databases in metropolitan cities.

The inaugural session concluded with the vote of thanks proposed by the convenor.

Session I was chaired by Mr M. N. Seetharaman, GIST, Bangalore. This session was devoted to CD-ROM scenario pertaining to databases and services in business, physical and engineering sciences, including patents and standards. The lead topic of the session was 'Trends in CD-ROM technology, world scenario'. Seven presentations were made in this session.

Session II was devoted to CD-ROM scenario pertaining to databases and services in biomedical and allied sciences (biotechnology, food sciences, full text databases, library applications, retrospective conversion). There were five presentations in this session. This session was chaired by Dr S. Kunthala Jayaram, CBT, Madras.

Session III was devoted to CD-ROM acquisition and copyright issues and was chaired by Dr S. S. Murthy, DESIDOC, New Delhi. The lead topic of the session was 'CD-ROM commercial issues concerning distribution, usage and scenario', followed by two presentations, viz. survey of CD-ROM databases and services in India and procurement of CD-ROMs.

Session IV was on 10th August 1994 and was devoted to CD-ROM hardware/software and networking. This session was chaired by Dr R. Srinivasan, NAL, Bangalore. The lead topic was 'CD-ROM hardware/software selection criteria and the issues concerned', followed by four presentations of CD-ROM standards and networking in this session.

Session V was devoted to CD-publishing and CD-ROM applications. This session was started with the chairperson's remarks on CD-publishing, options and opportunities by Mr N. V. Satyanarayana, Informatics (India), Bangalore. Two presentations on multimedia and hypertext were made in this session.

Session VI was devoted to online scenario. This session was chaired by Dr Anju Chadha, SPIC, Madras. The lead topic of the session was 'Online industry: trends and forecast', followed by six presentations on telecom options, NACIDs, INTERNET and user feedback.

Session VII was devoted to company presentations, wherein the following 11 companies participated; STN, USA; ESA/IRS, New Delhi; CMC, Bangalore; Informatics Group, Bangalore; GIST, New Delhi; Allied Publishers, Madras; Vans Information & Investors Services, Bombay; City Computers, Madras; Nexus Computers, Madras; World Trade Centre, Bombay; and C-DEC, USA. This session was chaired by Dr A. Lahiri, NISSAT, New Delhi.

The concluding session was chaired by Dr N. V. C. Swamy, IIT, Madras, who gave away the prizes to the three winners on the CD-ROM/Online Quiz sponsored by informatics Group. Dr Swamy recalled his research days when information had to be obtained manually, compared to the recent developments in information access. He expressed that networking of libraries is mandatory for effective information dissemination. Prof P. Soma Raju, Andhra University, Waltair, presented a bird's eye view of the proceedings of the meet, as a Rapporteur General. The meeting concluded with the vote of thanks from Ms Kamini Mishra, NISSAT, New Delhi, the co-convenor of the meet.

S. Subba Rao, Central Leather Research Institute, Madras

RESEARCH NEWS

New roles for RNA

K. K. Narayanan

Ribonucleic acid (RNA) is the most abundant form of nucleic acid in all cells; its concentration being five to ten times that of deoxyribonucleic acid (DNA). The principal and best understood role of RNA is as an intermediary in the translation of genetic information contained in DNA into proteins. In certain viruses, including the AIDS virus, RNA itself is the genetic material and gene expression is preceded by the copying of the RNA into complementary DNA. RNA, in association with certain proteins, is also known to be a structural component of subcellular bodies like the ribosomes—the centres of protein synthesis. Recent investigations[1,2] have shed light on the many more interesting ways in which RNA participates in cell function.

Types of RNA in the cell

The RNA molecules that carry the information from DNA to the actual sites of protein synthesis, the ribosomes, are the messenger RNAs (mRNAs). At any point of time, there will be several thousand kinds of mRNAs, each kind corresponding to a gene being expressed at that time. However, all the mRNAs together account for less than five per cent of the total cellular RNA. The most preponderant form of RNA in the cell is the ribosomal RNA (rRNA), which forms a structural component of the ribosomes. Three or four species of rRNAs make up nearly 80 per cent of the cellular RNA. Another 15 per cent of the cellular RNA is made up of nearly hundred kinds of transfer RNAs (tRNAs), whose primary function is to carry amino acids, the building blocks of proteins, to the ribosomes. Most, if not all, cells also contain a variety of other small cytoplasmic RNAs (scRNAs), and cells of higher organisms contain, in addition, a variety of small nuclear RNAs (snRNAs).

