

duly replenished, can restrict microbial activity and cause crisp dryness of litter biomass under low-humid conditions favouring forest fires.

In pine forests, needles decompose slowly due to its higher lignin content. Lignin resists microbial attack³ and is reported to accumulate in the litter, exerting a negative effect on its further degradation⁴. The leaf biomass therefore accumulates in pine forest.

The fires of summer 1995 in pine forests in western and central Himalayas is typical in enormity of magnitude and the extensive floral and avi-faunal losses it caused. The fire was reported along the broad distribution range of *P. roxburghii* from almost every district in Himachal Pradesh and various locations extending up to Garhwal Himalaya. In Himachal Pradesh, the Dharmshala Circle alone reported 226 forest fires between May to June⁵. The summer also recorded prolonged dry spell and a mean temperature rise of the order of 2–3°C above normal⁶.

The anomaly of temperature rise of 2–4°C has been widely discussed under the proposed climatic change, leading to

global warming by middle of next century⁷. Drought is one of the chief fears anticipated⁷, implying that vulnerability of pine forest to seasonal fire may increase under the situation.

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R. L. Semwal adds:

Our studies on chir pine forests and

associated grazing lands in Garhwal Himalaya deal with the effects of forest fire on soil, phytosociology, biomass and productivity, litterfall and litter decomposition and nutrient return through litter. Based on our work and available published literature from this region, presently we are not in a position to establish any precise relationship between forest fires and global warming phenomenon. However, as has been pointed out by Vats, it is true that warming of local atmosphere takes place during severe forest fires. Thus, in-depth studies need to be conducted in this direction to explore any such relationship. Nevertheless, we ought to have a well-thought programme to fight with the wild fires in Himalayan region which incurs environmental and social losses on an unmeasurable scale.

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RESEARCH NEWS

Classifying the kiwi

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Molecular genetics has, in recent years, become an invaluable tool for conservation biologists. Present thinking^{1,2} suggests that the higher the genetic variability within a species, the better are its chances for survival, and most work to date has centred around this. There has been substantial debate^{1–5} about the importance of genetics in conservation, but many ecologists⁶ still believe that population studies or behavioural studies are more useful. In the light of recent work^{2,7}, however, it seems clear enough that molecular genetics is here to stay in conservation. In a world with limited resources and an overloaded conservation schedule, tough choices have to be made as to which species, and specifically which populations, are to be conserved. These choices

would depend on our priorities and current opinion favours retention of genetic diversity^{1–5}. If we do assign priorities based on genetic diversity, we obviously need detailed studies in molecular genetics.

Baker and co-workers⁷ studied the molecular genetics of brown kiwis in New Zealand. The work is noteworthy for two reasons; firstly, they found levels of genetic differentiation between populations that had not been found in bird populations earlier. Secondly, they showed that the taxonomy of the brown kiwi needed to be reviewed and perhaps changed in the light of their study. This is important because the kiwi is an endangered bird and conservation priorities do need to be assigned.

Molecular genetics can help clarify taxonomic errors because traditional taxonomies depend on morphological characters which may not reflect true genetic distances between species². Since most work has depended on the subjective classification of taxonomists, it is likely to be riddled with errors. The case of the Camden County gopher clearly illustrates this².

In 1898, a distinct species of gopher was described in Camden County, Georgia, USA as *Geomys colonus*. The population consisted of very few individuals and was listed as endangered. However, a recent molecular genetic survey showed that this species was not genetically distinct from the more common *Geomys pinetis*, which is found all over USA. In

Table 1. Morphological characters used to classify the kiwi and the results of the allozyme and mtDNA work (from Baker *et al.*, 1995)

Character	Population					
	North Island	Okarito	Haast	Fiordland	Stewart Island	Spotted kiwis
Morphology						
Plumage colour	Brown	Grey	Rufous	Dark grey	Dark brown	Spotted fawn
Feather tips	Stiff	Soft	Soft	Soft	Soft	Soft
Large tarsal scutes	17	7	4	5	6	6
Facial bristles	Long	Short	Short	Short	Short	Short
Feather lice						
<i>Apterygon</i>	<i>A. mirum</i> ; <i>A. rodericki</i> on Little Barrier Island	New species	Absent	<i>A. dumosum</i>	<i>A. dumosum</i>	<i>A. hintoni</i> *
<i>Rallicola</i>	Absent?	<i>R. gadowi</i>	<i>R. gadowi</i>	<i>R. gadowi</i>	<i>R. gadowi</i>	<i>R. pilgrimi</i> † and <i>R. gracilentus</i> *
Allozymes and mtDNA						
AK-1	A > 0.9; C absent	A = 0.95; C = 0.05	B = 0.17; C = 0.83	A = 1.0	A = 1.0	A = 0.98
Hb-2	A = 1.0	A = 1.0	B = 1.0	B = 1.0	B = 1.0	B = 1.0
Ldh-2	A > 0.8; B and C rare	A = 0.4; C = 0.6	A = 1.0	A = 1.0	A = 1.0	A = 1.0
Cytochrome <i>b</i> [‡]	2-11	12 and 13	14	15 and 16	17-22	1 and 23

*Found only on little spotted kiwi; †Found only on great spotted kiwi.; ‡Numbers refer to haplotypes listed in Figure 2.

