Journal of Engineering and Applied Sciences 12 (15): 4005-4015, 2017
ISSN: 1816-949X

An Investigation of the Food Sources and Roosting Sites as Potential Factors of Hendra Virus Dispersion in South East Queensland, Australia

Jahnavi Burnham and Albert Chong
Department of Engineering and Surveying,
University of Southern Queensland, Toowoomba, 4350 Queensland, Australia

Abstract: Hendra Virus (HeV) was first identified in 1994 following the outbreak of a new disease which is fatally affecting horses and humans in South-East Queensland. Since, this outbreak, there have been subsequent incidents reported in South-East Queensland. Fruits Bats (*Pteropus sp.*) commonly known as flying-foxes have been identified as the natural host of the virus. In this study, an in-depth analysis is carried out to determine the correlation between food source vegetation and the flying-foxes roosting sites. This investigation may determine whether clustered or dispersed vegetation has more impact on the incidence. Using spatial analyst tools, the Major Vegetation Subgroups (MVS) present within 20 km buffer range of grey headed flying-foxes and black flying-foxes roosting sites are identified. The identification of abundance of food sources for individual species within their minimum foraging range indicated a strong correlation between their site locations and vegetation subgroups present. A 10 km range vegetation study on the incident locations identified the presence of 'food sources' of both species. The clustering of the food resource vegetation present near the incidence was studied using Getis-Ord General G Statistic method which indicated statistically high clustering with 99% confidence level at 3 km distance threshold. The findings suggest that the presence of potential 'food resource' of the flying-foxes within certain proximity increases the risk of Hendra virus disease transmission to horses.

Key words: Flying-foxes, vegetation, clustering, identification, certain, fruits bats

INTRODUCTION

Hendra virus is considered as one of the rarest diseases in the world. The scientific evidence suggests that the flying-foxes are the host of Hendra virus and the susceptible horses get infected by the virus, resulting in a 70% mortality rate (CSIRO, 2011). There are strong evidences suggesting the bat-to-horse to-human transmission of virus but there are no evidences suggesting the bat-to-human, human-to-human or human-to-horse transmissions. As there are subsequent incidents reported time to time since the outbreak in 1994, the government announced a pressing need for current research on the spatial and temporal occurrences of the virus outbreaks and further study into ecological and environmental factors causes of the disease (DAFF, 2012). As of December 2012, there were 80 confirmed outbreak events including equine and human cases (Smith *et al*., 2014).

A preliminary analysis of the relationship(s) between the Hendra virus outbreaks and the roosting sites of flying-foxes in the South-East Queensland revealed a strong relationship (92% of the incidents) between temporary and seasonal roosting sites (rather than the permanent continuous roosting sites) and the outbreak locations (Burnham *et al*., 2015). Spatial autocorrelation (Global Moran's I) revealed significant clustering of black and grey headed flying-fox species in the study area. Kernel density estimation analysis identified a greater association between black flying-foxes and the outbreak events in the study area. This study investigates the correlation between food sources and roosting sites of black and grey headed flying-foxes and the influence of vegetation on the incidents.

Flying-foxes largely depend on nectar and pollen from eucalypts, melaleucas and banksias; however they are attracted to a broad range of flowering and fruiting trees and vegetation as food sources (WPSQ, 2014). Department of Primary Industries (DPI), NSW investigated the type of vegetation present on some of the virus infected properties which included a range of fig trees, bottlebrushes, cocoas palm, stone fruits such as mangoes and papaws, palms, lilly-pillies and grevilleas (DPI, 2012). A cross-disciplinary study compared the

Corresponding Author: Jahnavi Burnham, Department of Engineering and Surveying, University of Southern Queensland, Toowoomba, 4350 Queensland, Australia

climatic and vegetation primary productivity variables for the dispersed and heterogenic outbreak sites. The study concluded that the dry season spill-over events that have significantly occurred suggested seasonal forcing of transmission across species/virus excretion by reservoir host. There are certain limitations mentioned for this study which indicated a need for further examination of flying-fox resource use in the urban-rural landscape to understand the Hendra virus transmission (Farlane *et al*., 2011). A study by Smith *et al*. (2014) included a vegetation variable (the dominant species of the tallest stratum) in the regression model but it was not found to be a significant risk factor. The study suggested that there were other 'unidentified' risk factors that exist at the property level.

A research on GIS applications in epidemiology stated that the most current researches used conventional methods and these methods can be further developed to design more sophisticated methods. GIS technology provides new opportunities to study the association between environmental exposure, spatial distribution of disease (Vine *et al*., 1997) and identification of high risk locations and populations (Bithell, 2000; Baum *et al*., 2010). A set of spatial analyst tools have been incorporated in this study to identify the major vegetation subgroups near the temporary and seasonal roosting sites of each flying-fox species. The potential food sources for both black and grey headed flying-foxes have been identified. The correlation between the food sources and roosting sites has been established. Using Getis-Ord General G Statistic tool, the clustering of the food source vegetation present near the incidence has been determined. This study serves as a base to determine the primary relationships between the vegetation subgroups/food sources, roosting sites and incidents to understand the virus dispersion in the study area.

MATERIALS AND METHODS

Study area: The study area for this research is South-East Queensland. There are 15 outbreak incidents recorded in the study area over the period of time. South-East Queensland is classified as an interim Australian bioregion which contains of 11 city and regional councils (DILGP, 2009). Figure 1 shows the map of the study area.