Cellular RNA is mostly single-stranded, although the genetic material of some viruses is made up of double-stranded RNA molecules that resemble a form of DNA. The single strands, almost invariably, form three-dimensional structures through base pairing between complementary regions within the same RNA molecule. The double helical structure at the paired regions is often short and interrupted because the base sequences

on the two interacting strands are rarely perfectly or continuously complementary. This secondary and tertiary configuration of the RNA molecule is implicated in the specialized functions that certain RNA molecules can perform in the cell. The dependence of a function on proper RNA structure is most typically exemplified in the case of tRNAs. In spite of their distinctive nucleotide sequences, the three-dimensional structure of all tRNAs is very similar and maintenance of their structure is critical for their biological function.

Catalytic RNAs

Till recently, it was believed that only proteins can make enzymes. However, this changed with the discovery, in the protozoan *Tetrahymena*, that an RNA sequence can catalyse the removal of intervening sequences of certain genes, or introns, from the pre-mRNAs and bring together the coding regions[3]; this process is called intron splicing. Since then, many cases of intron removal from the pre-mRNAs in lower animals and plants, and in cell organelles of higher plants and animals, have been attributed to the catalytic activity of the RNA. Such catalytic RNAs are often part of the intron sequence that is spliced and, therefore, such introns are called self-splicing introns. Many nuclear genes in higher plants and animals are interrupted by introns. Intron splicing for these genes occurs through a more complicated mechanism which involves a ribonucleoprotein complex, the spliceosome. Certain types of RNAs are active components of the spliceosome. A few enzymes that were earlier characterized were found to be associated with RNA molecules. RNA was thought to have only a structural role in such enzymes, but now there is increasing evidence to suggest a catalytic role for the RNA component as well. In most instances, the catalytic RNA sequences by themselves are capable of cleaving the substrate, which is always another RNA molecule, like any protein enzyme, and, therefore, these are called RNA enzymes or ribozymes.

The activity and specificity of ribozymes are, again, properties of their three-dimensional configuration. It has now been possible to design and synthesize ribozymes to cleave specific RNA substrates. This area of science is now under active investigation as ribozymes have a potential therapeutic value in treating diseases caused by RNA viruses, like AIDS.

RNA editing—a new twist in gene expression

It is generally accepted that all genetic information is contained in stretches of DNA in the form of specific sequence of nucleotides and this information is copied to RNA molecules, the mRNAs. The mRNA then directs the assembly of amino acids into protein, strictly in accordance with the genetic code contained in its nucleotide sequence. The genetic information, once transcribed into an mRNA was thought to be immutable, thus ensuring translation of a protein entirely based on the DNA sequence. This view underwent a radical change with the discovery, a few years ago, in *Trypanosomes* that some mitochondrial mRNAs underwent changes in their sequence resulting in the synthesis of proteins that were not entirely in accordance with what was encoded by the DNA[4,5]. This phenomenon has come to be known as RNA editing. RNA editing was so extensive for some of the mRNAs that the genes were unrecognizable at the DNA sequence level. RNA editing has now been reported in many organisms and it is very common in plant mitochondria and chloroplasts. While in *Trypanosomes* RNA editing results in the addition or deletion of a nucleotide residue (U), in plant organelles it generally results in the conversion of one nucleotide residue to another (C → U). RNA editing is a highly specific process and always results in the generation of a nucleotide sequence that codes for the correct protein. The exact mechanism of RNA editing in plants is not yet clear, but that in *Trypanosomes* has been thoroughly worked out. In this group of organisms, a chief component of the editing machinery is a specialized RNA molecule called guide RNA (gRNA). The gRNA associates with an unedited mRNA with the help of an 'anchor' sequence and directs the addition or removal of U residues at specific positions. Few to many gRNAs participate in the editing of one mRNA, depending upon the extent of editing required to generate the correct genetic sequence.

In most instances, RNA editing has been found to be necessary for the synthesis of functionally competent proteins. One disorder associated with fat metabolism has been attributed to improper editing of the nuclear apolipoprotein B gene transcript which is present in all mammals. In plants, recent reports have suggested that failure of RNA editing results in male sterility in tobacco and rice.

