Title: Understanding Peste des Petits Ruminants (PPR) Transmission Dynamics: A Network Analysis Approach in Pastoral and Agropastoral communities in Tanzania

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Abstract

Unregulated livestock movements pose a significant risk for the spread of diseases, which threaten their health and productivity, and has been cited as a potential driver of its spatial and temporal dynamics in the country. Formal evaluation of PPR spread linked to livestock migration is lacking. This study investigated the extent to which PPR spread can be attributed to livestock movement while accounting for risk factors such as production system, livestock population, geographical location and season. Data on livestock movement from Tanzania were collected to create network patterns that show the risk of PPR circulation across geographical areas and agroecological systems. Results demonstrate a notable variation in network structure. Compared to movement related to seasonality variation, trade-related movement reached 600km. Either, in the dry season, animals travel long distances compared to the wet season. The probability of contracting PPR infection was found to be half that of households with outgoing livestock (outdegree), indicating a lower risk of infection compared to households with more incoming livestock (indegree). Network pattern shows scale-free properties, negative and close to zero assortative mixing in Pastoral and agropastoral societies, respectively. From these findings it can be concluded that pastoral communities in northern Tanzania are prone to PPR infections, suggesting control methods targeting high-potential households in pastoral communities and districts with high livestock populations. The study suggests targeting the pastoral production system in these areas to impede PPR spread. Future research should focus on dynamic modeling and targeted control interventions.

Keywords: Pastoral, Agropastoral, livestock movement, scale-free property, network analysis, Peste des Petits Ruminants, short cycle stock

Introduction

The movement of livestock is crucial to the livestock trade, search for pasture and water, or relocation, yet it carries the danger of disease transmission. For example, in 1920 saw the return of rinderpest to Europe from Brazil, the disease, which was officially declared eradicated in 2011 (1,2). Improved livestock trade infrastructure like roads and railway networks and slaughter facilities show evidence of increased PPR risks. For example, in Asia and Africa , livestock movement in meat supply chain networks (herds-local small and big market central market) has been linked to the PPR outbreak (3,4).This is also true for Tanzania, where PPR spread throughout the northern part of Tanzania, where there is good trade-related infrastructure. International livestock market dynamics were linked to PPR spread, where outbreaks have been very common in regions with a high number of border markets (5). The health and sustainability of agricultural and pastoral production systems have been directly impacted by the unprecedented rapid spread of infectious diseases like Peste des Petits Ruminants (PPR), which pose a significant economic risk (6,7) Research efforts to gain a better understanding of the movement patterns of sheep and goats in different environmental settings have been spurred by the realization that the movement of livestock plays a significant role in the transmission and spread of contagious diseases (8,9). For sustainable agriculture, animal welfare, and effective resource use, it is essential to comprehend and optimize livestock mobility within various production systems. Every system has benefits and drawbacks, and the decision is frequently influenced by elements like the environment, the resources that are accessible, and the intended output (10).

1.1. Pastoral and Agropastoral

Tanzania's economy is rapidly developing, with agriculture accounting for 24.27% of the GDP(11,12). Livestock is essential for food, traction, revenue, savings, and social status in agropastoral and pastoral communities. Figure 1 illustrates that over 80% of production is accounted for by agropastoral societies, which include crop farming and livestock raising, and 14% by pastoral systems. Specialized or emerging practices, such as smallholder dairy systems, urban and peri-urban livestock production, and other mixed farming systems, make up the remaining 2-6% of production (10,13). The habitats of these communities are constantly shifting due to several factors including climate change(14). Climate change and other factors have led to a shift in pastoral communities to Agropastoralism due to unpredictable weather patterns and insufficient resources (15). Traditional coping techniques, such as livestock movement, are being adapted to include resilient breeds like drought-tolerant and short-cycle animals (16). However, developing disease management strategies is challenging due to the dynamic and interconnected nature of agropastoral and pastoral systems (17).

Figure 1: Agropastoral and Pastoral community distribution in selected disease surveillance zones

