade network in study areas was prone to the spread of PPRV due to the low epidemic threshold, the short diameter of the network and the presence of hub markets which can act as super-receivers and/or super-spreaders. Additionally, over 90% of the animals traded through the current small ruminant trade network came from PPR endemic and high-risk areas. Therefore, targeting those highly connected markets and nearby areas as sentinel during epidemiological surveillance could provide opportunities for early detection of threats enhance preparedness rapid response and minimize cost.

Key words: *Borena zone, Livestock market, Network analysis, PPRV, Small ruminants, Somali region*

1. INTRODUCTION

Movements between and within population are the main driving factors for wide-range spread of infectious agents. Livestock movement through trade is of particular importance since pathogens can spread long distance via movement of infected animal (Ortiz-Pelaez *et al.*, 2006; Dube *et al.*, 2010; Motta *et al.*, 2017). In order to achieve effective control of animal diseases and disease surveillance, understanding the structure of livestock contact patterns and studying the routes, volume, frequency and risks associated with animal movements is a fundamental step (Motta *et al.*, 2017). The spreading of animal diseases by trade involves different actors including farms, slaughterhouses and traders forming a complex system and it is crucial to understand this trade system (Lentz *et al.*, 2016). Several studies have used techniques adopted from social network analysis (SNA), to characterize animal movement patterns and identify network actors, for a better understanding of the main driving factors for spread of infectious diseases, to provide tools to localize high-risk areas, and identify potential sources of a disease (Kocho *et al.*, 2011; Charras-Garrido *et al.*, 2012; Júnior *et al.*, 2017; Menezes *et al.*, 2020; Negreiros *et al.*, 2020; Cardenas *et al.*, 2021).

Ethiopia has a substantial small ruminant population with an estimated 42.9 million sheep and 52.4 million goats (CSA, 2021). However, contribution of the livestock sector for foreign exchange earnings is much lower than expected for the given size of the livestock population (Gebremedhin *et al.*, 2007). This is due to presence of transboundary animal diseases, such as PPR, sheep and goat pox, and contagious caprine pleuropneumonia, with PPR considered a priority small ruminant disease in Ethiopia (Waret-Szkuta *et al.*, 2008; Magona *et al.*, 2016). Trans-boundary animal diseases (TADs) are those diseases that have significant economic, trade and food security importance for a considerable number of countries; they can easily spread to other countries and reach epidemic proportions; and where control measures including requirements of cooperation among several countries (Otte *et al.*, 2004). These diseases are highly contagious and have the potential for rapid spread irrespective of national borders, causing serious socio- economic consequences (Seine, 1998). With increasing globalization, the TADs in the world pose a serious risk to food security and jeopardize international trade (Seyoum and Teshome, 2017). Therefore, elimination of animal diseases in general and

transboundary diseases such as PPR in particular, should be priority for decision makers interested in making food value chain less risky for the people involved and the consumers they supply (OIE and FAO 2016).

Peste Des Petits Ruminants (PPR) is an acute, highly contagious viral disease that primarily infects sheep, goats, and wild small ruminants. The causative agent PPR is PPRV which belongs to the genus *Morbillivirus* of the family *Paramyxoviridae* (Gibbs *et al.*, 1979). The disease is endemic in several countries in Africa, the Arabian Peninsula, the Middle East, and India since it was first described in Côte d’Ivoire in 1942 (Banyard *et al.*, 2010). PPR has a severe impact on food security, livelihoods, and small ruminant trade for livestock-keeping communities (de Haan *et al.*, 2015) and is a World Organization for Animal Health (WOAH) listed disease (OIE, 2019). The annual economic loss of PPR-associated sheep and goat deaths for worldwide infected countries is estimated between 794 million and 2.7 billion US dollars (Jones *et al.*, 2016). Failure of sustaining control programs for PPRV resulted in the emergence of the virus in other regions and other animal species such as camels (Libeau *et al.*, 2014), despite the existence of a highly effective vaccine since 1989 (Diallo *et al.*, 1989). In 2013, the OIE and FAO jointly decided to embark upon the control of PPR on a global scale and develop a ‘PPR Global Control and Eradication Strategy entitled “PPR- Global Control and Eradication Strategy (GCES)” to eradicate PPR by the year 2030 (OIE and FAO, 2016).

Efficient disease control requires an understanding of the determinants and dynamics of disease spread in complex networks by analyzing large-scale structures (Lentz *et al.*, 2016). Recently, network based approach to study livestock movement has been emerged and tested in many African countries (Dean *et al.*, 2013; Motta *et al.*, 2017; Apolloni *et al.*, 2018; Mekonnen *et al.*, 2018; Nicolas *et al.*, 2018; Chaters *et al.*, 2019). Analysis of trade-related movements requires information extracted from official movement permits for improved identifications and traceability (González-Gordon *et al.*, 2023). In many developed countries maintaining digital data sets of animal movement between registered premises is enforced by law (Bowling *et al.*, 2008). However, gathering and maintaining comprehensive animal movement data to build network methods in developing countries is more challenging. The lack of systematic livestock recording in Africa has been a major obstacle in studying movement and disease spread (Ekwem *et al.*, 2022).

PPR has a widespread distribution in Ethiopia and major constraint for small ruminant production (Waret-Szkuta *et al.*, 2008; ESGPIP, 2009). Despite the widespread presence of virus and the high risk of transmission by animal movements through trade, well-organized data on small ruminant trade structures is limited for practical surveillance, control and communication intervention. Accordingly, it is necessary to characterize the current small ruminant trade network structure formed by the trading system, and its potential role in the epidemiology of PPRV in Borena zone and Somali region of Ethiopia. Thus, the objectives of this study were:

- To quantify the volume, frequency, and routes of small ruminants' movements through trade network and evaluate its change over the course of the year
- To evaluate the vulnerability of small ruminant trade network to the potential spread of infectious diseases using available small ruminant movement information
- To identify key markets and target areas for practical disease surveillance, control, and communication interventions
- To explore the association of market network properties with the epidemiology of PPRV

2. LITERATURE REVIEW

2.1. Animal trade as a mean for spread of infectious diseases

The role of animal movements and livestock trade network in the spread of animal disease has already been well recognized (Gilbert *et al.*, 2005; Kiss *et al.*, 2006; Nicolas *et al.*, 2013). Animal trade is usually driven by demand for animal products in other areas, and can potentially spread infectious diseases. Better understanding of factors influencing movement patterns in space and time could benefit control and prevention of diseases (Nicolas *et al.*, 2018). Livestock markets represent a strategic contact points and the contact between animals when herd meets together is conducive to disease transmission and rapid dissemination of pathogens across long distance (Fe`vre *et al.*, 2006; Motta *et al.*, 2017; Jahel *et al.*, 2020). Some examples include the spread of *Trypanosoma brucei rhodesiense*, one of the agents of Human African Trypanosomiasis, through cattle trade in Uganda (Hutchinson *et al.*, 2003) and highly pathogenic avian influenza H5N1 globally (Kilpatrick *et al.*, 2006). Understanding the dynamics of disease spread in complex networks requires analysis of their large-scale structures, because this is necessary to estimate incidence rate and size of a disease outbreak. With this information in hand, consequences of introduction of a contagious disease can be estimated and any control actions can be planned (Karthik *et al.*, 2014). Movements between premises are usually not homogeneously distributed. Instead, some premises/markets play key role in flow of animals and therefore either are having high risk of being exposed to infectious diseases or highly contributing to spread of infection (Ortiz-Pelaez *et al.*, 2001; Gilbert *et al.*, 2005). Therefore, identifying these key contact points in livestock trade is fundamentals step in effective disease surveillance and control (Apolloni *et al.*, 2018).

The contact structure of a population can affect disease transmission, for example, when variance in the number of potential contacts is high (Anderson and May 1991; Albert *et al.*, 2000) or when transmission is localized but occasional jumps over long distances occur (Watts and Strogatz 1998). Trans-boundary animal diseases have a multifaceted origin; factors include international trade and travel with increasing frequency and speed at local and international scales, facilitated by the globalization process that promotes the spread of microorganisms on a world scale, changes in agricultural practices (intensification of animal husbandry systems), climate change,

increased contact with wildlife, and the introduction of animals into new geographic areas where the disease is endemic and immunologically unknown to them (Chomel *et al.*, 2007; Brown, 2010).

The most common way of introducing TAD into a new geographic area is through the importation of infected or diseased animals or contaminated animal products, including animal production materials (Gongal *et al.*, 2022). The Horn of Africa is widely considered to be the region with the largest informal trans-boundary livestock movements in the world. In this geographic area, livestock are transported to their final destinations by both trek and truck. Well-known cross-border markets are: Wuchale, Dewele, Gashamo, Goladi and Ferfer in the east and Dolo Odo and Moyale in the south. Livestock trade networks extend deep into the Somali region of Ethiopia, where many of the animals are raised (Metaferiya *et al.*, 2021). The informal, cross-border livestock trading system in this region has survived and continued to thrive under the region's harrowing conditions of political rivalry, armed conflict, unpredictable border closures, and storms of other restrictive interventions (Desta *et al.*, 2011), the increasing prevalence of informal cross-border livestock trade in the peripheral countries of the region is arguably a simple restoration of the long-standing indigenous pattern of intensive barter and cross-border population migrations that predate colonial and postcolonial borders (Ogalo, 2010).

2.2. A network based approach to study Livestock movement through trade

Network-based approaches enable the description of livestock movements as a spatial network where nodes can represent villages, markets, herds, or individual animals, and edges define the movement of at least one animal from one node to another (Muwonge *et al.*, 2021). This approach is used for epidemiological purposes, particularly to understand the role of animal movement in disease spread and control strategies (Green *et al.*, 2008; Moslonka *et al.*, 2016; Chaters *et al.*, 2019). Geospatial networks are graphs whose nodes and edges can be associated with geographic locations (Schoettler *et al.*, 2021). The livestock marketing system can be studied as a network of actors or locations connected by livestock transportation. Livestock markets are distributed across regions and form a network of compounding and branching connections through which animals are purchased from rural areas, transported to wholesalers, and then sold in shortage areas, often across borders. Network analysis methods can help provide

insights into the structure and functioning of the livestock market and help policymakers shape agricultural development, trade policies, and disease control strategies (Valerio *et al.*, 2020).

Social network analysis is an approach based on the study of relationships among social units and the patterns and effects of those relationships (Wasserman and Faust, 1994). This approach is based on graph theory to examine pairwise relationships between objects in the same collection and has been used to analyze livestock movements (Christley *et al.*, 2005; Webb, 2005; Bigras-Poulin *et al.*, 2006; Kiss *et al.*, 2006; Webb, 2006; Bigras-Poulin *et al.*, 2007; Robinson *et al.*, 2007; Robinson and Christley, 2007). Network analysis can be used to examine the relationships between pairs of farms or livestock enterprises in the network and the sequences of animal movements that lead to pathways by which infectious diseases can spread. Livestock farms which are central to animal flows in the population, for example because they have a large number of trading partners, can be identified and targeted for action. Network analysis can also be useful for estimating the number of livestock farms potentially exposed during the silent spread phase of a disease, i.e., the period between the introduction of an infectious agent into a population and the first detection (Dube, 2009).

Construction of network models of livestock markets requires the use of animal movement records (Moslonka *et al.*, 2016). Recently, a network-based approach to study livestock movements has been developed and tested in many African countries (Dean *et al.*, 2013; Motta *et al.*, 2017; Apolloni *et al.*, 2018; Mekonnen *et al.*, 2018; Nicolas *et al.*, 2018; Chaters *et al.*, 2019). It consists of describing livestock movements as a directed and weighted spatial network, where the weight of a link is equal to the total number of animals exchanged (Guo *et al.*, 2012). Techniques from social network analysis (SNA) have been extensively used by veterinary epidemiologists to gain a better understanding of the spatiotemporal dynamics of animal diseases (Christley *et al.*, 2005; Webb, 2005; Bigras Poulin *et al.*, 2006; Bigras Poulin *et al.*, 2007; Dube *et al.*, 2009; Martínez López *et al.*, 2009; Buettner *et al.*, 2013; Rautureau *et al.*, 2012; Dutte *et al.*, 2014; Valdano *et al.*, 2015) and to identify network actors central to the spread of infectious diseases (Natale *et al.*, 2009; Natale *et al.*, 2011). SNA is a tool that defines relationships among entities of interest, which can be animals, people, or objects, either individually or in a group (Borgatti *et al.*, 2013).

Network data are defined by actors and by relationships (nodes and links). The node or actor part of network data seems to be fairly straightforward. Network analysis focuses on the relationships between actors rather than on individual actors and their characteristics. This means that actors are usually not interviewed independently, as is the case in many other studies (usually surveys). (Hanneman and Riddle, 2005). In veterinary epidemiology, SNA is a statistical tool for evaluating animal movements that have already occurred and extrapolating what might happen in the future. In this way, the impact of disease control measures can be evaluated using network structure and the potential magnitude of the epidemic can be predicted following the introduction of a highly contagious disease (Dube *et al.*, 2011). The SNA structure enables the identification of surveillance, intervention, and control targets (Menezes *et al.*, 2020).

A network is represented by a graph consisting of a set of vertices (nodes) and lines (links) (Watts, 2003; De Nooy *et al.*, 2005). Two problems that complicate the application of network theory to epidemiology are the typical assumptions that all potentially infectious contacts or links are equal (equally weighted) and that the network is static, i.e., that the potentially infectious links are fixed over the course of an epidemic. A potentially infectious link between two individuals (nodes) i and j has a transmission probability (p_{ij}) that is realistically time-dependent and weighted by the characteristics of i and j , the type of link, and the direction of contact (Kao *et al.*, 2006). However, analyses of weighted networks are complicated (Barrat *et al.*, 2004), because all links in an epidemiological network have the same weight and importance, standard network analyses become useful. An epidemic persists as long as an infected node can reach at least one uninfected node in a static network. A strongly connected component or strong component is a subset of a directed network in which all nodes can reach each other. A weakly connected component or weak component is a strong component plus all its sources and links. In a static epidemiological network, any disease originating from a strong component infects all elements of the strong component and also all connected nodes. Similarly, any epidemic emanating from a source node infects the strong component plus all the links, but not necessarily all the sources. Thus, the largest or giant strongly connected component (GSCC) is an estimate of the lower bound of the maximum epidemic size, while the giant weakly connected component is an estimate of its upper bound. The distributions of the sizes of the strong and weak components are estimates of the upper bound of the final epidemic size (Kao *et al.*, 2006).

In many developed countries, detailed digital records of animal movements between registered farms are maintained, often motivated by animal health concerns and enforced by regulation (Bowling *et al.*, 2008). These data have enabled extensive use of network epidemiological methods to rapidly respond to animal disease outbreaks through modeling and tracking (Kao, 2002; Dube *et al.*, 2009). The availability of these data has allowed methods to evolve, with network methods in veterinary epidemiology increasingly incorporating dynamic features of the network and detailed structural features (Bansal *et al.*, 2010). These methods have demonstrated that networks of animal movements are key for understanding and controlling a variety of pathogens in livestock. However, collecting and maintaining comprehensive livestock movement data in developing countries to establish network methods presents a significant challenge (Ekwem *et al.*, 2022). The unregulated nature of livestock movements and the lack of systematic livestock recording systems in Africa have been major obstacles in studying livestock movements and disease spread (Todaro and Smith, 2014). The absence of these critical factors provides an incomplete picture of the true extent and dynamics of movements. To overcome these difficulties, collecting data on livestock movements at the local level and approaches that rely on consultation with local communities are critical to understanding both the patterns of movements and their causes (Ekwem *et al.*, 2022).

2.3. Understanding Livestock markets from a network-centric perspective

Market can be formally described as a network of interaction of economic agents such as individuals, businesses or sovereign states (Eckehard and Rosenbaum, 2000; Goyal, 2012). Network perspective of agents corresponds to a node or vertex interacting with other nodes through links or edges. Exchanges of animals are directed and weighted since exchange occurs from suppliers to demanders, but often not in reverse direction and different numbers of animals are shipped per transaction. Total trade flow can also be calculated as it follows that trade flow has a direction; dissociated in- and out-trade flows. Markets are described by directed and weighted networks and form dynamic networks since exchanges occur at precise points in time. Dynamical networks are more difficult to analyze than static networks since, links can shift between nodes over time, and nodes can disappear or reappear, resulting in change of composition and size of components (Chaters *et al.*, 2019). Trade flow is the number of products (e.g. animals) traded from a supplier to a demander per unit time. Hence, trade flow can be

interpreted as the epidemiological contact rate (number of transactions per time unit) weighted by contact intensity (number of products exchanged per transaction) and can be route for transmission (Moslonka, 2016).

2.4. Importance of livestock movement studies and network analysis for surveillance disease control

Studying animal movements using network analysis techniques (SNA approach), enables researchers to explore interactions among pairs of livestock operations. The relationship created between a source and its destination premises becomes components of a complex web of connections, since the number of movements from a premise is not just an isolated attribute. This approach allows the epidemiologist to identify nodes or livestock operations in the web that are at high risk of incursion to infections and transmitting infection to many other operators (Dube, 2009).