Data: Hendra virus incident data was provided by the Queensland Department of Agriculture, Fisheries and Forestry (DAFF) under a data sharing agreement. For this study, a total of 15 equine related incidents that occurred from 1994-2011 in the study area are examined. The flying-fox occurrence spatial data set used in the study is obtained from the Department of Environment and Heritage Protection, Queensland (EHP). The collection of the data is continuous and is updated every three months by EHP. The Queensland vegetation data containing the Major Vegetation Subgroups (MVS) for the study has been obtained from the Department of Environment, Australia database.

Identification of vegetation subgroups near roosting sites and incidents: Buffer analysis was employed to select the area for further study of vegetation subgroups near the flying-fox roosting sites and the outbreak incidents. This is a simple yet important spatial technique used to determine the area or features covered within a specified location of a geographic feature. A 20 km range from the roosting sites has been chosen for the study which is the flying-foxes minimum foraging range and a 10 km range was chosen for the outbreak incidents for a detailed study. Using the area selected by buffer analysis, 'extract by mask' a geoprocessing tool in the spatial analyst toolset was used to extract the vegetation subgroups information near the roosting sites and incident locations.

Identification of food sources near roosting sites and incidents: Extract by attribute is a geoprocessing tool in the spatial analyst toolset that extracts the cells of a raster dataset based on a logical query. This tool was used to identify the food sources from the vegetation subgroups data of flying-foxes extracted earlier. Using the query builder, the food sources were obtained using their 'ID' and 'OR' clause was used for extracting multiple attributes at once.

Identification of vegetation clustering near the incident sites: High/low clustering method measures the degree of clustering for either high or low values using the Getis-Ord General G statistic. This method was employed to study the clustering of the food source vegetation near the incident locations. Global statistic like Getis-Ord General G assesses the overall pattern and trend of the data. It is an appropriate method if the values are fairly evenly distributed across the study area. As an inferential statistic tool, the results produced are interpreted within the context of null hypothesis which states that there is no spatial clustering of feature values. When p-value is statistically significant, the null hypothesis can be rejected. In case of null hypothesis rejection, the sign of the z-score becomes important. If the result is a positive z-score, it indicates that the high values are clustered together. If the result is a negative z-score, it indicates that the low values are clustered together.