1.2. Livestock movement analysis

It is possible to comprehend risk and investigate potential pathogen spread by closely examining livestock contact patterns (8). Various network analysis techniques have been applied to understand the structure and dynamics of livestock movements and their relevance to disease spread. Because livestock commerce is complicated and dynamic, it can be analysed using complex network analysis, which can handle bidirectional interactions such as animal movement, trade, and contacts (18,19). Network analysis allows us to determine centrality metrics, assess a node's significance within the network, and look into how a disease spreads(12). Some key measures that have been used include centrality, which identifies highly connected nodes or regions in the network, and community detection, which identifies groups of locations with strong internal connections(20). In addition, we can analyse the network structure to calculate the sizes of the epidemics and determine whether removing a node would allow for targeted surveillance or control (20–26). Risk-based interventions, directed towards high-risk nodes, have been shown to significantly reduce the explosiveness of acute infections that spread quickly, such as the PPR-virus (PPRV) (21). Few studies have been conducted to understand the impacts of movement of livestock in East Africa by looking at animal transaction records and sales records in conjunction with questionnaire surveys (12,24). For example, networks of local livestock mixing at communal areas have been developed using movement data gathered through community participatory mapping (10). In addition, livestock contact around communal areas of aggregation in a typical East African agropastoral community that was also examined through the use of Global Positioning System (GPS) data loggers (8,27–29), which allows the description of contact rates and identify factors that drive movements and contacts among local village herds. The study findings suggest that strategic interventions can be developed that will reduce infection without limiting livestock mobility (which is critical for their survival), by focusing on high risks points and times (10). Another study found that targeted interventions are a practical and efficient means of controlling disease, and that animal migrations can affect the patterns of disease transmission in the surroundings of livestock (30). Although these studies described livestock movements in the context of disease spread, they mostly focused on cattle in a small region in Tanzania. To date, no study has explicitly examined the various social and economic factors that influence small ruminant movements and the implication on the spread of PPR in both pastoral and agropastoral communities. This is particularly important in northern Tanzania where there is a shift in livestock typology, where more households now keep higher numbers of sheep and goats as compared to cattle because the former adapts better to increasing environmental and climatic challenges(31). This may result in increased risk of small ruminant diseases outbreaks like PPR in both pastoral and agropastoral communities (29. In this study, a network of movement of small ruminants (i.e. sheep and goats) was used to describe: (1) the role of livestock mobility in the spread and transmission of PPR in sheep and goats; (2) identify important hotspots PPR surveillance; and (3) how best PPR can be controlled in both agropastoral and pastoral production systems in Tanzania. Overall, the study findings have potential to improve our knowledge of the movement patterns of small ruminants within livestock-keeping communities and their function in network-based interventions for the surveillance and control of livestock diseases.

2. Methodology

2.1. Study area

A cross-sectional study was done in eight districts located in four surveillance zones of Tanzania, as described in the

Sup. Table 12: Definition of node and network metrics.

Sup. Material: 13 and Figure 2. Using a purposive sampling approach, risk factors for disease spread were considered in selecting the study area. Risk factors considered in this study include geographical location, husbandry system, animal population (32) and composition, species, season, vaccination, and source of the animal (33). Apart from risk factors, information from the Director of Veterinary Services (DVS) on the zones with recent outbreaks of PPR was considered during sample collection. Four surveillance zones, namely the southern, northern, lake, and central zones, were selected from seven surveillance zones established for animal disease control in Tanzania (5).

Figure 2: Map of Tanzania showing study area districts within four animal disease surveillance zones

2.2. Data collection

Data were collected between August and October, 2021. A semi-structured questionnaire was created to investigate the link between sheep and goat movements and the PPR outbreaks in the study area using the Kobo Toolbox (34). The primary unit of analysis in this study was the household because every household in the study owned animals. A household is a group of people living in the same homestead or compound, sharing cooking facilities, and reporting to the same household head (35).

2.3. Collection of Movement data

In this study, we documented both local movements to resource areas or trade related mobility; for the former, we defined agistment as taking livestock to acquire fodder and water in different sites during the dry season and wet season in exchange for payment while permanent involve trade related movement. Both trade-related and non-trade-related movements of animals were observed and documented. Using any of the aforementioned movement kinds throughout the study period, respondents were asked to name any animal destination by common name. In order to acquire locational data where wards were permanently recognized as opposed to the villages, it was necessary to identify both villages and a ward. A portable GPS embedded in the smartphone was used to record location information for each household surveyed and village/ward mentioned. The destination coordinates were picked through internet search where the mentioned name of village or ward was searched through Tanzania Postal code directory website(36) and google maps(37). To ensure all the information are included 121 sites which were involved in the study were extrapolated to 155 nodes to produce 471 connections. The extrapolation was done to meet three reasons of movement which include selling/trade, wet season and dry season.

2.4. Data Analysis

2.4.1. Network building

A movement network was constructed in our study using data on local movement resulting from resource seeking and trade-related mobility. Migration within a ward or district for specific purposes, like searching for pasture or water, can be classified as either dry or wet season migration. A third type of migration category was trade, in which animals moved between wards, districts, or market areas. (23). In the network a household or ward was represented by a node, and the movement of livestock between households or wards was represented by an edge. Centrality and network metrics at node and network level were calculated separately for individual district and the whole network (38). Two centrality metrics were computed at the node level: in and out-degree and betweenness, which are the pathways between nodes. At the network level, we computed the density, clustering coefficient, and giant strongly and weakly connected components. (39,40). These centrality metrics were used in locating important nodes that are thought to be PPR transmission hotspots. In addition, we created a composite network of all the movements in order to comprehend the high-ranking household in terms of degree.

