

The myth of wild dogs in Australia: are there any out there?

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Abstract. Hybridisation between wild and domestic canids is a global conservation and management issue. In Australia, dingoes are a distinct lineage of wild-living canid with a controversial domestication status. They are mainland Australia's apex terrestrial predator. There is ongoing concern that the identity of dingoes has been threatened from breeding with domestic dogs, and that feral dogs have established populations in rural Australia. We collate the results of microsatellite DNA testing from 5039 wild canids to explore patterns of domestic dog ancestry in dingoes and observations of feral domestic dogs across the continent. Only 31 feral dogs were detected, challenging the perception that feral dogs are widespread in Australia. First generation dingo × dog hybrids were similarly rare, with only 27 individuals identified. Spatial patterns of genetic ancestry across Australia identified that dingo populations in northern, western and central Australia were largely free from domestic dog introgression. Our findings challenge the perception that dingoes are virtually extinct in the wild and that feral dogs are common. A shift in terminology from wild dog to dingo would better reflect the identity of these wild canids and allow more nuanced debate about the balance between conservation and management of dingoes in Australia.

Keywords: admixture, Australia, *Canis dingo*, *Canis familiaris*, dingo, dog, domestication, feral dog, introgression, wild dog.

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Introduction

The occurrence of feral domestic dogs is rare, and distinct from the close to a billion free-breeding or village dogs that exist globally (Gompper 2013; Pilot *et al.* 2015). Free-breeding or village dogs are those that live in and around human settlements, rely upon anthropogenic food or water sources, breed freely with each other, and are not owned or cared for by people (Hughes and Macdonald 2013). Feral dogs are those that are living in a wild state not in the vicinity of human settlements: they may be escaped pets or self-sustaining populations. Empirical data from remote living free-breeding dog populations suggests these populations rely upon recruitment from stray or owned dogs because their reproductive success is low, i.e. pups rarely survive past 1 year (Boitani *et al.* 1995, 2006). The only acknowledged example of a true wild-living self-sustaining feral dog population occurred in the Galápagos; it was founded by a variety of breeds in the 1800s and persisted until the 1980s (Barnett 1986; Reponen *et al.* 2014). Despite there being a robust population of free-breeding or stray dogs associated with towns in the Galápagos, there was limited evidence of mixing between the free-breeding dog and feral dog populations based

on genetic analysis (Reponen *et al.* 2014). The Galápagos feral dog population was eradicated using 1080 poisoning of water and meat baits in the 1980s (Barnett 1986) and the population did not re-establish despite the presence of free-breeding and pet dogs in nearby human settlements.

Dingoes, including New Guinea singing dogs, form a discrete lineage from Eurasian and modern domestic dogs (Bergström *et al.* 2020; Surbakti *et al.* 2020; Cairns 2021). Their domestication status and taxonomic nomenclature is disputed, with some considering them *Canis familiaris*, a feral domestic dog (Jackson *et al.* 2017, 2019) and others calling them *Canis dingo*, a wild protodog (Crowther *et al.* 2014; Smith *et al.* 2019; Zhang *et al.* 2020). Globally, most free-breeding, village and breed dogs fall within the modern domestic dog lineage (Bergström *et al.* 2020; Surbakti *et al.* 2020; Cairns 2021). A close relationship between dingoes, Asian wolves, and some East Asian dogs has been observed, suggesting the dingoes' ancestor was of Asian origin (vonHoldt *et al.* 2010; Oskarsson *et al.* 2011; Freedman *et al.* 2014; Surbakti *et al.* 2020; Zhang *et al.* 2020; Cairns 2021). Dingoes and New Guinea singing dogs are examples of true wild-living dogs that are not reliant on artificial water or food sources.

Dingoes fill the ecological role of terrestrial apex predator on mainland Australia (Newsome *et al.* 2001; Letnic and Koch 2010; Letnic *et al.* 2012; Letnic *et al.* 2013; Marrant *et al.* 2017). Molecular dating indicates that dingoes and New Guinea singing dogs diverged from their ancestral population approximately 8000–12 000 years ago (Cairns and Wilton 2016; Cairns *et al.* 2017; Zhang *et al.* 2020). Dingoes remained reproductively isolated from domestic dogs until 1788.