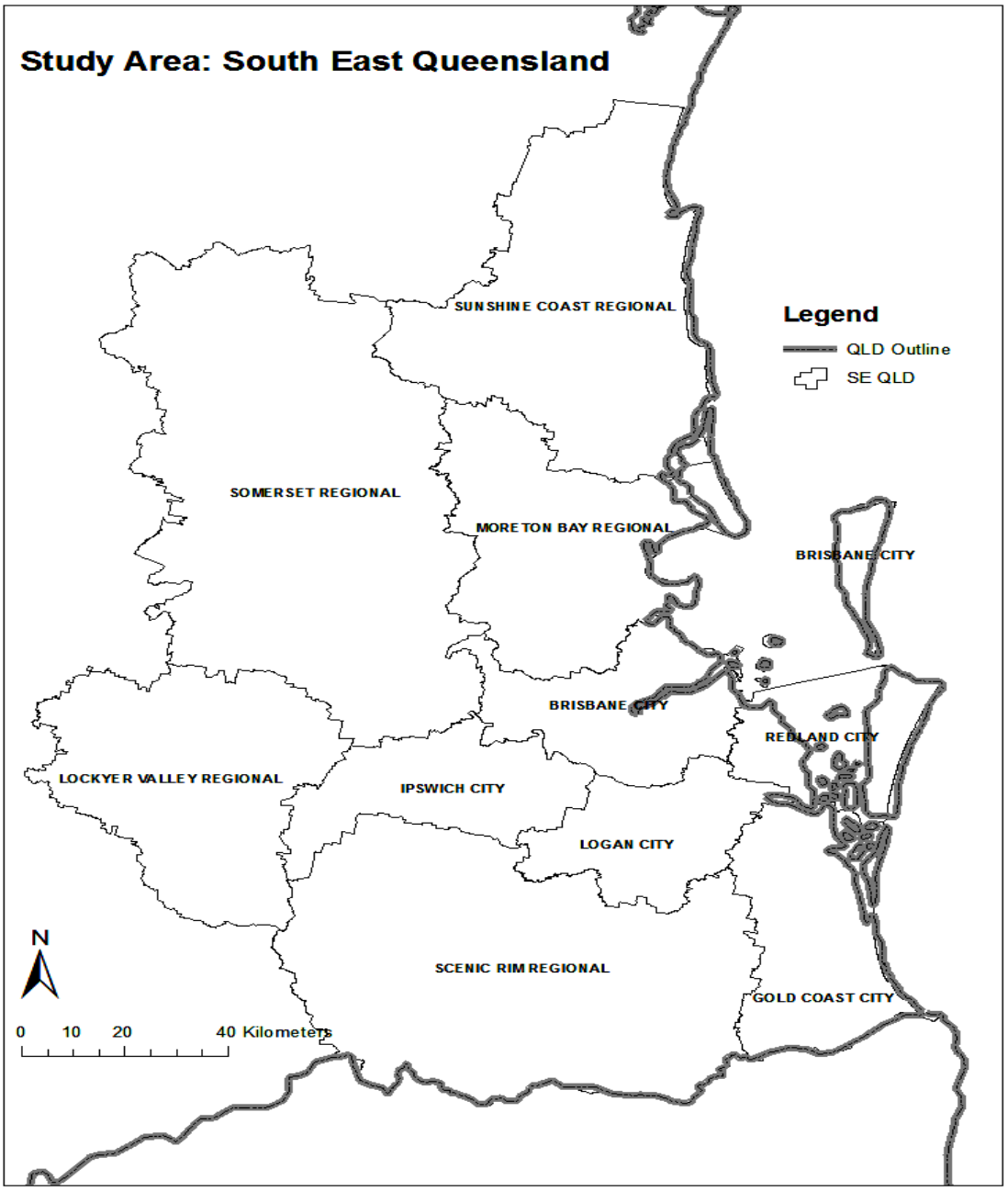


Fig. 1: Map of South-East queensland

Analysis: Using the buffer analysis and extract by mask tool, the vegetation subgroups near the black and grey headed flying-fox roosting sites and the outbreak incidents were identified. Area covering 20 km buffer range from the roosting sites was chosen for the study as it the minimum foraging range of both the species. For the vegetation subgroups identification near the incidence, a 10 km range was selected for a detailed study. Figure 2 shows the identification of major vegetation subgroups within 20 km buffer range of the black flying-fox roosting sites in the study area.

Figure 3 shows the identification of Major Vegetation Subgroups (MVS) within 20 km buffer range of the grey headed flying-fox roosting sites in the study area. The major vegetation subgroups identified on the incident locations indicated that 14 out of 15 incidents

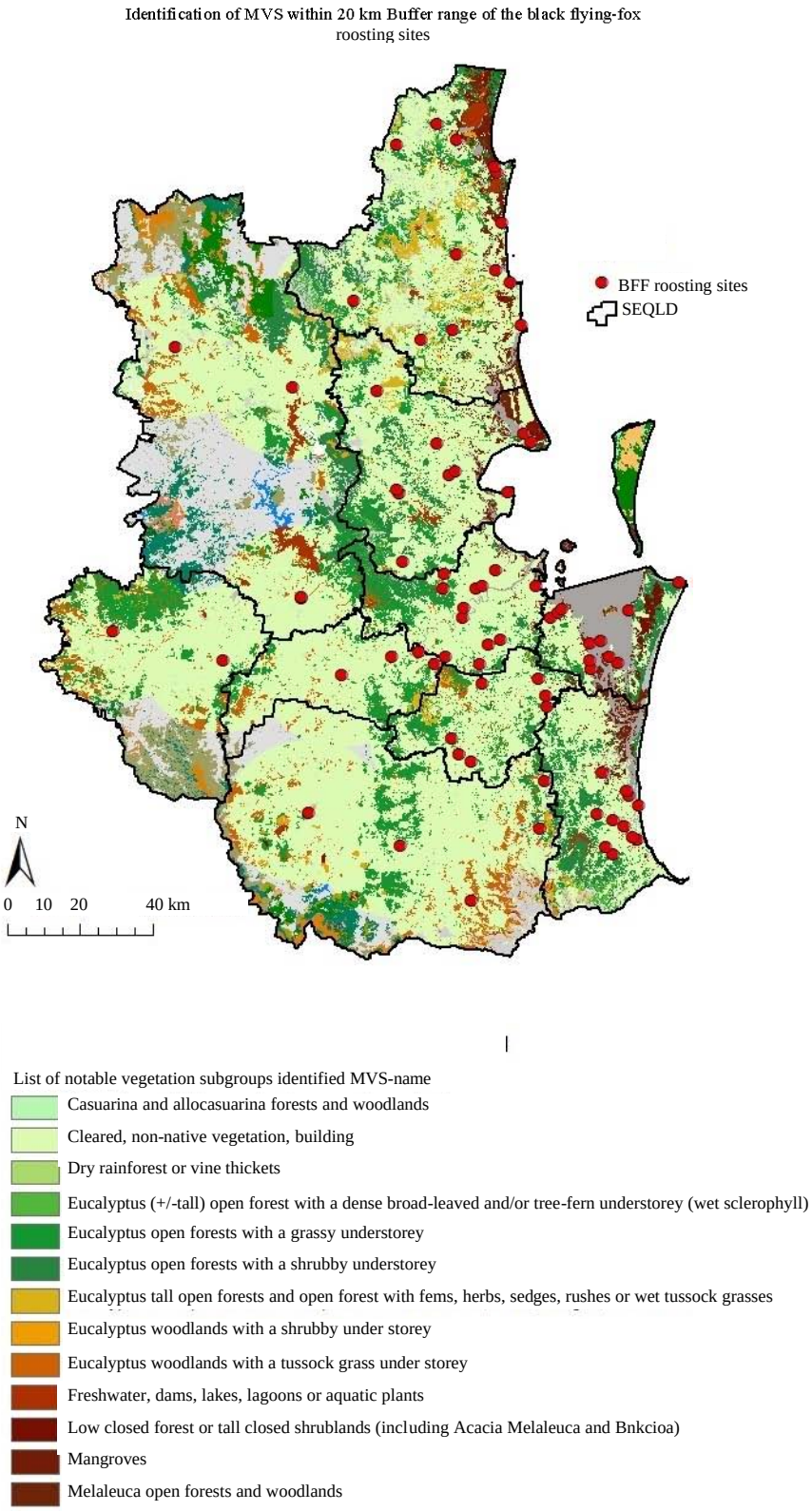


Fig. 2: Major vegetation subgroups within 20 km range of the black flying-fox roosting sites

