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Research Paper

Understanding PPR Transmission Dynamics: A Network Analysis Approach in Pastoral and Agropastoral Communities in Tanzania

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ABSTRACT

Introduction: Unregulated livestock movements pose a significant risk for the spread of diseases, threatening animal health and productivity. These movements have been cited as a potential driver of the spatial and temporal dynamics of disease spread in the country. However, a formal evaluation of peste des petits ruminants (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.

Materials & Methods: Data on livestock movement from Tanzania were collected to create network patterns illustrating the risk of PPR circulation across geographical areas and agroecological systems.

Results: Results demonstrate a notable variation in network structure. Compared to movement driven by seasonal variation, trade-related movement extended up to 600 km. Additionally, during the dry season, animals travel longer distances than in the wet season. The probability

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of contracting PPR infection was found to be half for households with outgoing livestock (outdegree), indicating a lower risk of infection compared to households with more incoming livestock (indegree). The network pattern shows scale-free properties, with negative and near-zero assortative mixing in pastoral and agropastoral societies, respectively.

Conclusion: These findings suggest 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 emphasize dynamic modeling and targeted control interventions.

1. Introduction

The movement of livestock is crucial for trade, search for pasture and water, or relocation. However, it also poses a significant risk for disease transmission. For example, in 1920, rinderpest returned to Europe from Brazil, a disease that was officially declared eradicated in 2011 [1, 2]. Improved livestock trade infrastructure like roads, railway networks, and slaughter facilities, show evidence of increased peste des petits ruminants (PPR) risks. For example, in Asia and Africa, livestock movement within meat supply chain networks (herds-local small and big market central market) has been linked to PPR outbreak [3, 4]. This pattern is also evident in Tanzania, where PPR spread throughout the northern part of Tanzania, which benefits from well-developed trade 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 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 has 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, available resources, and 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 plays a vital role for food, traction, revenue, savings, and social status in agropastoral and pastoral communities. As illustrated in Figure 1, 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].

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 explore the structure and dynamics of livestock movements and their relevance to disease spread. Given the complexity and dynamic nature of livestock commerce, complex network analysis is well-suited to 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 disease spread pathways [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 epidemics sizes and determine whether removing a node would allow for targeted surveillance or control strategies [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 examined the impacts of livestock movement of in East Africa by looking at animal transaction records, sales records, and questionnaire surveys [12, 24]. For example, networks of local livestock mixing at communal areas have been developed using movement data gathered from community participatory mapping [10]. In addition, GPS data loggers have been used to study livestock contact around communal aggregation areas of in a typical East African agropastoral community, helping describe contact rates and identify factors driving movement and interaction among village herds [27-29]. The study findings suggest that strategic interventions can reduce infection without limiting livestock mobility, critical for their survival, by focusing on high- risks points and times [10]. Another study found that targeted interventions are both practical and efficient means of controlling disease, and that animal migrations can affect the patterns of disease transmission in livestock environments [27]. Although these studies have explored livestock movements in the context of disease spread, they mostly focused on cattle in a small region of Tanzania. To date, no study has explicitly examined the various social and economic factors influencing small ruminant (SR) movements and implication for PPR spread in both pastoral and agropastoral communities. This is particularly important in northern Tanzania, where there is a shift in livestock typology and more households now keep higher numbers of sheep and goats compared to cattle because the former are better adapted to increasing environmental and climatic challenges [28]. This may result in increased risk of SR diseases outbreaks like PPR in both pastoral and agropastoral communities [29]. In this study, a network of movement of SRs (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) recommend strategies for controlling PPR in both agropastoral and pastoral production systems in Tanzania. Overall, the study findings have the potential to improve our understanding of SRs movement patterns within livestock-keeping communities and inform network-based interventions for diseases surveillance and control of livestock.