Sup. Table 12 lists the definitions of node and network level metrics as well as their importance in the spread of disease. All analyses were performed in R Programming Language using *Geosphere, igraph and ggplo*t packages (40,41).

2.4.2. How the degree of distribution and fitting look like

Although many writers claim that their studied networks have scale-free properties and a power-law distribution degree distribution, but this is extremely rare (42,43). Since node degree ‘k’ follows ‘a’ power-law distribution $k - \alpha$ where $\alpha > 1$, we considered in this study that many real-world networks are scale free. In order to manage complexity, the latter proposes that a small number of nodes handle the majority of connectivity. This is frequently connected to the hierarchical structure of real-world communication systems (42,44–46). This can have a substantial impact on the dynamics of disease at the population level and may indicate the presence of super-spreaders within the network (47,48). Maximum likelihood estimates (MLE) of the data for the given distribution are calculated by default by the Anderson-Darling test. The households data in the network were fitted with a power law distribution using the Anderson-Darling test in this study to determine the degree of data distribution.(23,49). Using the *ad.test* function from the *ADGof* Test package I performed the Anderson-Darling to test the data if they follow power-law distribution (50). A p-value (<0.05) from Anderson-Darling test results suggests that the data does not follow a power-law distribution, while a large p-value (>0.05) suggests that it does (49–51).

2.4.3. Small-world properties of the network

The "six degrees of separation" theory and other phenomena are explained by the small-world properties of networks, which strike a balance between local clustering and global connectivity and permit brief social connections between individuals on Earth (52). Through the computation of average path length and clustering coefficient and their comparison with a small world property model, the study assessed the small-world properties of a household network (23). Strong local connectivity is indicated by a high clustering coefficient, which is a feature of small-world networks (53). As mentioned in section 2.4.2 above small-world networks, the degree distribution typically resembles a power-law distribution (50). Furthermore, we generated random networks with the same number of nodes and links as actual networks by utilizing the Erdos-Renyl model.(54). We contrasted the generated networks' average path length and clustering coefficient with those of the real networks in order to find scale-free or small world characteristics.(55,56).

2.4.4. Analysis of the cohesion and fidelity of the network

The structural properties of the network and its overall connectedness were examined using interconnected sub-group analysis based on k-core decomposition. Every node in a subgroup known as a "k-core" is, on average, connected to at least k other nodes. The K-core decomposition method was used to identify the core and peripheral networks. Percolation analysis was used to determine the degree to which the network structure would be vulnerable to the targeted removal of household. In this study we investigated how the network structure would change if household were gradually removed one by one in descending order of a specific centrality value. These measurements of centrality -indegree, outdegree, betweenness, and eigenvector, were used for this study. The cohesiveness of the network supporting livestock movement was evaluated by computing the magnitude of the giant weakly connected component (GWCC) and the magnitude of the largest community visible in the residual networks at each removal phase.

2.4.5. Measurement of distance covered due to seasonal and commercial reason

Using the *Geosphere, ggplot* and *igraph* R packages, the geographic separation between the sender and recipient household/ward was calculated. Both the overall network data and the data for each individual district were measured. The distance covered in the whole network during wet and dry season were also measured using the R packages mentioned above. After being moved to Microsoft Excel, the data were further visualized.

2.4.6. Integration of network characteristics with PPR seropositivity

PPR is a highly contagious disease where infection of one animal means contamination of the whole flock. Household were classified as positive or negative to PPR based serological test using HPPR blocking ELISA (HPPR-b-ELISA) produced from AU-PANVAC Addis Ababa, Ethiopia. The assay is based on monoclonal antibodies against PPR virus hemagglutinin protein (H). HPPR-b-ELISA was used to detect antibodies from serum specimens according to the kit manufacturer's protocol (57). However, the test's ability to distinguish between animals that have not received vaccinations and those that have disease is limited. Regression modelling technique was used to explore the association between network characteristics and PPR seropositivity. For example, fit logistic regression models with PPR seropositivity as the outcome variable and network metrics as predictors, adjusting for covariates such as production system, geographical location, and season. PageRank is an algorithm used to measure the importance of nodes(household/ward) in a network and assigns a score to each node (household/ward) based on the number and quality of links connected to it, hence, due to its conceptualisation, it detects influential household/wards across the whole network. Household or wards with a higher PageRank were considered more central or influential in the network (58,59) Spearman correlation (Spearman's ρ) was computed by ranking the values of each household and ward and then calculating the correlation between their ranks (60). Relationship between household level risk and network characteristics as well as the correlation coefficient were determined by *lm*() function and *igraph* fitted R-package(61).