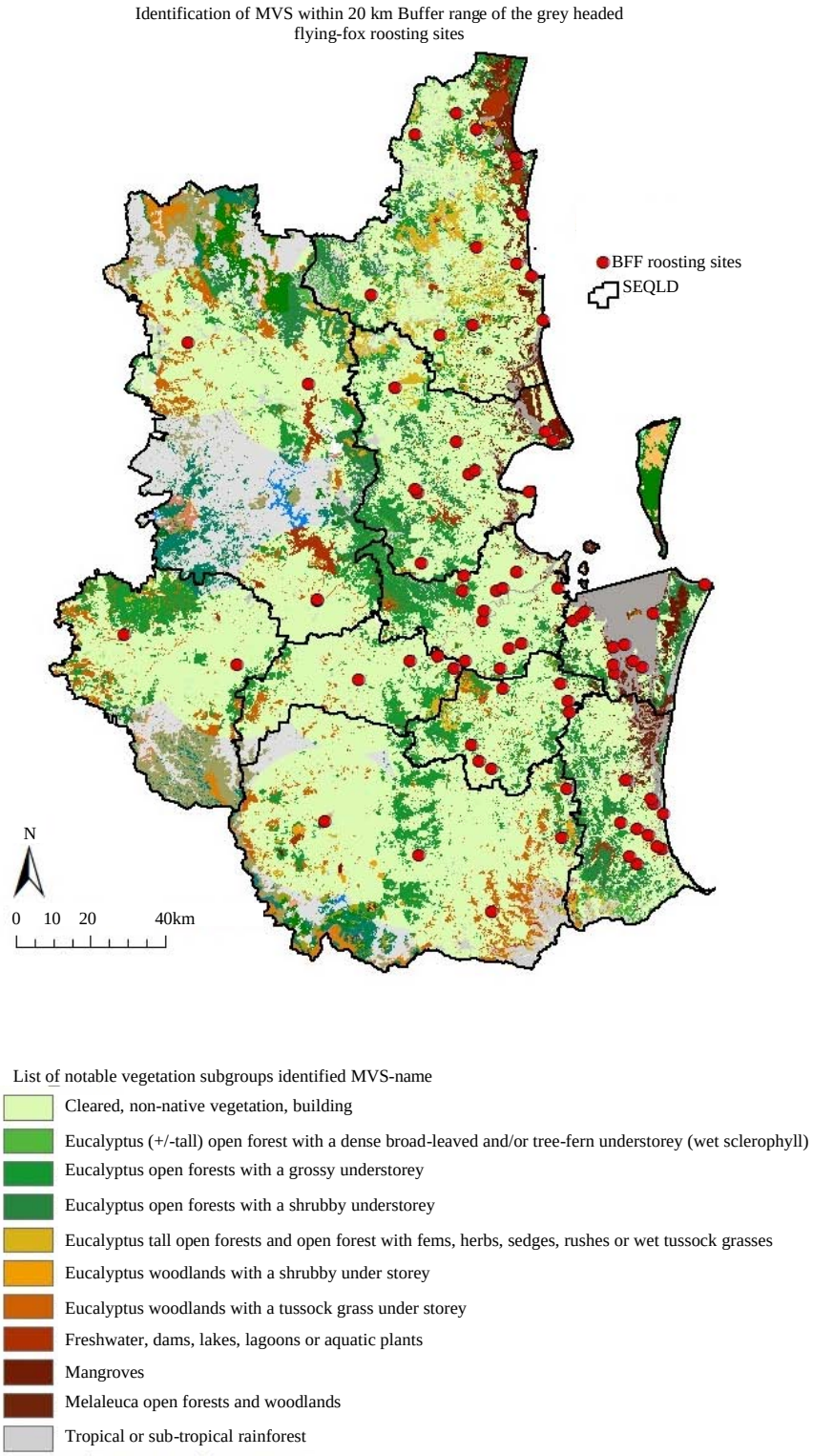


Fig. 3: Major vegetation subgroups within 20 km range of the grey headed flying-fox roosting sites

occurred on‘cleared, non-native vegetation, buildings’ subgroup. Figure 4 shows the identification of major vegetation subgroups within 10 km buffer rangeof the outbreak incidents in the study area.

