Record decrease of sea surface temperature following the passage of a super cyclone over the Bay of Bengal

A well-marked low pressure area that formed over Gulf of Thailand on 24 October 1999 intensified rapidly over the Andaman Sea by 26 October and further intensified into a very severe cyclonic storm by 27 October. Moving in a northwesterly direction, it intensified into a 'super cyclonic storm' over a hundred kilometres southeast of the port-town of Paradeep by 28 October. It crossed the coast at Paradeep on 29 October[1]. The system was practically stationary for 30 h after landfall and a record rainfall of 530 mm was observed at Paradeep on 30 October. The intensity of the storm increased from T4.5 to T7.0 from 28 to 29 October (i.e. 2.5 T/day), which is much higher than the usually recognized rapid rate of 1.5 T/day observed over the Atlantic Ocean[2]. The lowest central pressure of 912 hPa observed in this super cyclone was the minimum so far for any tropical cyclone in the Bay of Bengal.

The three-day TMI (Tropical Rainfall Measuring Mission (TRMM) Microwave Imager) SST images for the period 25 to 31 October 1999 have been examined to see the impact of the cyclone on the SST field. The sequence of TMI SST images before the intensification of the super cyclone is given in Figure 1. SST was more than 28°C during 25–27 October 1999 and cells of low SST (green patches) could be seen on 28 October over north Bay of Bengal. On 29 October, the lowest SST of 22.4°C could be seen at 17.4°N; 88.9°E, which suggests a cooling of about 6°C due to the passage of the super cyclone (Figure 2). Outside the storm area, the SST was greater than 27°C and a moored buoy at 13°N, 87°E recorded SSTs of 29.9 to 29°C during 25 to 29 October[3]. TMI SST data also show values more than 29°C at this location during the above period (Figures 1 and 2). It may be inferred that a decrease of 6°C occurred in SST due to the passage of this super cyclone, which was observed for the first time in the Bay of Bengal. From the IRS-P4 OCM data, the chlorophyll concentrations were of the order of 1 mg/m^3 before the super cyclone and enhanced to 20 mg/m^3 off Orissa coast after the passage of the super cyclone[4], which supports the above view. The signature of the super cyclone could be seen on the SST field over north Bay of Bengal on 30 and 31 October 1999 (Figure 3) and the low SST cell (green patch) could be seen in northwestern Bay of Bengal along the track of the cyclone. It may be mentioned here that 1–6°C decrease of SST

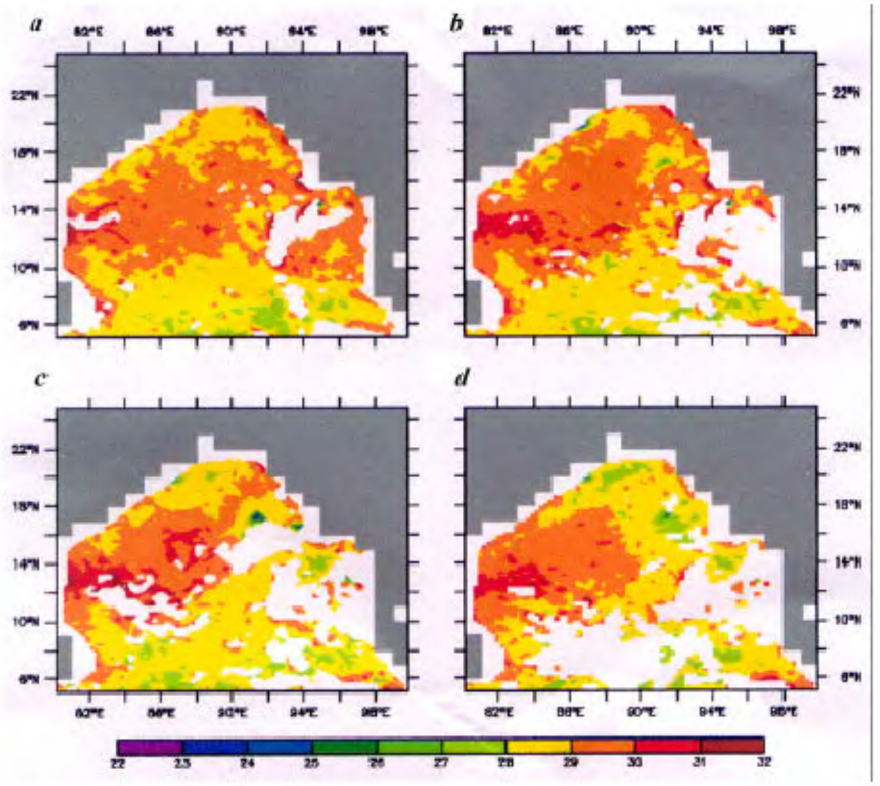

Figure 1. TMI SST images on (*a*) 25 October, (*b*) 26 October, (*c*) 27 October and (*d*) 28 October 1999.