3. Results

3.1. Descriptive statistics of the network

Table 1 displays the results of centrality measures at node and network levels which are also displayed in Sup. Table 9 and Sup. Table 10 separately. The livestock movement network topology for the full network is presented in Sup. Figure 8. Average degree of 6.077419 showing among household had at least six connections with any other households. According to the degree centrality, each household was found to have a median link of 1 (range: 1 to 18) with other households. The median outdegree centrality for every node in the entire network was also found to be 1, whereas the median indegree was found to be 0 meaning that few house hold have high number of incoming connections compared to outgoing connections. Greater household centrality as a result of closeness was seen throughout the entire network, meaning that it takes an average of just 1 step to access every other household from a particular household within the network. Higher reach_2 centrality nodes (>0.41) which means *are* significant in disease dissemination were detected in Hanang and Masasi districts showing the potential of PPR outbreaks within those districts Sup. Table 9. At the district level betweenness centrality measure for both districts were lower compared eigenvector centrality which takes into account the centrality of a node's neighbors. Nodes connected to other central nodes will have higher eigenvector centrality. High eigenvector centrality value (0.58) was detected in Simanjiro and Kiteto district meaning that those districts have PPR transmission potential. In comparison to subnetworks exclusive to the study districts, it was found that the probability of a well-connected household in the entire network

Table 1 present the findings of the livestock movement network analysis based on chosen node parameters in Table 1 network parameters. With only 1% of all potential links present, the entire livestock movement network showed a lower density of connections, indicating a very low level of network cohesiveness and highlighting the local and regional nature of livestock movement in Tanzania. District representing Pastoral societies according to the literature were Longido, Simanjiro, Kiteto and some wards of Hanang other districts were dominated by Agropastoral societies. Assortativity measurements which offer a quantitative way to understand how households in a network preferentially connect based on production system. According to Table 1 and

Sup. Table 10 assortativity based on degree close to negative was picked in those districts as was for the full network while all agropastoral society did have assortativity close to zero >0.004. Household in Agropastoral society were reachable compared to pastoral society as seen in Reach_2 and Reach_3 value (median >0.29) in Pastoral societies compared to agropastoral societies <0.29. According to the network diameter, there was a minimum of one step needed to connect the two most distant reachable households in the network. Degree centrality-based network centralization showed that the Masasi sub-network was more centralized although the overall network showed more of decentralized tendency. The district and overall livestock movement network's global clustering coefficient, which is the average of each household's local clustering coefficient, was zero (Table 1). A household may only need to take a few steps to connect with another household in the network because the average shortest path length for the entire and district networks was 1. Modularity which depends on network cohesion and network fragmentation was picked in both district level and full network at the range (0.6 to 0.76) and 0.9367 respectively. Network analysis base on justification for livestock movement as in Table 1 show that edge density was higher in trade related movement compared to season(wet/dry) related movement. Modularity and centralization by degree was constant throughout all the reasons. Assortativity close to negative (-0.1152909) was picked in dry season compared assortativity close to zero (0.002818196) was picked in wet season.

Table 1: The Network metrics parameters at node and Network level with network parameter determined uniquely for every purpose (Selling, Dry, Wet)

3.2. The appearance of the degree of distribution and fitting

The centrality degree of distribution shown in Figure 3 display high number of nodes with little connections while only few nodes which have many connections. This demonstrates that the network of livestock movement was not distributed normally. The data was left-skewed, suggesting that a relatively small percentage of households were highly connected in comparison to the majority of households. The distribution has been well described by a power-law distribution where after fitting the power law distribution with Anderson darling test it produces a *p-value* of 0.957 which is greater than 0.05 which means that the data are plausible.

Figure 3: The distribution of key centrality measures according to the number of nodes(households)

3.3. Small-world properties of the network and overall connectivity

The values of the clustering coefficient and average shortest path length were compared with those of the random network to determine whether the entire network showed a small world structure.(38,54). As in Table 2 the value was simulated at 156 as the number of vertices (nodes) in the graph and 0.3 as the probability of an edge existing between any pair of vertices. In light of this, the random network demonstrated a higher clustering coefficient of 0.3 and an average shortest path length of 1.7, indicating that the established livestock movement network was less clustered but still capable of reaching a large number of households easily. This suggested that the real network exhibited a small world structure.