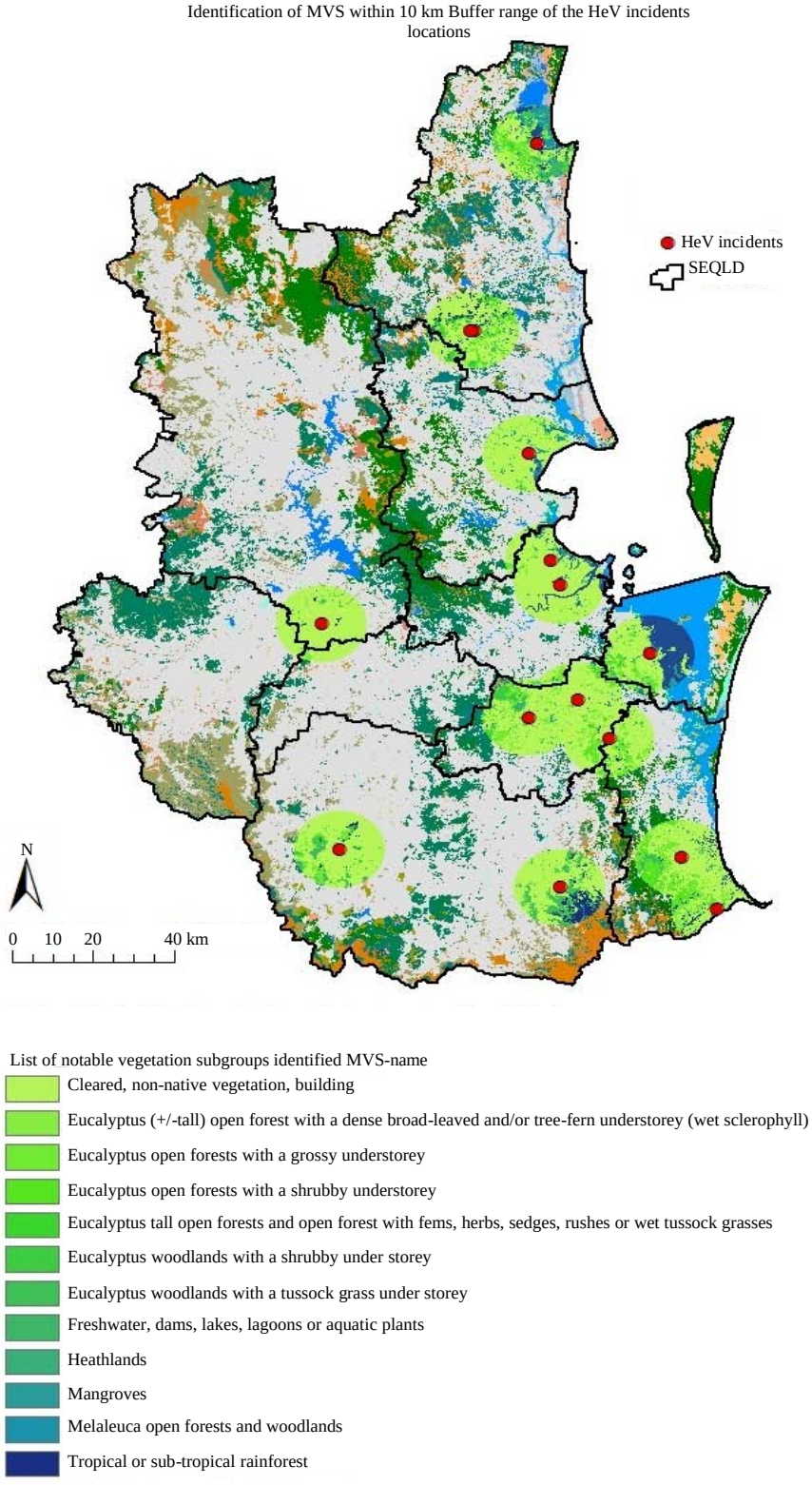


Fig. 4: Identification of major vegetation subgroups within 10 km of the incidents