There is rising global concern about the occurrence of hybridisation between wild and domestic canids or sympatric wild canids (Gopalakrishnan *et al.* 2018; Salvatori *et al.* 2020; vonHoldt and Aardema 2020). Hybridisation is the process of interbreeding between two species or varieties, generally F1 offspring would be referred to as hybrids and the offspring of F1 hybrids with animals from a parental species or variety would be called backcrosses. Interbreeding between varieties or species results in the exchange or mixing of genetic material (genetic admixture). The transfer of genetic material from one species into another through hybridisation and backcrossing is called introgression (Harrison and Larson 2014). The occurrence of genetic admixture may be modern or historical, and in some cases is the result of anthropogenic actions. In canids, the phenomenon of interspecific introgression has been observed between species such as grey wolves and dogs (Vilà and Wayne 1999; Anderson *et al.* 2009; vonHoldt *et al.* 2011, 2016; Schweizer *et al.* 2018), coyotes and wolves (Bohling *et al.* 2016; vonHoldt *et al.* 2016), red wolves and coyotes (Miller *et al.* 2003; Adams *et al.* 2007; Schmutz *et al.* 2007; Bohling and Waits 2015), jackals and dogs (Galov *et al.* 2015), dingoes and dogs (Newsome and Corbett 1985; Wilton 2001; Claridge *et al.* 2014; Stephens *et al.* 2015; Cairns *et al.* 2019).

One of the concerns raised by hybridisation is genetic swamping, whereby the genetic identity of a population is threatened by introgression of genes from another population or species. For example, the Scottish wildcat is threatened by hybridisation and subsequent introgression from domestic cats to the extent that contemporary wildcat populations exhibit extensive levels of domestic cat ancestry (Daniels *et al.* 1998; Kitchener *et al.* 2005; Macdonald *et al.* 2010). Indeed, most wildcats in Scotland carry significant domestic cat ancestry, and the occurrence of hybridisation is believed to have accelerated in the last 50–100 years (Mattucci *et al.* 2019; Senn *et al.* 2019). Similar concerns have been raised in Australia with many dingoes, particularly in southeastern Australia, exhibiting genetic, morphological or phenotypic evidence of domestic dog ancestry (Newsome and Corbett 1985; Daniels and Corbett 2003; Jones 2009; Stephens *et al.* 2015). There is also widespread concern that feral domestic dogs have established in the wild across Australia (Fleming *et al.* 2001; NSW Threatened Species Scientific Committee 2009).

Since the 1980s rising concern about domestic dog ancestry and the occurrence of hybridisation events has led to shifts in the management and conservation status of dingoes but also a duality in their identity. For example, in Victoria dingoes are now listed as a threatened species, but wild dogs are listed as a declared pest, where wild dogs are defined as feral or wild populations of dogs (*Canis familiaris*) and dingo \times dog hybrids (*Canis dingo* \times *Canis familiaris*) (DEPI 2013). In New South Wales (NSW), the listing of ‘predation and hybridisation by feral dogs (*Canis familiaris*)’ as a key threatening process

implies that dingoes are ‘under serious decline as a consequence of hybridisation’ (NSW Threatened Species Scientific Committee 2009). Indeed, there has been concern in NSW that feral dogs and dingo \times dog hybrids with low levels of dingo ancestry have essentially replaced dingoes in the wild (Claridge *et al.* 2014; Stephens *et al.* 2015). For example, the NSW key threatening process determination states that ‘due to the constant influx of Domestic Dogs into natural ecosystems, lasting eradication of even local populations of Feral Dogs is difficult’ (NSW Threatened Species Scientific Committee 2009). Accordingly, the term ‘wild dog’ is now used ubiquitously by state government and pest control organisations when communicating about management programs directed at controlling wild canids (Letnic 2012; Kreplins *et al.* 2019). However, it is clear from social studies of public perception and also expectations about the management of dingoes vs wild dogs, that the general public believe the term wild dog refers only to feral dogs and does not properly understand that the term wild dog is defined as including dingoes, dingo \times dog hybrids and feral dogs (van Eeden *et al.* 2020).