More to rRNA function

The translation of an mRNA sequence into proteins in the ribosome involves the interaction between the mRNA and tRNAs. The correct ordering of the amino acids in a protein is facilitated by the sequential interaction of the 'anticodon' region of tRNAs, each of which carries a specific amino acid, with the triplet nucleotide code (codon) on the mRNA. But the codon–anticodon interaction in itself is not sufficient to ensure efficient and accurate decoding of the genetic message and was long thought to be assisted by the protein components of the ribosomes. The rRNAs, which are also part of the ribosome complex, were not ascribed any function other than being mere structural components. Recent studies have shown that one species of rRNA, the 23S rRNA, plays a key role in peptide bond synthesis, the bond that connects two adjacent amino acids in a protein chain. Very recently, a report in *Nature*[6] gives evidence for the active involvement of another species of rRNA, the 16S rRNA, in decoding the genetic message carried by the mRNA. As more and more functions of the rRNAs in protein translation are unravelled, it may well turn out that the RNA species have as many, if not more, roles as the protein components in the whole process.

RNA and evolution of life

The quest for the elusive molecule whose appearance signalled the beginning of life on this planet has been going on for a very long time. The obvious candidates were DNA and protein; but in spite of endless debates, no satisfactory answer for the 'chicken or egg' question has emerged. But now, with the unravelling of more RNA-governed activities which are vital for cellular life[7], RNA is emerging as the most likely candidate for the first 'life molecule'. There is already a big group of scientists who believe that multifunctional RNAs were vital for the

existence and perpetuation of the first forms of life. Many of the cellular processes that are observed today, like RNA editing or intron splicing, they believe, are relics of the 'RNA world'.

1. Noller, H F, in *The RNA World* (eds. Gesteland, R. F. and Atkins, J. F.), Cold Spring Horbour Laboratory Press, New York, 1993, pp. 137–184
2 McCarthy, J. E. G. and Brimacombe, R., *Trends Genet.*, 1994, **10**, 402–407.
3. Cech, T. R., *Annu. Rev. Biochem.*, 1990, **59**, 543–568
4 Benee, R., Van Den Bing, J., Brakenhoff, J. P. J., Sloof, P., Van Boom, J. H. and Tromp, M. C., *Cell*, 1986, **46**, 819–826
5. Shaw, J. M., Feagin, J. E., Suart, K. and Simpson, L., *Cell*, 1988, **53**, 401–411.
6. Purohit, P. and Stern, S., *Nature*, 1994, **370**, 659–662.
7. Gray, M. W. and Cedergren, R., *FASEB J.*, 1993, **7**, 4–6.

K. K. Narayanan is in the Centre for Biotechology, SPIC Science Foundation, 110 Mount Road, Guindy, Madras 600 032, India.

OPINION

Genetic resource mapping and fisheries management

B. K. Padhi and R. K. Mandal

The Indian fisheries sector has witnessed two remarkable changes in the last four decades: (i) decline of natural fish populations in open waters[1], and (ii) development of aquaculture as a profitable business. Though fish production as a whole increased steadily during this period (0.7 million tonnes in 1951 to 4.5 million tonnes in 1993–94), the genetic and evolutionary consequences of these developments are less discussed and realized. We pointed out earlier[2] some genetically unsound practices which may affect aquaculture productivity and fish biodiversity. The effects of different anthropogenic factors on the fisheries resources are presented diagrammatically in Figure 1, which is self-explanatory.

In this article we emphasize the immediate and long-term importance of genetic resource mapping for safeguarding and utilizing more purposefully the fish biodiversity resources existing in India. We also elaborate here the concept of genetic resource mapping, the scientific approaches it needs, its approximate cost and utility.

Genetic resource mapping

Genetic variation in nature

Genetic variability occurs within and between the natural populations of a species occupying different geographical and ecological zones and is more prominent among freshwater fishes than in marine ones[3]. In population genetics terminology a 'stock' is defined as a randomly interbreeding, self-reproducing subset of a species that is geographically isolated from other such groups[4]. The genetic stocks (separate spawning populations) that make up a species represent the fundamental units of both reproductive and genetic diversity; thus, they determine the ecological and evolutionary potential of the species.

The genetic variation among stocks could be correlated with some adaptive, physiological and behavioural changes in them. These changes include differential spawning time, growth rate, disease resistance, heat and cold tolerance, pH tolerance, migratory behaviour, spawning performance and catchability. Genetic diversity is associated with immediate fitness and long-term evolutionary potential[5] and is also associated with enhanced mean fitness of fish populations[6]. Therefore, the stock concept has assumed tremendous importance for effective management and conservation of fisheries resources.

