



## A genealogical survey of Australian registered dog breeds

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### ABSTRACT

Breeding practices were analysed for 32 registered dog breeds representing very small registries (120 Central Asian shepherd dogs) through to very large registries (252,521 German shepherd dogs) in Australia. The vast majority (91%) of registered kennels in Australia that were sampled did not regularly employ either close breeding or popular sire usage in their kennels and the weighted mean inbreeding coefficient of Australian pedigree dogs was <5%. Australian breed mean inbreeding coefficients ranged from 0% (Central Asian shepherd dog) to 10.1% (Bichon Frise). Breed effective population sizes ranged from 26 (Ibizan hound) to 1090 (Golden retriever), comparable with other species of domesticated animals.

The relatively low levels of inbreeding suggest that pedigree dog disorders are unlikely to arise frequently from the use of popular sires or close breeding in Australian registered dog breeds. It is possible that deleterious allele fixation might be driven by founder effects, genetic drift or adverse selection practices, which were not assessed in this analysis. European popular sire definitions should be revisited for rare breeds.

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### Introduction

The pedigree dog community recently has been criticised in the media for using breeding practices unfavourable for population health, most notably selection for traits with adverse effects on health, close inbreeding and heavy use of popular sires. The actual application of these practices within breed registries currently is not well understood and allegations frequently are based on hearsay and presumption rather than on scientific analysis. To better understand the actual nature of pedigree dog population structure on a whole-population basis, we examined data records for a representative sample of recognised pedigree breed populations in Australia.

Using complete national pedigree data supplied by the Australian National Kennel Council (ANKC), this study examined the levels of inbreeding and popular sire use in 32 Australian dog breeding populations with different registry sizes. Dogs registered with the 205 breeds in the ANKC are estimated to account for 20% of puppies homed in Australia annually (ANKC, 2011). By studying both large and small populations of dogs, we can observe the relationships between base population size and inbreeding risk in real populations. The evaluation of data over the entire registration histories of breeds shows inbreeding trends over time.

We also assessed the relative application of risk practices between kennels with different levels of genetic contribution to these breeds. Kennels were separated into those that contribute more than 50 offspring to the breed (major kennels) and those with fewer than 50 registered offspring (minor kennels). The objective was to separate kennel behaviour according to commitment to breeding and genetic influence within the breeds and population-size cohorts of breeds examined. Understanding the behaviour of breeds and kennels according to simple discriminators (such as relative contributions to registrations) will enable better targeting of education to improve animal welfare practices.

### Materials and methods

Pedigree information for 32 Australian dog breeds (Table 1) was provided by the ANKC. The breeds were chosen as representative of the entire range of the number of registrations of Australian breeds, from very small registries to very large registries. Data were filtered to remove duplicate individuals and those with missing information. Animals that were recorded as their own ancestor or that were recorded as both dam and sire were omitted from the analysis. The pedigree data for analysed breeds commenced in years 1943 (Labrador retriever) to 1990 (Central Asian shepherd dog). The final represented year was 2008 or 2009 for all breeds. After filtering, the total number of registered dogs represented in the data was 1,234,475. The genders of animals were determined only from their positions in the pedigree and hence animals not used for breeding were recorded as having unknown gender.

Data for each of the 32 observed breeds, including the year from which data were available, the breed size grouping and the number of observed animals in each breed, are presented in Table 1. Breeds were divided into those with registration

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**Table 1**

List of dog breeds in alphabetical order, the year from which data were available, analysis group and the total number of animals in each breed.

Breed	Data available from	Analysis group	Registered animals
Australian cattle dog	1954	Large registry	74,290
Australian terrier	1955	Medium registry	22,460
Bichon Frise	1971	Medium registry	13,790
Border collie	1954	Large registry	68,535
Bouvier des Flandres	1975	Small registry	1769
Boxer	1955	Large registry	75,316
British bulldog	1956	Medium registry	16,207
Cavalier King Charles spaniel	1958	Large registry	77,108
Central Asian shepherd dog	1990	Small registry	120
English cocker spaniel	1952	Large registry	78,902
Collie (smooth)	1972	Small registry	1534
Dachshund (miniature wire-haired)	1962	Small registry	1991
Dandie Dinmont terrier	1963	Small registry	445
Fox terrier (smooth)	1955	Medium registry	19,302
German shepherd dog	1959	Very large registry	252,521
Golden retriever	1952	Very large registry	98,542
Harrier	1971	Small registry	134
Ibizan hound	1983	Small registry	130
Italian Spinone	1985	Small registry	190
Labrador retriever	1943	Very large registry	135,550
Lakeland terrier	1957	Small registry	1644
Leonberger	1988	Small registry	512
Nova Scotia duck tolling retriever	1989	Small registry	901
Papillon	1956	Medium registry	17,157
Pekingese	1958	Large registry	34,325
Polish lowland sheepdog	1984	Small registry	166
Poodle (miniature)	1954	Large registry	31,441
Rottweiler	1960	Very large registry	98,727
Samoyed	1955	Medium registry	20,290
Skye terrier	1958	Small registry	1739
Staffordshire bull terrier	1957	Very large registry	88,589
Sussex spaniel	1979	Small registry	148
Total			1,234,475

numbers <2000, 2001–25,000, 25,001–80,000 and >80,000, here named as 'small registries', 'medium registries', 'large registries' and 'very large registries', respectively.