Generally, the context of these network analysis studies can be categorized into:

- Descriptive studies of the contact structure of livestock movements (Webb and Sauter-Louis, 2002; Christley *et al.*, 2005; Webb, 2005; Bigras-Poulin *et al.*, 2006; Webb, 2006; Bigras-Poulin *et al.*, 2007; Robinson and Christley, 2007). Descriptive studies of livestock movements have mainly focused on the use of centrality measures of network to identify livestock operations that are important or central in the flow of animals in the network, and measures of cohesiveness which assess the level of connectedness in the network (Dube, 2009).
- Network analysis to assess the impact of livestock movement regulations. Study that demonstrates the role of some individual livestock holdings in controlling the flow from one part of the network to another part (Green *et al.*, 2006; Kao *et al.*, 2006; Robinson *et al.*, 2007).
- Characterizing the impact of the livestock contact structure on the spread of diseases, predicting epidemic size and developing network models for testing the validity of network concepts (May and Lloyd, 2001; Kiss *et al.*, 2005; Saramaki and Kaski, 2005;

Shirley and Rushton, 2005; Woolhouse *et al.*, 2005; Green *et al.*, 2006; Kao *et al.*, 2006; Kiss *et al.*, 2006; Duerr *et al.*, 2007; Kao *et al.*, 2007; Pautasso and Jeger, 2008).

- Using network analysis to understand past epidemics. The UK 2001 FMD outbreak has provided a network of contacts among infected premises that has been studied using network analysis (Shirley and Rushton, 2005; Ortiz-Pelaez *et al.*, 2006)

2.5. Network models in Epidemiological studies

Network model, often called graph model, is a technique or method of describing interaction in population. In this interaction, vertices (nodes) of network represent individuals, farms, markets etc. and edges (links) depict interaction between nodes that could potentially lead to transmission of infection. So, it is worth noting that network representations can be used in a number of contexts (Watts and Strogatz, 1998; Albert *et al.*, 1999; Newman *et al.*, 2001).

Many perceptions regarding the epidemiology of infectious diseases have been provided by network theory and mathematical modeling. The most notable one is threshold conditions, the so-called ‘basic reproductive number’, that describes when epidemics occur and persistence of infection is possible (Anderson and May, 1992; Diekmann and Heesterbeek, 2000; Hethcote, 2000). The use of simple models, such as deterministic compartmental models (SIR model) is the development of much of this theory. Deterministic compartmental model divide population into a small number of compartments based on infection status (susceptible, infected and recovered), and the flow between these compartments are described by a low dimensional set of ordinary differential equations (Lloyd and Valeika, 2007).

The use of network models in epidemiologic settings has a long history, including the study of sexually transmitted diseases (STDs), such as human immunodeficiency virus (HIV) and gonorrhoea. In this setting well-defined, network structures (sexual partnership networks), have been extremely studied by public health bodies in their attempts to track and control outbreaks of sexually transmitted diseases (Lloyd and Valeika, 2007). Different forms of idealized and simulated networks models have been studied in the context of disease transmission in order to explicit complex processes involved in network formation in real population (Keeling and Eames, 2005).

The most commonly used epidemiological network models are:

2.5.1. *Spatial Networks*

As the name suggests, spatial networks are generated by using the spatial location of all premises in the network, as such lattices and small worlds are a particular form of spatial network. The position of each premise i at specific location x_i is usually a randomly chosen location, but spatially clustered distributions have also been used (Badham *et al.*, 2008; Danon *et al.*, 2011). Spatial dimensions are very crucial when considering the management of infectious diseases. From an epidemiological perspective, outbreak of an epidemic is defined as any temporally unusual increase in numbers of new cases in a localized geographic area (Porta, 2008). Current technological advancements such as geographical information systems and sophisticated statistics can provide spatially more accurate information in terms of the direction and range of diseases spreading or locations of hot spots of diseases. Hence, disease control measures could be more effective. For a better understanding and management of infectious diseases, spatial approaches are necessary, and to be further integrated into the implementation of prevention and control measures against epidemics (Lin and Wen2022).

2.5.2. *Scale-free networks*

Scale-free networks formed dynamically by adding new vertices (nodes) to a network by one by one with connection mechanism that mimics natural formation of social contacts (Barabási and Albert, 1999). Each of new connected vertices that is added to the network preferentially connects to vertices that already have large number of contacts and this results in the number of contacts per individual vertices taking power law distribution. This extreme variation in number of contacts displayed by scale-free networks has long been interest to epidemiologists since it is possible to realize that having many contacts is greater risk for infection and once infected disease can transmit to many others (Keeling and Eames, 2005). This has been demonstrated several studies such as core groups of high-risk individuals helps to maintain sexually transmitted diseases in population (Hethcote and Yorke 2014) and significant portions of all infections in the SARS epidemic were caused by super-spreaders (Riley *et al.* 2003). Existence of vertices with arbitrarily large degrees makes random interventions (e.g. vaccination) not efficient to prevent an epidemic in scale-free network. However, targeted vaccination in scale-free

network is extremely efficient since targeting only highly connected individuals (super-spreaders) can be sufficient to prevent epidemics (Albert *et al.* 2000; Lloyd and May 2001; Pastor-Satorras and Vespignani, 2001).

2.5.3. *Small-world networks*

Small-world networks are characterized by their frequent short-range links (high clustering and short path length) and few long-range connections. Spread of disease through small-world networks has received considerable attention from both theoretical and applied epidemiological concepts. High level of clustering means that most infections are predominantly localized, but epidemic spread through the network is rapid due to short path length and the disease is unlikely to be limited within small regions of population (Watts and Strogatz, 1998). Percolation theory applied by Moore and Newman (2000), on small-world networks to calculate the threshold parameter at which epidemics can occur demonstrated that random long-range links can dramatically increase the likelihood of an epidemic (Moore and Newman, 2000).

2.5.4. *Contact Tracing Networks*

Contact tracing and network generated by this method have two distinctive forms; either contact-tracing is used for initiation of proactive control (Danon *et al.*, 2011) or when transmission pathway between all identified cases is wanted (Klovdahl, 1985; Haydon *et al.*, 2003; Riley *et al.*, 2003). In proactive contact-tracing, identified cases are asked about their recent contacts, and these contacts are traced and tested; if found infected repeated contact-tracing is conducted for secondary cases (Danon *et al.*, 2011).

Contact tracing forms of network have two main advantages. First, the network is supported by the test results of individuals within the network, which not only have contact process information but also contact is resulted in transmission of infection. Another advantage is the infection process itself defines the network of contacts, hence no need of human interpretation for defining an infection tree. However, major disadvantage of contact-tracing network is dependency on infection process to drive tracing that decreases its predictive power (Danon *et al.*, 2011).

2.6. Description of network and node level metrics and their epidemiological importance

A network is an assembly of units of interest that may or may not be connected. The units of interest are usually called vertices or nodes in physics and mathematics, or referred to as actors in the social sciences. Nodes are linked to each other through a connection of some sort. For example, animal movements from one farm to another link farms together in a network. Nodes may have some sort of attributes, such as type of species, geographical location, and size in terms of number of animals moved, and these attributes can be studied in the context of network analysis (Dube, 2009). A network is said to be connected when it is possible to travel between any pair of vertices (nodes) by moving along edges of the network. An epidemiological perspective of connectedness is that a single individual can transmit infection to any other individual in the population, typically via a number of intermediates. A variety of network metrics have been employed to describe the structure of a network. These have their origins in the mathematical theory of graphs, although some have been developed within the context of quite specific applications, such as social network theory or the exploration of large-scale technological networks. Many of these network metrics can describe properties that have a direct impact and implication on disease transmission dynamics (Lloyd and Valeika, 2007). A network and node level metrics employed to describe the structure of a network and extensively utilized in epidemiological study are:

2.6.1. Node (Vertex) level metrics

Degree of centrality

The degree of centrality or connectivity of a node, often written as k , is total the number of neighbors that a given node is connected to on the graph (that is, the number of people to whom our individual is directly linked) (Lloyd and Valeika, 2007). Average degree is a network-level parameter that quantifies the average number of links connected between nodes in a network. Besides these global measures, node`s in-degree is number of incoming links and node`s out-degree is number of outgoing links. All total degree of centrality, in and out-degree are weighed by volume of animals towards and from each node (total weight, in-weight or out-weight) (Nicolas *et al.*, 2018).

In livestock market context, centrality is the number of markets a specific market is connected to; standardized mean difference between degree of centrality of the most central market and the rest of the markets (Freeman, 2002). In- and out-degree refers to the number of markets that ship livestock to a market of interest, and the number of markets that the market of interest sends livestock to, respectively (Wasserman and Faust, 1994). In epidemiological terms, markets with higher out-degree act as the main animal suppliers within the network and they could function as major spreaders of infection. In the case of the weighted input degree markets that stood out for receiving more animals and are could be more vulnerable to an outbreak (Menezes *et al.*, 2020). Centrality measures can indicate the importance of a given market within a trading network (Bell *et al.*, 1999), and preferential protection, treatment or isolation of more central, or more influential, nodes might enhance disease control measures (Natale *et al.*, 2009; Volvoka *et al.*, 2010; Rautureau *et al.*, 2011). In general degree of centrality measurement indicates whether a livestock market can be a potential source of infection (high out-degree centrality) or receive most of the infection from other livestock markets (high in-degree centrality) (Okello *et al.*, 2021). The most central nodes in the networks are vulnerable in different ways and have a greater potential to infect a large part of the network in a possible outbreak. Therefore, during an outbreak, targeted surveillance for central markets (nodes) located in unaffected regions may have a greater probability of detecting the disease causing agent introduction into new areas. Likewise, movement restrictions directed at such markets may be more likely to prevent a wider spatial spread of the disease (Vanderwaal *et al.*, 2016).

Closeness centrality

Closeness centrality measure is based on the distance between a node and each other node in network. It extends degree centrality by looking at neighborhoods of all radii. The input into measures of closeness centrality is the list of distances between node i and other nodes j in the network, $\rho g (i, j)$. There are different variations of closeness centrality based on different functional forms based on distances between node i and all other nodes, $\sum_j \rho g (i, j)$. In that measure a higher score indicates a lower centrality (Bloch *et al.*, 2016). To overcome this inversion, and also to deal with the fact that this distance becomes infinite if nodes belong to two different components, Sabidussi (1966) proposed another approach to measure closeness

centrality measure as $1 / \sum_j \rho g(i, j)$. Hence, it is possible to obtain the closeness centrality measure by normalizing a measure that the highest possible centrality measure is equal to 1. So closeness centrality is given as:

$$c_i^{cl}(g) = n - 1 / \sum_{j \neq i} \rho g(i, j)$$

In the context of livestock trade, closeness centrality is number of markets a specific market is connected to; standardized mean difference between closeness centrality of the most central market and the rest of the markets (Freeman, 2002).

Betweenness Centrality

Betweenness centrality measures how often a given vertex is situated in paths between pairs of vertices. This measure is of particular importance in communication networks where a vertex v can attain a certain level of importance, responsibility, or status by bridging the flow of information across the network. In the simplest case, where there is a unique path between any pair of vertices, a vertex v can block or facilitate information flow between all pairs of vertices $\{x, y\}$ for which the unique path between x and y passes through v . It would be natural, then, to define $B(v) = B(v; G)$, the betweenness centrality index of the vertex v in the graph G , to be the number of exactly such pairs $\{x, y\}$ (Krnec and Riste, 2020).

In livestock trade, betweenness centrality measures the frequency a market lies in the shortest path between pairs of markets in the network (Freeman, 2002). It is the standardized mean difference between betweenness centrality of the most central market and the rest of the markets (Wasserman and Faust, 1994). Generally it measures how frequently a given livestock market (node) can act as a bridge between other livestock markets (nodes) in the network. In epidemiological terms, the higher the degree betweenness, the higher the potential of a livestock market to transmit the infection from a source livestock market (Okello *et al.*, 2021).

Eigenvector centrality

Eigenvector centrality assigns relative scores to all vertices in the network based on the concept that connections to vertices with high centrality contribute more to the score of the vertex in question than connections to low-scoring vertices (Krnec and Riste, 2020). Eigenvector centrality is computed by assuming that the centrality of node i is proportional to the sum of centrality of node i 's neighbors: $\lambda c_i = \sum_j g_{ij} c_j$, where λ is a positive proportionality factor. In matrix terms, $\lambda c = gc$. The vector $c_i^{eig}(g)$ is thus the right-hand-side eigenvector of g associated with the eigenvalue $\lambda \max(g)$ (Bloch *et al.*, 2016).

Eigenvector centrality measures the level of influence of a livestock market (node) within a network after assigning each score. In livestock market network context eigenvector centrality value is defined as the extent of how connected a market was to well-connected neighboring markets. It approximates the importance of each livestock market in the network by assuming that each market centrality is the sum of the centrality values of the markets that it is connected to. A high eigenvector score means that a market is connected to many markets, which themselves have high scores. In networks with high eigenvector centralization transmission of disease occurs more rapidly (Okello *et al.*, 2021).

2.6.2. Network (Graph) level metrics

Density

The density statistic represents the proportion of possible connections in the network that are actually present. The value ranges from 0 (no connection) to 1 (full connection), with the lower limit corresponding to networks with no relationships and the upper limit representing networks with all possible relationships. The closer the value is to 1, the denser is the network and the more cohesive are the nodes in the network (Nicolas *et al.*, 2018).

Density measures the ratio of links among livestock N number of markets in the network with respect to the maximum possible number of links ($2N(N-1)$); defined as $1/2N(N-1)$ (Wasserman and Faust, 1994). In epidemiological term, it is the degree of contact between pairs

of livestock markets in the network. Disease transmission may occur faster in high-density networks (Okello *et al.*, 2021).

Diameter and Average path length

The distance between two nodes is the length of the shortest path that connects them. The largest of these values when all pairs of nodes are examined is called diameter of network. Average path length or average shortest path length is a concept in network topology that is defined as the average number of steps along the shortest paths for all possible pairs of network nodes. It is a measure of the efficiency of information or mass transport on a network (Watts and Strogatz, 1998).

In livestock market context, diameter is the longest geodesic distance between any pair of livestock markets in the network using the shortest possible walk from one market to another (Wasserman and Faust, 1994); calculated considering (directed) and neglecting (undirected) link directions. Average path length is the shortest path between two livestock markets averaged over all pairs of livestock markets in the network; defined as $1/n(n-1) \sum_{i \neq j} d(v_i, v_j)$ where $d(v_i, v_j)$ is the geodesic path between markets i and j (Valerio *et al.*, 2020).

Network with lower average path length (PL) and significantly higher clustering coefficient (CC) when compared with random network of equivalent size and connections (that is with same number of nodes and links) is said to have a small-world structure (Wang *et al.*, 2012). Small-world networks are known to ease the spread of infectious diseases, thereby favoring rapid dissemination of pathogens through the network (Keeling and Eames, 2005; Shirley and Rushton, 2005; James *et al.*, 2009; Dube *et al.*, 2011).

Degree Assortativity (Connection preference)

Assortativity is a measure of the tendency of nodes within a network to have connections with similar (or dissimilar) nodes. Degree assortativity can be used as an indicator of the susceptibility of a network to random or targeted node isolation procedures, effectively removing them from the network. A disassortative network (negative assortativity value) is much more vulnerable to targeted node isolation than an assortative network (Newman, 2003). The assortativity

coefficient value lies between -1 and +1, a positive value of assortativity means that holdings with a high number of movements would be sending/receiving animals to/from other holdings with a high number of movements. A negative value of assortativity would mean the opposite; holdings with a high number of movements would be sending/receiving animals to/from other holdings with a low number of movements (Duncan *et al.*, 2022). According to Kao *et al.* (2007), it is expected that disease spread will be quicker on an assortative network than adissortative one. Assortatively mixed networks are less affected to random and even targeted removal of nodes and size of GSCC is unaffected unless a significant proportion of highly connected nodes are removed. Therefore, implementing control measures is difficult unless precise and effective targeted control is used. Disassortatively mixed networks are less resilient to random and targeted removal, and therefore implementing control measure is easier. Disease spread is disadvantage on disassortative networks compared to the assortatively mixed case, especially for low transmission rates (Newman 2002). However, if the network is disassortative, targeting highly connected nodes may still be effective, as they may act as bottlenecks in the transmission process (Kiss *et al.*, 2006).

Reciprocity

The reciprocity of a directed network is the proportion of edges $A \rightarrow B$ for which the reciprocal edge $B \rightarrow A$ also exists (Newman, 2010). A low value of reciprocity shows a highly directional network, meaning that trying to approximate with an undirected network would not be appropriate (Duncan *et al.*, 2022). In livestock market network topology, value of reciprocity indicates the proportion of reciprocal (bidirectional) connections among markets (Motta *et al.*, 2017).

