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GEOGRAPHIC PATTERNS OF GENETIC VARIATION IN BRUSHTAIL POSSUMS *TRICHOSURUS VULPECULA AND* IMPLICATIONS FOR PEST CONTROL

Summary: Two morphological types of brushtail possum *(Trichosurus vulpecula)* were introduced to New Zealand: smaller, grey possums from mainland southeastern Australia, and larger, black possums from Tasmania. Analysis of patterns of allozyme variation and allele frequencies of present-day possum populations in New Zealand and southeastern Australia indicates that populations comprised predominantly of black possums remain genetically similar to possums in Tasmania, whereas predominantly grey populations are genetically closer to Victorian and New South Wales possums. The distribution of possums in New Zealand can be accounted for at least partly by selection of stock types with respect to climate. Genetic differences between populations may have important implications for the control of possums, because Tasmanian possums have a greater resistance than mainland southeastern Australian possums to 1080 poison (sodium monotluoroacetate), which is commonly used to control possums in New Zealand.

Keywords: Genetic variation; allozyme electrophoresis; brushtail possum; *Trichosurus vulpecula;* introduced species; pest control; selection.

Introduction

Studies of the genetics of introduced species are often limited by lack of an historical context in which to interpret patterns of genetic change, because the origins, genetics, and history of introduced stock are seldom known. The introduction of the brushtail possum *(Trichosurus vulpecula* Kerr: Marsupialia) to New Zealand, on the other hand, has been relatively well documented, as has its morphology, distribution, and ecology (Morgan and Sinclair, 1983). These factors provide reference points for evaluating patterns of genetic variation, gene frequencies, and genetic change.

More than 200 possums were imported to New Zealand from Australia between 1837 and 1924 in order to establish a fur industry (Pracy, 1962). Although the possum is commercially important for its fur in New Zealand (Pracy, 1981), it is also a major pest. Possums cause damage to native and exotic forests (Bathgate, 1973), erosion control plantings (Jolly and Spurr, 1981), crops (Spurr and Jolly, 1981), pasture (Gilmore, 1965), orchards (Anon, 1968), and nectar sources (Anon, 1973), as well as being a reservoir for bovine tuberculosis (Ekdahl, Smith and Money,. 1970). The significance of the possum as a competitor of native birds has also been a cause for concern (Leathwick, Hay and Fitzgerald, 1983; Fitzgerald, 1984; Wardle, 1984).

The possums imported to New Zealand came from Victoria, New South Wales, and Tasmania (Pracy, 1962). These Australian populations differ in both the amount of heterozygosity and in the number of variable loci (Triggs, 1987). A Tasmanian

population had an overall observed heterozygosity of 0.029 and was fixed for the common allele at three loci which were variable in populations from New South Wales and Victoria. A Victorian population had a heterozygosity of 0.040 and was fixed at two loci variable in Tasmania and New South Wales, whereas a New South Wales population had a heterozygosity of 0.048 (Triggs, 1987). Thus the level of genetic (allozymic) variation in New Zealand populations should depend on the degree of mixing of these Australian stocks, as well as on any changes that have occurred during colonization.

According to historical records (Pracy, 1962), possums imported from mainland Australia *(Trichosurus vulpecula vulpecula)* were small and grey, whereas the Tasmanian stock *(Trichosurus vulpecula fuliginosa),* although probably polymorphic for colour (Kean, 1971), was larger and black. In New Zealand, possums can be classified as either 'black' or 'grey', although a range of shades occurs from black through brown, red-brown, and grey-brown to silver-grey. Mixed populations, having both grey and black individuals, occur in many parts of New Zealand, but the distribution of coat colours is not even in different parts of the country (Wodzicki, 1950; Kean, 1971). Some areas, such as Westland, have almost all black possums, whereas other areas, such as Northland, have only grey possums. Body size also varies between areas (Yom Tov, Green and Coleman, 1986; our study).

This mosaic of coat colours and body size may be the result of a) a non-random pattern of introduction

coupled with a subsequent lack of natural dispersal over long distances, b) a haphazard pattern of liberations followed by selection, c) random chance, or d) most likely, a combination of processes. There is some evidence that predominantly one colour morph was liberated in certain areas. Most possums liberated in Westland, for example, were black (Pracy, 1962). However, liberation records reveal that both black and grey possums were introduced to most areas of New Zealand (Pracy, 1962), suggesting that the pattern of distribution of possums in New Zealand has resulted at least partly from selection.