Table 2: Properties examined using Erdos-Renyl to verify compliance of real-world networks

3.4. Cohesive analysis and Network reliability

The Livestock movement network was organized in 9 core sub-groups as in

. One node was present in each of the three GWCCs among the network's participating households. It should be noted, though, that the network lacks a GSCCs. The livestock movement network's modularity, which was estimated to be 0.9367(Table 1), was used to assess the quality of the community structure. This indicates that there is a greater tendency for intracommunity connections than there would be if the connections were rewired under random network conditions. Within the connected network, 32 communities were found using a cluster walk trap algorithm for community detection (Sup. Figure 8). There were 18 households in the largest community, compared to just 2 in the smallest. Of the total number of households in the network, 3 of the largest communities had 41 households, making up 30% of the total. The remaining 70% of the communities had two to eight households each. In most cases, community distributions were contained to the study sites, although some communities did cross into neighboring districts. It was found that communities involving these households crossed over because fewer of the households in the Masasi districts (Mchauru, Sululu) had ties to the households in Bahi (Chiungutwa). A few other smaller communities in Meatu (Mwamalole) and Hanang (Dawari, Balagda Wards) were also seen to cross one another, despite the absence of any connected households in between as in Sup. Figure 8. A percolation analysis was carried out to assess the vulnerability of the cohesion of the network structure as measured by the size of GWCC and largest community. Figure 4 and

Sup. Figure 7 compare the impact of selective removal of households according to their centrality measures to random selection. Targeted removal of households in the network based on decreasing order of the betweenness, indegree, outdegree, closeness and eigenvector values showed remarkably faster changes in the network structure with faster reduction on the size of GWCC compared to random removal

Sup. Figure 7. Based on the fragmentation of the GWCC(Table 3) our study has shown that if we target the top 5% of highly connected households based on their degree centrality value, the cohesiveness of the network would be reduced by nearly 62%. Additionally, if we increase the target to 10% of the connected households, the cohesiveness would be further reduced by more than 83%. Household removal using betweenness centrality did not disintegrate the network structure. The largest community size in the network dropped promptly when households were removed based on the value of their eigenvector centrality followed by closeness centrality then out-degree and then indegree which shows slow disintegration (Figure 4).

Figure 4: Centrality measure changes during household(node) removal

Table 3: Fragmentation of the GWCC

Figure 5: Graph network on a Map of Tanzania showing livestock movement across different districts

3.5. Distance covered due to seasonal and commercial reason

The geographic distance between the sender and receiver household/ward as shown in B for all movement was between 0.0km and 617.59 km at both full network and district level. At full network level during dry season livestock movement was detected in several household with average of 10.62km. The maximum distance covered by movement of livestock as the result of selling was 617.6 km. Mean distance covered for commercial and seasonal purposes (dry and wet) in km were 10.62, 2.764 and 33.04 respectively. Seasonal livestock movement covered maximum distance of up to 258.16 km and 60.984 during wet and dry season, respectively. At district level there was zero livestock movement during dry and wet season in Bahi and Masasi while Hanang has zero livestock movement only in wet season. Livestock movement for commercial purposes was covered in all the districts but distance of >100km was covered in Longido (151.3km), Bahi(391.1km) and Meatu (617.6km)

B and Figure 6.

A

B Figure 6:The livestock movements distances covered A: seasonal and commercial reasons B: Overall livestock movement in the study districts

3.6. Important Network characteristics which show PPR Transmission Dynamics and Control

Through determination of the degree of correlation between PPR status and network characteristics as predictor variables the study has been able to find important PPR hot spots for surveillance and management (Table 4). Hub odds ratio of 0.01suggests that households identified as hubs (i.e., highly connected nodes within the network) have higher odds of PPR seropositivity compared to non-hub households. The degree odds ratio of 0.97 suggests that for every unit increase in the degree centrality of a household the odds of PPR seropositivity decrease by 3%. Conversely, households with one or more outgoing animals (outdegree ≥1) had a 52 percent lower likelihood of PPR seropositivity (adjusted OR = 0.48) compared to households that maintained their animals (indegree = 1.01). Households with higher closeness centrality values showed a 48% decrease in PPR seropositivity (adjusted OR 0.52) indicate a decrease in proximity to other households within the network. According to

Sup. Table 11 Page rank centrality measure by ward shows that Mbuyuni Chiungutwa and Sululu ward found in Masasi district were influential wards as ranked higher by page rank scores showing their importance in PPR spread during outbreak. It was further revealed that the Page rank centralities measure in the entire network using the page rank scores positively correlated (Spearman correlation, ρ = 0.6764416).