Clustering coefficient

The clustering coefficient is the probability that two nearest neighbors of a vertex (nodes) are nearest neighbors also of one another. The clustering coefficient of the network reflects the “cliquishness” of the mean closest neighborhood of a network vertex, that is, the extent to which the nearest neighbors of a vertex are the nearest neighbors of each other (Watts and Strogatz, 1998).

It is the ratio of the number of edges (links) that occur between a livestock markets (nodes) immediate neighbors and the maximum number of edges that could exist between them. Frequency of disease spread may increase with higher clustering coefficient (Okello *et al.*, 2021). However, Eames and Keeling (2003), stated that high degree of clustering can reduce the extent of an epidemic and can increase the efficacy of control measures such as contact tracing (Kiss *et al.*, 2006).

Component structure and Connectivity

A component is a section of the network where all nodes are connected to each other either through direct linkages or via intermediate nodes. In network analysis, “components” represent subgroups of nodes that are maximally connected between each other. By accounting (or not) for the direction of links in the network, components are generally two types may be either “strongly” or “weakly” connected (Motta *et al.*, 2017). A strongly connected component or Giant strongly connected components (GSCC) is a subset of a directed network in which all nodes can reach each other. A weakly connected component or Giant weakly connected components (GWCC) is a strong component plus all its sources and links (Kao *et al.*, 2006). Strongly connected components of node i is the set of all nodes that can be reached from node i and from which node i can be reached. All nodes in a strongly-connected component have the same in-component (i and all nodes from which i can be reached) and the same out-component (i and all nodes that can be reached from i). The weakly connected component of node i is the set of nodes that are connected to i when the direction of the edges is ignored (Kenah and Robins, 2007).

Strongly connected component (GSCC) of directed contact network plays crucial role in disease transmission (Newman *et al.* 2001). Any two nodes i and j of strong components are mutually reachable by following directed paths, and thus a disease introduced into any node in a strong component can potentially reach any other node in that strong component. A weakly connected component (GWCC) contains the GSCC plus all the nodes that connected to the GSCC in only one direction (Kiss *et al.*, 2006). In static epidemiological network an epidemic starting from nodes in the GSCC will infect all nodes in the GSCC and nodes in GWCC that are destinations

of directed connections starting from GSCC. Hence, GSCC and GWCC are often considered as an estimate of the minimum and maximum possible size of an epidemic, respectively assuming there are no changes or interventions (Kao *et al.*, 2006). The removal of specific nodes, and their links, causes the network to fragment in a set of smaller sub networks. The size of the largest component can be thought as the maximum extent a disease can spread after the implementation of the control measure (vaccination of animal in the areas surrounding the nodes, market closure, etc.) (Kiss *et al.*, 2006).

Communities and Sub-groups

Network systems are usually organized in compartments (sub-groups), which have their own role and/or function (Lancichinetti and Fortunato, 2009). These sub-groups are called communities or module, and occur in wide variety of networked systems (Girvan and Newman, 2002). Community detection (unfolding communities) in real network is widely used to determine structural properties of these networks and/or finding group of related nodes (communities), that are densely interconnected and have fewer connections with the rest of network (Moradi *et al.*, 2012). Different methods of community detection (clustering algorithm) have been developed; edge betweenness method (Girvan and Newman, 2002), eigenvectors of matrices method (Newman, 2006), Infomap method (Rosvall and Bergstrom, 2008) and spectral clustering method based on stochastic block models (Rohe *et al.*, 2011). However, there is no consensus on which algorithm is more suitable for which network. Therefore, it is important to incorporate empirical knowledge about network under investigation to select more suitable algorithm. Community detection identifies sub-group of markets which are more interconnected due to geographical proximity, natural barriers and regional/cultural communities (Motta *et al.*, 2017). Presence of subgroups on the network slows down disease transmission (Okello *et al.*, 2021).

2.7. Interpretation of epidemic threshold (q) and basic reproduction ratio (R_0) in the epidemiological network

The basic reproduction number, R_0 , of an infectious disease is the average number of secondary cases generated by a single primary case in a fully susceptible population (Diekmann *et al.*,

1990). R_0 is the most widely used epidemiological measurement of the transmission potential in a given population. Statistical estimation of R_0 has been performed for various infectious diseases, aiming towards understanding the dynamics of transmission and evolution, and designing effective public health (Becker, 1989; Dietz, 1993). Interpretation of the epidemiological network can be directly related to the basic reproduction ratio or R_0 . The persistence threshold associated with R_0 underpins modern theoretical epidemiology (Anderson and May, 1992). A pathogen will be successful when $R_0 > 1$. In that sense the introduction of a single infected individual into a wholly susceptible homogeneous population will on average infect more than one other. An equivalent interpretation can be made in terms of percolation theory for the epidemiological network. In general, a network percolation threshold can be defined by an increase in the average number of connections per node, below which there are only finite-sized strong components in an infinite network, and above which the GSCC is infinite (Stauffer and Aharony 2018; Moore and Newman 2000; Schwartz *et al.*, 2002). In a finite network, this is approximated by the sudden appearance of a large GSCC as the number of connections increases, by the joining of many prior strong components. In the context of a randomly connected epidemiological network (i.e. where the probability of connection is defined by the relative node degrees), a percolation threshold is defined when each node potentially infected over the network can subsequently infect on average, at least one other node. In an undirected network, this requires two links per node, while in a directed network, it requires that there be one outward link if a node has at least one inward link; in both cases this is equivalent to $R_0 = 1$. In the case of proportionate mixing, $R_0 = (K_{in} K_{out}) / (K_{in})$ (Schwartz *et al.*, 2002). Factors such as negative correlation between node centrality measures (where nodes of high out degree preferentially connect to nodes of low in degree) will of course change the expression for R_0 . Additional structure in the network could lower the estimated final epidemic size if connections are not random. If a network consisting only of sets of continuous loops or necklace of nodes will have $R_0 = 1$, but the GSCC will be equal to the length of the longest necklace. Comparing R_0 to the size of the GSCC can therefore be used to identify network structures and a percolation threshold more generally defined in terms of a value $R_0^{crit} \geq 1$, which defines when invasion by a novel pathogen can cause a large epidemic. A percolation value of $R_0^{crit} > 1$ implies localizing structures, such as spatial or social clustering (i.e. higher probabilities of links between nodes for reasons that are not related to the degrees of the nodes) (Kao *et al.*, 2006).

2.8. Epidemiological features of PPR virus in Ethiopia

2.8.1. PPR virus

Peste des petits ruminant (PPR) is an acute, highly contagious viral disease that primarily infects sheep, goats, and wild small ruminants. The causative agent PPR is PPRV which belongs to the genus *Morbillivirus* of the family *Paramyxoviridae* (Gibbs *et al.*, 1979). It is antigenically very similar to the rinderpest virus and other members of the genus such as measles virus, porcine distemper virus, canine distemper virus, and dolphin morbillivirus. Its name was driven by the French for “disastrous disease of small ruminants” as it is the fatal disease of sheep and particularly goats it is also called ‘goat plague’ (Bailey *et al.*, 2005). Phylogenetically, PPRV can be classified into four distinct lineages based on the fusion (F) protein gene and nucleoprotein (N) gene. Lineages I and II are mainly found in West and Central Africa; lineage III is found mainly in East Africa, Yemen and Oman; and lineage IV is found across the Arabian Peninsula, the Middle East, southern Asia, and recently, in several African territories (Banyard *et al.*, 2010; Muse *et al.*, 2012; Banyard *et al.*, 2014; Misinzo *et al.*, 2015). According to OIE Standards, 67 countries are infected with PPRV from 198 countries recognized by the United Nations (FAO/OIE, 2016). PPR is now present within a broad belt of sub-Saharan Africa, North Africa, the Middle East, and the Asia subcontinent. Recent outbreaks in Turkey, Morocco, Algeria, Tunisia, Tibet-China, Tanzania and Kazakhstan had signified the rising global spread of PPR and confirmed some of the hypotheses of PPR already circulating before being confirmed in some of those areas (Banyard *et al.*, 2010; Banyard *et al.*, 2014; Kardjadj *et al.*, 2015; Kock *et al.*, 2015).

2.8.2. Host range and transmission

A Peste des petits ruminant is primarily a disease of goats and sheep (Lefèvre and Diallo, 1990), although both cattle and pigs are susceptible to infection, but do not contribute to the epidemiology as they are unable to excrete virus. The existence of sylvatic reservoirs for PPRV with infections and deaths in captive wild ungulates from several species has been reported (Furley *et al.*, 1987; Ogunsanmi *et al.*, 2003; Elzein *et al.*, 2004; Kinne *et al.*, 2010). PPRV antigen has also been detected in camels (Khalafalla *et al.*, 2010) and lions (Balamurugan *et al.*, 2012). Severe clinical signs of PPR were seen in sheep and goats when kept with inoculated camels (Saeed *et al.*, 2022). However, the role of wildlife on the epizootiology of PPR remains to

be investigated. There is a possibility of some wild species can become dead-end hosts, when infected with the virus through spillover from domestic animals, but there is limited or no further transmission, and therefore, they do not maintain PPRV. Domestic cattle are also likely to be dead-end hosts through developing an immune response; however, experimental studies have not yet been able to demonstrate virus excretion or infection of in-contact susceptible cattle (Abubakar *et al.*, 2017; Couacy-Hymann *et al.*, 2019; Schulz *et al.*, 2019).

Transmission of PPRV from infected to healthy animal occurs through direct contact and indirectly through contaminated materials. The virus is secreted and discharged through tears, the nose and feces, and transmitted to other animals lick bedding, feed, water and through the milk of infected dams (Munir *et al.*, 2013). Oro-nasal discharges when small droplets released into the air facilitates spread of virus (Abubakar *et al.*, 2012). The virus can shed in the feces approximately 10 days after onset of fever (Zakian *et al.*, 2016). Congregation of flocks and mixing of species can increase risk of transmission (Biruk, 2014). Similarly, trans-boundary movements, sharing markets around border and animal movements in pastoral systems for search of feed and water might cause transmission of disease along border (Ullah *et al.*, 2022).

2.8.3. *Status of the disease in Ethiopia*

The first clinically suspected PPR in the country was in the 1977 in afar region (Abraham *et al.*, 2005). Later clinical and serological evidence of disease was confirmed in 1991 (Abraham *et al.*, 1994). Currently, available molecular epidemiological data confirms the presence of lineage III and lineage IV in Ethiopia (Banyard *et al.*, 2010; Muniraju *et al.*, 2016). According to national serological survey conducted in 1999 on 13651 serum samples from 7 regions, seroprevalence was found to be 21.35% in Somali, 15.3% in Afar, 15.3% in Tigray, 8% in Benishangul Gumuz, 4.6% in Amhara, 1.8 in SNNPR and 1.7% in Oromia (Waret-Szkuta *et al.*, 2008).

More recently, seroprevalence ranging from 1.3% to 83.33% d has been reported in different parts of Ethiopia (Table1)

Table1: Summary of recent seroprevalence studies on PPR reported from different parts of Ethiopia

Study areas	Prevalence (%)	References
Bench Maji and Kafa	2.1	Gebre <i>et al.</i> (2018)
South Omo	30.8	Mebrahtu <i>et al.</i> (2018)
Assosa Zone	75.7	Yalew <i>et al.</i> (2019)
North shewa	25.7	Agga <i>et al.</i> (2019)
Afar	2.1	Agga <i>et al.</i> (2019)
Silte and Gurage Zone	29.2	Hailegebreal, (2019)
Horu Guduru	5.71	Gelana <i>et al.</i> (2020)
Bale Zone	12.9	Gebresilassie <i>et al.</i> (2021)
South Ethiopia	54	Mohammed <i>et al.</i> (2022)

2.8.4. Challenges related with animal movements regarding PPR eradication

By 2030 PPR can be eradicated globally. After the successful eradication of rinderpest on global scale and the lessons learned from rinderpest eradication, OIE and FAO jointly set the goal for control and eradication of PPR by 2030 (OIE and FAO 2016). However, Transboundary nature of PPR is considered one of the main limitations in expanding the production of animals, particularly in enzootic regions of the world (Balamurugan *et al.* 2014). Seasonal occurrence of disease associated with agro-ecological conditions and movement of infected small ruminants within the country and cross-border particularly, the pastoral areas of Afar, Somali and Oromia in Ethiopia and cross-border seasonal movement of animals in search of pasture and water in pastoral areas of Kenyan border is also a great challenge to control widely spreading PPRV (Alemayehu *et al.*, 2015). Animal movement restrictions including the imposition of quarantine and sanitary measures are an integral part of most infectious disease control and eradication programs. However, strict movement control can stimulate unnecessary or illegal movement of animals to bypass quarantines and restriction orders. A major concern in several regions is pastoralist's keeps moving for the search of free vaccination whether vaccination is free or not. Vaccination team workers will be needed to come back to the same area several times to make sure that animals are immunized, if not informed. Cost of any animal disease control or

eradication campaign is higher, takes a long time, or even fails without comprehensive cooperation from stakeholders (Njeumi *et al.*, 2020).

2.9. Research Gaps

It is well understood that, livestock movement through trade play significant role for spread of trans-boundary animal diseases (TADs) including PPR virus; since pathogen can spread long distance via movement of infected animal (Lentz *et al.*, 2016; Motta *et al.*, 2017; González-Gordon *et al.*, 2023). Studying animal trade structure (Volume, frequency and trade routes) in network perspective has become popular approach to understand how disease can principally spread via livestock trade. Livestock trading points (markets) represent strategic contact nodes and are linked by movement of animals. In general structural characteristics of such networks are known to influence the potential dissemination of infectious agents, since some contact points (markets) are more connected than others (Barabasi and Albert, 1999; Christley *et al.*, 2005). Once these main contact points (highly connected nodes) are identified, implementation of control measures such as trade restriction, vaccination or animal testing can be modeled by node removal (Lentz *et al.*, 2016).

The organization of the pastoral trading system in peripheral areas is characterized by complex chain of several stages, actors, set of market corridors and trading routes (Berhanu, 2016). Hence, it is imperative to understand and characterize small ruminant trade movement pattern in network perspective for identifying main contact points and suggesting more suitable disease control strategy.

3. MATERIALS AND METHODS

3.1. Description of Study Area

The study was conducted in Borena and Somali areas of Ethiopia. The study sites are selected purposively based on their livestock number, presence of informal cross border livestock trade, and classified as a high-risk or endemic areas of major trans-boundary diseases in small ruminants (Waret-Szkuta *et al.*, 2008; Berhanu, 2016; Jilo *et al.*, 2016).

Borena Zone is located at 3° 26' - 6° 32' N latitude and 36° 43' - 40° 46' E latitudes. It is located in the southern part of Oromia region and its capital is Yabelo town. The zonal administrative area covers a total area of about 45,435 sq. kms and is divided into 13 districts, bordered by Kenya in the south, Southern Nations, Nationalities, and Peoples Regional State (SNNPRS) in the north west, Guji Zone in the north east and Somali region in the southeast. Most areas of Borena Zone lying below 1,500m above mean sea level and the climate is semi-arid with pockets of sub-humid zones. About 41% (18,712 sq. kms) of the area is grazing/browsing land, 34% (15,510 sq. kms) is bush and woodland, and 8% (342,040 ha) is cultivated land (Galgalo, 2015). The estimated livestock population of Borena Zone is 1,494,437 sheep, 2,306,672 goats, 2,338,998 cattle, and 355,837 camels (BZAO, 2022).

Somali Region is located in the south-eastern part of Ethiopia, between 4° and 11° N latitude and 40° and 48° E longitude. The altitude of region ranges between 400 – 1600 above mean sea level, with most areas lying below 900 masl. With a total area of 328,068 km² it is the second largest region in Ethiopia, with 9 administrative zones, 52 districts, and 703 Pas, and bordered by Kenya and Somalia to the south, the Republic of Djibouti and the Afar region to the north, Somalia to the east and southeast and Oromia region to the west (Wondimagegne, 2016). The region has an estimated livestock population of 6,034,887 cattle, 11,013,491 sheep, 16,464,505 goats, and 6,489,702 camels (CSA, 2021).