Conceptually, genetic resource mapping means identification and geographical localization of genetically differentiated populations (genetic stocks) of a species and assessing their evolutionary interrelationship by quantifying genetic identity/distance between them. In short, genetic resource mapping means documentation and cataloguing of intra-

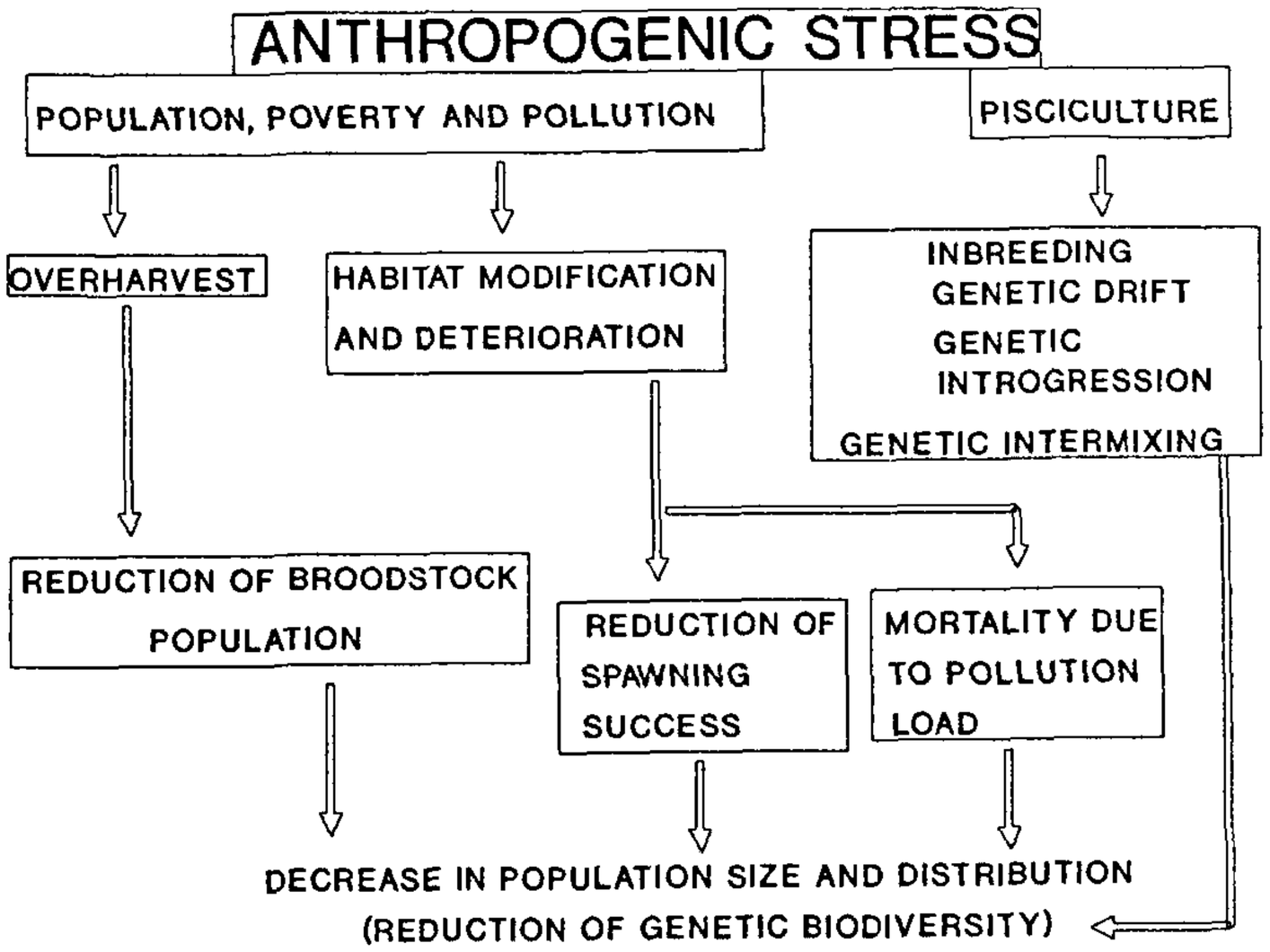

Figure 1. Anthropogenic factors operating in natural waters and aquaculture leading to the reduction of fish genetic biodiversity in the long run.