The main aim of our study was to use allozyme electrophoresis to determine whether the non-random distribution of colour morphs in New Zealand is accompanied by an associated pattern of allelic distribution which can be related to the different Australian stocks. If coat colour does reflect the origins of New Zealand populations with respect to Tasmanian and mainland Australian stocks, then two predictions' can be made: (1) that the amount of variation (heterozygosity and polymorphism) in each New Zealand population depends on the proportions of the two colour morphs in the population (in particular, predominantly black populations should have a lower level of variation than grey populations and mixed-colour populations a higher level of variation than non-mixed populations); (2) that allelic frequencies in predominantly black New Zealand populations are most similar to those of Tasmanian populations, whereas allele frequencies in

predominantly grey New Zealand populations are most similar to those of mainland Australian populations. A non-random distribution of Australian stocks in New Zealand may have implications for pest control, as Tasmanian possums are more resistant to 1080 poison at low temperatures than mainland Australian (New South Wales) possums (McIlroy, 1983). The analysis is complicated by any genetic changes that have accompanied the colonization of New Zealand by small founder populations (Triggs, 1987) and by the untestable assumption that the Australian populations that we sampled accurately estimate the allele frequencies of possums originally exported to New Zealand.

Methods

Samples of liver, muscle, and blood were collected from possums in four locations in southeastern Australia and 10 locations on New Zealand's North, South and Stewart Islands (Table 1). The sample from South Australia was collected for use as an outgroup, because possums are not known to have been exported to New Zealand from South Australia. Specimens were frozen on dry ice or in liquid nitrogen in the field and stored in an ultra-cold (-80°C) freezer for the duration of the study. For electrophoretic analysis small sub-samples of tissues were macerated in an equal volume of distilled water, then centrifuged at 2000 rpm for 5 minutes. The resulting supernatant fractions were subjected to starch-gel electrophoresis,

Table 1: *Sampling locations, sample sizes, and meteorological data (mean annual rainfall MAR and mean annual temperature MA T). Meteorological data are from New Zealand Meteorological Service Misc. Publ. 177 (1981) or the Tasmanian Year Book (1985).*Sample collected by Ecology Division, DSIR.*

Sample No.	Site	Location		Sample size	MAR (mm)	MAT (°C)
		Lat (°S)	Long (°E)			
Australia						
1.	Healesville, VIC	38° 01'	145° 08'	42	661	14.9
2.	Stonehenge, TAS	42° 21'	147° 42'	53	624	12.5
3.	Sydney, NSW	35° 55'	151° 13'	14	1215	17.5
4.	Adelaide, SA	34° 35'	139° 31'	22	531	17.1
New Zealand						
5.	Waipoua	35° 41'	173° 32'	50	1651	14.1
6.	Motu	38° 07'	177° 38'	36	1330	13.4
7.	Taupo	38° 34'	176° 10'	51	1178	12.0
8.	Wanganui	39° 57'	175° 16'	50	906	13.6
9.	Pararaki	41° 32'	175° 27'	50	1044	13.9
10.	Pounui	41° 12'	175° 20'	20	1109	12.7
11.	Woottons*	41° 24'	174° 56'	133	1804	12.3
12.	Haupiri	42° 35'	171° 49'	44	5042	9.9
13.	Mt Thomas	43° 09'	172° 19'	38	825	11.4
14.	Stewart I.	47° 00'	168° 12'	47	1467	10.6

using gels made of 14% Electrostarch (Madison, Wisconsin, lot no. 392) and modifications of the methods of Selander *et al*. (1971), Harris and Hopkinson (1976), and Allendorf *et al*. (1977), as described in Triggs (1987). The recommendations of Murphy and Crabtree (1985) were followed in labelling enzymes, genetic loci, and alleles.

For each population, the level of genetic variation was assessed by degree of polymorphism (P) and observed heterozygosity (H). Genetic differentiation between populations was estimated using Nei's (1978) unbiased genetic distance (D); populations were then clustered using the UPGMA algorithm (Sneath and Sokal, 1973). All data were analysed using the BIOSYS-l programme (Swofford and Selander, 1981).