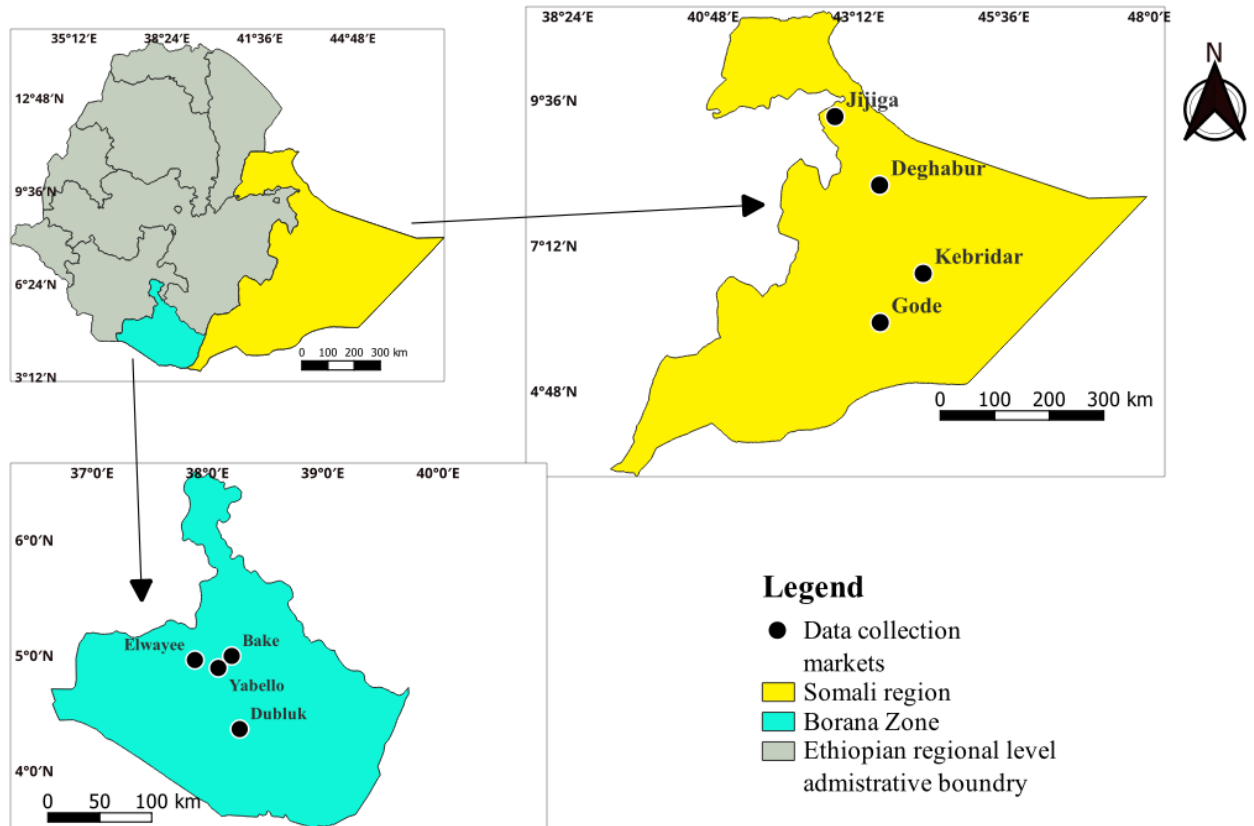


Figure 1: Map of Ethiopia with study areas and region

3.2. Study approach

The study used a network-based approach as a method to study the structure and patterns of small ruminant movements through trade. The network-based approach is a technique adopted from social network analysis (SNA) and enhances a better understanding of relevant network properties and its implication for pre-informed disease surveillance and control measures. This approach has been extensively used by veterinary epidemiologists in order to get a better understanding of spatio-temporal livestock disease.

3.3. Data collection methods

To gather relevant information on the small ruminant trade route, the quantity of movement and contact points in the network both primary and secondary data methods were applied.

3.3.1. Identification of markets for data collection

Identification of main livestock markets for recording small ruminant movement data in the study areas was conducted by interviewing key individuals (traders and livestock office experts). Structured questionnaire-based interviews were prepared, pretested, and personnel who have more knowhow about small ruminant trade were interviewed. Each individual for the interview was selected in consultation with the regional and Zone trade and Livestock office with detailed discussions.

3.3.2. Small ruminant movement data collection

Data on the number of animals traded during each market day was consistently observed and recorded by individuals who were assigned for this specific purpose in all selected markets. All necessary information related to traded animals such as source and destination points, type of movement (either by truck or walking), number of animals (volume of exchange), and purpose of movement were recorded. Information about animals traded in other markets is often gathered by direct phone calls by data collectors when market days are overlapping, far distant, and difficult to attend two markets at the same time.

Additionally, official animal movement records obtained from trade offices and control posts were included in data collection framework to catch the maximum possible movements and minimize possible missing in direct market recordings.

3.3.3. Retrospective epidemiological data of PPRV

To assess the potential role of small ruminant market network structure for PPRV incursion, the study utilized retrospective data on PPR outbreaks and PPR risk status in study areas for the year

2023, obtained from the Ministry of Agriculture (MoA). Since PPR is a reportable disease in Ethiopia, risk status is continuously monitored and all outbreaks of the disease must be immediately reported to MoA. Obtained data expected to provide inference of the current situation of PPR in study areas and its association with small ruminant trade network characteristics was analyzed accordingly.

3.4. Data Analysis and Markets Network Construction

Collected data containing all detailed information including data recorded from market points and secondary data from official records were manually extracted from field data records and entered in Excel spreadsheets for later data management and analysis. Based on these small ruminant trade movement data from January to December 2023, yearly aggregated fully weighted static directed network was constructed by using markets as the nodes of the network and the links between origin and destination markets as edges. Movements were described by direction of movement and weighted by the number of small ruminants traded over these links. In addition, due to hypothesized temporal variability of animal movements, monthly directed and weighed were constructed throughout the study year in order to capture potential seasonal variability in network structure and cohesiveness. All network metrics and summary statistics were estimated on the full annual and monthly networks to evaluate variations in both network cohesiveness and centrality metrics. Descriptive statistics was used to summarize the number of animals traded between different locations during the study period and general network properties, and visualized by using summary tables, graphs, and maps. All network visualization and analysis were performed by R statistical software (Version 4.2.2) and visualization of maps was performed by using *QGIS* (Version 3.30.2).

Characteristics of network structure were first described by general topology and then node-level metrics were further computed to evaluate the centrality of each market within the network. The general topology of the observed small ruminant trade network was described by using different network-level metrics such as density, diameter, average path length (PL), assortativity, reciprocity, and clustering coefficient (CC). To assess whether the observed network exhibited a small-world structure, measures of clustering coefficient and average path length were compared

with CC and PL from a set of 1000 randomly generated networks having similar sizes in terms of nodes and links. A network is said to have a small-world structure if its CC is significantly higher than that computed from a random network of equivalent size and connections while showing a lower value of PL (Wang *et al.*, 2012). Centrality measures of each market including in- and out-degree, betweenness, and eigenvector centrality were calculated to determine their distribution among markets in the network. Spearman correlation test statistic between nodes centrality measures was used to identify key markets and their practical role in cohesiveness of the network. The role of markets in observed network was classified depending on correlation between eigenvector and betweenness centrality as described by Valente *et al.* (2008). To detect group of markets sharing similarities in patterns of their connectivity, Infomap or Rosvall and Bergstrom community detection algorithm (Rosvall and Bergstrom, 2008) was applied. This algorithm uses a flow-based clustering approach, so called “maps of random walk” as a proxy for the flow in the network to identify its community structure. Estimations of all network-level and node-level metrics, community detection and network visualization were performed by using *igraph* package in R statistical software.

To assess the role of temporal change in trade network structure on the potential spread of disease epidemic threshold (q) described by Volkova *et al.* (2010) was computed. The epidemic threshold and its inverse, the Basic Reproduction Number (R_0) were computed for each of the monthly network snapshots throughout the year by using the mapMCDA R package. The epidemic threshold (q), quantifies minimal expected transmission coefficient necessary for the virus to spread through the network. This parameter depends on heterogeneity of network related to distribution of occasional links. Epidemic threshold for a network can be estimated as:

$$q_k = \frac{\bar{k}_{out}}{\bar{k}_{in} \times \bar{k}_{out}}$$

Where, \bar{k}_{out} is average out-degree and \bar{k}_{in} is average in-degree of all the nodes in the network at a specific month.

The impact of targeted node removal on the network's vulnerability was evaluated using percolation analysis. After each stage of node removal, based on decreasing order of centrality measures, the cohesiveness of the network structure was measured by the size of the GSCC and the largest community. The impact of targeted intervention on the structural vulnerability and connectivity of the network was further assessed by comparing targeted node removal with random node removal. Percolation analysis was conducted using the *igraph* package, and the *ggplot2* package was employed to visualize the graphs.

To explore the potential connection between market network characteristics and the spread of PPRV, retrospective epidemiological data and PPR risk status data from MoA was used. Markets were classified based on the risk status of the districts where they are located (endemic, high-risk, or risk-free). Since centrality metrics of markets were not assumed to follow normal distribution, Kruskal-Wallis test was used to determine whether there was significant difference in scale of small ruminants' trade among markets in different risk categories.

3.5. Ethical statement

The study was carried out in accordance with the Animal Research Ethics Review Committee of Addis Ababa University College of Veterinary Medicine and Agriculture. Ethical approval for the research was ensured by an approval certificate with reference number VM/ERC/03/15/2022 indicated in Annex 5. All methods were performed according to relevant guidelines. Informed consent was obtained from all subjects and the purpose of the interview was explained to all participants prior to the interview.

4. RESULTS

4.1. Market records collection

Based on information obtained from interviews, eight markets (four from each study area) were selected for direct recording of small ruminant movement data from each market day throughout the year (Table 2). These markets were selected due to their multiple and long-distance trade connections and are persistently active throughout the year. Livestock markets in study areas are organized in market channels that include different types of markets and with involvement of different actors. Movement of animals usually starts from bush markets in and/or around livestock-keeping communities and passes through different stages of markets until it reaches destination points. Smaller/village level markets located near livestock keepers were primary suppliers of animals for secondary markets located in cities and bigger towns. Animals traded in secondary markets were sent to final destinations such as slaughter houses, restaurants, or cross-border destinations. The main actors involved in the livestock trade are pastoralists, traders, brokers, and restaurants/ hotels.

Table2: Descriptions of selected markets for active recordings of small ruminant trade movements by volume of exchange (number of incoming and outgoing animals) from January to December 2023

Survey Markets	Location	Days active/week	Duration of recording	Volume of exchange (Count)	
				In volume	Out volume
Bake	Borena	1 day/week	12 months	9,496	11,185
Dubluk	Borena	1 day/week	12 months	9,862	11,394
Elwayee	Borena	1 day/week	12 months	9,772	10,277
Yabello	Borena	2 day/week	12 months	6,485	3,844
Deghabur	Somali	2 day/week	10 months	11,485	20,827
Gode	Somali	Whole week	10 months	30,929	35,134
Jijiga	Somali	Whole week	10 months	53,937	66,613
Kebridar	Somali	2 day/week	10 months	25,538	34,566

4.2. Summary statistics and general description of small ruminant market structure in study areas

During the study period between January 2023 and December 2023, a total of 365,261 animals (sheep and goats), were traded through 64 identified markets and 20 other destinations. From these movements, more than 54% (198,346 heads of animals) were to market destinations, while the remaining 166,915 records of movements were from secondary markets to final destination points including slaughter-houses and cross-border movements with neighboring countries (Table 3). Main cross border destination points were Hargiesa, Burco, and Berbera from Somaliland and Kenya through Moyale. The majority of slaughter-houses and cross-border destined movements (more than 85%) were transported by truck, while more than 55% of internal movements were by foot (Table 3).

The volume of exchange was highest from July to September, where nearly 42% of total year trade exchange (153,119 animals) occurred (Figure 2). This peak animal trade exchange period from summer to early autumn was also characterized by highest number of trade routes (Figure 3) and accounted for 46% of cross-border movement.

During the entire study period, on average each market was traded with 4.1 (range 1 - 32) other markets, with average incoming 1.96 (1 - 19), and outgoing links 2.2 (range 1 - 13). However, more 70 % of markets had only outgoing links (only sending animals). These are primarily district and village level markets close to pastoralist communities. Out of 172 small ruminant trading routes (links) recorded during entire study period, 12 were persistently remained for 10-12 months in the trade network throughout the year (“as back bones”); while 47 links were active for 6 - 9 months (“frequent”); 42 links remained in network for 3 - 5 months (“intermediate”); and the remaining 69 trade routes were only active for two month or less throughout the year (“occasional”) (Figure 4).

Table 3: Summary of animals head count by destination points and means of transportation from January to December, 2023

Survey areas	Transport		Count by destination points (Purpose of movement)			
			Internal Market	Slaughter Houses	Cross border (Export)	Total
Borena	Vehicle	Sheep	4,247	7,984	2,602	14,833
		Goat	5,325	12,097	4,624	22,046
	Foot	Sheep	15,419	-	-	15,419
		Goat	19,678	-	-	19,678
Somali	Vehicle	Sheep	33,917	3,612	51,289	88,818
		Goat	37,754	6,534	54,623	98,911
	Foot	Sheep	36,147	-	11,690	47,837
		Goat	45,859	-	11,860	57,719
Total			198,346	30,227	136,688	365,261

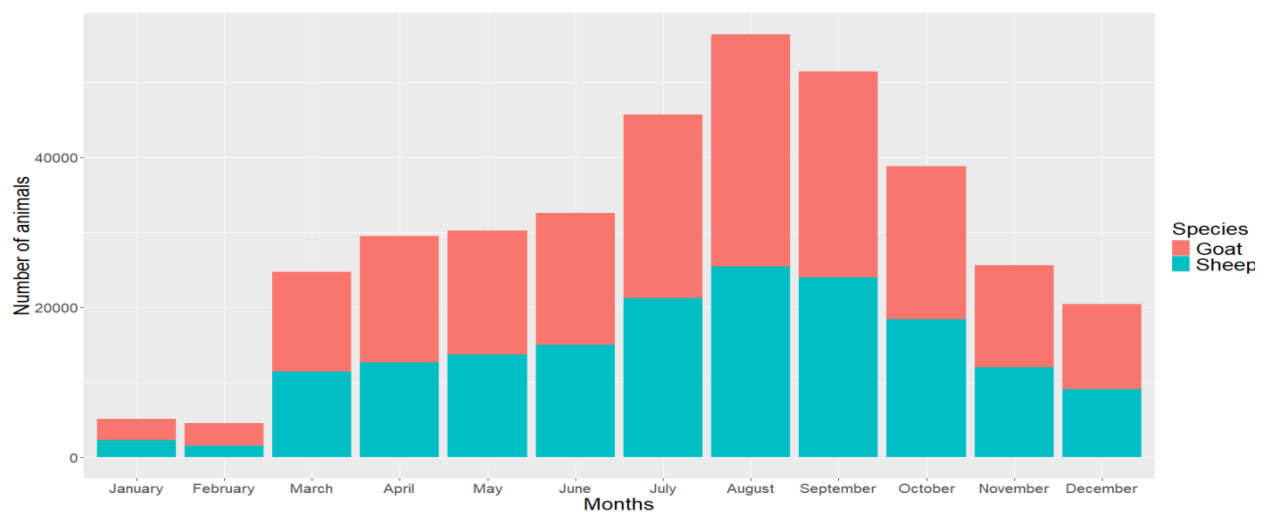


Figure 2: Volume of small ruminants traded through the network by month over 12 months

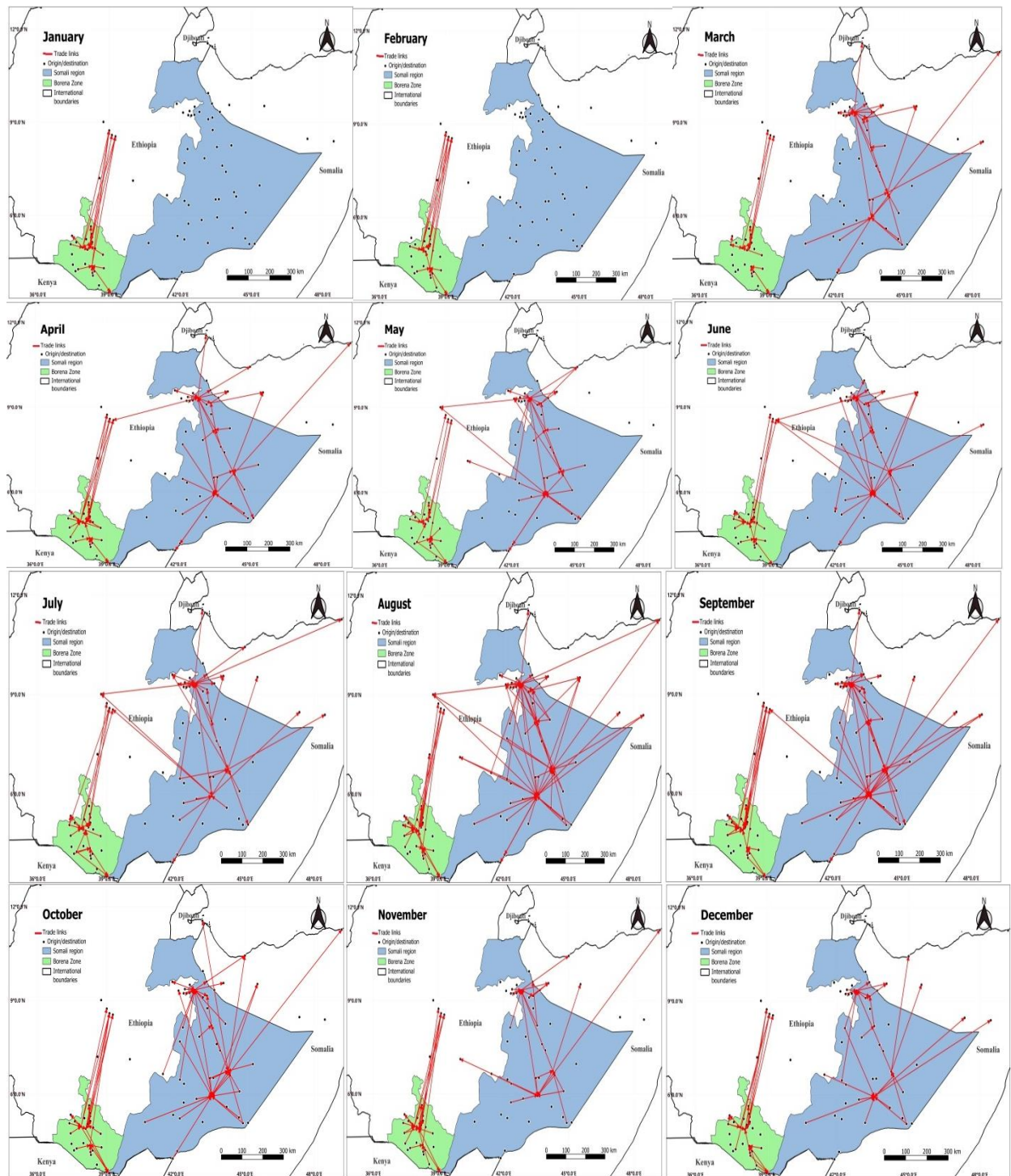


Figure 3: Monthly snapshot of small ruminant trade movement networks in Borena zone and Somali region from January to December 2023. Each black dot represents origin and destination points and arrows represents trade link with head of arrow indicating destination points.