Before the 2000s a majority of our knowledge about dingo \times dog hybridisation was based on assessment of skull morphology and physical appearance (Newsome *et al.* 1980; Newsome and Corbett 1985; Jones 1990; Corbett 2001; Fleming *et al.* 2001). A microsatellite DNA test for assessing the ancestry of dingoes was developed in 1999 (Wilton *et al.* 1999; Wilton 2001) and has since become widely used by wildlife managers and conservation groups. Studies assessing the reliability of morphological, physical and genetic methods of ancestry assessment in dingoes have highlighted the importance of using genetic data (Elledge *et al.* 2008; Parr *et al.* 2016). Stephens *et al.* (2015) undertook microsatellite DNA testing of wild canids across Australia and identified regional patterns of domestic dog introgression in dingoes, with dog ancestry particularly prevalent in southeastern Australia. However, a major limitation of Stephens *et al.* (2015) is the low number of samples (95) from NSW. A more detailed study using the same genetic markers and significantly higher density of sampling across northeastern NSW identified several key hotspots of high dingo ancestry (Cairns *et al.* 2019). Their finding that a majority of wild dingoes in NSW were pure dingoes or carried more than 75% dingo ancestry is a stark contrast to the common public perception that feral dogs are widespread and established in the wild (NSW Threatened Species Scientific Committee 2009; Claridge *et al.* 2014; ABC Landline 2019). Here we collate and analyse genetic ancestry data based on microsatellite DNA testing from 5039 samples to examine the occurrence of feral dogs and F1 or F2 dingo \times dog hybrids across Australia. Critically, this study includes a broader set of samples from southeastern Australia including from southern NSW filling knowledge gaps about the ancestry and identity of wild canids in southeastern Australia. Spatial patterns of domestic dog introgression across Australia are also examined using the dataset. These data inform ongoing debate about the appropriate terminology and management of wild canids in Australia.

Methods and materials

DNA testing based on a widely used 23 microsatellite marker set was used to estimate dingo ancestry in Stephens *et al.* (2015),

Cairns *et al.* (2019) and a previously unpublished dataset (available in the BioStudies database under accession number S-BSST501 <https://www.ebi.ac.uk/biostudies/studies/S-BSST501>). Briefly, a panel of 23 microsatellites were amplified and genotyped in the wild canid samples based on the original methodology of Wilton (2001) and Elledge (2008). Ancestry modelling was performed in STRUCTURE with reference populations of known dingoes and dogs using the admixture and correlated allele frequency models. Cairns *et al.* (2019) and the unpublished dataset used a set of 50 dingoes and 66 mixed breed dogs as reference populations; to account for regional variation these analyses included a set of 13 wild dingoes from northern and western Australia. Stephens *et al.* (2015) used a set of 322 post-priori identified reference dingoes and 102 domestic dogs. In all three studies simulations were run with 200 000 iterations, a 20 000 iteration burn-in period and 10 replicates of each $K = 2$ was performed. Previously, modelling demonstrated that $K = 2$ was the appropriate model for assessing ancestry in Australian wild canids and modelling was run with the USEPOPINFO flag to allow population allele frequencies to be updated only from the defined reference population individuals (Stephens *et al.* 2015; Cairns *et al.* 2019). STRUCTURE reports estimated ancestry proportions (q-values) for each genetic cluster for each sample (Stephens *et al.* 2015; Cairns *et al.* 2019). In a $K = 2$ analysis each individual has a q-value for the domestic dog

cluster and for the dingo cluster. The dingo cluster q-value is used to define animals as either a pure dingo, probable dingo, dingo with $>75\%$ ancestry, dingo with $65\text{--}75\%$ ancestry, dingo with $50\text{--}65\%$ ancestry, feral dog hybrid or feral domestic dog (Table 1; Stephens *et al.* 2015; Cairns *et al.* 2019). We define feral dog hybrids with a q-value between 0.25 and 0.49 to be possible F1 or F2 dingo \times dog hybrids (Stephens *et al.* 2015; Cairns *et al.* 2019). An F1 hybrid is defined as the offspring of a dingo \times a dog and an F2 hybrid is the offspring of two F1 dingo \times dog hybrids.

Raw microsatellite data could not be compared because of slightly different microsatellite amplification conditions. To confirm that ancestry estimates were equivalent between Cairns *et al.* (2019) and Stephens *et al.* (2015), a set of 13 wild canids were genotyped and ancestry estimates calculated by both laboratories (Table 2).

