

## In this issue

### Understanding and managing genetic diversity

The Rio conference of the early 1990s not only made 'biodiversity' a household word, but also put inventorying, monitoring and conserving biodiversity as an important item on the (non-hidden) agenda of most nations. Even then, for quite a while, biodiversity enthusiasts were seen as those who do little more than raise slogans about saving trees/rain forests/tigers, etc. However, as the possible immense commercial potential of biodiversity was realized (in terms of drugs from little known plants and animals, and strengthened with new patenting laws), study of biodiversity has started acquiring some respectability.

What, exactly, is meant by biodiversity? It comprises all the living organisms seen in a region. The 'all' actually means everything from viruses upwards, and the region could be anything from a 30' × 40' site to the whole of India. The ways in which the organisms differ from each other are also many. Thus there are large differences like those between broad taxonomic categories (plants vs animals) or sizes (trees vs herbs vs shrubs). There can be rather narrow differences like varietal (but commercially crucial) distinctions (basmati vs zeerkhamaba) and (sometimes even more critical) single locus genetic polymorphism (normal vs hemophilic humans).

As is well known (and has been very recently trumpeted in the aftermath of the triumph of the Human Genome Project), the fundamental difference between any two living organisms is the differences in their DNA sequences. This genetic diversity is thus the basis of all biological diversity. Understanding the factors and mechanisms that influence the origin, maintenance

and destruction of genetic diversity is therefore of crucial importance before one can formulate policies for the conservation of biodiversity.

In his authoritative article on [page 170](#) of this issue, Prem Narain provides a lucid and comprehensive overview of these diverse aspects. After giving a glimpse of some important facts and figures in this connection (e.g. an estimated 22,530 species of plants, fish, amphibians, reptiles, invertebrates, birds and mammals are threatened with extinction), the author gives a detailed description of what is meant by genetic diversity. This has been followed by an up-to-date account of the various methods of accessing genetic diversity in natural populations (this is one area where the two cultures of old fashioned natural historians and high-tech molecular biologists can most fruitfully interact!). Prem Narain has also discussed the factors that maintain genetic diversity under natural conditions, and those that lead to its decrease – mild ones like population bottlenecks and severe ones like extinction. Particularly novel is the next section that highlights the role of biotechnological methods (embryo collection and transfer) – procedures that can greatly aid the process of germ-plasm maintenance – preserving important varieties of plants and animals used in agriculture. On the basis of this technical background, the author next discusses the strategy and policy for the conservation of biodiversity. For a very readable and informative account of this complex subject of considerable contemporary interest, the reader can do no better than turn to [page 170](#) of this issue.

N. V. Joshi

### Lowest sea-level position during LGM

Due to increased greenhouse gas emissions, there is a justified possibility of atmospheric warming inducing sea-level rise during the next few decades. But geologists have known for a long time that global scale sea-level changes have occurred several times even in the relatively recent history of the earth. Numerous studies using a variety of evidence have confirmed that in the most recent past the sea-level was at its lowest position at the time of the Last Glacial Maximum (LGM) when large parts of the continent in higher latitudes and altitudes had accumulated glacial ice. As this ice melted and the water returned to the sea, its level rose to its present position. G. Gaitan Vaz ([page 228](#)) now reports the existence of a relict coral reef NE of the Karaikal coast in the Bay of Bengal. Its radiocarbon date ( $18,390 \pm 220$  yr before present) and the position at -125 m depth unambiguously suggest that the sea-level was about 120 m below the present-day sea-level at the time of the LGM. This is perhaps the most concrete evidence of the position of sea-level at the time of the LGM in the Indian context.

S. K. Gupta

### Induced male sterility in higher plants

Raising the ceiling to genetic yield is the only means to achieve the future production targets of crop commodities. Among the various technological options, exploitation of hybrid vigour is considered as the most reliable and readily adoptable strategy. This is why countries all over have identified hybrid technol-

ogy as the thrust area of research and development. Cytoplasmic-genetic male sterility (CMS) is the widely used system for production of hybrid seed across crops. Unlike genetic male sterility, and cyto sterility which are induced respectively by nuclear gene and cytoplasmic factor, CMS is induced by interaction of male sterility-inducing cytoplasmic factor (S) and pollen fertility-restoring nuclear gene in its recessive state (rf rf). The CMS line is essentially an alloplasmic line developed by placing nuclear genome in an alien cytoplasmic background by substitution backcrossing. The resultant CMS is attributed to complex 'nuclear-cytoplasmic interaction', a term often used to include all that are not explained by either nuclear or cytoplasmic inheritance. We have come a long way since then in defining the complexities of nuclear-cytoplasmic interaction.

Investigations made during the last 10 years have been to understand the biochemical-molecular basis of the nuclear-cytoplasmic interaction induced male sterility.

The findings reveal CMS phenotype to be a result of mitochondrial dysfunction. In maize, petunia, etc., the dysfunction-induced male sterility has been found to be associated with production of chimeric peptide(s). In plant mitochondria, post-transcriptional editing of mRNA is necessary for synthesis of functional protein. When this process of the RNA editing and post-transcriptional function are interfered by nuclear gene interaction, chimeric peptide is produced instead of functional protein resulting in sterility. It has been very well demonstrated through transgenic approach in tobacco, wherein splicing of unedited coding sequences of wheat ATP synthase subunit 9 (atp 9) made the plant male sterile as against the transgene with the RNA-edited sequence remaining fertile (Michael *et al.*, 1993). It appears from this and other studies that CMS results from 'acquisition' of a novel gene that produces a toxic product. The nuclear fertility restorer (Rf) allele by affecting either the abundance of the toxic gene or its expression suppresses the CMS phenotype. The

expression of CMS associated loci is affected by the presence of respective nuclear restorer alleles.

Following an extensive review earlier by Hanson (1991) on maternally inherited cytoplasmic male sterility, the present review (page 176) while updating our knowledge adds strength to the view that co-transcription of nuclear and mitochondrial genes is the molecular basis of cytoplasmic genetic male sterility in higher plants. The plant mitochondrial genome, now fully sequenced in *Arabidopsis* and the liverwort *Marchantia* may no longer be an enigma. Nevertheless, more and more knowledge on the intergenomic interaction relating to male sterility might help from applied angle diversification of CMS and extending the CMS-based hybrid technology to many crops that are still not amenable to heterosis breeding, besides providing better insight into the biogenesis and function of this important cytoplasmic organelle.

E. A. Siddiq