Correlation coefficients, r, were used to determine the relationships between allele frequency at each locus (Table 2), coat colour (given by "% black" - the percentage of black possums in a population; Table 3), mean adult body length and weight in each population (Table 3), latitude (Table 1), and climate (mean annual rainfall and mean annual temperature; Table 1).

Results

Allozyme loci

A total of 25 enzymes and 7 general proteins (including haemoglobin), encoding 45 loci, was resolved: aconitase (Acon 1-2, E.C. no. 3.1.3.2), adenylate kinase (Ak, 2.7.4.3), B-galactosidase (B-Gal, 3.2.1.23), creatine kinase (Ck, 2.7.3.2), diaphorase (Dia, 1.6.2.2), erythrocyte acid phosphatase (Eap, 3.1.3.2), esterase (list 1-6, 3.1.1.1), general proteins (Gp 1-6), glucose-6-phosphate dehydrogenase (Gd, 1.1.1.49), glucose phosphate isomerase (Gpi, 5.3.1.9), glucuronidase (Gus, 3.2.1.31), glutamate dehydrogenase (Glud, 1.4.1.3), glutamate oxaloacetate transaminase (Got 1-2, 2.6.1.1), glycerol-3-phosphate dehydrogenase (Gpd, 1.1.1.8), haemoglobin (Hb), isocitrate dehydrogenase (Icd 1-2, 1.1.1.42), lactate dehydrogenase (Ldh 1-2, 1.1.1.27), malate dehydrogenase (Mdh 1-2, 1.1.1.37), malic enzyme (Me, 1.1.1.40), mannose phosphate isomerase (Mpi, 5.3.1.8), peptidase (Pep 1-2, 3.4.11), phosphogluconate dehydrogenase (Pgd, 1.1.1.44), phosphoglucomutase (Pgm 1-2, 2.7.5.3), purine

Table 2: *Allele frequencies at polymorphic loci, % polymorphic loci (P), and observed heterozygosity (H) in southeastern Australian and New Zealand populations of* Trichosurus vulpecula. *(Populations numbered as in Table 1.) N = sample size.*

Locus and allele		Population						
		1	2	3	4	5	6	7
2N		84	106	28	44	100	72	102
Ck-1	a	0.524	1.000	0.571	0.438	-	-	1.000
	b	0.476	0.000	0.429	0.562	-	-	0.000
Est-1	a	0.575	0.794	0.867	0.119	0.575	0.708	0.990
	b	0.375	0.196	0.133	0.595	0.417	0.292	0.010
	c	0.050	0.010	0.000	0.286	0.008	0.000	0.000
Est-5	a	0.457	0.317	0.458	0.250	0.742	-	0.737
	b	0.543	0.683	0.542	0.750	0.258	-	0.263
Got-1	a	0.975	1.000	0.633	0.950	0.784	1.000	0.882
	b	0.025	0.000	0.367	0.050	0.216	0.000	0.118
Icd-2	a	0.905	1.000	0.948	0.750	-	0.956	0.918
	b	0.000	0.000	0.052	0.000	-	0.015	0.051
	c	0.095	0.000	0.000	0.250	-	0.029	0.031
Me-1	a	0.833	0.948	0.955	0.978	0.847	0.917	0.859
	b	0.167	0.052	0.000	0.022	0.153	0.041	0.130
	c	0.000	0.000	0.045	0.000	0.000	0.042	0.011
Pep-1	a	1.000	0.755	0.923	0.727	0.817	0.851	0.784
	b	0.000	0.245	0.077	0.273	0.183	0.149	0.216
Pgd-1	a	1.000	0.906	0.909	1.000	1.000	0.894	1.000
	b	0.000	0.094	0.091	0.000	0.000	0.106	0.000
Pgm-1	a	1.000	1.000	1.000	0.886	1.000	1.000	1.000
	b	0.000	.000	0.000	0.114	0.000	0.000	0.000
P		0.133	0.111	0.178	0.178	0.143	0.143	0.133
H		0.040	0.029	0.048	0.059	0.047	0.029	0.028

Table 2: *Continued*.