2. Materials and Methods

2.1. Study area

A cross-sectional study was done in eight districts located within four surveillance zones of Tanzania, as described in the Supplementary Materials S1 and Figure 2. A purposive sampling approach was employed, taking into account key risk factors for disease spread in selecting the study area. These risk factors include geographical location, husbandry system, animal population [30] and composition, species, season, vaccination, and source of the animal [31]. Apart from risk factors, information from the Director of Veterinary Services (DVS) on the zones with recent PPR outbreaks was considered during sample collection. The four selected surveillance zones, namely the southern, northern, lake, and central zones, were selected from the seven surveillance zones established for animal disease control in Tanzania [5].

2.2. Data collection

Data were collected between August and October, 2021. A semi-structured questionnaire was developed using Kobo Toolbox to investigate the link between sheep and goat movements and PPR outbreaks in the study area. 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 [32].

3.3. 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, often 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.

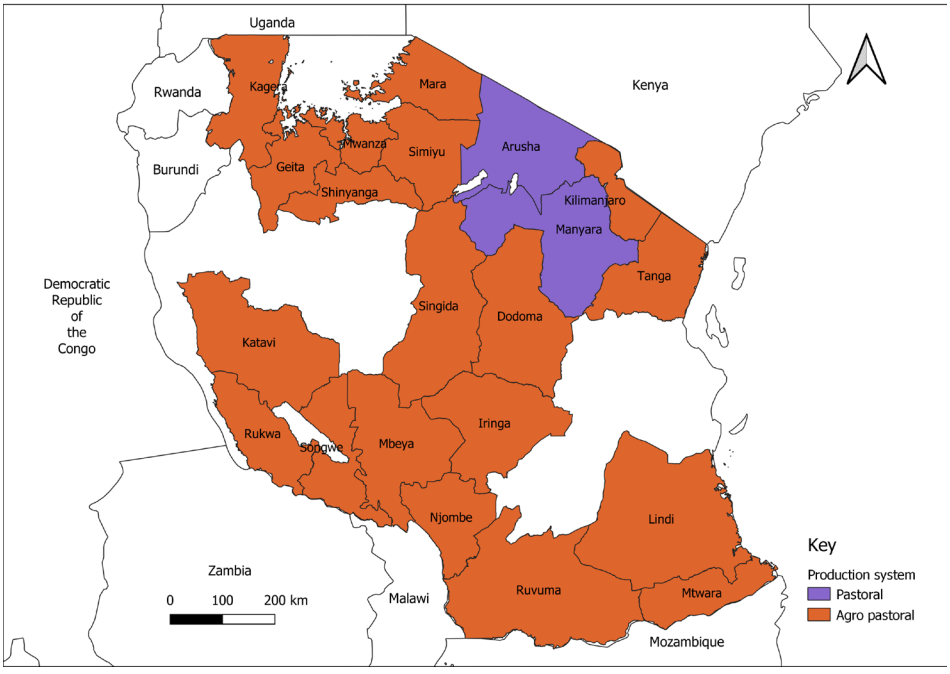

Figure 1. Agropastoral and pastoral community distribution in selected disease surveillance zones

The destination coordinates were picked through internet search, where the mentioned name of village or ward was searched through Tanzania Postal code directory website [33] and Google Maps [34]. To ensure comprehensive coverage, 121 sites involved in the study were extrapolated to 155 nodes to produce 471 connections. The extrapolation accounted for three reasons of movement, including 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 wards or districts for specific purposes, like searching for pasture or water, can be classified as either dry or wet season migrations. A third type of migration category was trade, in which animals moved between wards, districts, or market areas [23]. In the network, each 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 were separately calculated at both node and network levels for individual districts and the whole network [35]. 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 [36, 37]. 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. Supplementary Table S1 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 ggplot packages [37, 38].