Between the three-studies DNA ancestry estimates from 5039 wild canids collected by trappers, wildlife managers and government agencies across public and private lands in Australia were reported. A majority of the wild canids were trapped/shot as part of broadscale wild canid management to protect livestock from predation. Samples from the three datasets were collected between 1996 and 2014. We collated these DNA ancestry estimates (STRUCTURE q-values) together with location coordinates (Supplementary Material S1 dataset).

Table 1. Dingo purity categories and cut offs for average 3Q and STRUCTURE methods

Score	Category	Average 3Q ^A value and doglike allele cut offs	STRUCTURE ^B average q-value cut offs
1	Dingo 1 (dingo with no dog ancestry)	$3Q > 0.1$ and no doglike alleles	1.0–0.90
2	Dingo 2 (likely dingo with no dog ancestry)	$0.05 < 3Q < 0.1$ and ≤ 1 doglike alleles	0.89–0.80
3	Dingo with dog ancestry 1 ($>75\%$ dingo)	$0 < 3Q < 0.05$	0.79–0.70
4	Dingo with dog ancestry 2 ($65\text{--}75\%$ dingo)	$-0.1 < 3Q < 0$	0.69–0.60
5	Dingo with dog ancestry 3 ($50\text{--}64\%$ dingo)	$-0.25 < 3Q < -0.1$	0.59–0.50
6	Feral dog with dingo ancestry ($<50\%$ dingo)	$-0.5 < 3Q < -0.25$	0.49–0.25
7	Feral dog	$3Q < -0.5$	0.24–0.0

^AAccording to Wilton (2001) and Wilton *et al.* (1999).

^BAccording to Stephens *et al.* (2015).

Table 2. Comparison of STRUCTURE q-value ancestry estimates for 13 repeated samples from Stephens *et al.* (2015) and Cairns *et al.* (2019)

ID	Ancestry modelling from Cairns <i>et al.</i> (2019)		Ancestry modelling from Stephens <i>et al.</i> (2015)		Difference between Cairns <i>et al.</i> (2019) and Stephens <i>et al.</i> (2015) q-value	
	# markers	dingo ancestry (q-value)	ID	# markers		
W0021	23	0.87	wdi0053	23	0.83	0.04
W0022	22	0.88	wdi0163	23	0.89	-0.01
W0023	22	0.94	wdi0627	23	0.93	0.01
W0024	23	0.92	wdi0840	21	0.99	-0.07
W0025	22	0.89	wdi1736	23	0.96	-0.07
W0026	22	0.92	wdi1811	23	0.89	0.03
W0027	23	0.92	wdi1884	23	0.94	-0.02
W0028	22	0.77	wdi2397	23	0.77	0.00
W0029	22	0.96	di0910	23	0.92	0.04
W0030	23	0.89	di1050	23	0.9	-0.01
W0031	23	0.89	di1270	23	0.88	0.01
W0033	22	0.94	de013	22	0.94	0.00
W0034	23	0.92	de017	22	0.94	-0.02

The distribution of feral dogs with no dingo ancestry and possible F1 or F2 dingo \times dog hybrids was mapped using QGIS ver. 3.01 (QGIS 2020). We also explore the distribution of dingoes with varying degrees of dog ancestry across Australia as follows: the location of 5039 samples with DNA ancestry results were mapped in QGIS, a 0.3×0.3 degree hexagonal grid was drawn and the mean and median 'q-score' of the samples within each grid cell was calculated (using the join attributes by location tool). We also mapped the occurrence of feral dogs with no dingo ancestry and possible F1 or F2 dingo \times dog hybrids across Australia.

Results

We collated the ancestry results of 3641 samples from Stephens *et al.* (2015), 753 samples from Cairns *et al.* (2019) and 611

samples from the unpublished dataset. Ancestry estimates were consistent between Stephens *et al.* (2015) and Cairns *et al.* (2019) based on comparison of results for 13 repeated samples (Table 2). Out of 5039 samples that were DNA tested the breakdown of dingo ancestry results are as follows: 33.7% pure dingoes, 30.4% probable dingoes, 19.8% greater than 75% dingo ancestry, 11.7% greater than 65% dingo ancestry and 3.2% greater than 50% dingo ancestry (Table 3). Feral dogs and F1 or F2 dingo-dog hybrids were rarely collected from the wild and made up less than 1.2% of the wild canid population (Table 3). In total, only 31 feral dogs with no evidence of dingo ancestry were observed and 27 probable F1 or F2 dingo \times dog hybrids (q-value between 0.25 and 0.49) were identified in the sample. The occurrence of dog introgression differed between states (Fig. 1) and was more prevalent in southeastern Australia.

