

USING A COMPUTER SIMULATION PACKAGE FOR PVA TO MODEL THE DYNAMICS OF SUB-DIVIDED POPULATIONS: AN EXAMPLE USING HYPOTHETICAL META-POPULATIONS OF THE MOUNTAIN BRUSHTAIL POSSUM

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1. INTRODUCTION

Population sub-division is one of the many potentially detrimental consequences of habitat fragmentation [1]. Ensembles of sub-populations of organisms that occupy dispersed patches of suitable habitat remaining within highly fragmented landscapes may exhibit markedly different patterns of population behaviour than a single isolated population of equivalent initial size [2], [3].

Here, we use the computer simulation program VORTEX [4] to model the dynamics of hypothetical meta-populations of the forest-dependent arboreal marsupial, Mountain Brushtail Possum, *Trichosurus caninus* Ogilby. We simulated the dynamics of meta-populations of different sizes that were sub-divided to varying degrees and connected by different rates of inter-patch migration.

2. METHODS

2.1. Simulation model and input data used in the analysis

VORTEX was written by [4] and it has been applied widely in many studies of endangered taxa [5], [6]. A range of input data are required to run VORTEX including detailed information on the life history attributes of the study species [3]. Data on *T.caninus* that were used in our analyses are presented in Table 1 and they have been derived from several field studies of the species [7], [8].

2.2. Scenarios explored in the analysis

The behaviour of an array of meta-population structures was examined and they were selected to correspond to the size of populations of *T.caninus* that are predicted to occupy suitable old growth habitat patches remaining within extensively disturbed timber production montane ash forests in the Central Highlands of Victoria, south-eastern Australia [9]. Meta-populations ranging in total size from 100 to 400 *T.caninus* were modelled. These were sub-divided into one, two, five and ten sub-populations. A sub-model for migration in VORTEX [3] was invoked for those scenarios with two or more sub-populations. Rates for the annual probability of migration

to each other individual sub-population ranged from 0, 0.01 and 0.05. The actual number of individuals moving between pairs of sub-populations in any given year is intimately linked with the structure of the meta-population. This is because it is function of the number and size of sub-populations that are being modelled. In summary, the study encompassed four levels of population sub-division and three rates of migration for each of the three meta-population sizes that were modelled. A time horizon of 100 years was used in the analyses and a total of 500 simulations was completed for each scenario to stabilize our results.

TABLE 1

A summary of the biology and life history attributes of *T.caninus*.

BIOLOGICAL ATTRIBUTES

Family	:	Phalangeridae
Mean Body Weight	:	2670g
Diet	:	foliage and fungi
Home range	:	2-6 ha
Social system	:	pairs
Adult sex ratio	:	1M:1F

MODEL INPUT PARAMETERS

Breeding system	:	monogamous
Percent of adult males in breeding pool	:	100%
Breeding age of males	:	3 years
Breeding age of females	:	3 years
Max. no. of young per year	:	1
<i>Distribution of reproductive success</i>		
% of adult males producing	:	0 young 20%
	:	1 young 80%
Ann. mortality of males	:	0-1 years old 70%
	:	1-2 years old 7.5%
	:	2-3 years old 10%
	:	> 3 years old 4.5%
Ann. mortality of females	:	0-1 years old 70%
	:	1-2 years old 15%
	:	2-3 years old 10%
	:	3 years old 2%
Maximum longevity	:	17 years
Deterministic pop. growth	:	1.002
Generation time	:	9.23 years

3. RESULTS AND DISCUSSION

Figure 1 summarises some of the inter-relationships between the probability of sub-population and meta-population extinction and:- (1) total meta-population size, (2) the severity of population sub-division, and (3) the rate of inter-patch migration. Our analyses showed that sub-division had a negative impact on the demographic stability of populations of *T.caninus*. In those scenarios with a total of 100 and 200 *T.caninus*, the probability of extinction for a single large population was lower than recorded for an ensemble of sub-populations that were initially of similar size. The negative impacts of sub-division were most pronounced in scenarios where very small sub-populations of 10-20 *T.caninus* were created. In these cases the probability of sub-population extinction exceeded 50% for the 100 year time frame employed in the study. Our findings are likely to be associated with the array of factors that destabilise small populations of animals such as demographic stochasticity [10], and inbreeding depression [11].