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 degree distribution, but this is extremely rare [39, 40]. 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 [39, 41-43]. 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 [44, 45]. Maximum likelihood estimates (MLE) of the data for the given distribution are calculated by default by the Anderson-Darling

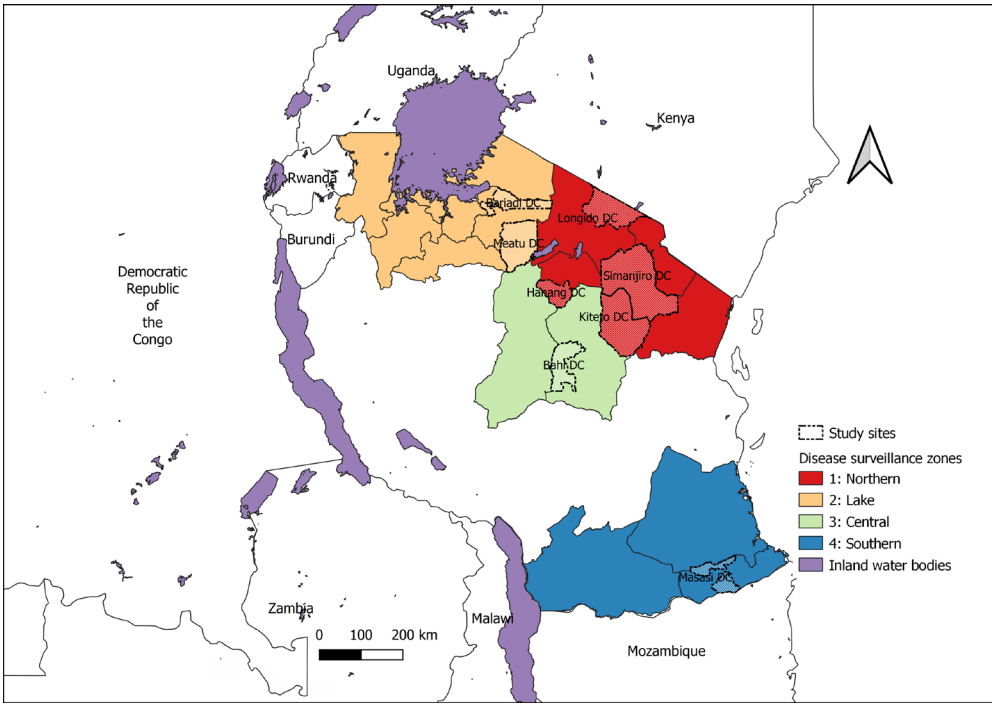

Figure 2. Map of Tanzania showing study area districts within four animal disease surveillance zones

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, 46]. Using the ad.test function from the ADG of test package I performed the Anderson-Darling to test the data, if they follow power-law distribution [47]. A P <0.05 from Anderson-Darling test results suggests that the data don't follow a power-law distribution, while a large P>0.05 suggests that it does [46-48].

2.4.3. Small-world properties of the network

The "six degrees of separation" theory and other phenomena are explained by the small-world networks properties, which balance between local clustering and global connectivity and permit brief social connections between individuals on Earth [49]. 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, a feature of small-world networks [50]. As mentioned in section 2.4.2, the degree distribution typically resembles a power-law distribution [47]. Furthermore, we generated random networks with the same number of nodes and links as actual networks, by utilizing the Erdos-Renyl model [51]. We contrasted the generated networks' average path length and clustering coefficient with those of the real networks to find scale-free or small world characteristics [52, 53].

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 subgroup 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 in 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, was calculated the geographic distances between the sender and recipient household or ward. These measurements were performed for both the overall network data and the data for each individual district. The distance covered in the whole network during wet and dry seasons were also measured using the R packages mentioned above. After moving 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 PPR- positive or negative based on serological test using the HPPR blocking ELISA (HPPR-b-ELISA) produced from AU-PANVAC Addis Ababa, Ethiopia. This 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 [54]. However, the test's ability to distinguish between unvaccinated animals and naturally infected animals 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, an algorithm that measures 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 conceptualization, 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 [55, 56] Spearman correlation (Spearman's ρ) was computed by ranking the values of each household and ward, and then calculating the correlation between their ranks S [57]. Relationship between household level risk and network characteristics, as well as the correlation coefficient were determined by lm() function and igraph fitted R-package [58].