Locus and allele		Population						
		8	9	10	11	12	13	14
2N		100	100	40	266	88	76	94
Ck-1	a	1.000	0.633	0.625	0.701	1.000	0.844	1.000
	b	0.000	0.367	0.375	0.299	0.000	0.156	0.000
Est-1	a	0.674	0.738	0.467	0.602	0.833	0.684	0.864
	b	0.326	0.214	0.300	0.303	0.167	0.276	0.136
	c	0.000	0.048	0.233	0.095	0.000	0.040	0.000
Est-5	a	0.956	0.727	0.567	0.534	0.608	-	0.458
	b	0.044	0.273	0.433	0.466	0.392	-	0.542
Got-1	a	0.970	0.590	0.842	0.795	1.000	0.961	1.000
	b	0.030	0.410	0.158	0.205	0.000	0.039	0.000
Icd-2	a	0.560	0.883	0.928	0.844	0.944	0.750	0.968
	b	0.010	0.000	0.024	0.066	0.056	0.250	0.032
	c	0.430	0.117	0.048	0.090	0.000	0.000	0.000
Me-1	a	0.663	0.977	0.895	0.891	0.900	0.961	0.862
	b	0.304	0.023	0.079	0.073	0.067	0.000	0.138
	c	0.033	0.000	0.026	0.036	0.033	0.039	0.000
Pep-1	a	0.980	1.000	0.568	0.783	0.982	1.000	0.630
	b	0.020	0.000	0.432	0.217	0.018	0.000	0.370
Pgd-1	a	0.980	0.977	0.857	0.912	0.862	0.974	0.734
	b	0.020	0.023	0.143	0.088	0.138	0.026	0.266
Pgm-1	a	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	b	0.000	0.000	0.000	0.000	0.000	0.000	0.000
P		0.156	0.178	0.178	0.178	0.133	0.171	0.133
H		0.032	0.043	0.065	0.056	0.027	0.039	0.040

Table 3: *Morphological characteristics of New Zealand populations of brush tail possum. Equal numbers of adult females and adult males were sampled.*

Population	% Black individuals	Mean total body length (mm)	Mean Weight (g)
Waipoua	0	758	2300
Motu	66	844	3380
Taupo	61	878	3320
Wanganui	2	757	2410
Pararaki	39	765	2260
Pounui	32	807	2630
Woo lions	34	785	2310
Haupiri	100	814	3060
Mt Thomas	53	813	2530
Stewart I.	73	870	3550

nucleoside phosphorylase (Np, 2.4.2.1), sorbitol dehydrogenase (Sordh, 1.1.1.14), superoxide dismutase (Sod 1-2, 1.15.1.1), and unidentified dehydrogenase ('Udh').

Allozyme variation in New Zealand populations
No alleles were detected in New Zealand that were not found in at least one Australian population (Table 2).

Mean estimates of allozyme variation in New Zealand (P = 0.155, H = 0.041) were slightly, but not significantly, greater than those of the Australian stock populations (P = 0.141, H = 0.039; Table 4). Comparisons of polymorphism and heterozygosity among Australian and New Zealand populations (Table 4) suggest that the amount of variation in New Zealand depends to some extent on the proportion of each colour morph in the population. New Zealand populations with more than 50% black individuals had a significantly lower level of variation than predominantly grey populations (t = 2.37, p < 0.05 for P; t = 3.4, p < 0.01 for H), in parallel with the lower level of variation in Tasmanian compared to mainland Australian populations (Table 4). Mixed colour populations in New Zealand had a higher level of variation than non-mixed populations, as expected from the mixing of stocks fixed for different loci, although the difference in variation was not significant between mixed and non-mixed populations (t = 2.07, P = 0.07 for P; t = 1.30, p = 0.2 for H). The difference in variation between mixed New Zealand

Table 4: *Mean and standard deviation of polymorphism (P) and heterozygosity (H) for brush tail possum populations of similar geographic origin or coat colour, and for Australian stocks (.*excludes Adelaide sample).*

Populations	n	P	Std Dev.	H	Std Dev.
Australian stocks*	3	0.141	0.034	0.039	0.012
Mainland Australia*	2	0.156	0.032	0.044	0.006
Tasmania	1	0.111	-	0.029	-
New Zealand, all populations	10	0.155	0.020	0.041	0.013
New Zealand mixed colour (32-66% black possums)	6	0.164	0.020	0.043	0.015
New Zealand non-mixed (0-2%, 73-100% black possums)	4	0.141	0.011	0.037	0.008
New Zealand grey (0-39% black possums)	5	0.167	0.016	0.049	0.013
New Zealand black (53-100% black possums)	5	0.143	0.016	0.033	0.006

and Australian stock populations was not significant ($t = 1.31$, $p = 0.2$ for P; $t = 0.4$, $p = 0.5$ for H) (Table 4).