Table 3. Ancestry of 5039 wild canids across Australia according to STRUCTURE modelling by Stephens *et al.* (2015), Cairns *et al.* (2019) and this study

Category	WA	SA	NT	Qld	NSW	Vic.	ACT	Australia
Dingo 1 (dingo with no dog ancestry)	61.9% (1414)	34.5% (51)	88.2% (112)	21.9% (78)	2.2% (29)	1.1% (8)	5.8% (6)	33.7% (1698)
Dingo 2 (likely dingo with no dog ancestry)	35.0% (799)	56.8% (84)	10.2% (13)	46.6% (166)	23.8% (314)	16.8% (118)	35.6% (37)	30.4% (1531)
Dingo 1 and 2 (dingoes with no dog ancestry detected)	96.9% (2213)	91.2% (135)	98.4% (125)	68.5% (244)	26% (343)	17.9% (126)	41.3% (43)	64.1% (3229)
Dingo with dog ancestry 1 (>75% dingo)	2.3% (52)	8.8% (13)	0.8% (1)	23.6% (84)	39.5% (521)	40.5% (284)	41.3% (43)	19.8% (998)
Dingo with dog ancestry 2 (65–75% dingo)	0.02% (1)	0	0.8% (1)	4.8% (17)	25.6% (337)	32.1% (225)	10.6% (11)	11.7% (592)
Dingo with dog ancestry 3 (50–64% dingo)	0.02% (1)	0	0	2.2% (8)	7.4% (97)	7.7% (54)	1.9% (2)	3.2% (162)
Feral dog with dingo ancestry (<50% dingo)	0.2% (5)	0	0	0.6% (2)	0.9% (12)	1.1% (8)	0	0.5% (27)
Feral dog	0.5% (12)	0	0	0.3% (1)	0.6% (8)	0.7% (5)	4.8% (5)	0.6% (31)

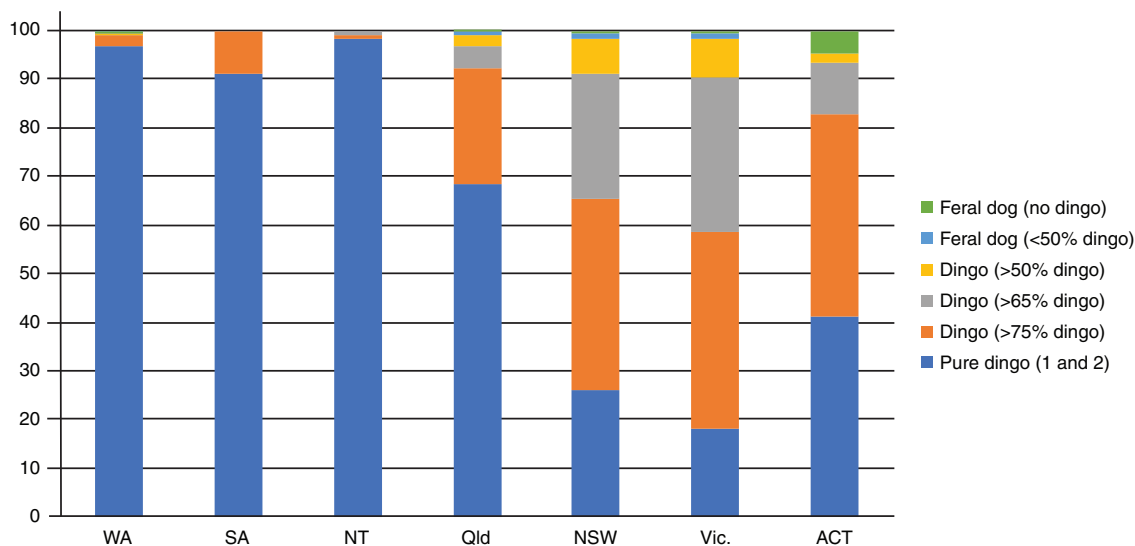


Fig. 1. Proportion of Australian wild canids that were pure dingoes, dingoes with domestic dog introgression, possible F1 dingo \times dog hybrids, and feral domestic dogs, by state.

