Cochran, Stow et al 1987

clear; the issue raised is not without interest. But by allowing individual replies to each criticism of the original idea, Dessler placed the burden of proof on critics to show that their objections were valid. The debate has thus been turned inside-out. The burden of proof should have been squarely on Frank *et al.* to examine other data sets or otherwise to find positive evidence for the existence of these objects.

This is precisely what Donahue *et al.*, in their paper in this issue, have done[4]. Previously, Donahue[8] had shown that even at the low rate claimed by Frank *et al.* for the outgassing of water by the CLO, the number of hydrogen atoms produced by the dissociation of water by solar ultraviolet light would far exceed the known abundance of these atoms derived from many years of observations of the interplanetary Lyman-$\alpha$ glow[9]. But when he and his colleagues searched the records from the ultraviolet spectrometer experiments on Voyagers 1 and 2, they found that the concentration of hydrogen atoms between the orbits of Earth and Mars is indeed greater than that produced by the motion of the Solar System through the interstellar medium. By using a size distribution that matches the known rate of lunar cratering, Donahue *et al.* can produce the required hydrogen-atom abundance with 10 million times fewer CLOs per minute than Frank *et al.* and in so doing avoid many of the pitfalls in the hypothesis of Frank *et al.*.

The catch? These CLOs are the absolute inverse of the CLOs of Frank *et al.*. They have refractory cores surrounded by mantles of pure water ice. These, too, escape detection by ground-based astronomers, whose charge-coupled-device detectors would be sensitive to sunlight scattered from the smallest amount of dust impurities released by evaporation from a dirty surface (as happens with real comets). Moreover, the CLOs of Donahue *et al.* would account for all the lunar cratering, leaving no allowance for cratering by non-icy asteroidal debris.

The virtue of the analysis of Donahue *et al.* is that it is testable by instruments that are either available or that soon will be. The Galileo mission to Jupiter and its moons, postponed as a result of the Challenger accident, will reach the planet via a swing-by of Venus and two of Earth. Thus, the ultraviolet spectrometer on the spacecraft will be able to measure the Lyman-$\alpha$ emission between Venus and Jupiter. The most appropriate evidence would be the direct detection of a CLO or several CLOs, which would be difficult because of their proposed flux. In fact, Donahue *et al.* have deliberately described a CLO that would avoid detection by any of the several current search programmes for faint, slow-moving asteroids.

Fluorescent emission by hydroxyl (OH) radicals, produced by the dissociation of water, could also reveal the CLOs. This emission, at a wavelength of about 310 nm, is produced by real comets[10], and is more intense than Lyman-$\alpha$ emission, especially near the cometary nucleus. It is difficult, although not impossible, to see the fluorescence from Earth, because of attenuation by ozone in the atmosphere. NASA's comet rendezvous asteroid flyby mission now being planned will have cameras with narrowband OH filters that could be used to search for CLOs on the journey to the periodic comet Tempel-2.

What is the origin of CLOs, whatever their form? Presumably they are primordial remnants from the formation of the Solar System and share many of the known characteristics of the observed comets. It is difficult, however, to imagine that kilometre-sized comets were formed by aggregation of the CLOs proposed either by Frank *et al.* or by Donahue *et al.*. Anticipating this problem, Frank and his group have come up with a model of the Oort cloud which carefully segregates the different types of objects in the cloud, thus allowing them to respond differently to different stellar perturbations. The bottom line of this model, which was presented at the recent meeting of the Division for Planetary Sciences of the American Astronomical Society (Pasadena, 10–13 November 1987), is the prediction of periodic extinctions of terrestrial flora and fauna by showers of the more massive members of the cloud. Is there any wonder that the community remains sceptical? □

1. Raup, D.M. & Sepkoski, J.J. *Proc. natn. Acad. Sci. U.S.A.* **81**, 801–805 (1984).
2. Whitmire, D.P. & Jackson, A.A. *Nature* **308**, 713–715 (1984).
3. Davis, M., Hut, P. & Muller, R.A. *Nature* **308**, 715–717 (1984).
4. Donahue, T.M., Gombosi, T.I. & Sandel, B.R. *Nature* **330**, 548–550 (1987).
5. Frank, L.A. *et al. Geophys, Res. Lett.* **13**, 303–306 (1986).
6. Frank, L.A. *et al. Geophys. Res. Lett.* **13**, 307–310 (1986).
7. Seabrook, W. *Doctor Wood* (Harcourt Brace, New York, 1941).
8. Donahue, T.M. *Geophys. Res. Lett.* **14**, 213-215 (1987).
9. Ajello, J.M., Stewart, A.I., Thomas, G.E. & Graps, A. *Astrophys. J.* **317**, 964 (1987).
10. Feldman, P.D. *Science* **219**, 347–354 (1984).