In the genealogical analysis, animals with known parents born from 2000 to 2009 inclusive were used as the reference population. The completeness of pedigree information was determined by complete equivalent generations (EqG) in the reference population. Founders ( $f$ ) were defined as animals with unknown parents (typically imported dogs with known parentage but outside of the Australian registry) contributing to the gene pool in the reference population. To account for differing relative contributions of each true founder, the effective number of founders ( $f_e$ ) was determined based on the concept of 'equivalent founders' (Lacy, 1989) using the algorithm of Boichard et al. (1997), as instituted in the programme prob\_orig in the Pedig package (Boichard, 2002).

The effective population size ( $N_e$ ) was estimated from the rate of inbreeding per generation, using the formula  $N_e = 1/2\Delta F$  (Wright, 1923; Falconer and Mackay, 1996).  $\Delta F$  was calculated following Maki (2010) as  $\Delta F = (b * I) / (1 - (Fly - b * I))$ , where 'b' is the regression coefficient of the average inbreeding coefficient on year of birth, 'I' is the average generation interval and 'Fly' is the average inbreeding coefficient in the last year of birth available for the study. An inbreeding coefficient was calculated for each animal, including those in the reference population, by the method of Meuwissen and Luo (1992), using CFC software (Sargolzaei et al., 2006). The purpose of including the reference population was to see if there were recent changes in inbreeding trend.

Pedig programmes ngen, segreg and intgen were used to calculate complete equivalent generations (EqG), the number of founder genome equivalents ( $N_g$ ) and generation interval ( $I$ ), respectively. The Pedig programme prob\_orig was used to calculate the total number of founders ( $f$ ), the effective number of founders ( $f_e$ ) and the effective number of ancestors ( $f_a$ ), the latter being taken as the lower boundary of the marginally contributing ancestors after 100 iterations.  $N_g$  was calculated using 500 iterations.

Kennels were divided into major kennels (registering 50 or more progeny) or minor kennels (registering <50 progeny). Kennels were defined in the data by the use of a kennel prefix. The purpose of this comparison was to differentiate breeders demonstrating a longer-term influence on breed genetics from those breeding few litters. We were interested to know whether the major and minor kennels behave differently with respect to breeding practices, including the use of close breeding and popular sires. For this purpose, we defined kennels as being 'close-breeding' kennels when more than 50% of the progeny born to the kennel had inbreeding coefficients >10%. We defined a kennel as a regular user of popular sires when

>50% of progeny in the kennel were sired by dogs that had in turn sired >5% of progeny registered in the breed (over all kennels of that breed) in the previous 5 years (Fédération Cynologique Internationale [FCI], 2011). Restricted maximum likelihood (Genstat; Payne et al., 2008) was used to assess the significance of fixed effects (breed, breed size, kennel type, close-breeding and popular sire usage) in the kennel behaviour analysis.

## Results

Pedigree information, determined by the number of generation equivalents (EqG), varied among breeds, ranging from almost no information content to highly informative pedigrees (Table 2). Among the breeds studied, the Central Asian shepherd dog, Polish lowland sheepdog and Sussex spaniel had values of EqG < 3 and so provided the poorest pedigree information. The Australian cattle dog, Australian terrier and Bichon Frise breeds had EqG values >9 and so provided the richest pedigrees for analysis. Two of the most informative breeds (Australian cattle dog and Australian terrier) were derived in Australia.

Estimated effective population sizes ( $N_e$ ) ranged from 26 (Ibizan hound) to 1090 (Golden retriever). The number of observed founders ( $f$ ) ranged from 12 (Central Asian shepherd dog and Harrier) to 1893 (German shepherd dog), while the number of effective founders ( $f_e$ ) ranged from 8 (Harrier and Ibizan hound) to 258 (Cavalier King Charles spaniel) (Table 2). Results comparable to those of previous studies were observed for effective number of ancestors ( $f_a$ ) and the effective number of founder genomes ( $N_g$ ) (Leroy et al., 2006; Maki, 2010).

As expected, the number of observed founders ( $f$ ) was greater than the number of effective founders ( $f_e$ ) in all breeds, with the latter term indicating the number of founders that could account for the observed genetic diversity if each founder contributed equally. The ratio ( $f_e/f$ ) is relatively high (mean 0.5) in 'small regis-

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