3. Results

3.1. Descriptive statistics of the network

The results of centrality measures at the node and network levels are presented in Supplementary Tables S2 and S3, respectively. The livestock movement network topology for the full network is presented in Supplementary Figure S1. The average degree was 6.077419, indicating that each household had,on average, 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 1, while the median indegree was 0, meaning that only a few households 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,on average, it took just 1 step to access every other household from a particular household within the network. Higher reach_2 centrality nodes (>0.41) which are significant for disease dissemination, were detected in Hanang and Masasi districts, showing the potential of PPR outbreaks within those districts (Supplementary Table S2). At the district level, betweenness centrality measure for both districts were lower compared to eigenvector centrality, taking 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, indicating that those districts have PPR transmission potential. In comparison to subnetworks exclusive to the study districts, it found the probability of a well-connected household in entire network

Table 1 presents the findings of the livestock movement network analysis based on selected node- and network-level 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. According to the literature, Longido, Simanjiro, Kiteto and some wards of Hanang represent pastoral societies, while the other districts were agropastoral societies.

Assortativity measurements, which offer a quantitative way to understand how households in a network preferentially connect, based on production system. According to According to Table 1 and Supplementary Table S3, assortativity, based on degree close to negative, was picked in those districts as for the full network, while all

agropastoral society did have assortativity close to zero >0.004. Households 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 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 levels and full networks at the range (0.6 to 0.76) and 0.9367, respectively. Network analysis, base on justification for livestock movement as in Table 1, shows 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 the assortativity close to zero (0.002818196), picked in wet season.

3.2. The appearance of the degree of distribution and fitting

The centrality degree of distribution shown in Figure 3 displays high number of nodes with little connections, while only few nodes 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, while after fitting the power law distribution with Anderson darling test it produces a P of 0.957, greater than 0.05, which means that the data are plausible.

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 [35, 51]. 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 pairs 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.

3.4. Cohesive analysis and network reliability

The livestock movement network was organized in 9-core sub-groups as shown in Supplementary Figure S1

One node was present in each of the three GWCCs among the network's participating households. It should be noted that the network lacks a GSCCs. The livestock movement network's modularity, 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 what 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 (Supplementary Figure S1). 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 connections 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 Supplementary Figure S1.

A percolation analysis assessed network vulnerability of the cohesion of the network structure as measured by the size of GWCC and largest community (Figure 4). Supplementary Figure S2 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 Supplementary Figure S2. Based on the fragmentation of the GWCC

Table 1. 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
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 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 will drop by nearly 62%. Additionally, if we increase the target to 10% of the connected households, the cohesiveness will drop 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 showing slow disintegration (Figure 4). The spatial livestock movement network is shown in Figure 5.

3.5. Distance covered due to seasonal and commercial reason

The geographic distance between the sender and receiver household/ward as shown in Figure 5 for all movement was between 0.0 km and 617.59 km at both full network and district level. At full network level during dry season, livestock movement was detected in several households with average of 10.62 km. 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

Table 2. 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 3. 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

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 showed zero livestock movement only in wet season. Livestock movement for commercial purposes was covered in all the districts but distance of >100 km was covered in Longido (151.3 km), Bahi (391.1 km) and Meatu (617.6 km) Figure 5.

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 ould find important PPR hot spots for surveillance and management (Table 4). Hub odds ratio of 0.01 suggests 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 sug-

Table 4. Estimation of node characteristics by logistic regression model for household level PPR risk

PPR-risk Factor	OR	95% CI	P
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	0.0, 0.0	0.001
Reach_3	0	0.0, 0.0	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

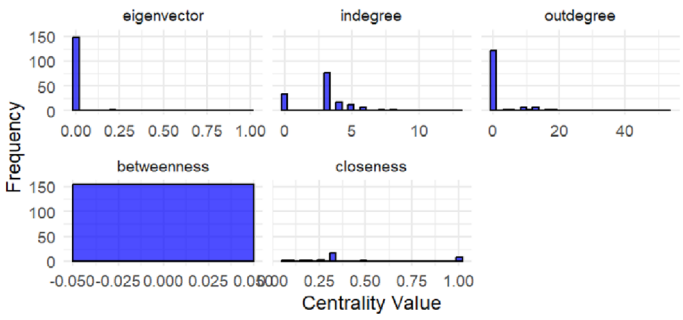

Figure 3. The distribution of key centrality measures according to the number of nodes (households)

gests 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 52 percent lower likelihood of PPR seropositivity (adjusted OR=0.48) compared to households maintaining their animals (indegree=1.01). Households with higher closeness centrality values showed 48% decrease in PPR seropositivity (adjusted OR 0.52), indicating decrease in proximity to other households within the network. According to Supplementary Table S4 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).