*Paul D. Feldman is Professor of Physics and Astronomy at the Johns Hopkins University, Baltimore, Maryland 21218, USA.*

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## Ocean Drilling Program

# Collisions in the Indian Ocean

*Leg 116 shipboard scientific party*[*]

On Leg 116 of the Ocean Drilling Program, we investigated the tectonic and sedimentological effects of the continental collision between India and Eurasia near the equator in the central Indian Ocean, over 3,000 km from the Himalaya collision zone (Fig. 1). We found that major uplift of the Himalayas had begun by the early Miocene, earlier than previously reported. We also investigated the timing and nature of faulting within a wide area of intraplate deformation and studied sediment sources and depositional processes on the distal Bengal Fan.

Continental collision began in the Eocene with a 'soft' collision, probably between continental India and an island arc seawards of Asia[1,2]. Convergence between the two continents continued, perhaps consuming a back-arc basin. The 'hard' continent–continent collision is thought to have begun later, resulting in the first main uplift of the Himalayas[3,4]. Continued seafloor spreading at the Southeast Indian Ridge combined with growing resistance to shortening between India and Asia implies that the central Indian Ocean is under a large north–south compressive stress regime.

Classical plate tectonics assumes that large lithospheric plates behave as rigid units that deform only at their boundaries. The Indian–Australian Plate seems not to be behaving in this manner, rather it has been compressively deformed in its interior[5-7]. The most spectacular and direct evidence from this deformation is the large-scale folding and faulting between the Chagos–Laccadive Ridge and the Ninetyeast Ridge and from 5° N to 10° S. Within the affected region, the oceanic crust and the overlying sediments are deformed into long-wavelength (100–300 km) folds with peak-to-trough amplitudes of 1–3 km. Superimposed on the long-wavelength undulations are faulted and deformed blocks, bounded by high-angle faults 5–20 km apart, which offset the top of the crust by up to 500 m (Fig. 2).

Rapid terrigenous sedimentation on the

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[*] Co-chief scientists: James Cochran (Lamont-Doherty Geological Observatory, Palisades, New York) and Dorrik A.V. Stow (Department of Geology, Nottingham University). ODP Staff Scientist: Christian Auroux (Ocean Drilling Program, Texas A&M University, College Station). Also, Kazuo Amano (Department of Earth Sciences, Ibaraki Univ.), Peter S. Balson (British Geological Survey, Keyworth), Jacques Boulegue (Laboratoire de Geochimie, Univ. Pierre et Marie Curie), Garrett Brass (Univ. Miami), Jeffrey Corrigan (Dept. Geological Sciences, Univ. Texas, Austin), Stefan Gartner (Dept. Oceanography, Texas A&M University), Stuart Hall (Dept. Geosciences, Univ. Houston), Silvia Iaccarino (Istituto di Geologia, Univ. Parma), Toshio Ishizuka (Ocean Research Institute, Univ. Tokyo), Irena Kaczmarska (Mount Allison Univ. Sackville, New Brunswick), Heidemarie Kassens (Geologisch-Palaeontologisches Institut, Univ. Kiel), Gregory Leger (Dept. Oceanography, Dalhousie Univ.), Franca Proto Decima (Istituto de Geologia, Univ. Padova), Venkata Challagundla Raman (Dept. Geology, Andhra Univ., Visakhapatnam), Will Sager (Dept. Oceanography, Texas A&M Univ.), Kozo Takahashi (Woods Hole Oceanographic Inst.), Thomas Thompson (580 Euclid Avenue, Boulder), Jean-Jacques Tiercelin (Oceanologie et Geodynamique, Univ. Bretagne), Mark Townsend (Dept. Geology, Univ. Nottingham), N.P. Wijayananda (Oceanography Unit, Natn. Aquatic Resources Agency, Colombo), Andreas Wetzel (Geologisches Inst., Tubingen), Colin Williams (Lamont-Doherty Geological Observatory).

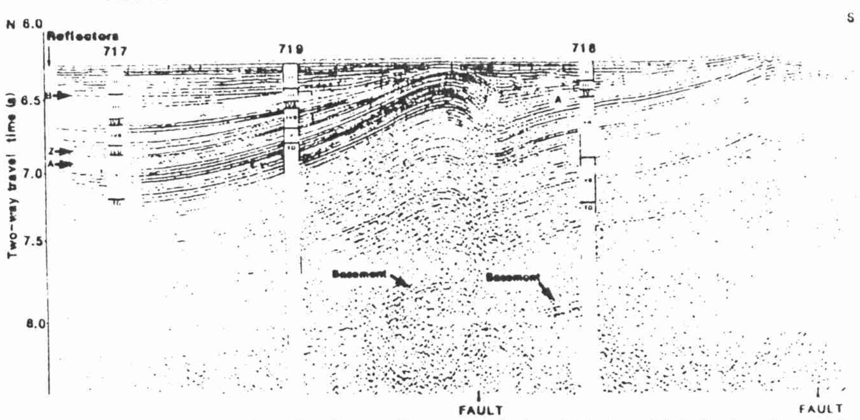

**Fig. 2** Single-channel seismic reflection profile across the Leg 116 sites. Lithologic units are shown at location of sites with depth converted to two-way travel time. Unconformities A and B and reflector Z are noted to left of the profile. Total length of the seismic line, 18.5 km.