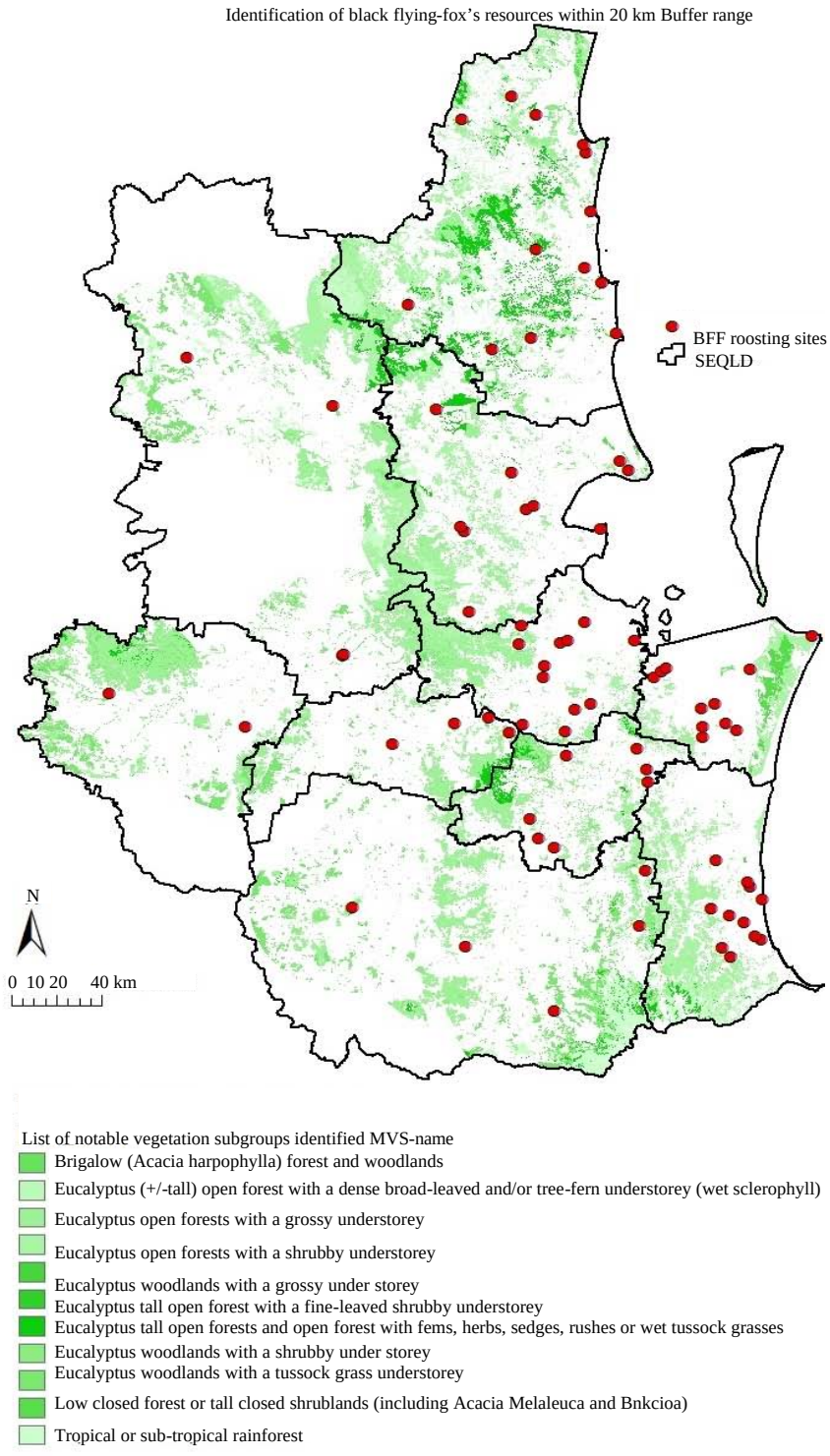


Fig. 5: Identification of food sources of black flying-foxes within their minimum foraging range

Using extract by attributes tool, the possible food sources for individual species near the roosting sites was identified. The possible food sources for the flying-foxes near the incident locations were identified. Figure 5 shows