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 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) showed 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 [60-63]. 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, ρ=0.6764416) PageRank centralities measures emphasize 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 indegree, eigenvector, outdegree distribution and power law fit (Figure 3). 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 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

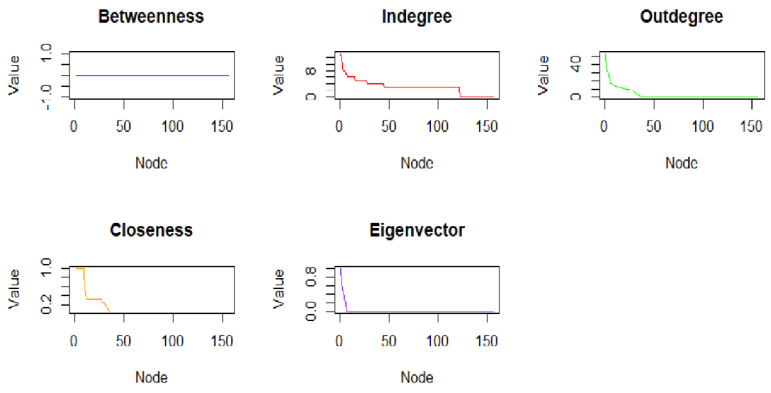

Figure 4. Centrality measure changes during household (node) removal

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, 64, 65]. 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 compared to networks exhibiting 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 [66].

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 linked to high modularity [67]. 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

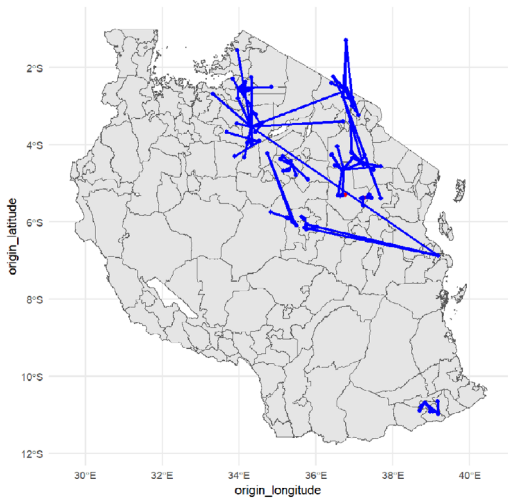

Figure 5. Graph network on a map of Tanzania showing livestock movement across different districts

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 Figure 5, 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 [68]. 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 [69]. The risk of PPR spreading to a wide area, including neighboring countries, increases with the increase in vehicular movement [66]. Previous research demonstrating the significance of animal movement in the transmission of infectious diseases supports this observation [9, 70]. 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 [70, 71]. 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, 35, 72]. 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 will drop by nearly 62%. Additionally, if we increase the target to 10% of the connected households, the cohesiveness will drop 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 SR populations.

5. Conclusion

While this study provides valuable insights into the spread and transmission of PPR among SRs, 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 exclusively on SRs, 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 SR diseases.

Ethical Considerations

Compliance with ethical guidelines

The authors hereby declare all ethical standards have been respected in preparation of the submitted article.

Data availability

The data that support the findings of this study are available upon request from the corresponding author.

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Authors' contributions

Supervision: Gerald Misinzo, Augustino Chengula, Sharadhuli Kimera, George Omondi Paul, Devine Ekwem, and Satya Parida; Methodology: Julius Joseph Mwanandota and Daniel Mdetele; Conceptualization, investigation and writing the original draft: Julius Joseph Mwanandota; Data collection and analysis: Julius Joseph Mwanandota and Daniel Mdetele; Review and editing: Gerald Misinzo, Augustino Chengula, Sharadhuli Kimera, George Omondi Paul, Devine Ekwem, Satya Parida, and Daniel Mdetele.