The level of variation was not entirely consistent among New Zealand populations with similar proportions of each colour morpho For example, Waipoua 0% black) had a 50% greater heterozygosity than Wanganui (2% black), presumably as a result of genetic drift in small founder populations. Changes in levels of variation associated with colonization are discussed by Triggs (1987).

Genetic relationships among New Zealand and Australian populations

Two main clusters of populations were identified by phenetic clustering, based on Nei's D (Fig. 1). New Zealand populations with a high proportion of grey possums (0-53% black) and grey Australian populations were closely associated, as were predominantly black New Zealand populations (61-100% black) and the Tasmanian population. The inclusion of New South Wales in the former cluster may be due to either the small genetic distance
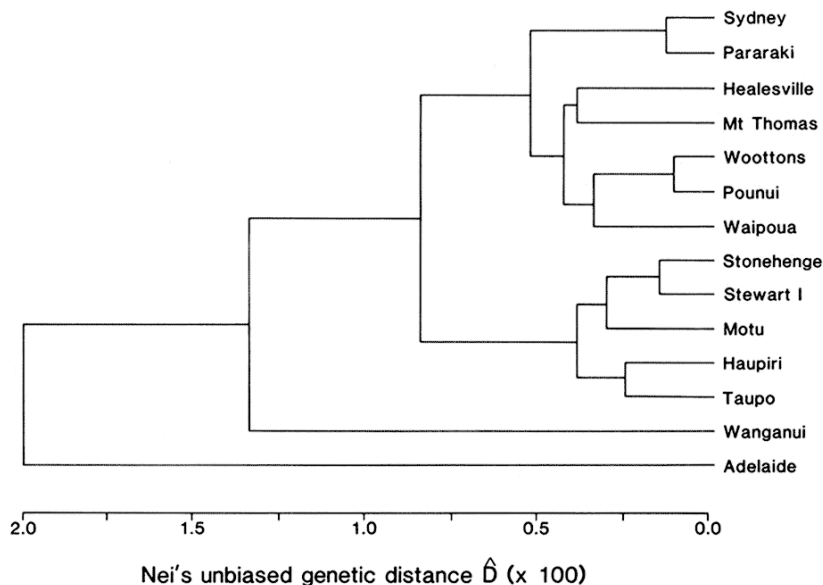

Figure 1: *UPGMA phenogram of genetic relationships among southeastern Australian and New Zealand populations of brushtail possum.*

between Victoria and New South Wales or confirmation that some possums were imported from New South Wales. The Me-1(c) allele found in many New Zealand populations was also found in 'possums from New South Wales but not in the sample from Victoria, although it is also possible that this allele was present at low frequency in Victoria. However, the greater genetic similarity of New Zealand grey populations to Victoria (Fig. 1) and the presence in New Zealand of several alleles not found in the New South Wales sample [Est-1(c), Idh-2(c) and Me-1(b)] suggest the predominance of Victorian stock in New Zealand.

South Australian possums did not closely resemble those from New Zealand. This result was expected, because no possums were imported to New Zealand from South Australia. One population, Wanganui, did not fall into either cluster, possibly due to genetic drift, if the Wanganui population had a small founder size.

Although the genetic distances involved are very small (the 'black/grey' separation occurs at D = 0.008), our analysis suggests that the origins of New Zealand populations are still reflected in their allele frequencies and may be roughly estimated by coat colour. The relationship between coat colour in New Zealand populations and position within the genetic cluster is by no means perfect. Presumably random genetic drift in the relatively small founder populations has led to changes in gene frequency in many populations. However, the general pattern that emerges, grouping predominantly black populations with the Tasmanian sample and grey with mainland Australia, is unlikely to have arisen by chance (that is, by random drift). The implication is that either interbreeding of stock types for 150 years has been insufficient to establish a panmictic unit, or that selection has acted differentially on stock types to produce genetic structuring of allozymes and colour types.

