

Domestic dog roaming patterns in remote northern Australian indigenous communities and implications for disease modelling



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ABSTRACT

Although Australia is canine rabies free, the Northern Peninsula Area (NPA), Queensland and other northern Australian communities are at risk of an incursion due to proximity to rabies infected islands of Indonesia and existing disease spread pathways. Northern Australia also has large populations of free-roaming domestic dogs, presenting a risk of rabies establishment and maintenance should an incursion occur. Agent-based rabies spread models are being used to predict potential outbreak size and identify effective control strategies to aid incursion preparedness. A key component of these models is knowledge of dog roaming patterns to inform contact rates. However, a comprehensive understanding of how dogs utilise their environment and the heterogeneity of their movements to estimate contact rates is lacking. Using a novel simulation approach – and GPS data collected from 21 free-roaming domestic dogs in the NPA in 2014 and 2016 – we characterised the roaming patterns within this dog population. Multiple subsets from each individual dog's GPS dataset were selected representing different monitoring durations and a utilisation distribution (UD) and derived core (50%) and extended (95%) home ranges (HR) were estimated for each duration. Three roaming patterns were identified, based on changes in mean HR over increased monitoring durations, supported by assessment of maps of daily UD's of each dog. *Stay-at-home* dogs consolidated their HR around their owner's residence, resulting in a decrease in mean HR (both core and extended) as monitoring duration increased (median peak core and extended HR 0.336 and 3.696 ha, respectively). *Roamer* dogs consolidated their core HR but their extended HR increased with longer monitoring durations, suggesting that their roaming patterns based on place of residence were more variable (median peak core and extended HR 0.391 and 6.049 ha, respectively). *Explorer* dogs demonstrated large variability in their roaming patterns, with both core and extended HR increasing as monitoring duration increased (median peak core and extended HR 0.650 and 9.520 ha, respectively). These findings are likely driven by multiple factors that have not been further investigated within this study. Different roaming patterns suggest heterogeneous contact rates between dogs in this population. These findings will be incorporated into disease-spread modelling to more realistically represent roaming patterns and improve model predictions.

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1. Introduction

Domestic dogs are responsible for >90% of human rabies cases (WHO, 2013). In most rabies-endemic regions – such as Africa and Asia – the domestic dogs that are responsible for rabies endemicity and spill-over to humans are those that are free-roaming. Therefore, efforts are focussed on controlling rabies in these populations (Knobel et al., 2005; Hampson et al., 2009; Tenzin and Ward, 2012; Morders et al., 2014).

To support preparedness planning and control of rabies, transmission models of canine rabies spread are needed. Ideally, such models should incorporate dog behaviour and ecology information from free-roaming domestic dog populations. A critical parameter in disease spread models is the probability that individuals make contact sufficient for disease transmission. Variation in roaming patterns and behaviours has previously been observed in populations of free-roaming dogs (Meek 1999). It is known that a range of factors influence dog roaming patterns, including scavenging for food, interaction with humans, and the sex and breeding behaviour of the dog (Newsome et al., 2014; Sparkes et al., 2014; Ruiz Izaguirre et al., 2015; Dürr et al., 2017). These factors might cause some dogs to roam more extensively than others, resulting in heterogeneity

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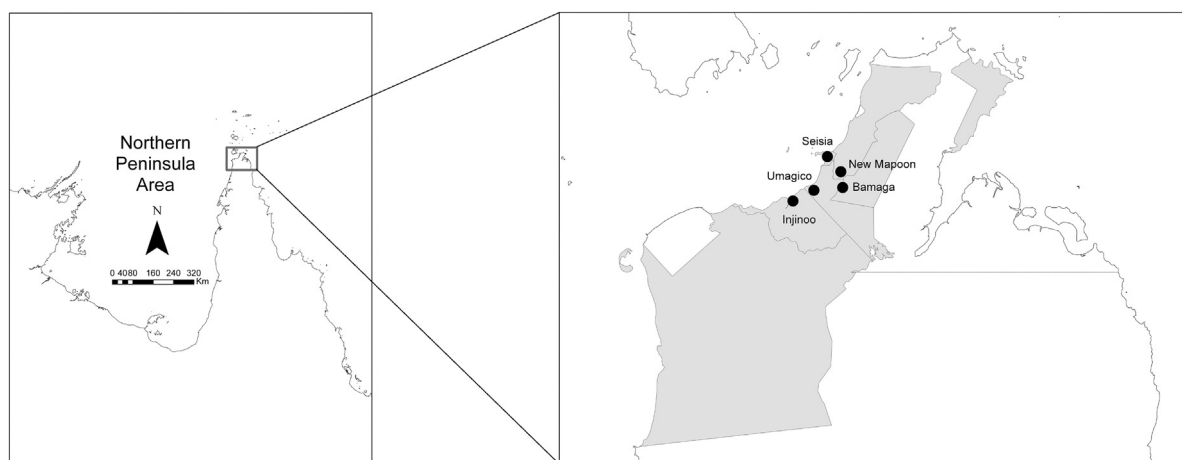


Fig. 1. Map of the study site – the Northern Peninsula Area (NPA) – and its five communities where GPS units were deployed in 2014 and 2016 on free-roaming domestic dogs. Left: the NPA in relation to the rest of Australia. Right: The NPA and the five communities. Grey sections represent the NPA local government area.

of individual roaming patterns. Consequently, an understanding of how dogs utilise their environment and thus, how they contact each other, could provide useful insights that can be used to develop more realistic disease-spread models.