Conflict of interest

The authors declared no conflict of interest

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1. Supplementary files

Supplementary Table S1. Definition of node and network metrics

Parameter	Definition	Epidemiological Sig.
	Node-Level Metrics	
Betweenness	The frequency of any pair of pairings in the observed network along the shortest path between any two wards.	Wards with a high betweenness are closer to the network and are more likely to be infected sooner. They could be good intervention targets one of its assumptions, i.e. the contributions of all shortest paths are equal, is inconsistent with variations in spatial interactions along these paths and has been questioned when applied to spatial networks. Hence, this paper proposes a spatial interaction incorporated betweenness centrality (SIBC)
In and out-degree	The total number of other wards from which or to whom a ward sent or received animals.	In the network, a higher in-degree ward is viewed as a sink (correlated with a higher risk of disease introduction), whereas a higher out-degree ward is viewed as influential (higher probability of spreading disease)
Undirected path	The pathway between nodes (households/wards) ignoring the direction of the contacts.	A movement from household to a ward/market area or vice versa thus defines the same pathway in disease transmission.
Directed path	The pathway between nodes (households/wards) accounting for the direction of the contacts (i.e. livestock movements).	A movement from household to a ward/market area or vice versa thus defines two different pathways in disease transmission.
	Network-level Metrics	
Clustering coefficient	Probability that any two wards connected to a third ward in common are also connected to one another in the network to form a triangle.	This describes the spatial or social organization of a network, with high clustering being hypothesized to lessen transmission.
Giant strongly/ weakly connected component	A set of households that are all reachable from each other by existing directed edges is referred to as a strongly connected component in a network. The term “weakly connected component” refers to a region of the network where all wards are connected to one another but not all wards can be reached from every other ward in the network.	The size of the GSCC is a measure of the potential size of an epidemic in the network because any ward in the giant strongly connected component can be reached from every other ward. The size of the GWCC is frequently interpreted as the maximum size for an epidemic within the system because the GWCC relaxes the assumption that all wards can be reached from any other ward by directed paths in the connected component.
Clustering coefficient		

Supplementary Table S2. The authority, eigenvector, degree, and reach-2 and reach-3 metrics, which indicate how central the node is in the livestock movement network

Centrality	Centrality Values (Ranges)								
	Bahi	Bariadi	Hanang	Kiteto	Longido	Masasi	Meatu	Simanjiro	Full Network
Degree	1(1,5)	1(1,4)	1(1,4)	1(1,3)	(1,4)	1(1,18)	1(1,4)	1(1,3)	1(1,18)
Indegree	0(0,5)	0(0,4)	0(0,4)	0(0,3)	0(0,4)	0(0,18)	0(0,4)	0(0,3)	0(0,18)
Outdegree	1(0,2)	1(0,1)	1(0,2)	1(0,1)	1(0,1)	1(0,2)	1(0,2)	1(0,1)	1(0,2)
Closeness	1(0.5,1)	1(1,1)	1(0.5,1)	1(1,1)	1(1,1)	1(0.5,1)	1(0.5,1)	1(1,1)	1(0.5,1.0)
Reach_2	0.16 (0.08,0.32)	0.28 (0.1,0.28)	0.3 (0.13,0.6)	0.33 (0.33,0.33)	0.29 (0.14,0.36)	0.29 (0.11.0.52)	0.28 (0.11,0.5)	0.29 (0.14,0.29)	0.03 (0.013,0.15)
Reach_3	0.24 (0.08,0.32)	0.28 (0.1,0.28)	0.4 (0.13,0.6)	0.33 (0.33,0.33)	0.29 (0.14,0.36)	0.41 (0.15,0.74)	0.33 (0.11,0.67)	0.29 (0.14,0.29)	0.03 (0.01,0.22)
Eigenvector value	0(0.1)	0.16(0,1)	0.45(0,1)	0.58(0.58,1)	0(0.1)	0.01(0,1)	0.35(0,1)	0.58(0,1)	0(0,1)
Betweenness	0	0	0	0	0	0	0	0	0
Hubs	0(0,1)	0(0,1)	0(0,1)	1(0,1)	0(0,1)	0.01(0,1)	0.12(0,1)	1(0,1)	0(0,1)
Authority	0(0,1)	0(0,1)	0(0,1)	0(0,1)	0(0,1)	0(0,1)	0(0,1)	0(0,1)	0(0,1)