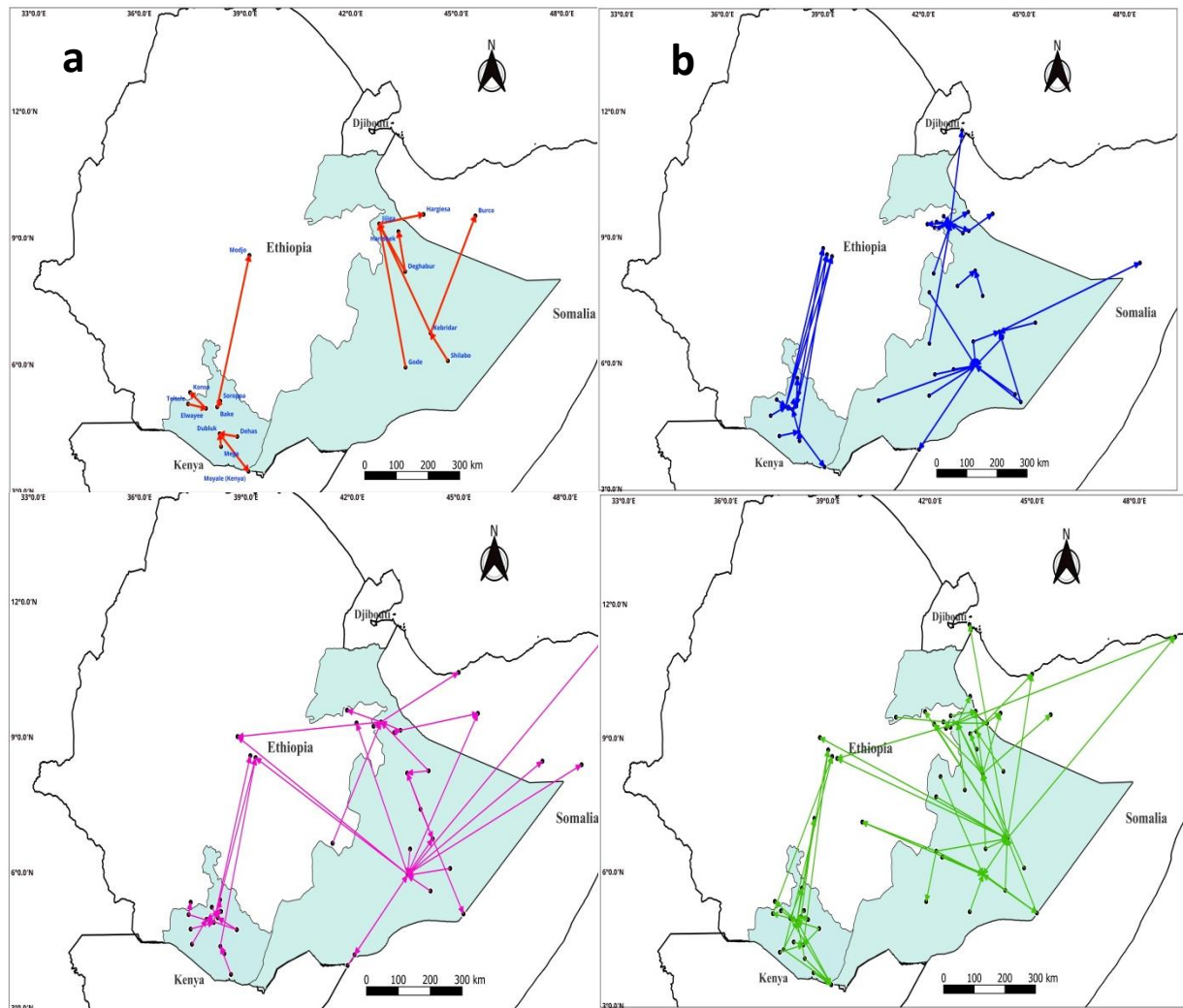


Figure 4: Geographical representation of small ruminant trade network links by frequency of activities over the year. **a.** backbone links (active for 10 -12 months), **b.** frequent links (active between 6 to 9 months), **c.** Intermediate links (active 3 - 5 months), and **d.** occasional links (active only for two months or less). Black dots represent origin or destination points.

4.3. General Network Description and Network Topology

Results of selected network (graph) and nodes (market) level parameters for full and sub-networks are presented in Table 4 and Table 5. The network displayed sparse connectivity (density = 0.02437), with only 2.4% of possible node pairs were actually connected. The reciprocity of the network was 0.104, indicating that only 10% of animal trade among markets are reciprocal (bidirectional), while the majority of the flow was in a specific direction from livestock keepers to the final destination. The degree of assortativity (connection preference) was -0.52. This negative degree assortativity value indicating that markets with a high degree of centrality (bigger markets) tended to preferentially traded with a markets of lower degree of centrality (smaller markets) more often than bigger markets. On average 2.21 steps were needed to connect two random pair of markets in the network (average path length = 2.212), and a minimum of five steps were required to connecting most distant reachable markets in the network (diameter = 5). Visualization of the actual path of the network diameter began at Fafan, extended across Jijiga, Deghabur, Kebridar, and Gode and ended at Madera in Kenya. All markets along the path of diameter were located in Somali region.

All in-degree, out-degree, and total degree distribution of all markets involved in the small ruminant trade network was right-skewed (Figure 5). Only a small portion of markets (Table 6), were exhibiting a relatively high degree of connectivity; the top 10% of markets with a high degree accounted for 50% of connections, while 90% of markets held 50% of connections. The majority of markets (83%) had either out-degree (only sending animals) or in-degree (only receiving animals) (Figure 6). The clustering coefficient and average path length for full small ruminant trade network were 0.729 and 2.216, respectively. While in comparison average path length and clustering coefficient of 1000 simulated random networks with the same number of nodes and links was 3.22 (range = 3.07 – 3.457) and 0.047(range = 0.01322 – 0.0927), respectively.

Table 4: Summary table of graph (network) level small ruminant trade network metrics

Network level metrics		Borena	Somali	Full network
Number of nodes (Markets)		31	55	84
Number of links (Routes)		64	107	171
Density		0.0667	0.037	0.0242
Diameter		3	5	5
Average path length		1.846	2.31	2.31
Clustering Coefficient		0.61	0.808	0.729
Degree of assortativity		-0.549	-0.649	-0.517
Reciprocity (%)		6.25%	12.3%	10.4%
Component size	% of markets in GSCC	93.55%	88.9%	90.47%
	% of markets in GWCC	6.45%	11.1%	9.5%

Table 5: Summary table of node (market) level small ruminant trade network metrics (Centrality measures)

Centrality measures		Borena	Somali	Full network
In-degree	Median	0	0.5	0
	Max	10	19	19
Out-degree	Median	1	1	1
	Max	8	13	13
Betweenness (average)		6.225	20.27	15.57
Closeness(average)		4.35×10^{-2}	2.1×10^{-2}	3.51×10^{-2}
Eigenvector (average)		3.67×10^{-2}	2.26×10^{-1}	1.56×10^{-1}

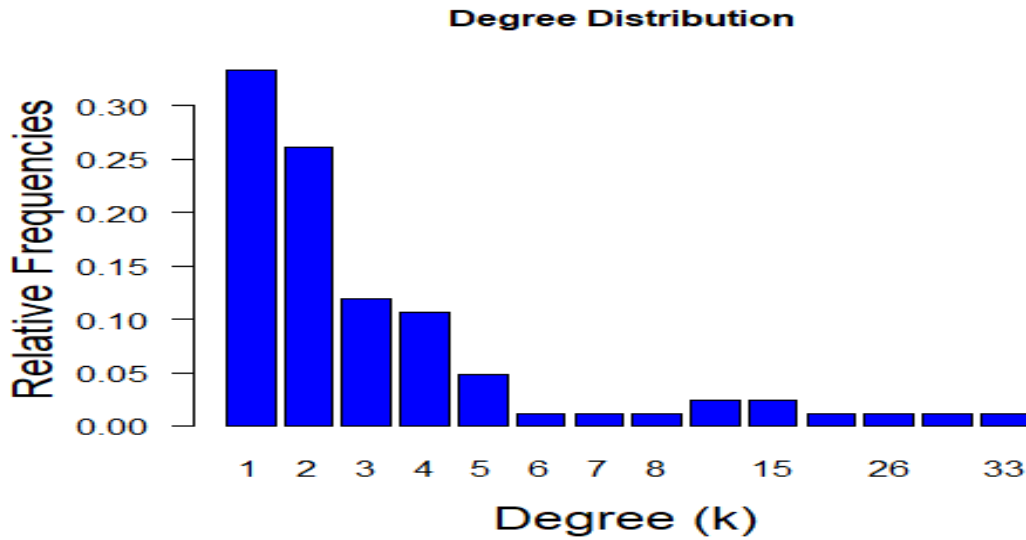


Figure 5: Network degree distribution (right skewed and heavy-tailed, with a small number of markets exhibiting relatively high degree of connectivity).

Table 6: Node level centrality measures of top-ranked markets and their contribution in connectivity for respective network in Borena and Somali livestock market system

Markets	Location	Out-degree	In-degree	Betweenness	Closeness	Eigenvector	% Share of connectivity
Gode	Somali	13	19	337.33	0.0323	0.94	14.5%
Jijiga	Somali	13	17	341.16	0.02381	0.91	13.6%
Kebridar	Somali	13	14	248.5	0.03226	1	12.3%
Yabello	Borena	7	10	60.25	0.14286	0.089	12.9%
Deghabur	Somali	7	8	157	0.02439	0.67	6.8%
Dubluk	Borena	6	9	58.083	0.0833	0.066	11.45%
Bake	Borena	7	7	49.416	0.0909	0.066	10.7%
Elwayee	Borena	8	6	25.25	0.1	0.074	10.7%
Hartshek	Somali	4	4	8	0.017	0.039	3.6%

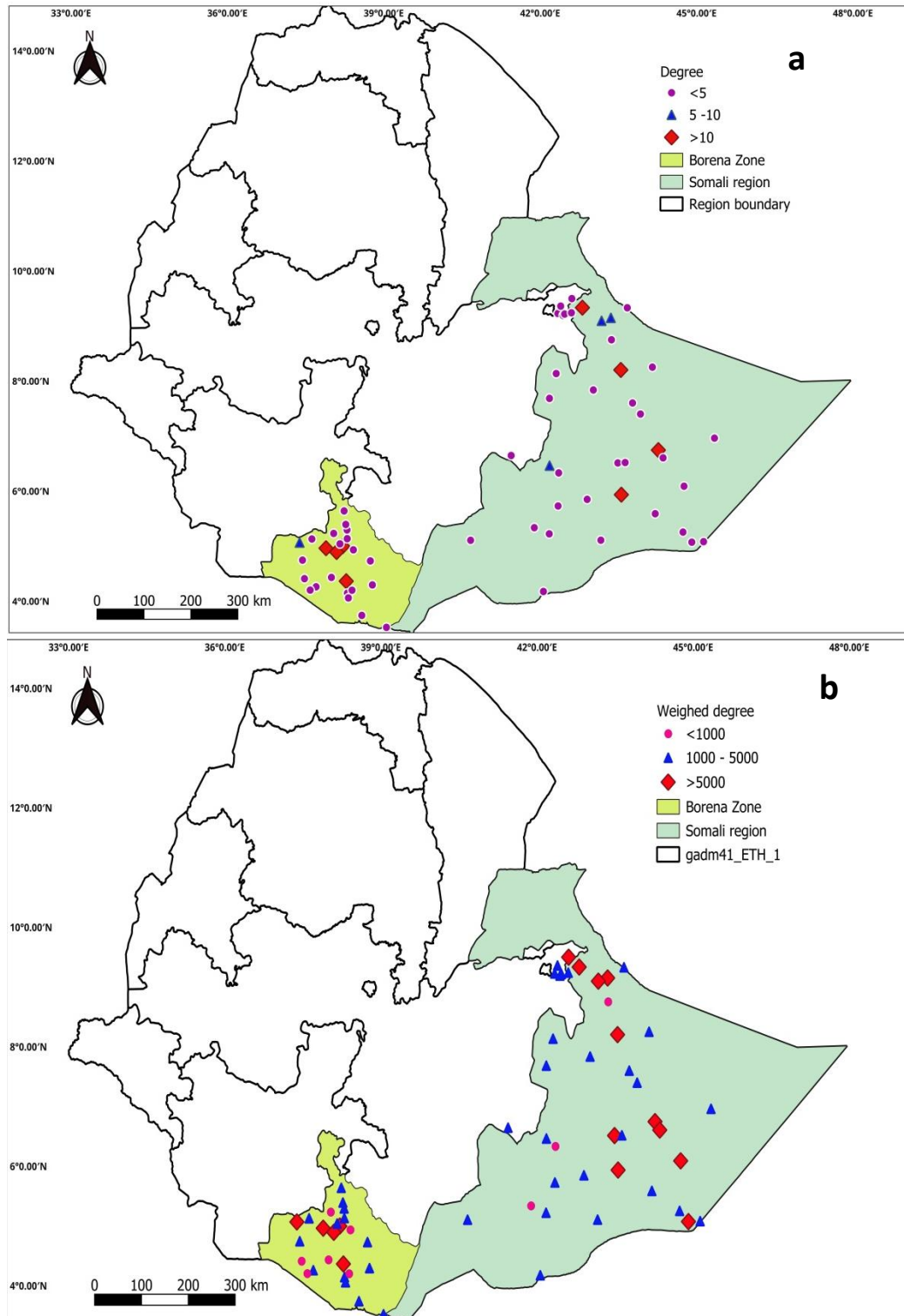


Figure 6: Maps depicting degree distributions of markets. **a.** un-weighted degree **b.** weighed degree; markets are weighed by the number of animals traded (volume of exchange)

4.4. Network cohesiveness and Key actor analysis

Small ruminant trade network in Borena zone and Somali region was organized around eight core markets and involved 76 periphery markets (Figure 9) which are connected to different cores. All markets in the network were included in giant weak component (GWCC). On the other hand there were 76 strongly connected components (GSCC). The largest GSCC included 7 markets (Figure 8), while two strongly connected components contained two markets each and the remaining 73 contained only one market. Community detection based on Bergstrom community detection algorithm identified 8 communities (sub groups 1 -8) within the network (Figure 7). The three top largest communities accounted for more than 75% of markets. Each community included between 1- 26 markets. The largest community (sub-group 5) located in southern part of Somali regional state involved 26 markets, while the smallest communities (subgroups 6, 7 and 8) only contained one market each.

