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Tracey L. Kreplins

Danielle Stephens

N Laing

C Oskam

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# An assessment of dingo ancestry in camp dogs in Western Australia

T. L. Kreplins<sup>A,\*</sup> , D. Stephens<sup>B</sup>, N. Laing<sup>C</sup> and C. Oskam<sup>D</sup>

For full list of author affiliations and declarations see end of paper

**\*Correspondence to:**

T. L. Kreplins  
Department of Primary Industries and  
Regional Development, PO Box 483,  
Northam, WA 6401, Australia  
Email: [tracey.kreplins@dpid.wa.gov.au](mailto:tracey.kreplins@dpid.wa.gov.au)

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## ABSTRACT

Hybridisation between Australian dingoes and domestic dogs is a controversial area of interest and research. An ongoing canine sterilisation programme in rural and remote Western Australia provided an opportunity to assess the dingo ancestry of camp dogs and opportunities for hybridisation. Blood samples were collected from 345 individual community dogs at 21 locations. Dogs were screened using 23 microsatellite loci and ancestry percentage assigned using an iterative Bayesian assignment algorithm. A single individual was a dingo, 96% were domestic dogs and 3.5% were hybrids. Camp dog and dingo hybridisation in these areas is of little concern in terms of conserving dingo purity.

**Keywords:** Australian dingoes (*Canis familiaris*), camp dog, dingo, domestic dog, hybridisation, Western Australia.

## Introduction

Dogs are one of the most widespread domesticated species and are found on all continents (Balme and O'Connor 2016) except Antarctica. Australian dingoes (*Canis familiaris*) (Jackson *et al.* 2017) are adaptable wild-living canids that are found across the breadth of Australian landscapes, from deserts to alpine, forests to peri-urban. Dingoes have been present in Australian landscapes for approximately 4500 years (Balme *et al.* 2018; Zhang *et al.* 2020). Surveys of dingoes by DNA across the continent have revealed that few domestic dogs live away from urban settlements, and even dingo–dog hybrids with low dingo ancestry seem rare (Stephens *et al.* 2015). Despite being a single species, dingoes and domestic dogs differ in a few phenotypic characteristics. The proposed explanations for this finding are that behavioural and/or social factors make domestic dogs unsuited to life without humans, either through an inability to survive directly, or inhibition/hostility from dingoes (Wilton *et al.* 1998). Dingoes are valued culturally (Hyttén 2009) and conservation of their purity is valued in some parts of the Australian community (van Eeden *et al.* 2017). There is an alternate view that dingoes are their own species (Smith *et al.* 2019), but this has recently been questioned (see Supplementary material; Jackson *et al.* 2021).

A major concern of dingo conservation is the hybridisation with domestic dogs (Stephens *et al.* 2015; Cairns *et al.* 2020). ‘Camp-dogs’ are populations of domestic but often free-living dogs residing in and around remote or regional human settlements. These camp dogs exploit human resources and have close associations with the human residents (Smith and Litchfield 2005; Newsome *et al.* 2014). In previous studies where camp dogs have been included in surveys of dingo ancestry (Newsome *et al.* 2013; Bombara *et al.* 2017), the camp dogs have shown low percentages of dingo ancestry, both within individuals and in the population as a whole.

Understanding the relationship between dingoes and free-roaming dogs will provide knowledge around the potential animal and human health risks. Free-roaming dogs residing in and around human settlement not only pose a genetic risk to dingoes but can also introduce parasite and disease risks (Barker *et al.* 2012; King *et al.* 2012). Many of the free-roaming dogs have poor health due to lack of veterinary support and resources in remote areas (Sparkes *et al.* 2014). This pathogen risk can also be transferred to livestock, native species, and even zoonotic risks to humans.