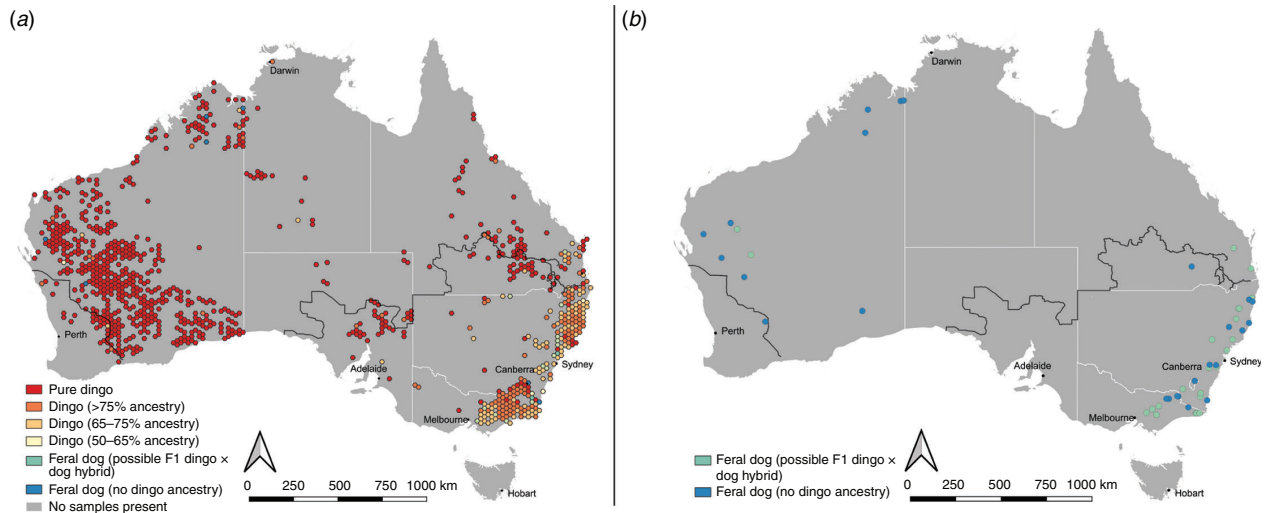


Fig. 2. Spatial patterns of dingo ancestry across Australia based on microsatellite DNA testing. (a) Median ancestry calculated for all samples within each hex grid. As the results were consistent between mean and median ancestry, the map depicting mean ancestry is presented in Supplementary Material S2. (b) Distribution of 31 feral domestic dogs and 27 feral dog hybrids (possible F1 or F2 dingo \times dog hybrids) across Australia. The positions of the national dingo exclusion fence and the Western Australian dingo exclusion fence are depicted by solid black lines.

Mapping of wild canid ancestry across Australia indicates that domestic dog introgression is largely restricted to southeastern Australia (Fig. 2; Supplementary Material S2). Across northern, central and western Australia, the dingo population is genetically intact, i.e. with limited or no domestic dog introgression. In southeastern Australia there are regions with dingo populations that are genetically intact (Fig. 2) and most populations maintain a dingo-dominant identity (median ancestry is greater than 75% dingo). Feral dogs were restricted mostly to southeastern Australia and were captured in relatively close proximity to human settlements (Fig. 2). Interestingly, no feral dogs were identified in central Australia.

Discussion

Extensive DNA testing across Australia detected very few feral dogs. Out of the 5039 wild canids that were sampled just 31 (0.61%) were inferred to be feral dogs (Table 3). Similarly, there were only 27 animals identified as likely F1 or F2 dingo \times dog hybrids. Contrary to widespread understanding, our results show that feral dogs and feral dog \times dingo hybrids were very rare across mainland Australia. This suggests that feral dogs have not established a self-sustaining population in the wild and that interbreeding between dingoes and dogs may occur infrequently.