The role of markets in the cohesiveness of network was identified by correlation analysis of node centrality measures (Table 7). The overall correlation coefficient among node centrality measures varied from low to high. The largest correlation coefficient was observed between Eigenvector and Betweenness centrality ($r = 0.7$), while the smallest correlation coefficient resulted between Closeness and Eigenvector ($r = -0.1413$). The role of markets in trading network was identified by correlation analysis between Eigenvector centrality and Betweenness centrality nodes. Ten Markets were detected as critical in the structural functionality of the small ruminant trade network (Figure 10). Two markets (Deghabur and Yabello) were identified as “gate-keepers”, due to their unique role of bridging more isolated markets to wider community of trade network; Three markets (Elwaye, Kebribeyah and Hartshek) had easy access to other central markets as well as to the rest of the trade network due to their shortest paths (acted as “pulse takers”); Five markets (Bake, Dubluk, Jijiga, Gode and Kebridar) had role of both as “pulse takers” and “gate-keepers”.

COMMUNITIES

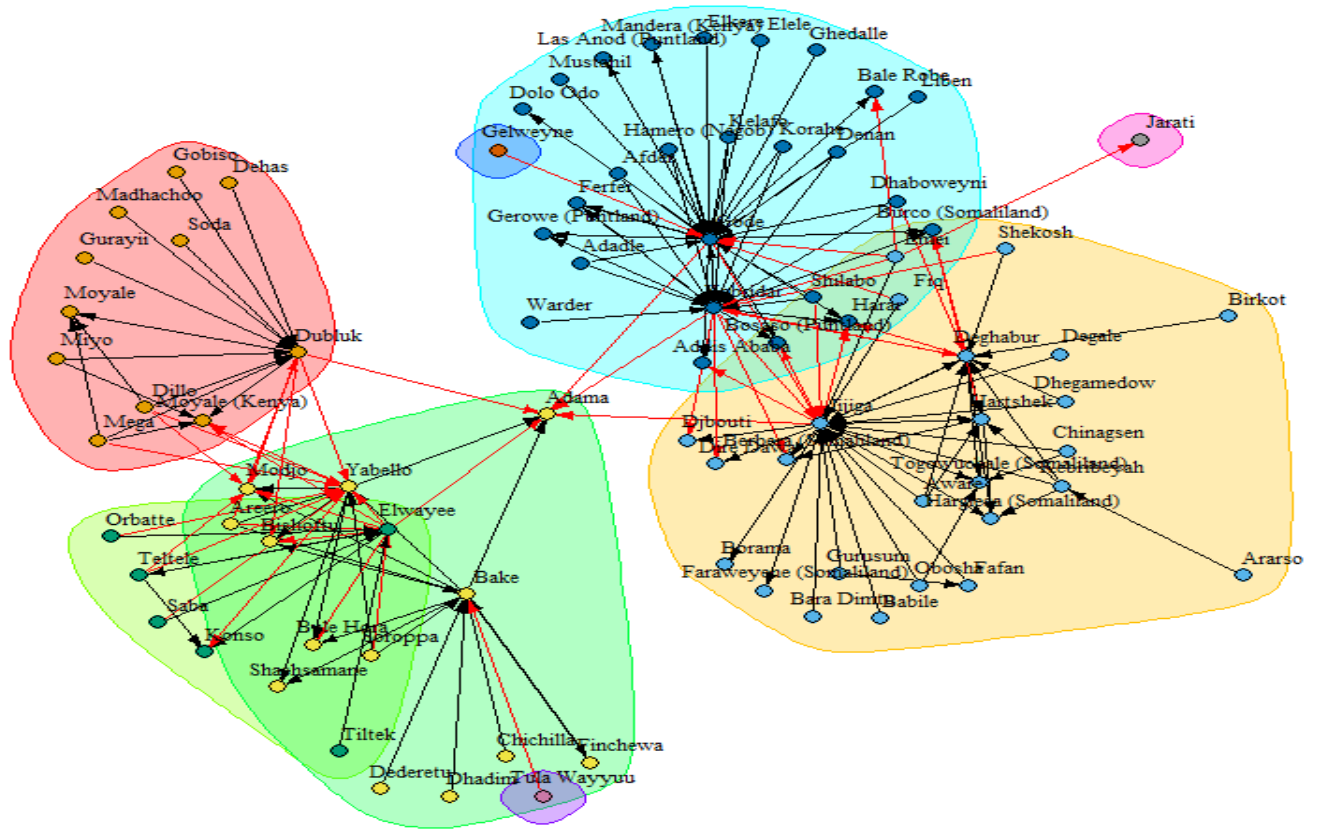


Figure 7: Community structure of small ruminant trade network in Borena and Somali region

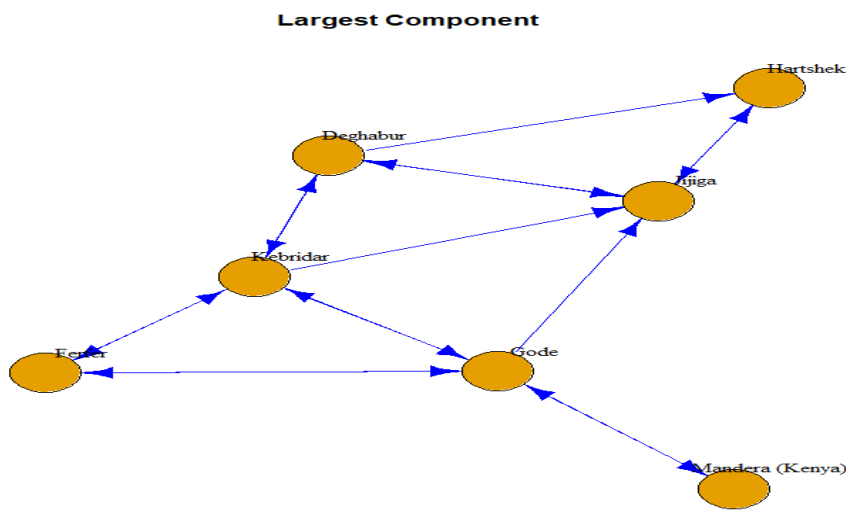


Figure 8: The largest giant strongly connected component of small ruminant trade network

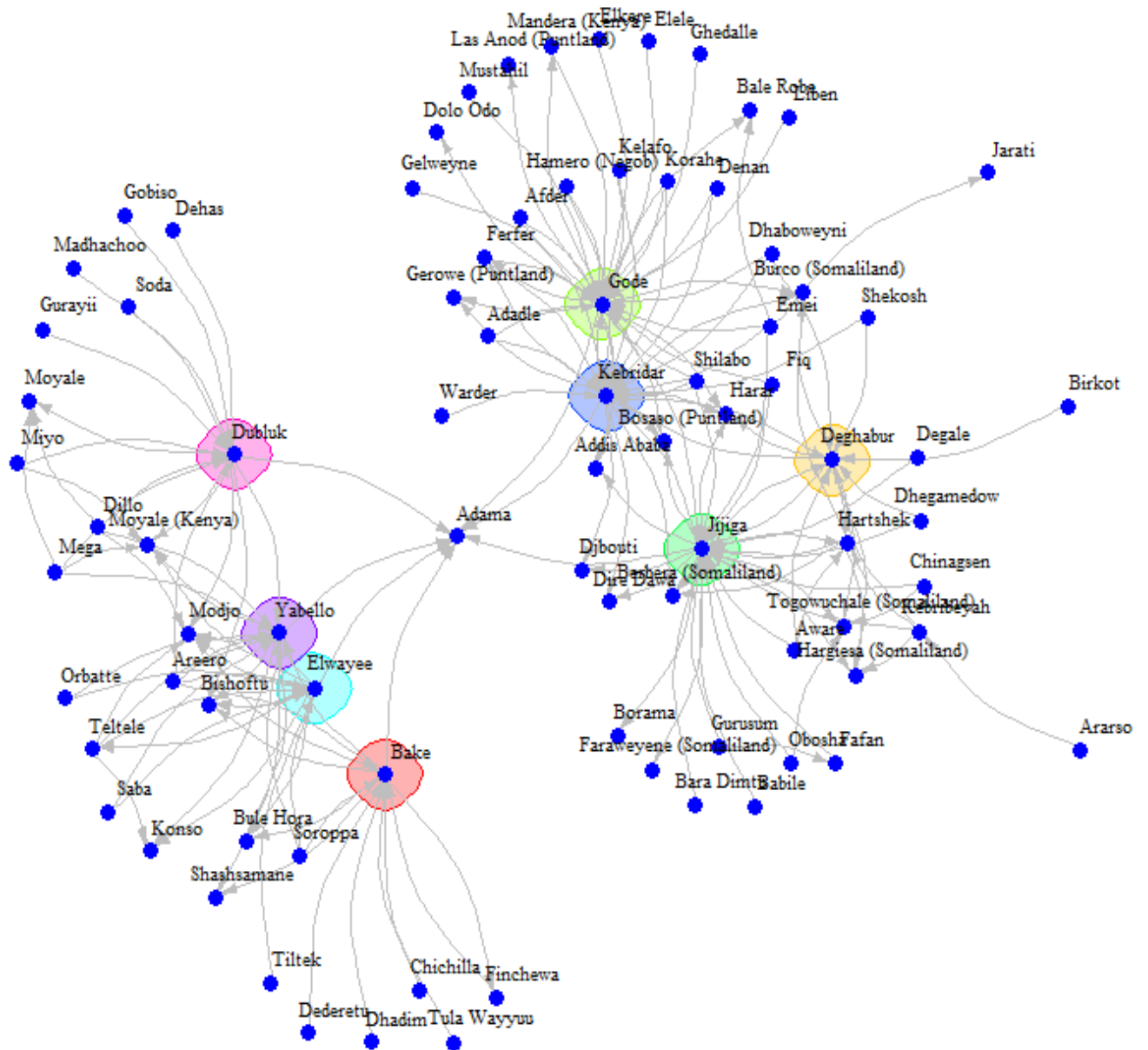


Figure 9: Core –Periphery structure of small ruminant trade network in Borena (bottom left) and Somali region (top right). Markets colored with smooth polygon are core markets

Table 7: Correlation coefficients between nodes centrality measures

	Out degree	In degree	Closeness	Betweenness	Eigenvector
Out degree	1	0.731417	0.533526	0.760929	0.620612
In degree	0.731417	1	0.183046	0.877367	0.71614
Closeness	0.533526	0.183046	1	0.13625	-0.14135
Betweenness	0.760929	0.877367	0.13625	1	0.839014
Eigenvector	0.620612	0.71614	-0.14135	0.839014	1

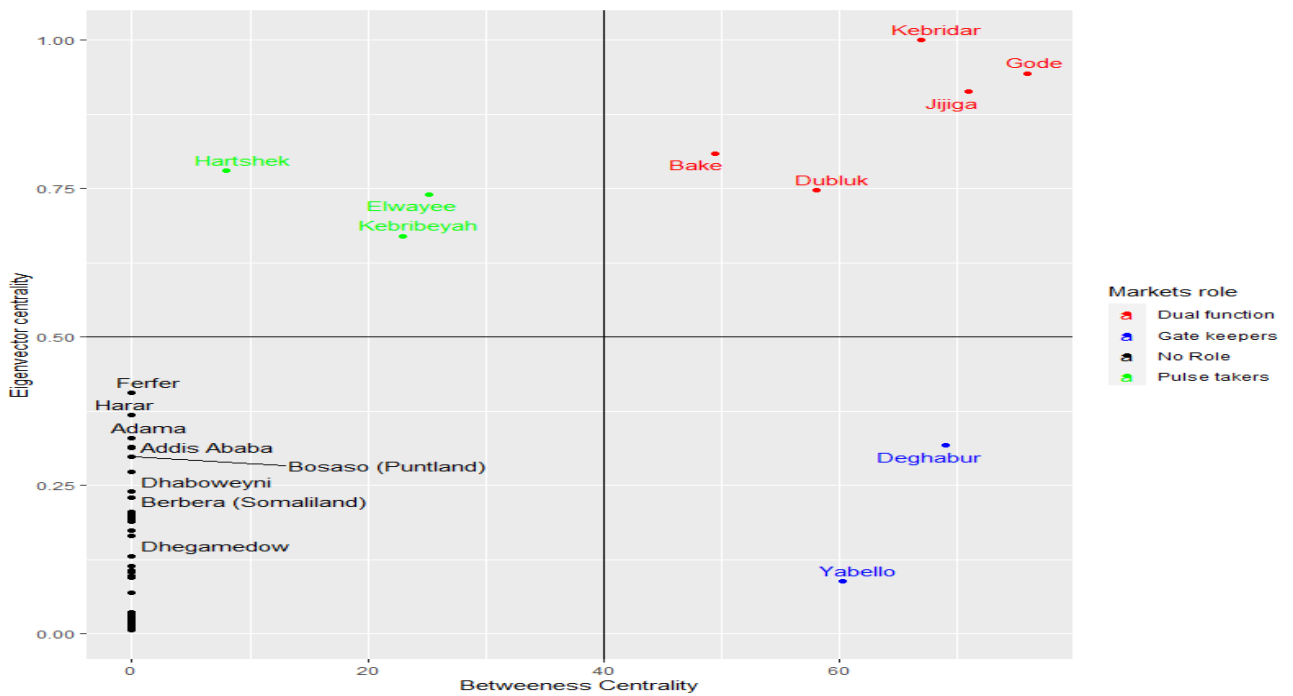


Figure 10: Key actors analysis. Markets in the top-left quadrant have unique access to central actors and are well-connected actors at the core of the network (“Pulse takers”), in the bottom-right quadrant, were being fundamental in connecting actors to the network that would otherwise be isolated from the core (“Gate keepers”), Markets in the top-right quadrant have both abilities and in the bottom left quadrant tend to have no particular role.

4.5. Risk of disease diffusion over the course of the year

The role of temporal change in trade network structure on potential spread of disease was estimated by the variation of the epidemic threshold (denoted q), for each of monthly network snapshots throughout the year. Analysis of threshold parameter (q) suggested that, the whole small ruminant network was prone to the risk of disease spread throughout the year (average epidemic threshold (q) = 0.392 and its inverse (R_0) = 2.75) (Figure 11 b and c). In animal trade context Basic Reproduction Number (R_0) = 2.75, indicates any high prevalence and highly contagious disease ($\beta \approx 1$) can spread to approximately 3 markets from a single infectious market without considering volume of exchange (number of animals traded between markets).

High risk period was between July and October ($q < 0.4$, $R_0 > 3$), with its peak in August where single infectious market had potential to infect 5 susceptible markets through trade (Figure 11 c). This high risk period was also characterized by highest trade movement both in terms of connections (new trade routes) and volume of exchange (Figure 2, Figure 4 and Figure 11 a). About 45% (328 out of 725 recorded movements) and more than 50 % of occasional links (market routes active for two months or less/ year) occurred between July and October. The volume of exchange was also highest in already existing and new links, 52.8% (192,812 animals) traded during this time.

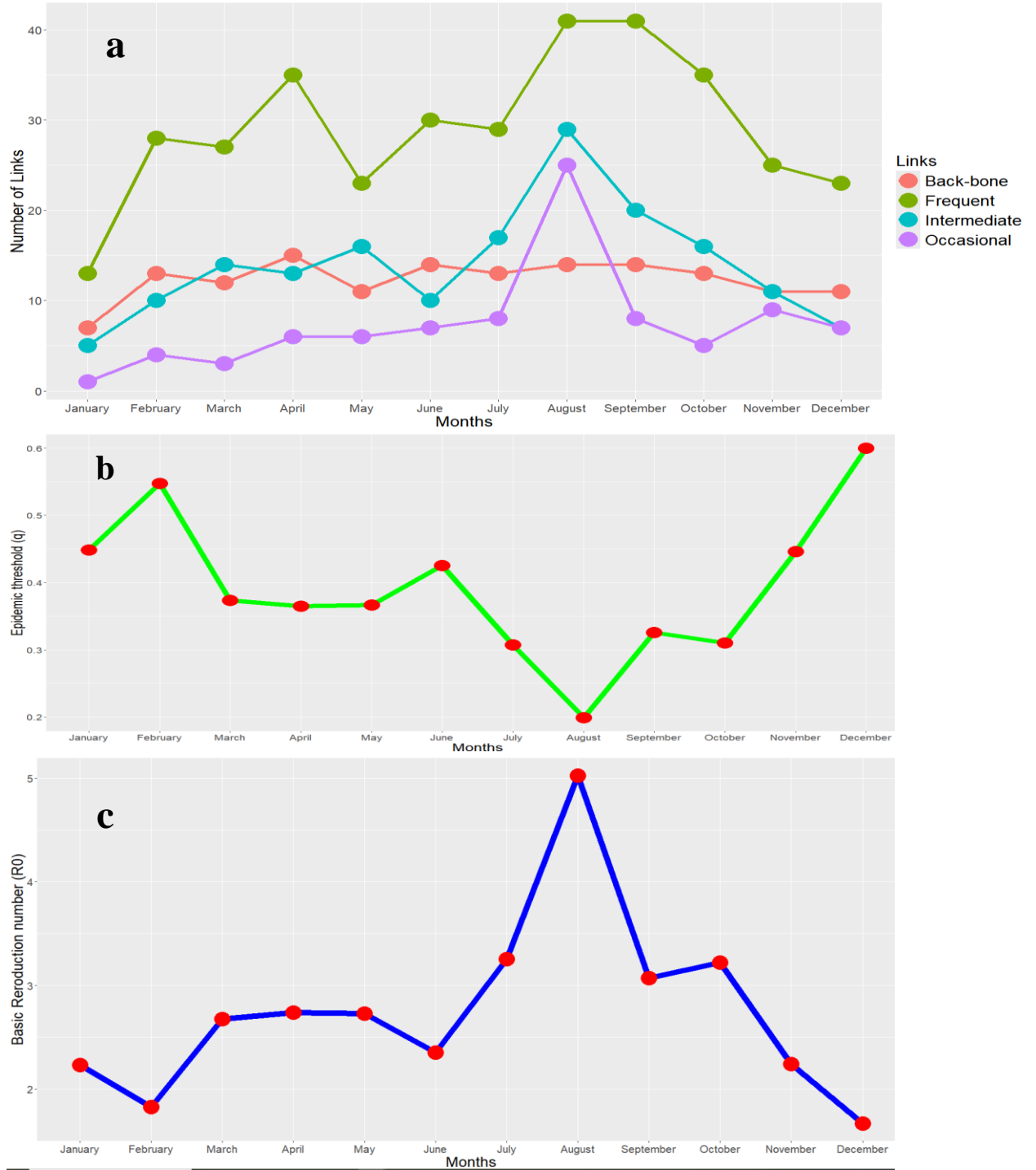


Figure 11: Monthly variations of small ruminant trade networks structures; and related epidemic threshold (q) and R_0 along the year. **a.** Trade links, **b.** epidemic threshold, **c.** Basic reproduction number (R_0).