Here we surveyed 21 sites with 1–70 individuals per site (345 total individuals) where there is coexistence between humans and semiowned camp dogs. We aimed to identify the

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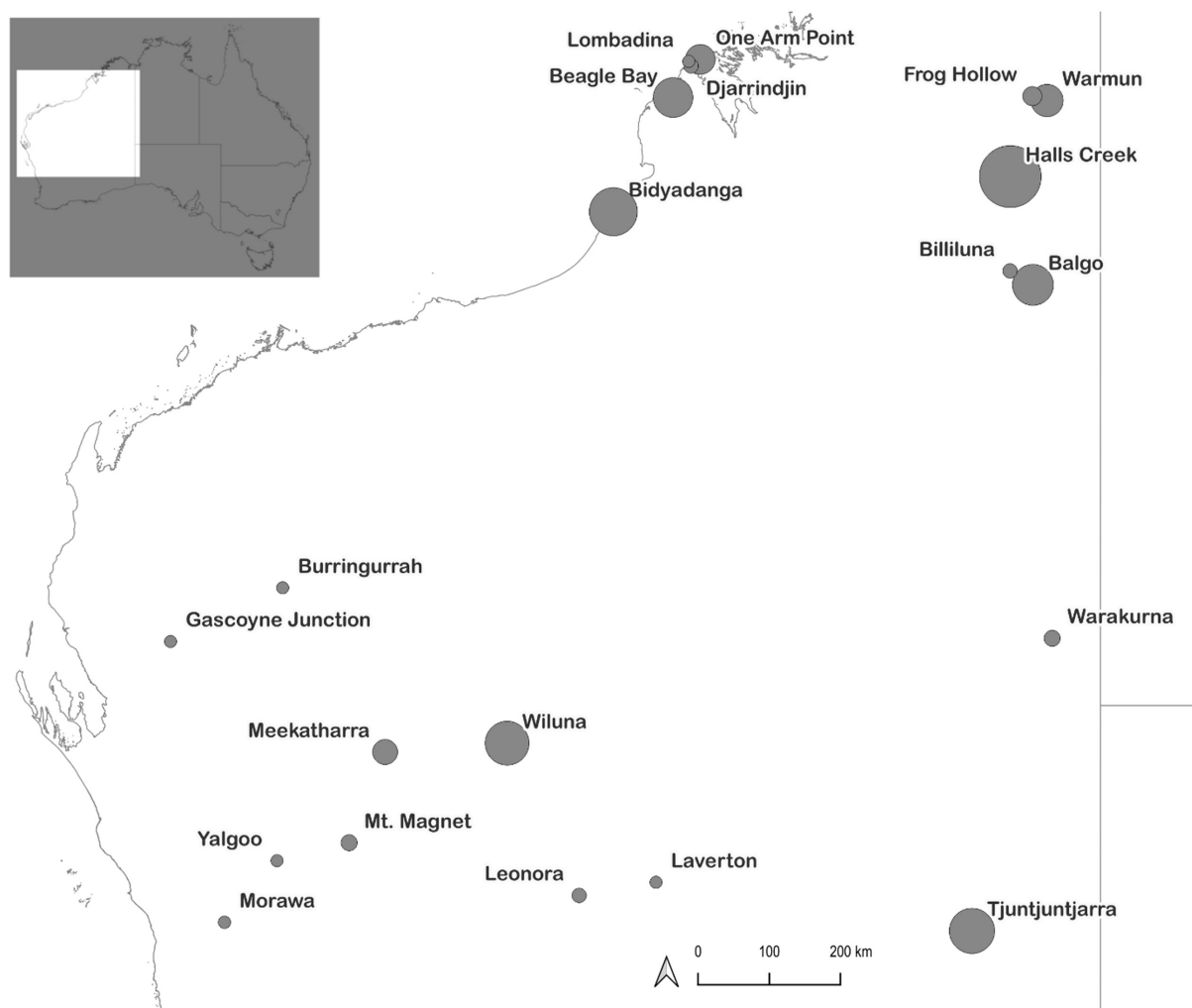
percentage of free-roaming camp dogs with dingo ancestry or identify pure dingoes at the sites.

## Methods

The camp dogs were part of a canine sterilisation programme in which they were health screened, sterilised and treated for illness by Murdoch University veterinarians in training at a range of communities across Western Australia (Fig. 1).