The utilisation distribution (UD) and home range (HR) are two measures that are used to describe the roaming patterns of many species, including dogs (Burt, 1943; Winkle, 1975; Walton et al., 1999; Millspaugh et al., 2006). The UD incorporates the relative time frequencies during which the various areas of a HR (a spatial measure) are used. Several studies have reported UD or HRs for wild canine species such as wolves and dingoes (Claridge et al., 2009; de Almeida Jácomo et al., 2009; Eriksen et al., 2009; Chadwick et al., 2010; Allen et al., 2013; Newsome et al., 2013; McNeill et al., 2016), and others have focused on free-roaming domestic dog HR size and roaming patterns (Meek, 1999; Vaniscotte et al., 2011; Dias et al., 2013; Van Kesteren et al., 2013; Sparkes et al., 2014; Molloy et al., 2017). There have also been a few studies conducted in which free-roaming dogs were investigated in the Northern Peninsula Area (NPA) (Dürr and Ward, 2014; Bombara et al., 2017; Dürr et al., 2017). Home range estimates for domestic dogs have varied within these studies. Within the NPA population, studies have estimated a wide range of HR sizes despite similar median HR sizes. For example, Dürr and Ward (2014) estimated core and extended HR ranges of 0.2–1.1 ha and 2.1–40.5, respectively (median 0.4 and 5.3 ha, respectively), and Bombara et al. (2017) calculated core and extended HR ranges of 0.05–2.33 ha and 1.09–131.02 ha respectively (median 0.33 and 4.54 ha, respectively). These highly varied HRs could reflect different roaming groups within populations. However, only Meek (1999) grouped study dogs based on HR size into sedentary and wandering. Also, most of these previous studies have only estimated a single HR for each dog based on short monitoring durations (usually 1–4 days), with Sparkes et al. (2014) and Meek (1990) monitoring for longer periods (7-day periods and one 21-day period, and five one-week periods, respectively). Comparing multiple HRs from the same dog calculated from different monitoring periods and the insights into roaming patterns that this could provide have not been explored yet.

Although Australia is currently canine rabies free, a recent eastward spread along the Indonesian archipelago has brought rabies within 300 km of mainland Australia, increasing the risk of a rabies incursion (Tenzin and Ward, 2012; Ward, 2014). Due to this proximity and the large populations of free-roaming domestic dogs in Indigenous communities in northern Australia (Sparkes et al., 2015), an agent-based, stochastic simulation model of domestic dog rabies spread was recently developed (Dürr and Ward, 2015). This model was parameterised using GPS data from short-term

field studies in the NPA of Cape York, Queensland. We hypothesise that the accuracy of model predictions could be improved if dog contacts were parameterised using data from longer-term GPS studies in which the characteristics of dogs' roaming behaviour were more comprehensively described. Therefore, the objective of this study was to measure changes in HR size with increased monitoring duration using a novel simulation method applied to GPS data, and characterise different roaming patterns within the NPA free-roaming dog population. We aimed to improve understanding of dog movements and potential for heterogeneity of contacts within the free-roaming dog population in the NPA by categorizing dogs into distinct roaming groups. This can be used to further refine contact parameters in the rabies-spread model. The findings of this study could also have relevance to modelling and understanding disease spread of other infectious diseases within free-roaming dog populations.

2. Methods

2.1. Study site

The studies were conducted in the five coastal communities of the NPA, a local government area (www.nparc.qld.gov.au) located in Cape York Peninsula, Queensland, Australia (Fig. 1). The five Aboriginal and Torres Strait Islander communities that comprise the NPA are – from north to south – Seisia, New Mapoon, Bamaga, Umagico and Injinoo. Almost the entire human population (approx. 2230) in the NPA (1057 km²) live in one of these five communities, occupying a land area of 32 km² (3% of the NPA) (ABS, <http://www.censusdata.abs.gov.au>, accessed 28 February, 2017). Each of these communities is located 4 km or less from a neighbouring community and all are surrounded by dense tropical forest.

2.2. GPS units and data collection

Data were recorded (first to last GPS fix) during two periods: 2–9 September 2014 (15 days) and 8 May to 15 July 2016 (68 days), with different dogs sampled in 2014 and 2016. The 2014 data has been recently used for home range analysis addressing different research questions (Bombara et al., 2017). Small, lightweight GPS units enclosed within a robust plastic casing (CatLog and CatLog2™; <http://www.mr-lee.com>) attached to nylon dog-collars were used to record dog locations throughout the studies. GPS units were deployed on 46 and 29 dogs in NPA communities in 2014 and 2016, respectively. Dogs within all five NPA communities that were >6 months of age were the target population, and were eligible for

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