Our finding that feral dogs were rare and are unlikely to have established a self-sustaining population on mainland Australia is backed up by the rarity of true feral dog populations globally. In Tasmania, there is a similar mix of European derived dog breeds to mainland Australia and a similar environment to southeastern Australia but there is little evidence that a feral dog population has become established (DPIPWE 2013). The rarity of true feral dogs both globally and in Australia suggests that domestic dogs have not retained the ability to persist in the wild in the absence of anthropogenic derived resources. Indeed, the Galápagos remains an isolated exemplar of domestic dogs establishing a feral population (Barnett 1986; Reponen *et al.* 2014). However, free breeding ('village or camp dogs') that rely on anthropogenic

food and water sources are of widespread occurrence in many regions of the world (Gompper 2013; Home *et al.* 2018). In Australia, free-breeding dogs are largely restricted to the fringes of Indigenous communities (Collins and Mills 2013; Newsome *et al.* 2013, 2014; Hudson *et al.* 2018; Brookes *et al.* 2020; Ma *et al.* 2020).

Our collation of DNA ancestry testing results suggests that most wild canids in Australia are pure dingoes (Fig. 1). Dog introgression is uncommon in Western Australia, the Northern Territory and South Australia, with more than of 90% of dingoes tested in those states being pure dingoes. Of the dingoes which did show domestic dog introgression, most carried more than 75% dingo ancestry. No F1 or F2 dingo \times dog hybrids were observed in the Northern Territory or South Australia. In Queensland, 68.5% of wild canids were pure dingoes and a majority of the remaining carried greater than 75% dingo ancestry. Only 7% of wild canids in Queensland were less than 65% dingo, and 0.8% were feral dogs or possible F1 or F2 dingo \times domestic dog hybrids.

As highlighted by Stephens *et al.* (2015), dog introgression is most widespread in southeastern Australia (Fig. 2). Despite this, the occurrence of possible F1 or F2 dingo \times dog hybrids was low in southeastern Australia, making up less than 2% of the total population in these regions. It may be that dingo \times dog hybridisation events are rare in the wild or that the survival of wild canids with less than 50% dingo ancestry is poor. The widespread introgression of dog genes in southeastern Australia may reflect backcrossing of F1 dingo \times dog hybrids, facilitating the spread of dog genes into the wider dingo population over long periods of time rather than a high occurrence of dingo \times dog hybridisation in the wild. As emphasised by Stephens *et al.* (2015), dog introgression in dingoes may be more common in southeastern Australia due to the earlier and more intensive European settlement, resulting in increased contact between domestic dogs and dingoes in these regions. Cairns *et al.* (2019) added that the widespread occurrence of intensive lethal control, particularly aerial baiting, may increase the likelihood of dingo \times dog hybridisation by

fracturing dingo social structures. Although this admixture from dogs into the dingo population is a concern, it is important to note that the dingo population still maintains a genetically and morphologically dingo dominant identity (Parr *et al.* 2016; Cairns *et al.* 2019; Crowther *et al.* 2020).

There are several key knowledge gaps about the identity of dingoes in Australia that bear consideration. First, we still lack information about the genetic identity of dingoes across large regions of Australia, particularly central and northern Australia (Fig. 2). Morphological research about the phenotype of dingoes with low levels of dog ancestry may assist on-ground management and conservation efforts, particularly if distinguishing features could be identified. Management plans should be careful not to assume that a given population does or does not carry domestic dog ancestry without the necessary genetic data. Despite this, the broad pattern of dingo ancestry across Australia suggests that in western, central and northern Australia, dog introgression is likely to be limited and feral dogs extremely rare. There is some concern that current microsatellite testing methods may be biased by regional genetic variation within dingoes (Cairns *et al.* 2017, 2019). It is important to consider that ancestry testing methods rely on the assumption that dingoes form a single homogeneous population (Elledge *et al.* 2008; Stephens *et al.* 2015; Cairns *et al.* 2019), an assumption we now know to be false (Cairns and Wilton 2016; Cairns *et al.* 2018; Koungoulos 2020). Robust dingo ancestry assessments require broad sampling across Australia to capture regional genetic variation (Cairns *et al.* 2019). Possibly some dingoes are misclassified as hybrids because of regional variation. As argued by Cairns *et al.* (2019), the type and number of genetic markers limits accuracy of genetic testing and estimates based on 23 microsatellites may not reflect genome-wide ancestry. Genome-wide SNP genotyping may offer a cost-effective and high-throughput alternative to address the limitations of microsatellite genetic testing in the future. Thus, we caution managers and researchers to evaluate the reliability of ancestry estimates and urge end-users to explore technology improvements for ancestry testing into the future.