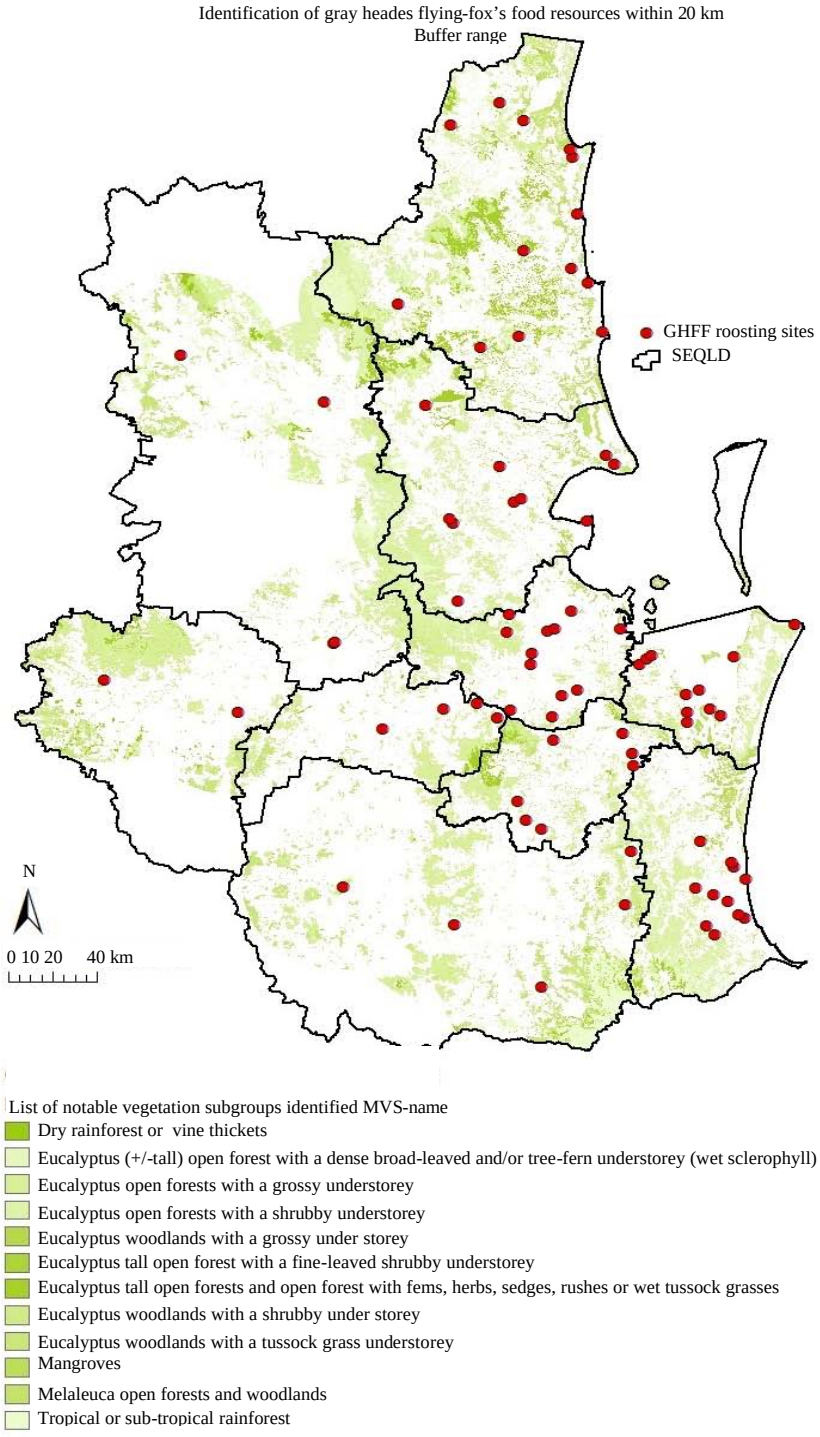
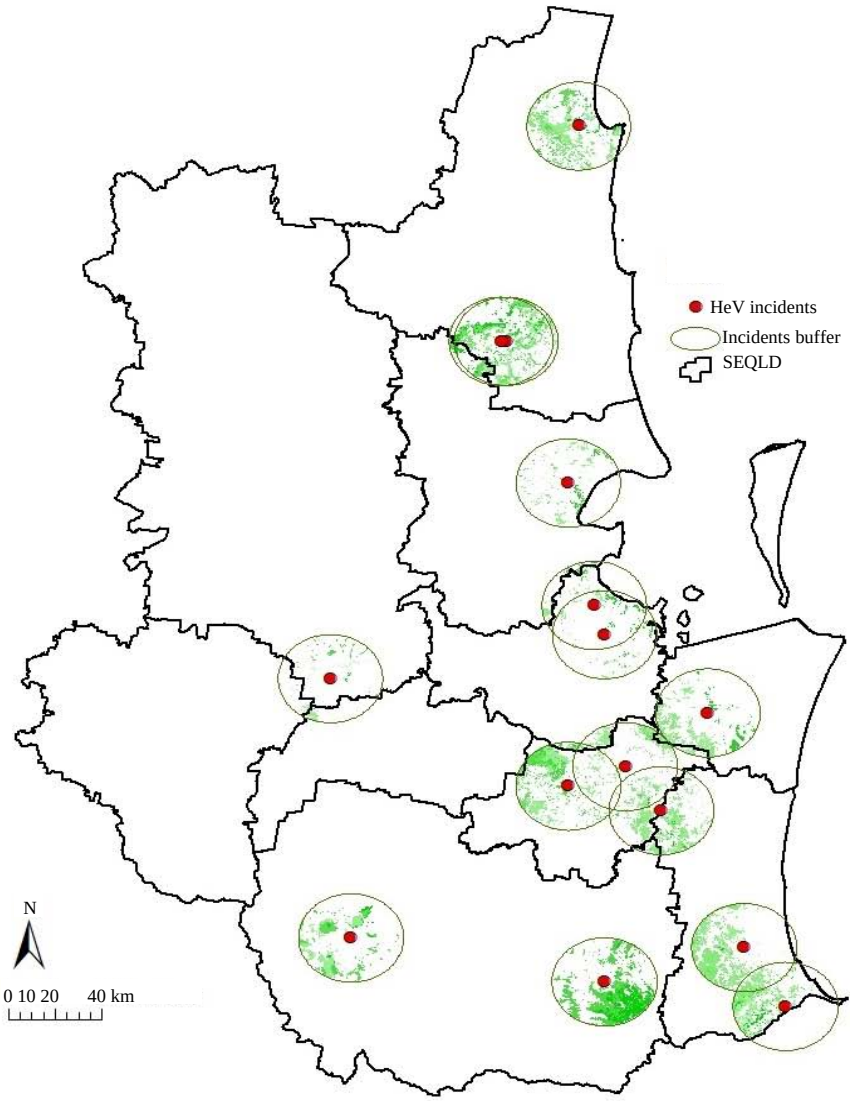


Fig. 6: Identification of food sources of grey headed flying-foxes within their minimum foraging range

the food sources identified within the minimum foraging range of the black flying-foxes. Figure 6 shows the food sources identified within the minimum foraging range of the grey headed flying-foxes.

Figure 7 shows the food sources identified within 10 kilometre range of the outbreak incidents in the study area. Using high/low clustering (Getis-Ord General G Statistic) method, the clustering of the food source

Flying-fox's food resources within 10 km buffer range of the incidents



Flying-fox's food resources present within 10km range of the incidents MV S_NAME

- Banksia woodlands
- Brigalow (Acacia harpophylla) forest and woodland
- Dry rainforest or vine thickets
- Eucalyptus (+/-tall) open forest with a dense broad-leaved and/or tree-fern understorey (wet sclerophyll)
- Eucalyptus open forests with a grossy understorey
- Eucalyptus open forests with a shrubby understorey
- Eucalyptus woodlands with a grossy under storey
- Eucalyptus tall open forests and open forest with fems, herbs, sedges, rushes or wet tussock grasses
- Eucalyptus woodlands with a shrubby under storey
- Eucalyptus woodlands with a tussock grass understorey
- Low closed forest or tall closed shrublands (including acacia, melaleuca and banksias)
- Mangroves
- Tropical or sub-tropical rainforest

Fig. 7: Identification of flying-fox food sources near the outbreak incidents

vegetation near the incidents was examined. The report suggested high clustering at 3 km distance threshold with a p-value of 0.002.