Selection as an explanation for the mosaic of colour morph distribution in New Zealand is supported by evidence of correlations between coat colour (% black possums in a population), allele frequencies, body size and weight, and climatic variables. A significant correlation (r = 0.642, p < 0.01) exists between coat colour and rainfall in New Zealand (R.E. Brockie, pers. comm.). Data from our 10 mainland New Zealand study areas showed a similar, although non-significant, correlation between colour (% black) and rainfall (r = 0.58, P < 0.10). A significant correlation in our data was found between

colour and mean daily temperature (r = -0.77, p < 0.01), but not with latitude (r = 0.48, p > 0.05).

Several significant correlations were also found between allele frequencies, coat colour, latitude and climate in New Zealand. A total of 56 correlations was calculated. With a 5% chance of a type II error, only 2.8 significant correlations were expected by chance, but 7 were observed. Colour (% black) was significantly (p < 0.05) correlated with allele frequency for Est-1(a), Est-1(b), Icd-2(a), Icd-2(c), and Pgd-1(a). Mean annual temperature was significantly correlated with Pgd-1(a) (p < 0.05) and associated with Est-1(b), Est-5(a) and Got-1(a) (p < 0.10). Latitude was correlated with Pgd-1(a) (p < 0.05). No significant correlations were found between allele frequency and rainfall. Colour and allele frequency appear to be the most closely associated; selection of one or both may be linked to temperature. No significant correlation (r = 0.012, P > 0.05) was found between overall heterozygosity and latitude, in contrast to the result for Australia (Triggs, 1987).

Body length and weight were also correlated with coat colour in our study populations (r = 0.68 and r = 0.64 respectively; p < 0.05). Yom Tov (1984) and Yom Tov et al. (1986), in an extensive morphological survey of possums in New Zealand, found significant negative correlations between many skull and body length measurements and mean annual temperature. However, they did not consider coat colour, and our reanalysis of data on body and skull measurements in Yom Tov (1984) with respect to coat colour produced better correlations between body size and % black than between body size and mean annual temperature for all characters except distance between bullae (Table 5).

Table 5: *Correlations (r) between body and skull measurements, coat colour (% Black), and mean annual temperature (MA T). Body and skull measurements and correlation coefficients of measurements vs MAT are from Yom Tov (/984). % Black (the proportion of black possums in a population) values are from our data. Significance levels of r: .*p < 0.05, .**p < 0.001.*

Measurements	r:MAT	r: % Black
Body length	-0.723	0.823*
Tail length	-0.716	0.809*
Skull length	-0.751**	0.859**
Upper tooth row length	-0.739**	0.763*
Width at jugular arches	-0.786**	0.853**
Distance between bullae	-0.583	0.486
Skull width at tympanic region	0.735*	0.753*

Discussion

The introduction of possums from at least two regions of Australia, followed by hundreds of largely undocumented liberations of New Zealand-bred stock, has produced a complex pattern of genetic relationships in New Zealand possums, upon which selective and random genetic changes have been superimposed.

Our results generally conform to the prediction that if coat colour of New Zealand populations indicates origin, then (1) the level of genetic variation in New Zealand populations should be related to the proportion of each colour morph in a population, and (2) allele frequencies of New Zealand populations with different proportions of each coat colour should reflect allele frequencies of the Australian stock types. Thus, mainland Australian and Tasmanian stocks are not distributed at random in New Zealand. Black and grey populations also differ in average body size (Yom Tov *et al.,* 1987; our study), as they do in Australia (Yom Tov and Nix, 1986).

Selection with respect to climate appears to be an important determinant of the distribution of possum types in New Zealand, although deliberate introductions of possums of different stocks to suitable habitats probably also played a part in determining present distributions. In New Zealand, cold, wet areas tend to harbour large, black possums most similar to the Tasmanian type, whereas warm, dry areas harbour small, grey, mainland Australian-type possums. Areas of intermediate climate have mixed populations. The significant correlations between temperature and allele frequency, colour and body size of possums in New Zealand suggest that these were either directly selected for or acted as markers for other characteristics selected as possums colonized New Zealand. The correlation between colour and rainfall has been found even within a single valley with a steep rainfall gradient (R.E. Brockie, pers. comm.), emphasizing the strength of selection. An association between coat colour and rainfall has also been documented in Tasmania (Guiler, 1953), black possums being more common in areas of high rainfall. A physiological basis for different climatic tolerances is suggested by the differences in water metabolism between black and grey morphs (Williams and Turnbull, 1983).