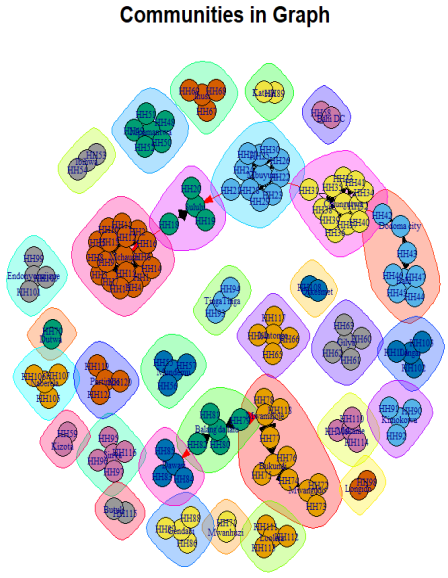
Supplementary Table S3. Network metrics calculated for every district and network as a whole

Parameter	Metrics Values								
	Bahi	Bariadi	Hanang	Kiteto	Longido	Masasi	Meatu	Simanjiro	Full Network
Diameter	1	1	1	1	1	1	1	1	1
Average shortest path length	1	1	1	1	1	1	1	1	1
Edge density	0.132	0.16	0.171	0.32	0.21	0.06	0.173	0.214	0.01
Reciprocity	0	0	0	0	0	0	0	0	0
Assortativity (based on degree)	0.626	0.492	-0764	0.658	-0.0896	0.0038	0.066	-0.0804	-0.04317455
CC	0	0	0	0	0	0	0	0	0
Modularity	0.75	0.76	0.7045	0.651	0.713	0.668	0.703	0.7469	0.9367
Giant components (GC)	8	5	9	4	4	46	12	4	4
Centralization (by degree)	0.4704861	0.2352941	0.2372449	0.4876033	0.4319527	0.5283951	0.2525952	0.2248521	0.1524662

Supplementary Table S4. Page rank score by ward

Ward	Page Rank Score
Bahi	0.022558335
Balang'da lalu	0.014317109
Bukundi	0.013767694
Butuli	0.007174714
Chiungutwa	0.040139616
Dawari	0.014866524
Dodoma city	0.007174714
Dutwa	0.007174714
Endonyongijape	0.013767694
Gendabi	0.013767694
Gilya	0.017064185
Ibihwa	0.010471204
Ihusi	0.013767694
Katesh	0.007174714
Kimokowa	0.013767694
Kizota	0.007174714
Langai	0.013767694
Longido	0.007174714
Loolera	0.013767694
Makame	0.013767694
Matongo	0.017064185
Mbuyuni	0.036843126
Mchauru	0.061017387
Mpamantwa	0.020360675
Mundemu	0.013767694
Mwamalole	0.014097343
Mwangudo	0.0117898
Mwanhuzi	0.007174714
Naberela	0.013767694
Orkesmet	0.007174714
Partimbo	0.013767694
Sinya	0.017064185
Sululu	0.013767694
TingaTinga	0.010471204