There has been ongoing debate about the appropriate terminology for wild canids in Australia, i.e. dingo or wild dog (Letnic 2012). Kreplins *et al.* (2019) found that the term wild dog was more commonly used in studies funded by livestock industry organisations, compared to conservation-based studies which predominately used the term dingo. van Eeden *et al.* (2020) studied public understanding of the terms dingo and wild dog. They found that only 19.1% of respondents were aware that wild dog control programs targeted dingoes and furthermore respondents were generally not supportive of lethal dingo management. At the 2019 Royal Zoological Society of NSW symposium titled 'Dingo Dilemma' there was strong opposition to the term wild dog, with many participants asserting that the term wild dog disguises lethal management practices on dingoes from the public and hinders debate about dingo management in Australia (Dickman 2019). We add that the term wild dog does not accurately represent the ancestry of wild canids in Australia, particularly as the dominant genetic identity is dingo and feral domestic dogs are virtually absent from the landscape (Fig. 2). Although there are dingoes carrying domestic dog ancestry, particularly in southeastern Australia, there are few F1 or F2

hybrids. The term hybrid generally refers to only F1 crosses, i.e. the offspring of a dingo and domestic dog but F2 animals which are the offspring of two F1 hybrids may also be referred to as hybrids (Hansson *et al.* 2012). We suggest that dingoes that carry domestic dog ancestry but are not F1/F2 hybrids should be referred to as dingo backcrosses or admixed dingoes.

The finding that feral dogs have not established populations has implications for the management of wild canids in Australia. Dingoes and stray or roaming domestic dogs can cause serious impacts for livestock graziers (Fleming *et al.* 2001). Management of feral, stray or roaming domestic dogs should focus on responsible pet ownership including spaying and neutering of pet animals, keeping pet and working dogs under control and confined during the night. As feral dogs do not represent a significant portion of the wild canid population, it should be clear in legislation and policy that lethal control programs are targeting dingoes (including admixed dingoes) rather than feral dogs. Although hybridisation is a concern in southeastern Australia (Stephens *et al.* 2015; Cairns *et al.* 2019), responsible pet ownership and continued exclusion of domestic dogs from National Parks and conservation areas can reduce the occurrence of future dingo \times dog hybridisation events. The low number of F1 or F2 hybrids detected indicates that dingo \times dog hybridisation events are uncommon. Despite historical domestic dog introgression, the dingo population maintains a dingo dominant identity, even in southeastern Australia (Fig. 1). It is possible that widespread lethal control programs have increased the likelihood of dingo \times dog hybridisation events and facilitating the spread of introgressed dog genes into the wider dingo population. Lethal control has been identified as a factor increasing the likelihood of interspecific hybridisation in other wild canids including coyotes and red wolves by fracturing social structures and altering demographic patterns (Bohling and Waits 2015). Management programs that maintain stable dingo social structures present a better balance to managing the risks to stock predation and dingo conservation (Allen 2014, 2015; Wallach *et al.* 2017). Additionally, lethal control programs should not occur during the dingo breeding season (winter) as this may facilitate dingo \times dog hybridisation events, by fracturing pack structures and reducing the availability of dingo mates. Baiting has also been linked to an increase in the body-size of dingoes, possibly increasing their impact on livestock (Letnic and Crowther 2020).

The lack of public engagement and debate on dingo conservation on private and public lands in Australia has allowed agricultural industry priorities to dominate government policy and decision making on dingo management. Social science studies show the general public are largely unaware of the current threats wild dog control programs have on the remaining dingo populations in Australia (van Eeden *et al.* 2020). The lack of engagement by the public on dingo conservation can in part be attributed to the renaming of the Australian dingo as a wild dog in government literature and allowing the general misunderstanding that all wild dogs are feral dogs to persist. We propose that a terminology shift is required to reflect the identity of wild canids in Australia: the term dingo needs to be reinstated because genetic testing demonstrates that a majority of animals are of high dingo ancestry and feral dogs are virtually absent. The term wild dog does not reflect the ancestry of wild canids in Australia and is poorly understood by the public, it should be retired from use.

Conflicts of interest

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