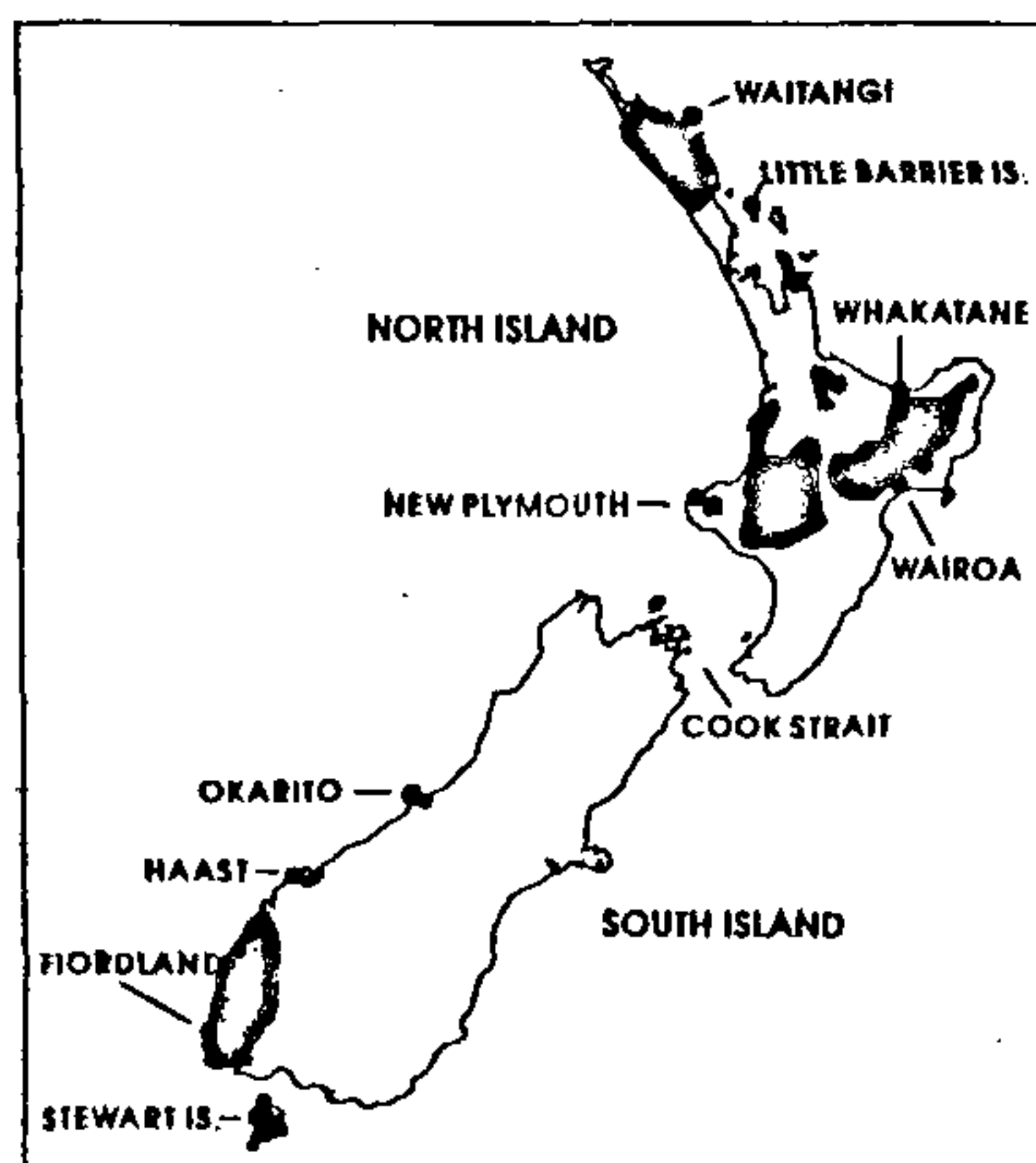


Figure 1. Distribution of the various populations of brown kiwis in New Zealand (from Baker *et al.*, 1995).

fact, there were wider genetic differences across different populations of *G. pinetis*. Hence, *G. colonus* did not warrant recognition as a separate species. Either a mistake had been made in the original classification or *G. colonus* had gone extinct and was replaced by the common *G. pinetis*. In either case, incorrect taxonomy led to an inappropriate conservation priority for the Camden County population of gophers.

