CORRESPONDENCE

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 attack and is reported to accumulate in the litter, exerting a negative effect on its further degradation. 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 avifaunal losses it caused. The fire was reported along the broad distribution range of *P. roxburghii* from almost every district in Himalachal Pradesh and various locations extending up to Garhwal Himalaya. In Himachal Pradesh, the Dharmshala Circle alone reported 226 forest fires between May to June. The summer also recorded prolonged dry spell and a mean temperature rise of the order of 2-3°C above normal.

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 century. Drought is one of the chief fears anticipated, implying that vulnerability of pine forest to seasonal fire may increase under the situation.


S. K. VATS

CSIR Complex,
P.B. No. 6,
Palampur 176061, India

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.

R. L. SEMWAL

G.B. Pant Institute of Himalayan Environment and Development,
Garhwal Unit, P.B. No. 92,
Srinagar (Garhwal) 246174, India

RESEARCH NEWS

Classifying the kiwi

*Kartik Shanker*

Molecular genetics has, in recent years, become an invaluable tool for conservation biologists. Present thinking 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 about the importance of genetics in conservation, but many ecologists still believe that population studies or behavioural studies are more useful. In the light of recent work, 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. If we do assign priorities based on genetic diversity, we obviously need detailed studies in molecular genetics.

Baker and co-workers 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 species. 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 goopher clearly illustrates this.

In 1898, a distinct species of goopher 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)

<table>
<thead>
<tr>
<th>Character</th>
<th>North Island</th>
<th>Okarito</th>
<th>Haast</th>
<th>Fiordland</th>
<th>Stewart Island</th>
<th>Spotted kiwis</th>
</tr>
</thead>
<tbody>
<tr>
<td>Morphology</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Plumage colour</td>
<td>Brown</td>
<td>Grey</td>
<td>Rufous</td>
<td>Dark grey</td>
<td>Dark brown</td>
<td>Spotted fawn</td>
</tr>
<tr>
<td>Feather tips</td>
<td>Silt</td>
<td>Soft</td>
<td>Soft</td>
<td>Soft</td>
<td>Soft</td>
<td>Soft</td>
</tr>
<tr>
<td>Large tarsal scutes</td>
<td>17</td>
<td>7</td>
<td>4</td>
<td>5</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td>Facial bristles</td>
<td>Long</td>
<td>Short</td>
<td>Short</td>
<td>Short</td>
<td>Short</td>
<td>Short</td>
</tr>
<tr>
<td>Feather lace</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Apterygous</td>
<td>A. mirum</td>
<td>New species</td>
<td>Absent</td>
<td>A. dumosum</td>
<td>A. dumosum</td>
<td>A. hintoni*</td>
</tr>
<tr>
<td>Rallidae</td>
<td>Absent?</td>
<td>R. gadowi</td>
<td>R. gadowi</td>
<td>R. gadowi</td>
<td>R. gadowi</td>
<td>R. pilgrimi* and R. gracilentus*</td>
</tr>
</tbody>
</table>

Allozymes and mtDNA

<table>
<thead>
<tr>
<th>Character</th>
<th>Population</th>
</tr>
</thead>
<tbody>
<tr>
<td>AK-1</td>
<td>A = 0.95; C = 0.85; B = 0.17; A = 1.0; A = 1.0; A = 0.98</td>
</tr>
<tr>
<td>Hb-2</td>
<td>A = 1.0; B = 1.0; B = 1.0; B = 1.0</td>
</tr>
<tr>
<td>Ldh-2</td>
<td>A = 0.8; B and C rare</td>
</tr>
</tbody>
</table>
| Cytochrome b | 2-11  
14 and 15  
14 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 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 lace, 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 lineages. 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.\(^7\) 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
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 form 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.


Kartik Shanker is in the Centre for Ecological Sciences, Indian Institute of Science, Bangalore 560 012, India.