Table 4: Estimation of node characteristics by logistic regression model for household level PPR Risk

4. Discussion

Livestock movements play a significant role in the spread of PPR by influencing the contact structure of livestock populations, which in turn affects the transmission of PPR in small ruminant (SR). By pinpointing the locations of PPR hot spots, network-based risk assessment can help to shape animal health policy. These places can then be targeted to lessen the burden of disease and the chance of PPR spreading. The movement networks of livestock in pastoral and agropastoral districts were described in this study using network analysis. According to our hypothesis, the wet season, dry season, and trade have an effect on the cohesiveness and structure of the network, which in turn affects the likelihood of PPR transmission and the efficacy of outbreak containment and response strategies. In this study, network structure showed a higher degree of variation in the number of connections per household, indicating the heterogeneity of links per household. The observed variation is partly due to production systems. As observed in all the districts, Kiteto1 (0,1) and Simanjiro 1 (0,1) had higher concentrations of highly connected households, or "hubs," which could act as super spreaders of PPR once infected. Lower outdegree is typically found in households with higher indegrees, indicating a lack of households that are both more likely to contract an infection and spread it to others, which is crucial in promoting PPR transmission throughout the network (9). Eigenvector values have been used to identify super spreaders, in which Kiteto and Simanjiro with high eigenvector values can be considered PPR hot spots (62). While some risk factors show associations with PPR seropositivity, such as outward livestock movement due to a high tendency to sell animals as a result of extended dry season and other social and economic factors, none of the associations are statistically significant at the conventional significance level ($p < 0.05$). This indicates that the observed relationships may be due to random variation or confounding factors, highlighting the need for further investigation and larger sample sizes to draw definitive conclusions.

Through PageRank scores, it was revealed that wards with higher scores, like Chiungutwa, Mbuyuni and Sululu, are influential in the event of PPR during outbreaks. These wards connect other wards, potentially serving as hubs for disease transmission. Positively correlated (Spearman correlation, $\rho = 0.6764416$) pagerank centralities measures emphasizes the importance of network centrality measures in predicting disease spread and identifying hotspots for targeted control and management strategies. A scale-free property is also suggested by the livestock movement network's right-skewed (Figure 3 indegree, eigenvector, outdegree distribution and power law fit. Fewer homes with many connections, the bulk of which act as hubs, are more likely to become infected with PPR, and once they do, they may become potential super spreaders to many other homes that are connected to them (9). Kiteto and Simanjiro districts identified as hubs can not only play a role as super spreaders but also as maintainers of PPR infection. Prior research on infectious disease epidemics on scale-free networks has shown that the presence of hubs accelerates the spread of epidemics (63–66).

Livestock production system variation in the districts involved in the study area shows higher-order relationships between households in the full network and in the districts level. Negative assortative mixing is seen in both full networks and districts with pastoral production systems, suggesting that households with higher levels of connectivity tend to interact with those with lower levels of connection. It was found that the latter relationship was more pronounced in pastoral societies, suggesting that PPR could spread quickly within those communities (21,67,68). Previous studies have demonstrated that frequent connections between households with high and low levels of connectivity can effectively inhibit the spread of infectious diseases in comparison to networks that exhibit positive assortative relationships, which is true for Bahi and Masasi (9). Identifying negative assortative relationships in networks as seen in the dry season (-0.1152909) can aid in PPR control by implementing control measures like movement restriction, culling, and increased biosecurity during the respective season (69).

Livestock groups exhibit modular structure when subsets of conspecifics habitually engage in more interactions with one another than with other members of the group, hence creating subgroups. Reduced disease burden is caused by structural delay and the trapping of pathogens that propagate across social networks due to strong subgroup cohesion and fragmentation, both of which are linked to high modularity (70). Despite the network's weak cohesiveness, its high fragmentation structure has boosted its modularity at both the district and entire network levels. The scale of the epidemic impact may be greater on the tiny subgroups with strong cohesion seen in the Masasi district, which has been recognized as a hotbed of future PPR outbreaks. Subgroups with high modularity can be easily connected over long distances for a variety of reasons, which can result in PPR outbreaks. According to
B and Figure 6 very short distances were covered by animals during the wet season compared to the dry season. However, livestock was transported very far for trade purposes compared to seasonal purposes as a result of water and pasture searches. The higher distances covered in the dry season compared to the wet season increase due to variations in the heterogeneous contact rate between animals. Livestock movement rate is related to an increase in PPR risk, in which areas with a road/railway density of 5000 m/km^2 have a higher risk of PPR spread (71). In the study area, vehicular livestock movement was mostly preferred compared to tracking, resulting in long distance movement, as shown in pastoral and agropastoral societies located in accessible areas (72). The risk of PPR spreading to a wide area, including neighboring countries, increases with the increase in vehicular movement (69). Previous research that demonstrated the significance of animal movement in the transmission of infectious diseases supports this observation (9,73). Long-distance livestock travel is a major contributor to the nationwide PPR epidemic, making it difficult to control. Therefore, finding an ideal way to quickly split up a network into isolated components at the lowest feasible cost is crucial and fascinating for managing the spread of PPR (73,74). One useful tactic to identify households that are crucial to the spread of disease is to remove specific households from the livestock movement network in order to break up the cohesiveness of the network. Then, you can implement disease control measures like movement restrictions and vaccinations (9,24,38,75). Based on the fragmentation of the GWCC (Table 3) this study has shown that if we target the top 5% of highly connected households based on their degree centrality value, the cohesiveness of the network would be reduced by nearly 62%. Additionally, if we