RESULTS AND DISCUSSION

This study identified the major vegetation subgroups present within the minimum foraging range (20 km) of the black and grey headed flying-foxes temporary and seasonal roosting sites. From the identified subgroups, the potential food sources for each species were identified. The abundance of food sources for each species within their minimum foraging range indicates a positive relationship between the roosting site locations and the vegetation subgroups present near them. The vegetation subgroup identification on the incident locations indicated that 14 out 15 incidents are rather located on 'cleared, non-native vegetation, buildings' subgroup and one incident is located vegetation subgroup 'Eucalyptus open forests with a grassy understorey'. This suggested a further need to study the vegetation near the incident sites.

A study on the vegetation subgroups within 10 km range from the incident sites identified a range of vegetation including a decent amount of potential food sources for both black and grey headed flying-foxes. High/low clustering method was employed to study the clustering of the food sources near the incident sites which indicated a significant high clustering at 3 km distance threshold. The p-value of 0.002 indicates 99% significance and the positive z-score indicates clustering among the high values. However, the clustering started dispersing as the distance threshold increased. At 4 km distance threshold, the clustering was still statistically significant with 90% confidence level. At 5 km distance threshold, the clustering is random and at 8 km distance threshold, the result is dispersed.

CONCLUSION

This study serves as a base to examine the primary relationships between the vegetation subgroups/food sources, roosting sites and the incidence for understanding the virus dispersion in the study area. Using spatial analyst tools, the Major Vegetation Subgroups (MVS) present within 20 km buffer range of both grey headed flying-foxes and black flying-foxes roosting sites were identified. The identification of abundance of food sources for individual species within their minimum foraging range indicated a strong correlation between their roosting site locations and vegetation subgroups present. A 10 km range vegetation study on the incident locations identified the presence of food sources of both species. The clustering of the food source vegetation present near the incidence has been studied using high/low clustering/Getis-Ord General G Statistic tool which indicated statistically high clustering with 99% confidence level at 3 km distance threshold. The findings suggest that the presence of potential 'food sources' of the flying-foxes within certain proximity increases the risk of Hendra virus disease transmission.

RECOMMENDATIONS

The next stage of the research concentrates on the most re-occurring food sources (at least 3 vegetation subgroups) near the roosting sites and the outbreak incidents to identify the individual correlations. This may help identify if the virus dispersion could be linked to a particular major vegetation subgroup(s) in the study area. Equine population with respect to the vegetation subgroups and outbreak incidents will be examined to identify possible spatial relationships and/or patterns. The research focuses on identifying the accurate combination of parameters/factors to yield the most suitable predictive model for the Hendra virus outbreaks in the study area.

ACKNOWLEDGEMENT

We would like to thank Dr Xiaoye Liu from the University of Southern Queensland, Australia and Dr Antoni Moore from University of Otago, New Zealand for their advice, guidance and comments on the manuscript.

REFERENCES

Baum, S., E. Kendall, H. Muenchberger, O. Gudes and T. Yigitcanlar, 2010. Geographical information systems: An effective planning and decision-making platform for community health coalitions in Australia. Health Inf. Manage. J., 39: 28-33.

Bithell, J.F., 2000. A classification of disease mapping methods. Stat. Med., 19: 2203-2215.

Burnham, J., A.K. Chong, X. Liu and A. Moore, 2015. Preliminary spatial analysis of hendra disease outbreaks in South East Queensland. Globe, 76: 39-45.

CSIRO., 2011. Hendra virus. Common wealth Scientific and Industrial, Canberra, Australia. http://www.csiro.au/Outcomes/Food-and-Agriculture/Hendra-Virus.aspx/.

DAFF, 2012. National hendra virus research program. Department of Agriculture, Forestry and Fisheries, Pretoria, South Africa. https://www.daff.qld.gov.au/animal-industries/animal-health-and-diseases/a-z-list/hendra-virus/intergovernmental-hendra-virus-taskforce/national-hendra-virus-research-program.

DILGP., 2009. South East quee nsland regional plan 2009-2031. Department Of Infrastructure, Local Government and Planning, Brisbane, Queensland. http://www.dsdip. qld.gov. au/resources/plan/seq/regional-plan-2009/seq-regional-plan-2009.pdf.

DPI., 2012. Hendra virus-frequently asked questions. Department of Primary Industries, Orange, Australia. http://www.dpi.nsw.gov. au/agriculture/livestock/horses/health/general/hendra-virus/faqs.

Farlane, M.R., N. Becker and H. Field, 2011. Investigation of the climatic and environmental context of hendra virus spillover events 1994-2010. PloS One, Vol. 6,

Smith, C., C. Skelly, N. Kung, B. Roberts and H. Field, 2014. Flying-fox species density-a spatial risk factor for Hendra virus infection in horses in Eastern Australia. PLoS One, 9: e99965-e99965.

Vine, M.F., D. Degnan and C. Hanchette, 1997. Geographic information systems: Their use in environmental epidemiologic research. Environ. Health Perspect., 105: 598-605.

WPSQ., 2014. Flying foxes. Wildlife Preservation Society of Queensland, Highgate Hill, Queensland. www.wildlife. org. au/wildlife/speciesprofile /mammals/flyingfox/.