A



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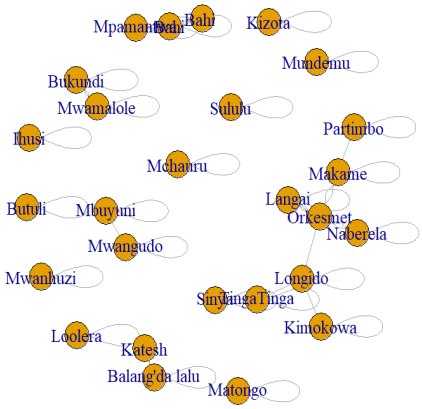
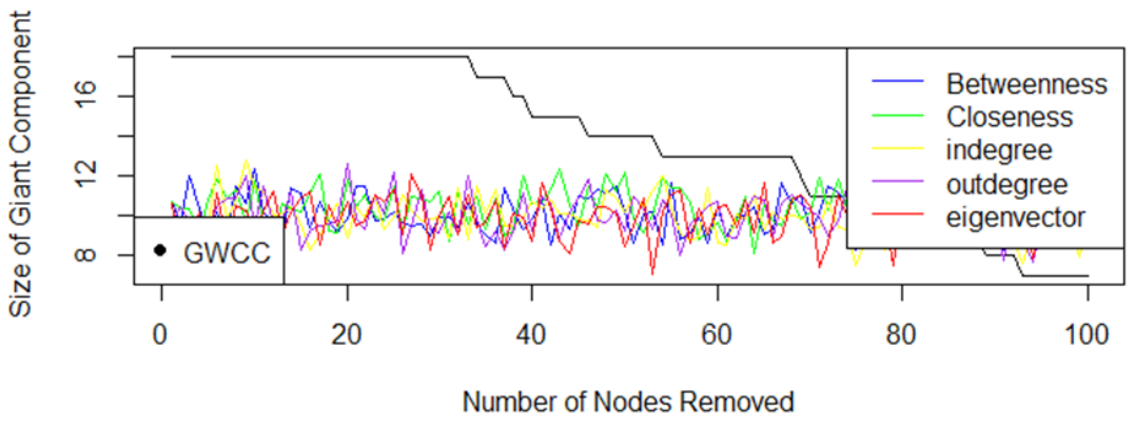


Supplementary Figure S1. A network graph that displays the network (Communities (A) , wards (B)) and their connections

A



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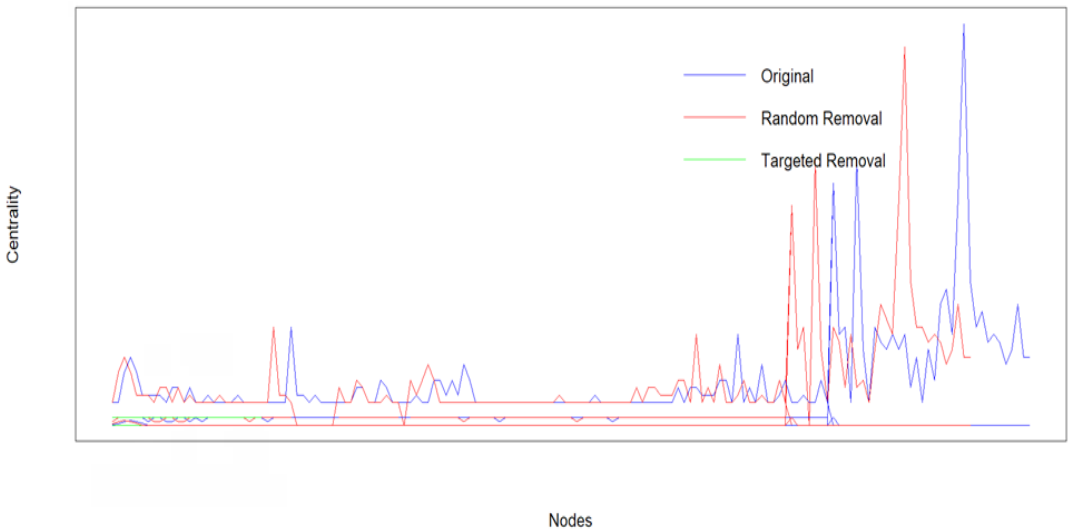

Supplementary Figure S2. Changes of centrality measures from random and targeted node removal

A) Showing the GWCC decreasing with other centrality measures, B) Showing metric changes between random and targeted node removal

Supplementary Material S1: 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. [73].

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 [73].

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 [74]. 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 [74]. 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.

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