increase the target to 10% of the connected households, the cohesiveness would be further reduced by more than 83%. Though at a slower rate than the effect on GWCC, a measure of network resilience, targeted removal based on the degree centrality value also demonstrated a positive effect on the fragmentation of the largest community. The relatively rapid fragmentation of the cohesiveness of the network implies that there may be a limit to the rate at which PPR spreads among household networks. The removal of households by fragmentation indicates that targeted interventions may be an option for disease control. However, because PPR is infectious, it may be easier to attain effectiveness and detect the intervention's impact in a shorter period of time than chronic infections. Thus, control efficacy can be improved by implementing good biosecurity measures and restricting livestock movement from PPR-endemic areas. These findings could inform policymakers and veterinary authorities about the need to implement more effective surveillance and intervention measures to mitigate the spread of PPR in small ruminant populations.

Conclusion

While this study provides valuable insights into the spread and transmission of PPR among small ruminants, several limitations must be acknowledged. The use of static, non-weighted networks simplifies analysis but does not account for the temporal nature of livestock movements or variations in link weights, such as the quantity of livestock, which could influence outcomes. Furthermore, the study considered all livestock species rather than focusing solely on small ruminants, the primary hosts of PPR, potentially affecting the precision of findings. Limitations in smartphone GPS data accuracy, influenced by signal interference and device variability, may have introduced data inconsistencies. Despite these limitations, the findings identified pastoral districts as hotspots for PPR transmission and emphasized the need for targeted control measures, particularly in southern Tanzania, where dynamic livestock mobility driven by climate change and other factors heightens disease spread risk. Future research should integrate temporal network modeling and evaluate focused control interventions, accounting for production systems, transmission pathways, seasonal variations, and contact rates, to construct dynamic models for PPR and other small ruminant diseases.

Conflict of interest:

No conflict of interest

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Authors' contributions

JM led the research, including developing the research question, designing the study, conducting the literature review, laboratory work, data collection, data analysis, and drafting and revising the manuscript. GM, AC, SK, GO, DE, and SP mentored JM throughout the research process, assisting with study design, data interpretation, and manuscript review. DM supported study design, data collection, findings interpretation, and manuscript preparation, while RS contributed to laboratory work and reviewed the drafts. All authors reviewed and approved the final manuscript.

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Tables

Table 5: The Network metrics parameters at node and Network level with network parameter determined uniquely for every purpose (Selling, Dry, Wet)

Node level Parameters		**Network level Parameters**	
Parameter	**Values**	**Parameter**	**Values**
Degree	1(1,18)	Diameter	1
Indegree	0(0,18)	Average shortest path length	1
Outdegree	1(0,2)	Edge Density	0.01
Closeness	1(0.5,1.0)	Reciprocity	0
Reach_2	0.03(0.013,0.15)	Assortativity (based on degree)	-0.04317455
Reach_3	0.03(0.01,0.22)	Global clustering coefficient (CC)	0
Eigenvector value	0(0,1)	Modularity	0.9367
Hubs	0(0,1)	Giant Components (GC)	4
Authority	0(0,1)	Centralization (by degree)	0.1524662

Parameter	**Metrics values uniquely for every purpose**		
	Dry	**Wet**	**Selling**
Diameter	1	1	1
Average shortest path length	1	1	1
Edge Density	0.005593663	0.005684109	0.007880124
Reciprocity	0	0	0
Assortativity (based on degree)	-0.1152909	0.002818196	0.007293846
Global clustering coefficient (CC)	0	0	0
Modularity	0.952315	0.9515618	0.9597036
Components (GC)	18	19	18
Centralization (by degree)	0.04920694	0.05196965	0.05013149

Table 6: Properties examined using Erdos-Renyl to verify compliance of real-world networks