Other studies of introduced species have also documented associations between colour or size and climate. These studies include house sparrows (Baker, 1980), mynas (Baker and Moeed, 1979), and stoats (King and Moody, 1982) in New Zealand, and house

sparrows in North America (Johnson and Selander, 1964). In all cases, these associations have developed very rapidly, within a few hundred years, suggesting that selection for local adaptation may be very strong, even in small populations in which random forces are likely to be powerful.

Our results have important implications for the control of possums in New Zealand. Currently, large-scale control of possum numbers is by aerially-sown cereal baits or carrots with 1080 (sodium monofluoroacetate) poison. One serious concern is the dosage level of 1080 required to kill a possum. Bell (1972), Rammell and Fleming (1978), and McIlroy (1983) experimentally determined an LD_{50} of about 0.8 mg 1080 kg^{-1} body weight for possums. In contrast, the New Zealand Forest Service found an LD_{50} of 1.3-2.1 mg kg^{-1} (Anon, 1978), requiring a toxic loading of 0.15% w/w on baits of mean weight of 4 g. The higher dose not only adds to the cost of poisoning operations and the risk to non-target species, but also leads to a high aversion rate as some possums can detect and reject 1080 at concentrations of 0.1 % w/w or more (Morgan, 1982). At present, flavours such as cinnamon are used as masks to disguise the poison (Morgan, Batcheler and Peters, 1986), and baits are loaded either at 0.08% w/w or 0.15% w/w (D.R. Morgan, pers. comm.) as a result of the ambiguous data published on the possum's sensitivity to 1080 poison. The cause of differences in LD_{50} between laboratories is still not clear, although variation in the techniques for handling 'and acclimatising possums were probably partly responsible (Anon, 1979). McIlroy (1983) found neither acclimatisation nor stress had any effect on the LD_{50} but he did find significant differences between possums from different regions of southeastern Australia. At low temperature (10°C) Tasmanian possums were more resistant to 1080 than mainland (New South Wales) possums. The LD,. for Tasmanian possums was 0.92 mg kg^{-1}, while New South Wales possums had an LD_{50} of 0.42 mg kg^{-1}, (McIlroy, 1983). Decreased sensitivity to 1080 at low temperatures has also been found in racoons (Eastland and Beasom, 1986). Much higher tolerances to 1080 occur in brushtail possums and other mammals in Western Australia, where high levels of fluoroacetates occur naturally in some plants (King, Oliver and Mead, 1978).

The possums used in the original New Zealand Forest Service trials (Anon, 1978) were from an area of predominantly black possums, and were therefore likely to be of the Tasmanian type, whereas the

possums used in the Ministry of Agriculture and Fisheries trials (Bell, 1972) were from an area of grey possums and were therefore likely to be of the mainland Australian type. A higher tolerance would therefore be expected in the New Zealand Forest Service results. However, a reciprocal exchange of possums between the two testing laboratories still resulted in different LD_{50} estimates (Anon, 1979), suggesting that some other factor, such as handling technique, was also involved. The temperature regime used in each laboratory was not given and could have been a factor.

If Tasmanian possums are more resistant to 1080, as found by McIlroy (1983), then there is a good case for using a higher dose rate of 1080 in cold, wet areas, where Tasmanian-type possums predominate, than in warm, dry areas, where mainland-type possums predominate. Tasmanian possums are also heavier and larger (Yom Tov and Nix, 1986; Triggs, 1987, Appendix II). In order to receive a lethal dose they would need to consume more baits at the same toxic loading than would smaller, lighter, mainland-type possums. As a hypothetical example, assuming that a totally grey population has an equivalent LD_{50} and mean body weight to mainland Australian possums (i.e. 0.42 mg 1080 kg^{-1} and 2.3 kg) and a black population is equivalent to Tasmanian possums (0.92 mg 1080 kg^{-1} and 3.1 kg), then 50070 of the grey population would be killed with 0.97 mg 1080 per possum, whereas the black population would require an average of 2.9 mg 1080 per possum.

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