incipient Bengal Fan began in the Eocene as a response to the first interplate collision[1,2] and has continued to the present, producing the world's largest submarine fan. The Bengal Fan is more than 2,500 km long and is at least 16 km thick under the northern Bay of Bengal. The sediment is 1.5–2 km thick under the distal part of the fan near the Leg 116 sites.

We investigated the timing and development of the intraplate deformation by drilling a pair of companion sites on one of the fault blocks that make up the tectonic fabric of the region (Fig. 2). Site 717 is in the thickest part at the axis of a syncline in the sediments between the faults. It was designed to obtain a complete section of sediments where the unconformity marking the onset of deformation seems to have become conformable on seismic-reflection records. Site 719 is partway up the block in an area where the syndeformation sediments are thinner.

Sediments at both sites consist almost entirely of fan turbidites. The sedimentary sections correspond closely, and many distinctive individual turbidites and turbidite sequences between the two sites can easily be correlated. Attenuation of the section between sites 717 and 719 seems to have occurred by the pinching out of beds and the thinning of individual turbidites. Some intervals show marked reduction of thickness, whereas others are less attenuated. But in general it seems that the process has continued steadily ever since the onset of faulting, and therefore motion on the fault has been gradual and fairly constant. The rate of motion may have increased slightly with time. We penetrated the seismic horizon marking the onset of deformation (A in Fig. 2) at all the Leg 116 sites, and we find it is about 7 Myr old. There has been about 350 m of uplift across the fault, so that the average rate of motion has been about 50 m Myr$^{-1}$.

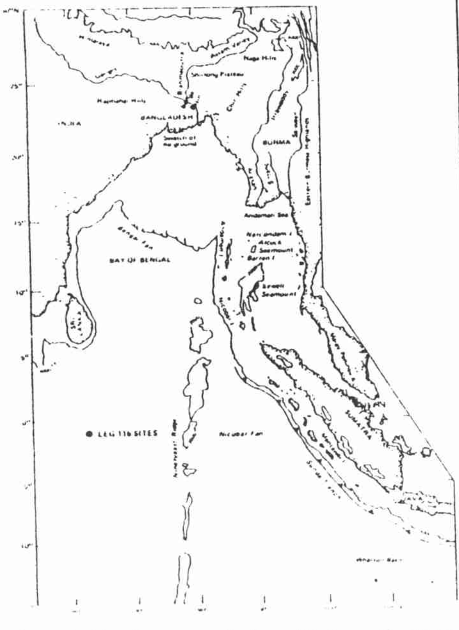

Fig. 1 Northeastern Indian Ocean, showing the location of the Leg 116 sites.

The limiting factor in determining the deformation history is the resolution that can be obtained on stratigraphic ages. Biostratigraphic control at all the Leg 116 sites is provided primarily by calcareous nannofossils, because the other microfossil groups are either absent or poorly preserved. But, subject to the resolution provided by the nannofossil zones, the data from sites 717 and 719 will allow us to determine the detailed history of the motion of the fault block. This will in turn provide constraints for theoretical modelling of the deformation process.

These two sites, particularly site 717, where the section appears complete, also yield a record of sedimentation on the distal Bengal Fan since the late Miocene, showing the nature, thickness and vertical succession of turbidites that have been transported as much as 2,500 km from the head of the fan. A thin layer of mud and clayey ooze overlies a sequence dominated by micaceous silty turbidites which accumulated very rapidly during the late Pleistocene at greater than 350 m Myr$^{-1}$ (Fig. 2, Lithologic unit II). This region constitutes a distinctive seismic stratigraphic unit which, in places, truncates lower reflectors. These relatively coarse-grained, rapidly deposited turbidites probably reflect the Quaternary uplift of the Himalayas, which provided a massive source of sediments. The silty turbidites overlie a thick section of mainly mud turbidites and thin interbedded pelagic clays that accumulated at a slower average rate of about 70 m Myr$^{-1}$ from the late Miocene to early Pliocene (Fig. 2, Lithologic units III and IV). We have tentatively identified at least three distinct sources of turbidites: silts and muds from the Ganges–Brahmaputra delta, which constitute the largest component; dark grey organic-rich muds with up to 5 per cent terrigenous plant debris from the upper slope of the Bay of Bengal; and almost white, carbonate-rich, biogenic turbidites, probably from a local seamount.