DNA was extracted from 200  $\mu$ L of each blood sample using the Qiagen QIAMP mini blood kit. Samples were processed according to the recommended protocol, with 150  $\mu$ L final elution. Extracted DNA was amplified by PCR using the following conditions: 15 min at 95°C, 35 cycles of 30 s at 94°C, 90 s at 55°C and 60 s at 72°C, then 30 min final extension at 60°C at 23 microsatellite loci in five multiplexes. PCR primers used were as described in Stephens (2015; table 1). PCR products were visualised using an Applied Biosystems 3730

at the Australian Genome Research Facility (AGRF, Adelaide, Australia). Data from the amplified fragments were analysed using Structure ver. 2.3.4 (Pritchard *et al.* 2000) along with 322 reference dingoes and 109 domestic dogs, with allele frequencies updating and initialising from these reference populations. The selection of these reference individuals is detailed in Stephens *et al.* (2015). The number of populations was fixed at  $K = 2$  for 10 replicates to produce a percentage genotype for each individual assigned to either the dingo or domestic dog ancestral group. Replicates were combined and averaged using pophelper (Francis 2017; R Core Team 2023). Stephens *et al.* (2015, 2022, 2023) has published many times using the stricter dingo purity definitions; using an error of  $\pm 10\%$  based on this previous work was used to assign individuals to categories of dingo ( $>90\%$  dingo ancestry), hybrid (11–89% dingo ancestry) or domestic dog ( $<10\%$  dingo ancestry) for comparison between sites. This margin of error also covers the mean difference between microsatellite and single nucleotide polymorphism (SNP)



**Fig. 1.** Locations where dogs were sampled for this study within Western Australia. Grey dots are scaled by the number of animals collected at each site. The inset shows location of the study area within Australia.

testing in the study area (9%) as demonstrated by Cairns *et al.* (2023: table 5). Principal coordinates analysis was performed for comparison with the Structure results, and was calculated using GenAlEx ver. 6.51b2 (Peakall and Smouse 2012).

## Results

A genotype was obtained from all of the 345 animals tested, and only one was classified as a dingo, with 94% dingo

**Table 1.** Number of dingoes (90–100% dingo ancestry), hybrids (11–89% dingo ancestry) and domestic dogs (<10% dingo) identified by genetic testing at each site.

Location	Dingo	Hybrid	Dog
Balgo	0	0	32
Beagle Bay	0	1	30
Bidyadanga	0	0	44
Billiluna	0	1	3
Burringurrah	0	0	2
Djarrindjin	0	1	3
Frog Hollow	0	0	7
Gascoyne Junction	0	0	1
Halls Creek	0	3	70
Warmun	0	0	20
Laverton	0	0	1
Leonora	0	0	4
Lombadina	0	0	2
Meekatharra	0	0	12
Morawa	0	0	3
Mount Magnet	0	1	4
One Arm Point	1	0	17
Tjuntjuntjarra	0	3	36
Warakurna	0	0	5
Wiluna	0	2	35
Yalgoo	0	0	1
Total	1	12	332
Percentage	0.3	3.5	96.2

ancestry (Table 1). There were 12 dingo–dog hybrids with mostly domestic dog ancestry, but the majority of individuals (96%) were domestic dogs. Of the hybrid animals, all had less than 50% dingo ancestry, and nine of the 12 were less than 25% dingo ancestry (range 11–43%).

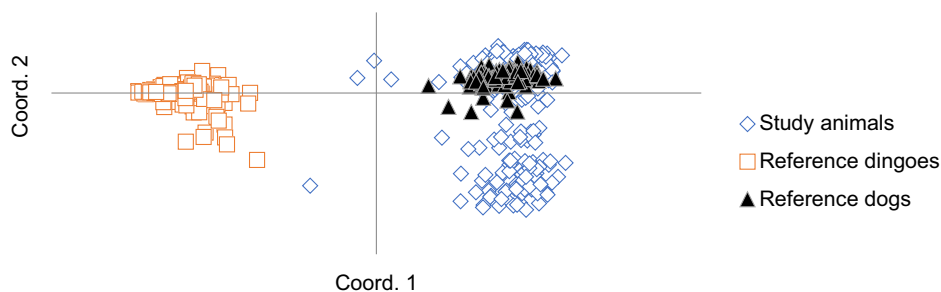
Separation of the study animals from the reference dingoes in the PCoA also indicates the lack of hybridisation between dingoes and community dogs (Fig. 2).

## Discussion

How ‘wild’ and genetically pure dingoes are, is under constant debate. Dingoes most likely arose in Asia around 5000–12,000 years ago (Filios and Tacon 2016) through either descent from Asian wolves or hybridisation with Asian wolves, although the literature is unclear on this point (Corbett 2001; Savolainen *et al.* 2004). After arriving with humans, dingoes quickly spread across Australia and their relationships with dogs throughout the continent is becoming better understood.