4.6. Network vulnerability and resilience

The impact of targeted node removal on vulnerability and cohesion of network was tested by the sequential deletion of markets from trading network according to their centrality scores. After each removal step cohesion and vulnerability of the network were measured by the size of GSCC and number of communities involved in network. Targeted removal of markets based on centrality score of in-degree, out-degree, and betweenness centrality showed remarkably faster change in network cohesion with faster reduction in connected component size (GSCC). Targeting only 10% of the most central nodes based on in-degree, out-degree, and betweenness scores resulted in approximately 80% decrease in size of GSCC. While random removal of more than 50% of nodes is required to achieve the same effect on size of GSCC (Figure 12). Removal of markets based on their closeness centrality was effective during early stage of disruption, but then out performed by in-degree, out-degree and betweenness centrality. It is important to note that largest or giant strongly connected component (GSCC) is indirect estimate of lower bound of maximal epidemic size, for epidemics spread in the considered network (Kao *et al.*, 2006).

Node removal based on in-degree, out-degree, and betweenness centrality showed fast increase in number of communities during early stage (Figure 13). Removal of 20 % highly connected nodes triggered more than four-fold increase in number of communities. However, betweenness centrality based removal was less effective than other centrality scores in decomposing network into multiple communities.

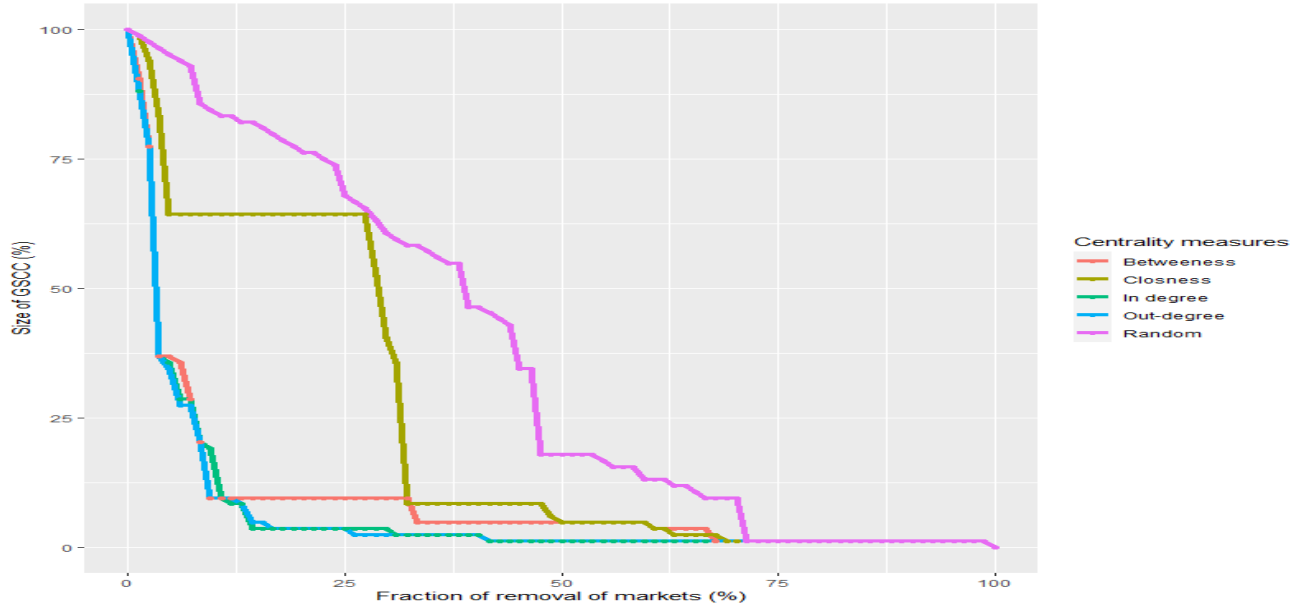


Figure 12: Plot of node centrality measures based percolation showing effect of targeted removal on connected component size compared to random removal

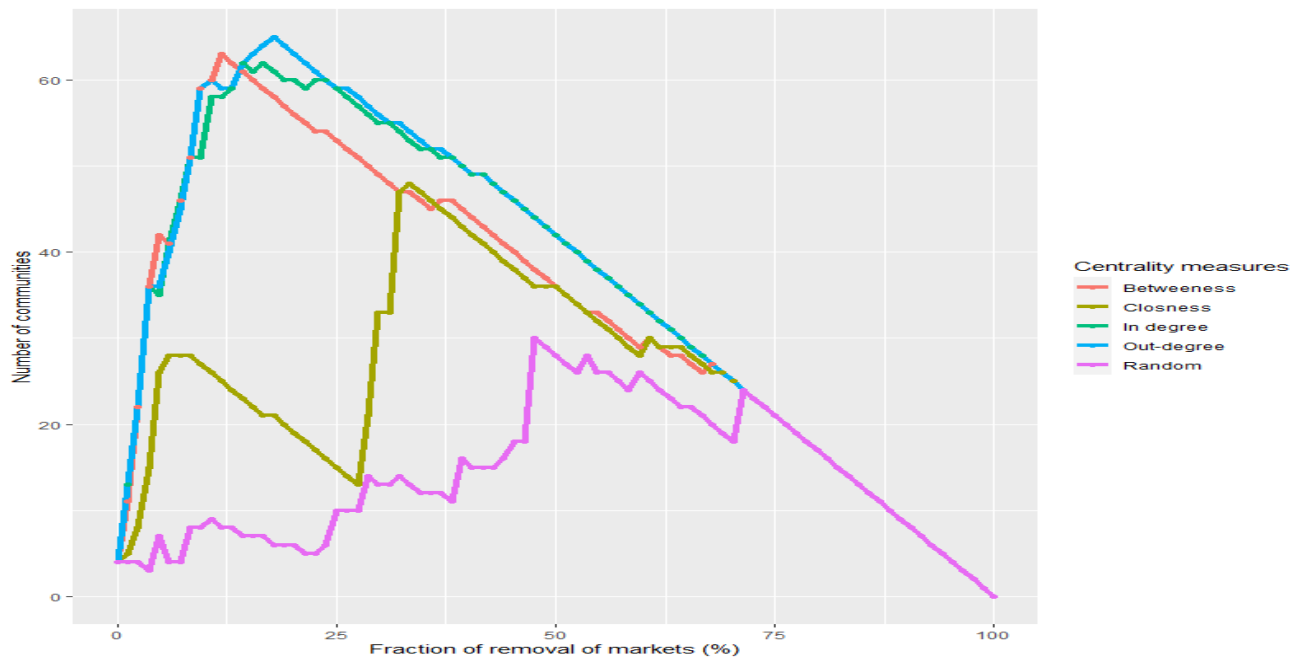


Figure 13: Effectiveness of node lever centrality measures based targeted removal of nodes on number of communities in the small ruminant trade network

4.7. PPR outbreaks and risk status, and relations with features of small ruminant trade network

According to national disease surveillance data for the year 2023 by the Ministry of Agriculture, PPR outbreaks were reported from 22 districts in study areas (3 in the Borena zone and 19 districts in the Somali region) (Figure 14). Based on participatory disease surveillance, outbreak investigation and Disease Outbreak and Vaccination Reporting (DOVAR) 19 districts are endemic to PPR, 32 districts are at high risk and 12 districts are relatively risk-free in the year 2023(Figure 15).

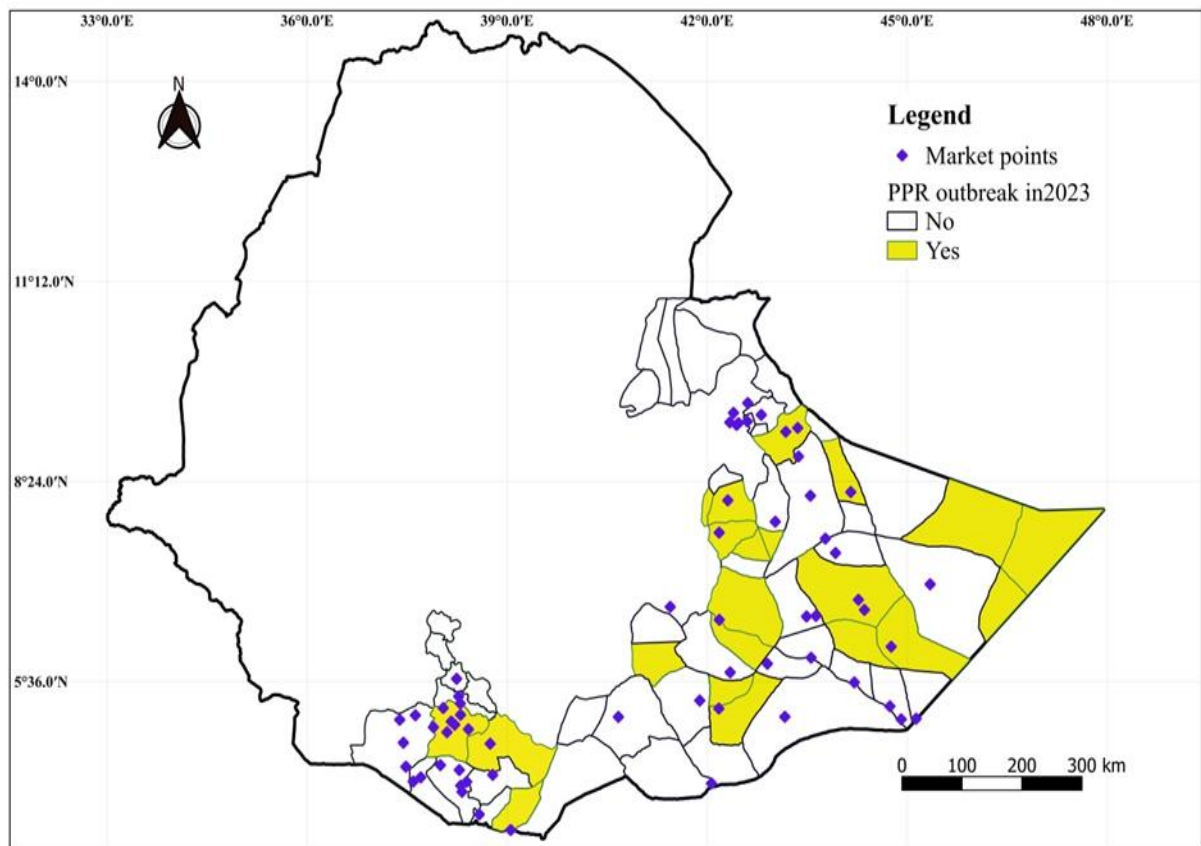


Figure 14: PPR outbreaks distributions in 2023 and livestock markets

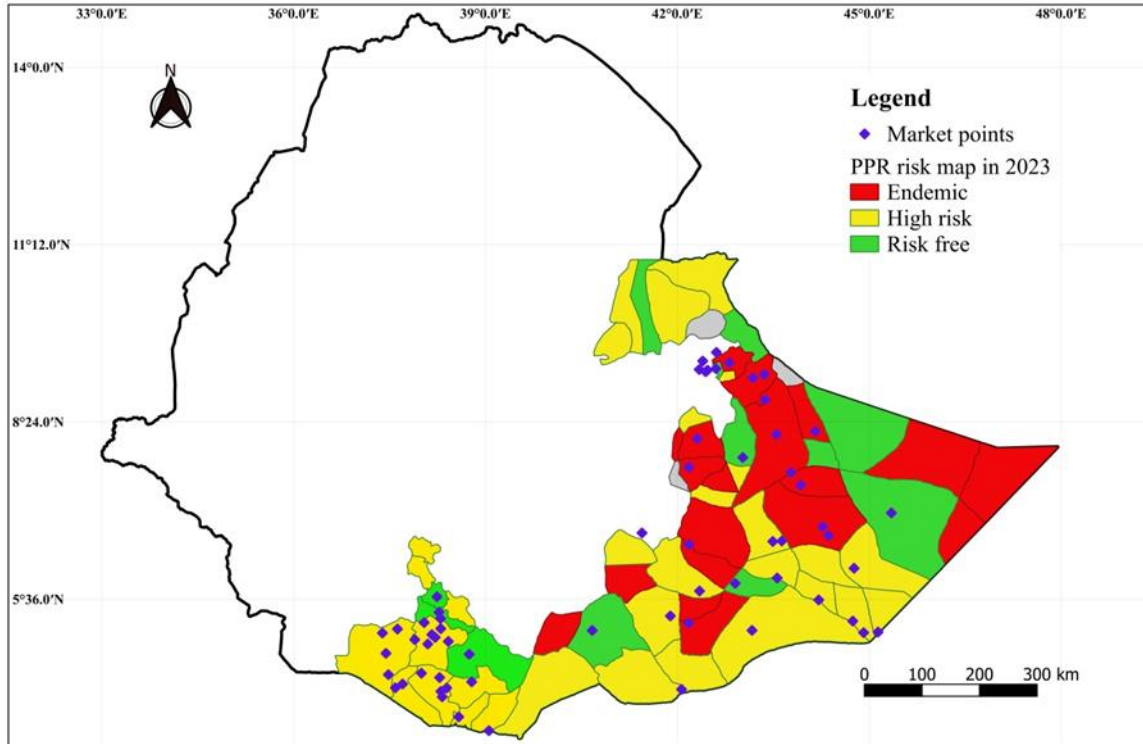


Figure 15: PPR risk status of Somali region and Borena zone in 2023 and livestock markets distribution

From a total of 64 livestock markets of different sizes located in the study areas, 53 are situated in PPR-endemic and high-risk districts, while 11 markets are in relatively PPR risk-free districts. There was a strong association between PPR risk status and out-degree ($X^2 = 7.82$; $p = 0.02$), out-weight ($X^2 = 6.1$; $p = 0.047$), and eigenvector centrality ($X^2 = 13.6$; $p = 0.001$) (Table 9). The markets in areas with a high risk and endemic of PPR accounted for over 90% of the annual volume of animal trade, with 343,423 individual animals being traded in these areas. Additionally, more than 92% of the recorded trade routes, specifically 158 out of 171 existing trade links, either originated from or were within PPR endemic and high-risk areas (Table 8).

Table 8: PPR risk status and small ruminant trade movements

PPR Risk	Number of districts (Woredas)	Number of Markets	Number of trade links (routes)	Trade volume (animals head count)
Endemic	19	16	62	188,878
High risk	32	38	96	154,545
Relatively risk free	12	10	13	21,838
Total	63	64	171	365,261

Table 9: Kruskal-Wallis test for markets (node) centrality metrics by PPR risk status

Market (node) level centrality metrics	Chi squared (X^2)	p-value
Out-degree (Outgoing links)	7.8208	0.020**
Out-weight (Outgoing volume)	6.1099	0.047**
In-degree (Incoming links)	0.7961	0.671
In-weight (Incoming volume)	1.2309	0.541
Betweenness	5.1526	0.076
Closeness	3.0079	0.222
Eigenvector	13.665	0.001**

5. DISCUSSION

Network-based approaches are widely applied in veterinary epidemiology to study role of animal movements in spread of disease, aiming to develop suitable strategies for disease surveillance and control (Dube *et al.*, 2009; Motta *et al.*, 2017). Network-based approach describes livestock movement as a spatial network, where nodes representing livestock markets, farms, administrative units or herds and links are created each time when animals move from one node to another. The implication of livestock trade movement for disease spread is particularly getting more attention since pathogens can be transmitted over long distance via movement of infectious animals (Motta *et al.*, 2017). To achieve goal of identifying potential paths and understanding the dynamics of disease spread in complex networks, it is essential to analyze contact patterns between actors in the system and their large scale structure. The application of techniques adopted from social network analysis (SNA), has been widely implemented by veterinary epidemiologists to identify actors in the network that are central to the spread of infectious diseases (Lentz *et al.*, 2016). In this study, small ruminant trade network and its vulnerability to potential diffusion of PPR virus was investigated in major pastoral regions of Ethiopia, namely Borena zone and Somali region using social network analysis in combination with epidemiology of PPRV in study areas.