Kiwis are small, non-flying birds, found only in New Zealand. Unfortunately, kiwi populations have been fragmented by

hunting, habitat destruction and introduced mammalian predators. They are now found in small, discrete populations that are unlikely to exchange genes. Brown kiwis are found on North Island, South Island and the smaller Stewart Island (south of South Island) (Figure 1). Initially, the North and South Island populations were recognized as separate species (*Apteryx mantelli* and *Apteryx australis*, respectively) on the basis of morphological characters. Subsequently, they were clubbed as a single species and accorded the status of subspecies (*A. australis mantelli* and *A. australis australis*). The Stewart Island population was also recognized as a subspecies (*A. australis lawryi*). Although this classification was widely accepted, reports of differences in feather lice, blood proteins and possibly calls shed some doubt on its validity (for a review, see ref. 7 and references therein). Baker *et al.*⁷ attempted to resolve the issue using molecular genetic techniques.

A number of studies in recent times have been done on maternally inherited mitochondrial DNA, because they provide an excellent source of genetic markers and can be used to reconstruct intra-specific phylogenies of matriarchal lineages⁸. Baker *et al.*⁷ examined differences in the cytochrome *b* gene from mitochondrial DNA. In the 60 kiwis studied, 654 bp of mtDNA was sequenced; there were 21 types of sequences due to variation at 42 sites. Based on these 21 types, the brown kiwis could be separated into five

populations – the North Island population, the Stewart Island population and three different populations on South Island. Remarkably, *none of the populations shared any sequence type.*

As one might expect, the North and the South Island birds were clearly divided. However, the northernmost South Island population (the Okarito population) turned out to be a sister group of the North Island population. Baker *et al.*⁷ suggest that the two sub species can now be reinstated as separate species. This is based on the result that the genetic distance between the two populations is as great as that between the two species of spotted kiwi (*A. haastii* and *A. oweni*) (Figure 2). Also, the Okarito population of the South Island can be classified as the same species as the North Island population.

The most remarkable aspect of their result, however, was the extreme structuring of the matrilineal lineages of cytochrome *b*, with virtually every population showing private alleles (Table 1). This is a first for mtDNA studies in vertebrates. Baker *et al.* also looked at genetic differences between populations by studying the variation in enzymes. The results from the allozyme study confirmed the results of the mtDNA work, showing levels of subdivision seen only in vertebrates such as salamanders, cave-dwelling fishes and small mammals, all animals with very poor dispersal power and disjunct populations.