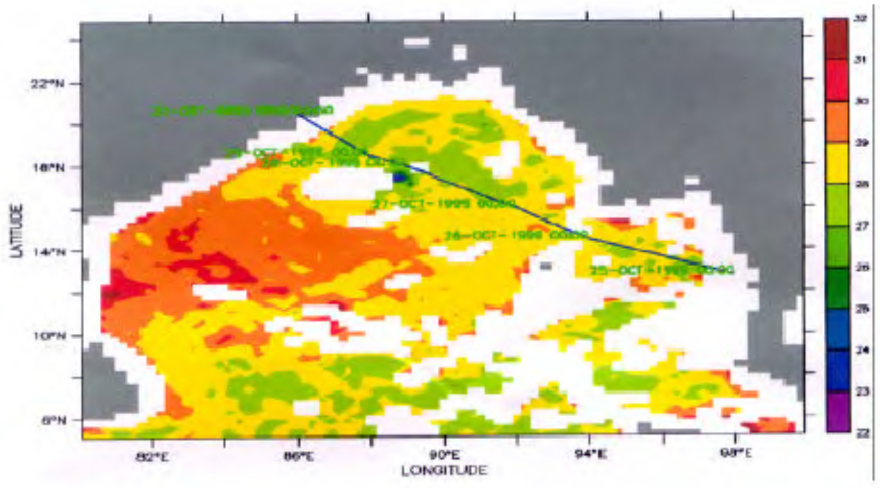

Figure 2. Track of the super cyclone in the Bay of Bengal from 25 to 29 October 1999 (thick blue line). Lowest SST of 22.4°C at 17.4°N; 88.9°E could be seen from the third day TMI SST data ending with 29 October, which suggests a cooling of about 6°C after the passage of the super cyclone.

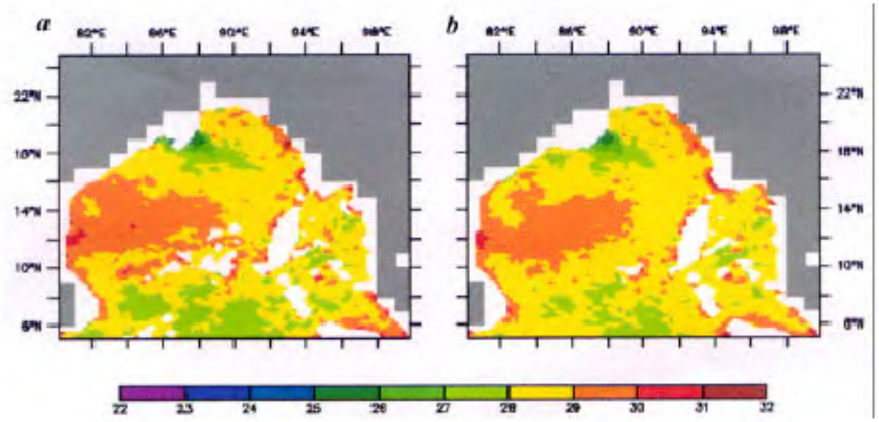

Figure 3. TMI SST images on (*a*) 30 October and (*b*) 31 October 1999.

is quite common in the Atlantic Ocean and Gulf of Mexico, following the passage of a hurricane[5].

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Interlocus homogenization of ribosomal DNA repeat units in barley

Eukaryotic ribosomal RNA genes that encode 18S, 5.8S and 26S ribosomal RNAs (rRNAs), are found as parts of repeat units that are organized as tandem arrays, located at the chromosomal sites known as nucleolar organizing regions (NORs). These ribosomal repeats at one or more loci constitute what is described as ribosomal DNA (rDNA). The ribosomal repeat units at an individual NOR are present in hundreds to thousands of copies[1]. Each rDNA repeat unit consists of a highly conserved coding region (for 18S, 5.8S and 26S rRNAs) and a variable non-coding intergenic spacer (IGS) region. Each IGS in its turn contains a set of subrepeats which range in size from about 100 bp to about 4000 bp in different plant species[2]. Generally, variation in the length of rDNA repeat units occurs due to variation in the size of the IGS region that itself depends on the variation in the number of intergenic spacer subrepeats. This variation in the number of subrepeats alters the length of the whole spacer region, leading to the occurrence of spacer-length-variants (slvs). These slvs at a locus are described as rDNA alleles and can be identified by restriction enzyme digestion coupled with Southern hybridization[3–9].

Barley has two major rDNA loci (*Rrn1* on chromosome 6 or 6H and *Rrn2* on chromosome 7 or 5H). Each barley rDNA repeat unit has two restriction sites for *Sac*I, one in the 18S and the other in the 26S region. Consequently, on digestion with *Sac*I, each ribosomal repeat will produce two DNA fragments; one of them containing the coding region would be constant in size, and the other containing full IGS and a part of the coding region would be variable in size. Such a feature is easily resolved as two bands that are visualized on Southern blots after hybridization with a ribosomal DNA probe. If there are two loci, as in barley, they will each produce a constant band and a variable band, so that one denser constant band is observed along with two lighter variable bands, which represent two slvs. Sometimes, three to five slvs are also observed in barley accessions either due to presence of complex loci or due to heterozygosity, but a solitary slv associated with two loci is only rarely observed.

For a study of ribosomal DNA polymorphism, we used 42 wild barley accessions collected from four eco-geographically contrasting microniches (sun-deep soil, sun-shallow soil, shade-deep soil and shade-shallow soil) of Newe Ya'ar microsite (3182 m^2) in Israel and supplied to us by E. Nevo from Haifa (Israel). We digested appropriate amounts of DNA of each of these 42 wild barley accessions with *Sac*I restriction enzyme. Digested DNA was fractionated by electrophoresis on 1% agarose gel for 16 h at 4 V/cm, blotted to nylon membrane (Hybond N+) and subsequently hybridized with α^{32}P-labelled wheat rDNA probe pTA71. Membranes were exposed to X-ray films for

Table 1. Frequencies of different rDNA slv phenotypes in 42 accessions of wild barley (*H. spontaneum*) from Newe Ya'ar, Israel

slv phenotype	No. of accessions	Frequency
105	2	0.0476
106	2	0.0476
107	11	0.2619
108a	4	0.0952
108	4	0.0952
109	12	0.2857
110	2	0.0476
108a, 110	3	0.0714
108, 113	1	0.0238
109, 113	1	0.0238
Total	42	1.00