

## In this issue

### Molecular biology comes of age in India – at last!

Over the last four decades, a number of innovative experimental techniques have allowed us to investigate the molecular biology of many simple organisms including viruses, bacteria, yeasts and amoebae. These molecular techniques have also been used to understand the cellular biology of many higher organisms – both for fundamental knowledge and for application in the fields of medicine, agriculture, and industry.

What became rapidly apparent at this time was that these same techniques could also be used to screen large numbers of individual plants and animals for genetic variability at the molecular level. And that such knowledge was of crucial importance in other, less fashionable, areas of biological research. Estimates of genetic variability often become essential if one is to address problems in organismic biology including those in behavioural ecology and evolutionary biology, molecular taxonomy and phylogenetics, and in the conservation and management of biodiversity.

In the field of taxonomy and phylogenetics, molecular genetic information can be used in the appraisal of phylogenetic and evolutionary discontinuities within and among species. Our understanding of evolutionary relationships at these levels has traditionally depended on small numbers of morphological characters, and these continue to provide the systematic framework within which different taxa are recognized. But these often give inadequate or even incorrect partitions of phylogenetic diversity. Updated taxonomic and phylogenetic data, drawn from molecular inputs, are therefore invaluable in providing a firmer foundation not only for comparative studies in evolution, but also for the management of biotic diversity. A fine example of work of this kind is the paper by Parani *et al.*, on page 1235 of this issue. This study has examined the polymorphic variation in certain sequences of ribosomal DNA in several species and varieties of pigeonpea (*Cajanus cajan*), one of the major grain legumes in India and several other tropical countries of Africa and Latin America. In addition to exploring the genetic divergence between the cultivated varieties of this species and their

wild relatives, this study also provides insight into the genomic variation within the different cultivated species of pigeonpea. This is extremely important information not only for plant breeders interested in hybridization programmes for agricultural improvement, but also for conservation biologists keen on documenting, characterizing and preserving the germplasm of our indigenous crop species. What is even more promising is that this research group is currently involved in investigating the mitochondrial and chloroplast genomes of pigeonpea and its related genera as well; their findings will definitely be of great importance from the perspectives of both agricultural genetics and evolutionary biology.

In conservation biology, most discussions of genetics have invariably focused on how best to preserve genetic variability within populations of threatened species. What we often tend to overlook are the many other problems – less visible, but equally vital – that molecular genetic studies can potentially address in the field of wildlife research and conservation. One striking example of this is provided by the paper of Prakash *et al.*, on page 1239 of this issue. An extremely important problem that conservationists frequently have to deal with (and it almost always appears to be an uphill struggle) is that of wildlife poaching and the underground trade in wildlife products. While, on the one hand, it is necessary to physically and legally protect our wildlife from being converted into wallets, handbags and aphrodisiacs, it is also important to identify the actual species that are being targeted, the specific populations under maximum threat, and hence, the exact locations where protection has to be prioritized. It is the latter class of problems that pose maximum difficulty for wildlife protection agencies – they thus often have no idea where a particular victim of poaching has originated. The paper by Prakash *et al.* addresses precisely a very closely related issue, and one that is of great importance. Using sequence analysis of a particular stretch of mitochondrial DNA and its comparison with the known sequences of the same DNA from other species, they have been able to genetically identify what was allegedly a piece of processed tiger skin to be actually that from do-

mestic cattle! This is indeed a most remarkable demonstration of science as a detective – and one, which in its myriad applications, is likely to have profound implications for wildlife forensics.

An explanation of the rather dramatic title to this short piece may now be in order. We have made remarkable progress in research areas involving molecular biology, not only in furthering our basic understanding of molecular mechanisms, but also in developing products in different areas of human welfare. Notwithstanding some excellent individual efforts, however, there seemed to have been a lacuna in our use of molecular techniques in the areas of evolutionary biology, phylogenetics, behavioural ecology and conservation science. Although, in all fairness, there have been a few isolated papers addressing these problems in earlier issues of *Current Science*, two fine examples of the kind included here – together in the same issue – have definitely been rare. They give us hope that the days of organismic biology are far from over as some skeptics and pessimists had thought they were. And they also demonstrate how powerful indeed are these new molecular techniques – they transcend all our frail attempts at compartmentalizing our science!

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### Image histograms of RBCs

Digital images of normal erythrocytes have characteristic image histograms which depend on the concentration of light absorbing elements (Hb) and the overall optical path distance associated with the biconcavity of the erythrocyte surface. In the paper 'Digital indicators for red cell disorder' by A. K. Dasgupta and P. Lahiri (page 1250), for each cell the morphological parameters – area, perimeter, elongation, roundness, Feret diameter and compactness are determined. Based on these parameters the abnormal cells obtained from patients such as that of thalassemia and iron deficiency anemia are clearly identified. This technique can further be applied to classify erythrocytes with varying abnormalities associated with the interior and membrane of these cells.

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