Unlike small mammals, bird populations were not expected to be genetically

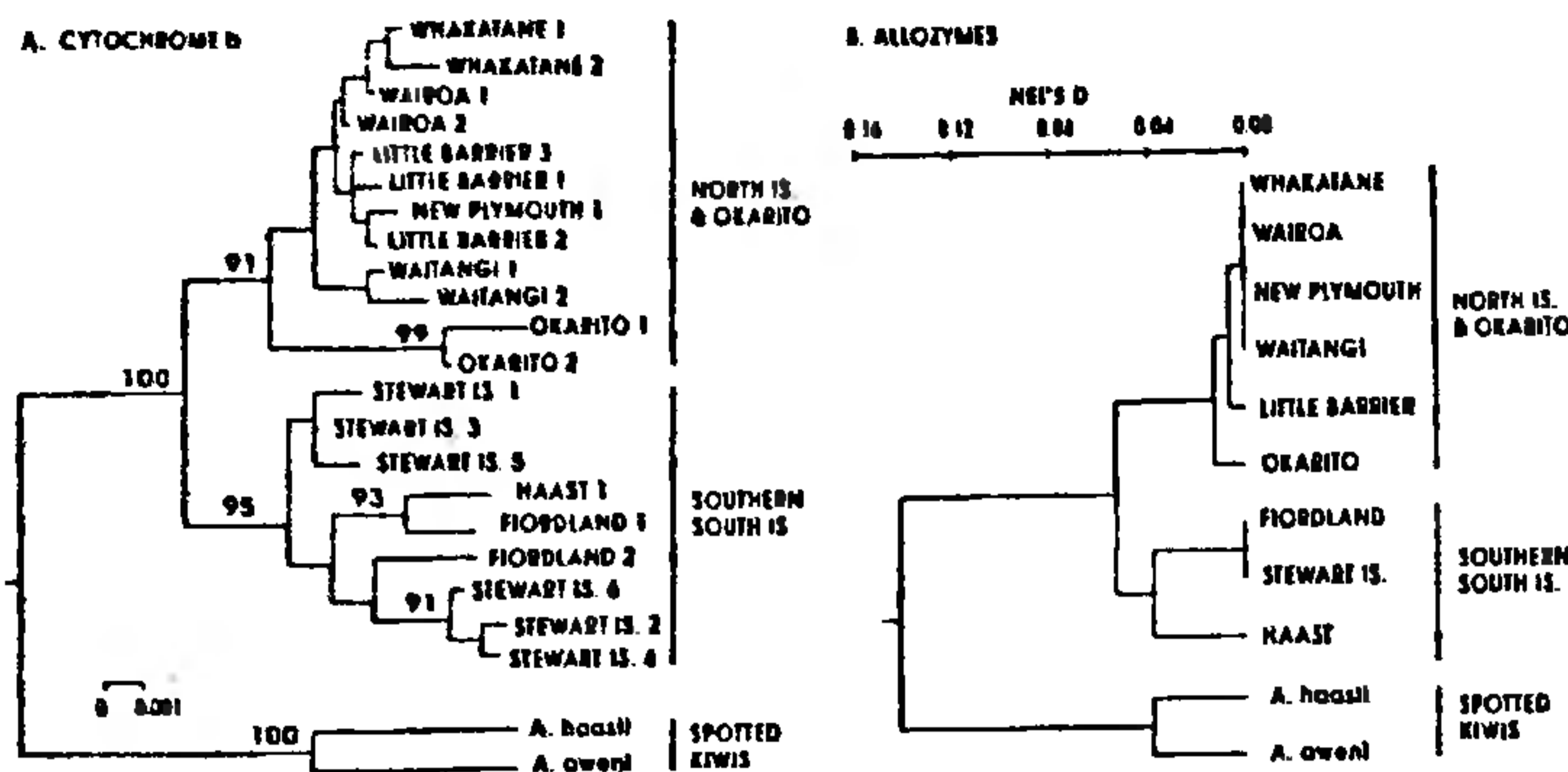


Figure 2. The mtDNA and allozyme trees constructed for the kiwi populations (from Baker *et al.*, 1995).



Figure 3. A great spotted kiwi (*Apteryx owenii*); the brown kiwi (*Apteryx australis*) is a little smaller and its body colour is a streaked dark brown and light brown. [The *Encyclopedia of Birds* (eds Perrins, C. M. and Middleton, A. L. A.), George Allen and Unwin, London, 1985.]

different from each other. Their ability to disperse (due to flight) would result in greater exchange of genes between populations and less genetic difference between populations⁹.

Kiwis, however, seem to be more like small mammals than birds (Figure 3). They are the smallest of the seven families of ratite birds. Ratites are non-flying birds that lack the keeled breastbone to which the pectoral muscles are attached. Kiwis, like other ratites, have an adult plumage that is the same in structure as the juvenile down of other birds. They live in burrows, and are essentially nocturnal. These and

other features such as hair-like feathers, facial bristles, two functional ovaries, a well-developed sense of smell and absence of flight make them more like small mammals in their ecology¹⁰.

The brown kiwis were once widely distributed in New Zealand. Range fragmentation must have accelerated since the arrival of humans ca 1000 years ago, due to both loss of habitat and hunting. A simple biogeographical hypothesis suggests that the southern South Island population is a remnant of the original population. This then colonised northward and diverged⁷.

The kiwis are an ancient lineage, judging from Gondwanaland distributions, and have had 40–80 million years to evolve in the isolation of New Zealand. Baker *et al.* used the RFLP (restriction fragment length polymorphism) clock of 2% sequence divergence per 1 million years to estimate divergence in New Zealand. They estimate that the basal population diverged from the Okarito population 900,000 years ago. The divergence between the Okarito and North Island populations would have occurred 500,000 years ago and that within the North Island populations, 200,000 years ago.

To summarize, the truly remarkable finding of this work is the fact that each population has private alleles for cytochrome b. The value of their work lies in their re-classification of the brown kiwi, which sheds new light on its status and makes it necessary to reevaluate conservation priorities. This work emphasizes the role of molecular genetics in conservation biology and stresses the need to continuously assess and review conservation practices. Certainly various other factors such as population ecology, behaviour and even aesthetic value may need to be taken into consideration, but this should in no way detract from the role that molecular genetics has in the conservation biology of tomorrow.

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