Properties	**Actual**	**Simulation**
Total number of households (Nodes)	155	155
Size of GSC	0	13
Size of GWC	27	13
Average path length	1	1.7
Clustering coefficient	0	0.3

Table 7: Fragmentation of the GWCC

Parameters	**Values**		
Fragmentation %	5%	10%	30%
GWCC-Before Fragmentation	53	53	53
GWCC-After Fragmentation	20	9	3
Remaining nodes	33	44	50
Remaining nodes (%)	62%	83%	94%

Table 8: Estimation of node characteristics by logistic regression model for household level PPR Risk

PPR-Risk factor	**OR**	**95% CI**	**P-value**
Degree	0.97	0.73, 1.17	0.8
Eigenevector	0		0.2
Hub	0.01		0.2
Authority	0		0.9
Closeness	0.52	0.18, 1.52	0.2
Reach_2	0	0.00, 0.00	0.001
Reach_3	0	0.00, 0.00	0.001
Inward livestock movement (Indegree)	1.01	0.82, 1.19	0.9
Outward livestock (Outdegree)	0.48	0.19, 1.15	0.11

6. Supplementary files

Sup. Table 9: The authority, eigenvector, degree, and reach-2 and reach-3 metrics, which indicate how central the node is in the livestock movement network

Sup. Table 10: Network metrics calculated for every district and network as a whole

Sup. Table 11: Page rank score by ward

Sup. Figure 7: Changes of centrality measures from random and targeted node removal A: showing the GWCC decreasing with other centrality measures B: showing metric changes between random and targeted node removal.

Sup. Figure 8: A network graph that displays the network (A: communities B. Wards) and their connections

Sup. Table 12: Definition of node and network metrics.

Sup. Material: 13: Study area Description

Tanzania, an East African country south of the equator, covers 945,087 km^2, with 883,749 km^2 land and 59,050 km^2 inland water bodies, including the Indian Ocean. (Chang'a et al. 2017).

Tanzania's rainfall regimes are categorized as unimodal or bimodal, with bimodal rainfall occurring in northern regions and unimodal in Central, South, and Western districts. These distributions impact pasture, water availability, and animal migration. (Chang'a et al. 2017).

Our study area covers five regions found in the southern (Mtwara), central (Dodoma), and northern (Manyara, Arusha) Lake Victoria basin (Simiyu) where sheep and goat populations are considerable high, except Mtwara (Tanzania National Bureau of Statistics and NBS 2017). Eight districts were chosen from the regions based on PPR risk factors, including climate change vulnerability. Sheep and goat populations, wildlife and livestock interactions, social economics, and international border proximity Longido, Meatu, and Bahi districts with unimodal rainfall patterns and low annual rainfall represent the areas with PPR risk due to continuous shortages of pasture and water. Meatu, Simanjiro, Kiteto, Hanang, and Longido have large populations of sheep and goats, increasing the risk of PPR through social and economic activities. Masasi, Bahi, and Bariadi reported the incidence of PPR during the study period. Meatu and Bariadi share the Serengeti ecosystem, with previous incidences of PPR within the regions and the country bordering the ecosystem. Simanjiro, Kiteto, and Longido districts have wildlife and forest protected areas where there is sharing of grazing land with wildlife. Longido and Masasi districts were in close proximity to the international borders of Kenya and Mozambique, respectively. Hanang, Kiteto, and Simanjiro districts are inhabited by agropastoral and pastoral groups that own agricultural areas, with some areas demarcated for grazing, as seen in Simanjiro and Kiteto districts. Hanang district, on the other hand, has limited grazing areas where seasonal cropping allows the use of agricultural areas for grazing during the dry season. The Simiyu region within the Lake Victoria ecosystem was represented by Meatu and Bariadi. The latter two districts are within the Serengeti National Park North ecosystem in the eastern part of lake victoria. Wildlife-livestock interaction in the districts of Longido, Simanjiro, Kiteto, Bariadi, and Meatu is very common due to their proximity to wildlife and forest conservation areas. In those districts, various types of animals, including small ruminants, can be found grazing together with sheep and goats. During the dry season, poor water and pasture availability leads to increased animal interaction. In the Simiyu region, illegal activities in Serengeti National Park and Butuli Forest Conservation Area are very common, thus increasing PPR risks to the domestic small ruminant population. Livestock trade increases, involving up to 9 million sheep and goats annually. (Tanzania National Bureau of Statistics and NBS 2017). Most of the animals are transported by vehicles to the secondary markets located in the major cities of Mwanza, Dar es Salaam, and Arusha. Non-vehicular transportation has been reported for short-distance travel toward or from primary markets. Long-distance travel has been reported during the pasture shortage, when animals have been moving from one district to another in search of water and greener pasture.