Dingo purity, and in turn their conservation, is only at risk if camp dogs and dingoes intermix freely (Elledge *et al.* 2008). A reduction in dingo purity is unlikely if the dingoes and camp dogs do not intermix. The pattern of domestic dogs being largely absent from wild landscapes seems to exist in the inverse in human settlements. Dingoes are almost completely absent from the settlements in this study (except Allen *et al.* 2013), indicating that either the dingoes are not favoured by the humans present, or the dingoes themselves do not choose to remain in the settlements. Domestic dogs, on the other hand, seem able to persist in these areas as long as there is some assistance from humans or human resources, even without direct ownership.

Transmission of disease or pathogens could potentially be very high between all canids. Contact rates between free-roaming dogs of Indigenous communities in Northern Australia (of unknown ancestry) were 8–147 direct contacts (i.e. licking, mouthing, playing) between dogs within 24 h. Often this occurred in urban settings but also in the bush and beach lands (Bombara *et al.* 2017). However, if there is minimal hybridisation or socialisation between camp dogs and dingoes, as recorded from the lack of hybridised individuals, transmission of disease and pathogens is low. Parasites are known to be



**Fig. 2.** PCoA of reference dogs, reference dingoes and animals from this study. Dingoes and dogs are separated on the x-axis.

common among free-roaming camp dogs of Indigenous communities in Australia, in particular ectoparasites such as ticks (Newsome *et al.* 2013; Bombara *et al.* 2017). However, anecdotally, dingoes are not parasitised by ticks (Koungoulos and Contos 2019).

Other studies in Australia have found variable results in relation to roaming dogs of a range of ancestry. For example, a study on hair samples found approximately one-third of dogs were classified as hybrids (Bombara *et al.* 2017). However, the percentage of the samples differed between the regions: 41% for Galinwin'ku and 6% for Northern Peninsula Area. These dogs were also tracked and were demonstrated to stray into nearby bushland and may potentially interact with dingoes. Another study comparing the ancestry of dogs of mine sites and neighbouring communities found that 89% of samples from the mine were dingoes and there was minimal dingo ancestry in the community dogs. Only one of the studied communities showed the potential for interactions between community and dingoes (Newsome *et al.* 2013).

The next step in this research is to understand why there is a lack of hybridisation. Is the lack of intermixing between camp dogs and dingoes by choice or because camp dogs never encounter dingoes? Is there anything occurring differently in the Kimberly region compared to the Nullarbor region leading to a few more hybrids? Or is this an artefact of sampling (i.e. dogs that can be handled for sterilisation)? In other words, do the community dogs remain within the community bounds or do they enter the bushland where dingoes reside and choose to not interact? Studies that have investigated urban roaming domestic dogs indicate that each individual dog has a preference for roaming or not roaming (Meek 1999). However, domestic dogs that did roam made similar choices to dingoes and were active along waterways that had high prey activity (i.e. kangaroos). Is the 'roaming' dog moving further because of food availability regardless of its ancestry? Furthermore, is the persecution of dingoes in Western Australia for their predation of livestock creating a learned aversion to human settlements (Stephens *et al.* 2023)?

While dingoes are of high value to some Australians, camp dogs themselves are of high cultural importance to community members (Hyttén 2009; Balme and O'Connor 2016). Although the companionship between dogs and humans covers 30,000 years, with dogs being in Australia for only approximately 4500 years, their significance is cherished by the entire Australian community, regardless of their ancestry (Filios and Tacon 2016). This study adds to previous research showing a lack of hybridisation occurring, which indicates that dingo purity is not of conservation concern at the present time in Western Australia and possible disease transmission pathways are minimal.

## Supplementary material

Supplementary material is available [online](#).

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**Data availability.** Data have been uploaded to Dryad.

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#### Author affiliations

<sup>A</sup>Department of Primary Industries and Regional Development, 75 York Road, Northam, WA 6403, Australia.

<sup>B</sup>Zoological Genetics, Inglewood, SA, Australia.

<sup>C</sup>School of Veterinary Medicine, Murdoch University, 90 South Street, Murdoch, WA 6050, Australia.

<sup>D</sup>School of Medical, Molecular, and Forensic Sciences, and the Centre for Biosecurity and One Health, Harry Butler Institute, Murdoch University, 90 South Street, Murdoch, WA 6050, Australia.