Over the study period, there was a clear seasonality both in trade flow and volume of exchange of small ruminants through livestock trade chain in study areas. The highest volume of exchange was recorded between July and October 2023, with 192,812 sheep and goats (more than 50 % of annual exchange) was traded during these four months. This highest animal trade movement in late summer and early autumn is associated with seasonal factors that influence both supply and demand of livestock market. Seasonality in trade volume in Borena zone might be due to prolonged drought until 2023 springtime in Borena pastoral area and seasonal fluctuation in demand and price associated with festive periods (Galgalo, 2015). According to traders, in Somali region the demand in market is higher in autumn (“dayr”) season (Awoke *et al.*, 2015). Another possible reason might be availability of quality animals for market and export is influenced by seasonal factors such as drought, and seasonal demand for livestock is influenced

by festive periods within country and annual Hajj to and in Saudi Arabia which increase demand in cross border destination markets (Majid, 2010).

In the current study, full small ruminant trade network displayed low density of connection, with only 2.4% of possible links (routes) among markets. This sparse connectivity suggests that traded animals in Borena and Somali pastoral areas are predominantly local in nature and had limited number of destinations. This observation in agreement with Mekonnen *et al.* (2019), on dairy cattle movement suggested regional/local level nature of animal trade in Ethiopia. The current small ruminant trade network displayed short diameter (diameter = 5) and average path length (PL = 2.2), indicating only few steps are required to connect any possible pairs of markets. This small value for network diameter, presence of highly connected markets (hubs) and low epidemic threshold value (average $q = 0.39$), indicates small ruminant trade system could be prone to the spread of infectious diseases. Once any communicable disease introduced into trade system, it could reach other markets in a short period of time due to small diameter of network. Earlier studies supported this observation and indicated the role of network diameter, epidemic threshold and presence of hubs on spread of infectious diseases (Nicolas *et al.*, 2018; Ciss *et al.*, 2023; Puspitarani *et al.*, 2023).

The degree distribution of markets in small ruminant trade network was right-skewed, with large variation in number of connections. Only small fraction (less than 10 %), top highly connected markets held 50 % of connection, while the remaining majority of smaller markets(90%) accounted for only 50% of connections in network. This heterogeneity in number of connections, among markets was due to bigger livestock markets located urban areas are main destination for animals from many surrounding smaller/village level markets, and attract long-distance connections including export abattoirs and cross-border destinations; while majority of small markets are trading only with nearest big markets. Hence, due to this heterogeneous distribution of connectivity markets could play a distinct roles based on their structural position in the small ruminant trade chain. Since current small ruminant trade network is directed (direction of movement is defined), spread of disease depends of correlation between the in-degree and out-degree of markets (Schwartz *et al.* 2002). The high correlation between the in-degree and out-degree ($r_0 = 0.73$), indicating presence of markets that are both likely to become infected and to transmit infection, facilitating disease transmission (Schwartz *et al.* 2002; Kao *et*

al., 2006). Markets with high out-degree and high betweenness centrality can act as super-spreaders of disease (Puspitarani *et al.*, 2023). These core groups and super spreaders could play critical role in the spread and maintenance of infection because once disease is introduced to these groups can be transmitted into many others (Keeling and Eames, 2005). For early disease detection (targeted surveillance) and to implement effective disease control interventions such as targeted vaccination; and for enforcing regulation of live animal trade (GoE, 2014), targeting markets with high out degree and betweenness (“gate-keepers”), could minimize risk of disease spread through market chain, and could improve early reaction and response capacity for any emerging disease (Hitchcock *et al.*, 2007). Markets with high in-degree and betweenness (“pulse takers”) are at position of high vulnerability for infection (super-receivers) from other markets. Enhancing and enforcing biosecurity measures and laboratory-based surveillance in these high-risk groups would greatly reduce the structural risk and favors early warning (timely detection) of pathogens (Dube *et al.*, 2011, Guinat *et al.*, 2016; González-Gordon *et al.*, 2023). However, these findings would certainly require further empirical verifications through testing for their real-world implications and practical applicability.

Global clustering coefficient and average path length of observed small ruminant trade network were 0.73 and 2.21, respectively. In comparison sets of 1000 randomly simulated networks having the same number of nodes and edges with current network displayed $CC = 0.047$ and $PL = 3.22$. This significantly higher global clustering coefficient and shorter path length of small ruminant trade network when compared to randomly generated networks indicates, the network characteristic was consistent with small-world network topology. Small-world networks known for their multiple interconnected subgroups of markets through with presence of few long-distance connections (Watts and Strogatz, 1998; Wang *et al.*, 2012; Motta *et al.*, 2017; Hasahya *et al.*, 2023). Many previous studies suggested that small-world type networks are prone to rapid and easy spread of infectious diseases (Keeling and Eames, 2005; Shirley and Rushton, 2005; Dube *et al.*, 2011; Motta *et al.*, 2017). This susceptibility of small-world networks for rapid dissemination of infectious diseases is due to small diameter (easy to reach out) and high clustering within subgroups of markets (Nicolas *et al.*, 2018). However, according to previous theoretical epidemiological studies, Watts and Strogatz (1998), high clustering means that most

infections are predominantly localized in some areas, but wide-scale dissemination is still possible due to some long-range links (Moore and Newman, 2000).

The higher-order interaction among markets in full network displayed negative assortative mixing (degree assortativity = -0.517). This disassortative relationship indicates bigger markets (markets with high degree of centrality) tended to trade more often with less connected (smaller) markets than highly connected counterparts. When compared with assortatively mixed case, the main disadvantage of disassortatively mixed networks is that sustaining disease spread especially for small transmission rates (Kiss *et al.*, 2006). However, implementing control intervention is easier in disassortatively mixed networks than assortatively mixed networks. This is because; disassortatively mixed networks are easily disrupted by targeted and even random removal of nodes (Figure 13). On the other hand, assortatively mixed networks are more resilient to random and even targeted attack, and the size of GSCC is unaffected unless a significant portion of highly connected nodes are removed (Newman, 2002). Hence, negative assortative relationship observed in current small ruminant trade network could be beneficial for implementing disease control intervention. Implementing control measures such as targeted vaccination, movement restriction and biosecurity measures to highly connected markets could limit disease transmission and, is a resource-friendly method for cost-effective disease control strategy (Lentz *et al.*, 2016; Mekonnen *et al.*, 2019; González-Gordon *et al.*, 2023).

Analysis of threshold parameters showed an average epidemic threshold ($q = 0.392$) and Basic Reproduction Number ($R_0 = 2.75$) indicating that the whole small ruminant trade network was prone to spread of disease. Basic Reproduction Number ($R_0 = 2.75$), in livestock market context interpreted as highly contagious diseases like PPRV can spread to approximately three other markets that are trading with one infected market, by a single batch of movements irrespective of number of animals exchanged (Volkova *et al.*, 2010). Lowest observed risk time was December ($q = 0.6$, $R_0 = 1.66$); but was still enough to trigger epidemics. Maximum risk period was between July and October, with its peak at August ($q = 0.199$, $R_0 = 5$). This highest risk from late summer to early autumn might be due to high animal trade movement related with festive periods (Majid, 2010; Awoke *et al.*, 2015; Galgalo, 2015). Previous studies by Lancelot *et al.* (2017), Nicolas *et al.* (2018) and Ciss *et al.* (2023) demonstrated same high risk of disease spread (low threshold

value) related to increased volume of trade exchange and appearance of new links (market routes) during festive periods.

According to PPR risk status update by the Ministry of Agriculture in the year 2023, 19 districts are endemic to PPR, 32 districts are at high risk and 12 districts are relatively risk-free in Somali region and Borena zone. A strong association was observed between PPR risk status and out-degree, out-weight and eigenvector centrality ($p < 0.05$). This strong association suggests markets with high degree of outgoing trade connections (both in terms of links and volume of exchange) were primarily located in PPR endemic and high-risk areas. The PPR endemic and high-risk areas were source for more than 90 % of animals traded through the small ruminant trade network. And the majority of these animals were destined for different regions of the country and neighboring countries through cross-border animal trade. Hence, the risk of PPRV through live animal trade is high due to the direct and indirect contact transmission nature of the virus; congregation of animals and mixing of species can increase the risk of transmission; cross-border movements; and sharing markets around border in pastoral systems (Munir *et al.*, 2013; Biruk, 2014; Ullah *et al.*, 2022).

Targeted removal of nodes (markets) based on their in-degree; out-degree and betweenness centrality measures was an effective method for faster fragmentation of network cohesiveness and reduction in connected components size than randomly targeting markets (Figure 12). Removing top 10 % ranked markets sequentially based on decreasing order of these centrality measures reduced size of GSCC by approximately 80%. At the same time, randomly targeting markets required removing of more than 60 % of markets to achieve same size of reduction (80%) in connected component size. The size of GSCC is indirect estimate of a lower bound of the maximum number of markets that a newly introduced infectious agent might reach (Schwartz *et al.* 2002). It is worth noting that removing markets based on their position does not mean that they are not active in trade, rather making them effectively cannot transmit disease to other markets by implementing control measures (Lentz *et al.*, 2016). This observation suggests that any intervention such as movement restriction or vaccination implemented on top 10% ranked markets can limit epidemic spread by 80%, since GSCC is considered as indirect measure for lower bounds of maximum epidemic size (Kao *et al.*, 2006). Current observation agrees with

previous findings and theoretical studies suggested targeting nodes based on their centrality values in disassortatively mixed networks can be considered as an effective way to identify markets playing critical role in disease transmission and to implement efficient disease control measures such as movement restriction, vaccination or diagnostic testing (Kiss *et al.*, 2006; Motta *et al.*, 2017; Mohr *et al.*, 2018). Hence, this study suggests highly connected markets in Borena and Somali pastoral areas presented in Table 6 are at higher risk of disease incursion and rapid dissemination over long distance. Even though control strategies may be difficult to implement on ground, it is important to note that targeting those markets could provide opportunities for targeted disease risk mitigation interventions and minimize cost and time, rather than randomly implementing control interventions and disease surveillance.

6. CONCLUSION AND RECOMMENDATIONS

This study provides a first assessment and quantitative description of small ruminant movement patterns through markets in Borena zone and Somali region. The current analysis of small ruminant trade network offers insight into structure of small ruminant mobility by analyzing the annual and monthly patterns of shipments for trade and slaughter houses. It is widely known that the trade of live animals is a major pathway for the spread of infectious diseases, including Transboundary Animal Diseases (TADs) such as PPR. Current empirical observation and analysis suggest that small ruminant trade movement pattern is organized around small fraction of highly connected hub markets which serve as main destinations points for majority of less connected smaller and village level markets, and sending animals to final destinations such as slaughter houses and cross-border destinations. Furthermore, small-worldness network topology and disassortative mixing (assortativity degree = -0.517) indicate geographical clustering of markets with few long-distance connections, and tendency of highly connected markets more often trade with less connected smaller markets than highly connected counter parts. This negative assortative relationship could provide opportunity for targeted disease control interventions such as movement restriction and biosecurity measures to highly connected markets. This assessment is further supported by effectiveness of node-level centrality metric driven percolation, which shown faster fragmentation of network structure by significantly decreasing size of GSSC. The entire trade network for small ruminants was at risk of contagious diseases such as PPRV due to its small diameter, low epidemic threshold value throughout the year, and the presence of highly connected markets that can act as super-receivers and/or super-spreaders. The current study and its outputs are only focusing on empirical observation and small ruminant movements through markets and interpreted with caution. Over all, this study could improve our general understanding of the small ruminant movement and its potential role in epidemiology of TADs including PPRV in Borena zone and Somali region.

Based on above conclusions, the following recommendations are forwarded:

- ❖ Animal movement through trade should be considered as key component when planning and implementing national or regional-level epidemiological surveillance and disease control activities.
- ❖ Targeting highly connected markets and nearby areas for systematic market surveillance and disease inspection could provide opportunities for early detection of threats, tracing the source and destination of agents, and enhancing preparedness and rapid response.
- ❖ Increasing biosecurity, reinforcing health checks during transportation; and improving community health education could minimize the risk of transmission of disease even though, these strategies may be difficult to implement on ground.
- ❖ For future evidence-based decision-making and effective disease control, characterizing multilayer networks of all movements, including grazing-oriented mobility, transhumance and movement of other animal species should be aim for future investigations.

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8. ANNEXES

Annex 1. Number of respondents involved in Key informant interview

Survey Sites	Number of respondents involved in Key informant interview					Total
	Local Traders and Brokers	Long Distance Traders	Livestock, Office personnel	Trade office personnel		
Borena	12	3	1	1		17
Somali	12	8	2	1		23

Annex 2. Key Informant Interview Guide

Respondent Information

Name _____ . Address _____

Education level _____

Organization/Job _____ . Position _____

Phone _____ Date of interview _____

Introduction

Hello,

Thank you for taking the time to talk to me.

My name is _____. I am MSc student in Addis Ababa University College of Veterinary Medicine and Agriculture. I am working my MSc thesis on Spatial Mapping and Network Analysis of Small Ruminant Trade Routes to Inform Disease Control Strategies in Somali and Borena Pastoral Regions of Ethiopia. The information we collect will help to identify major markets, border crossing points and change in

market trends over season. This interview is completely anonymous and is an informative exercise. It will take approximately 15-30 minutes. The objective of this interview is to obtain information from relevant stakeholders and people who have more knowhow small ruminant trade. The answer to all the questions is voluntary. Continue only if you want to participate.

Your personal data and your answers to questions will be kept confidential. No names will appear in the final report.

- Are You willing to give interview? Yes No
- Do you have any questions before we start our discussion/interview?
 Yes No

Interview Questions

Assessment of small ruminant trade and its status in the regions

- Is there livestock market in your district? 1. Yes 2. No
- Where is the main market?
- Can you tell us the market route?
- How big is the demand per annum?
- How often animals traded in the market?
- Is there change in market trends over season?
- Have any major events altered the volume and frequency of market?
1. Yes 2. No
- If yes, what are events/factors altering the volume and frequency of market?
- Based on your experience, can you tell most frequent sources, transit and destinations of animals traded in the market?
- Is there cross border small ruminant trade in your district? 1. Yes 2. No

- If yes, what is its trend in terms of volume, frequency and direction?
- What are the policies, rules and regulations that regulate the livestock market in your district?
- Any remarks that you would like to suggest?

Annex 3. Format for small ruminant market data Collection

Name of data collector _____, Signature _____

District_____. Zone_____, Region_____

Name of market place _____	Geographic coordinates		Latitude_____					
			Longitude_____					
Date of quantification	Number of animals sold		Origin			Destination point		
	Sheep	Goat	Name	Latitude	Longitude	Name	Latitude	Longitude

Annex 4. Sample pictures indicating some key informant interview and market data collection procedures

1. Key informant Interview



B. Gode market (Somali Region)



C. Bake market (Borena Zone)



D. Yabello livestock market (Borena zone)



E. Kebridar (Somali region)



Annex 5. Research Ethical Clearance Certificate

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ADDIS ABABA UNIVERSITY
College of Veterinary Medicine
and Agriculture
Bishoftu

Animal Research Ethical Review Committee

Ethical clearance certificate

Certificate Ref. No: VM/ERC/03/14/15/2024

Name of Applicant: **Asrat Arke Ashango (DVM, MSc student)**

Address: Department of Clinical Studies, College of Veterinary Medicine and Agriculture, Addis Ababa University

Title of the project: *Mapping and network analysis of small ruminants trade in Somali Region and Borena zone, Ethiopia: Implication for potential spread and control of PPR virus*

Date of application: **December, 2022**
 Nature of the project: **Questionnaire survey**
 Target animal species: **None**
 Number of animals involved: **None**
 Study area: **Somali Region and Borena Zone- Ethiopia**

Minutes No. and date of review: **VM/ERC/03/15/022, 08/03/2023**

The Institutional Animal Care and Use Committee of the College of Veterinary Medicine and Agriculture of the Addis Ababa University has reviewed the above research project and unanimously approved the application of **Asrat Arke Ashango**.

Professor Getachew Terefe (DVM, PhD)

Chairman

(Signature)
Signature



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 Please quote Our Ref. No. when replying

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Annex 6. Status of plagiarism reports