The results of analyses examining the impact of migration on sub-population and meta-population dynamics were complex. They demonstrated that the relative benefits of migration were closely allied with meta-population structure, particularly the number, and thus the size, of sub-populations that were created (Figure 1). Accelerated rates of migration generally had a positive impact on meta-population stability in scenarios with sub-populations of 40 or more animals. This is highlighted by comparing the results for scenarios with five sub-populations of 40 *T.caninus*. Here, the probability of extinction declined from 33% amongst isolated sub-populations to 1% when they were connected by frequent migration events (Figure 1). The results suggest the existence of a "rescue effect" [12] where dispersing individuals supplemented local populations and reduced their risk of extinction.

Perhaps surprisingly, some of the positive effects of migration were reversed where the meta-population structure was comprised of sub-populations of 10-20 *T.caninus*. In these cases, increased migration reduced both sub-population and meta-population persistence (Figure 1). It is likely that a series of negative feedback processes resulting from the inherent demographic and genetic instability of very small sub-populations could have produced some of these phenomena [10], [13].

VORTEX outputs information on a wide range of other population indicators such as variations in expected heterozygosity and sub-population and meta-population growth [3]. However, only predictions of the probability of sub-population and meta-population extinction have been described in this paper. More detailed descriptions of the results of the study are outlined elsewhere [14], [15].

Probability of Extinction over 100 Years

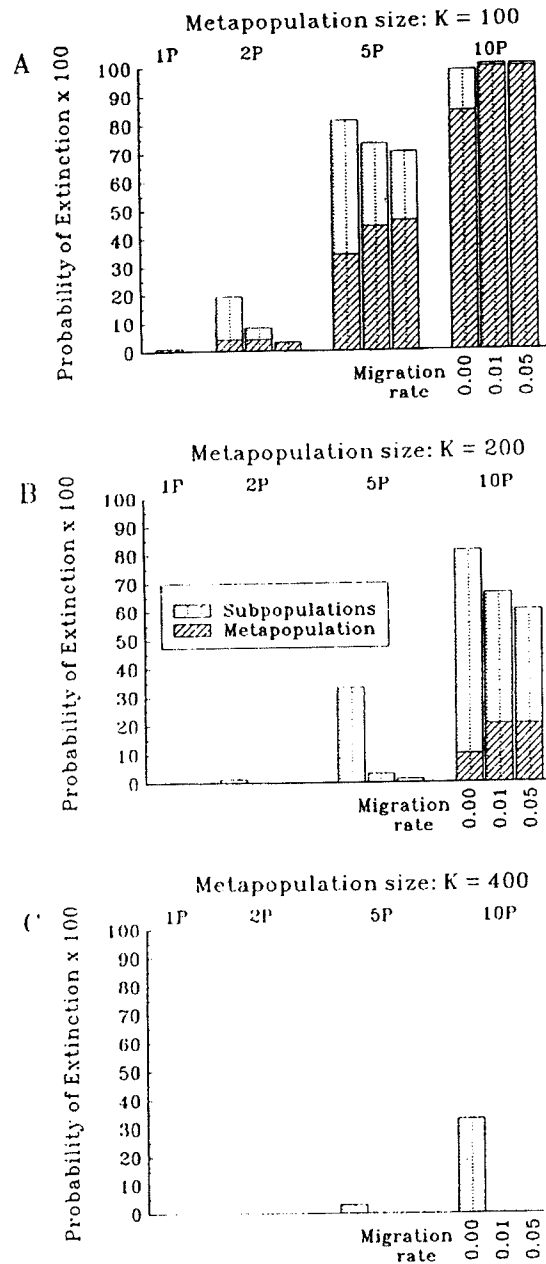


FIGURE 1

The probability of extinction of meta-populations of 100, 200 and 400 *T. caninus*, subjected to varying levels of population sub-division (1 Patch [1P], 2 Patches [2P], 5 Patches [5P], 10 Patches [10P]) and connected by different rates of inter-patch migration.

4. CONCLUSION

Our application of PVA has indicated that sub-division of populations of *T.caninus* into fragments containing 20 or fewer animals may lead to meta-population instability resulting in elevated rates of extinction. It has also been particularly instructive in identifying the potential impacts of migration on population persistence within different meta-population structures that may exist in highly fragmented timber production forests in central Victoria. The results of the analysis have also indicated that many more successful migration events may be required to reverse the negative effects of sub-division on population demography than previously speculated [16]. Finally, our investigation has identified key gaps in our understanding of the biology and ecology of *T.caninus*. In particular it has confirmed the results of field studies [17], [18] that there is a need for further detailed investigations of the patterns of dispersal and movement between habitat remnants.

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