Site 718, on the next fault block south from sites 717 and 719, where the post-Miocene section is greatly attenuated (Fig. 2), provided an opportunity to probe further back into the sedimentary history of the distal Bengal Fan. At this site, we obtained a sedimentary section to a depth of 960 below the sea floor, penetrating 775 of the approximately 1,200 m of pre-deformation sediment. One surprising result is the age and thickness of the fan. At the base of the hole, fan sediments of early Miocene age (17 Myr old) were still being penetrated with no evidence of approaching the base of the fan. Almost the entire Miocene section consists of silt and silty mud turbidites. Intervals up to 20 m thick of reddish brown pelagic clay and thin greenish silt-clay turbidites occur below a depth of 600 m below the sea floor. These intervals represent periods of slowed sedimentation and, possibly, the influx of turbidites from a different source such as the eastern Indian or Sri Lankan margin. The average sedimentation rate was about 70 m Myr$^{-1}$ throughout the Miocene. The Bengal Fan was well established at the Leg 116 sites (2,500 km from the Ganges delta) by the early Miocene and has been receiving sediment, including wood fragments and even coarse sand-sized grains ever since, suggesting that the main uplift of the Himalayas occurred earlier than is generally assumed.

A second surprise came from downhole temperature measurements. Site 718 is on an area of high local heat-flow to enable study of the effects of high heat flow on sediment and of hydrothermal circulation. We found dramatic evidence of vigorous hydrothermal circulation in the form of a temperature inversion. Temperatures in the silty turbidites of Lithologic unit II were scattered and were actually higher than in the upper part of underlying clay turbidites of unit III. Warm water appears to be rising up the fault to the north of site 718 (Fig. 2) and to be spreading laterally through permeable layers in the upper silty turbidites. At the same time, cooler sea water must be flowing downwards through silt layers within the clayey turbidites, which appear on seismic records to crop out several kilometres to the south at the tip of the fault block. Our conclusions are supported by geochemical studies of interstitial waters, which show the effects of mixing between two end-members, one of which is sea water and the other a water chemically altered by basement rocks or by diagenetic processes.

Several factors influence sedimentation on the distal Bengal Fan. A primary control is the uplift history of the Himalayas, which are the main source of the sediments. This is seen, for example, in the pulse of coarser-grained silty turbidites in the Pleistocene following a significant phase of mountain building. A second influence is variations in sea level: a sharp rise in sea level near the Miocene/Pliocene boundary[8] could have contributed to the change from silty to more muddy turbidite deposition at that time. A third influence is tectonic activity related to the intraplate deformation. The block containing site 718 has been elevated relative to the block containing sites 717 and 719 (Fig. 2), and as a result the post-Miocene sedimentary history of the two blocks differs considerably. Normal fan processes such as channel migration and lobe switching have also influenced sedimentation. ☐

1. Curray, J.R. & Moore, D.G. *Bull. geol. Soc. Am.* **82**, 563–572 (1972).
2. Curray, J.R. *et al.* in *Ocean Basins and Margins* (eds Nairn, A.E.M. & Stehli, F.G.) Vol 6, 399–450 (Plenum, New York, 1972).
3. Gansser, A. *The Geology of the Himalayas*, (Wiley-Interscience, New York, 1964).
4. Powell, C.M.A. & Conaghan, P.J. *Earth planet. Sci. Lett.* **20**, 1–12 (1973).
5. Eittreim, S.L. & Ewing, J. *J. geophys. Res.* **77**, 6413–6421 (1972).
6. Weissel, J.K. *et al. Nature* **287**, 284–291 (1980).
7. Geller, C.A. *et al. J. geophys. Res.* **88**, 1018–1032 (1983).
8. Haq, B.U. *et al. Science* **235**, 1156–1167 (1987).

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**Molecular endocrinology**

# Growth-hormone receptor cloned

*Michael Wallis*

LIKE most polypeptide hormones and growth factors, pituitary growth hormone (GH) acts by binding to plasma membrane-associated receptors on its target cells. But the mechanisms by which the GH–receptor complex then exerts intracellular effects are poorly understood. GH receptors have been characterized[1] in some detail from several tissues, but the field is a complex one because of species specificity[1], receptor heterogeneity[2-4], and the presence of soluble GH-binding proteins in both cytosol and plasma[5-7]. The paper by Leung *et al.* on page 537 of this issue[8] should help to resolve many of these issues. These authors have cloned complementary (c)DNA encoding GH receptors from rabbit and human liver, have obtained expression of the cDNA clones in cultured monkey COS 7 cells, and show that the amino-terminal sequence of the GH-binding protein in rabbit serum is very similar to that of the membrane-bound receptor in liver.

The authors purified detergent-solubilized GH receptor from rabbit liver and characterized it by SDS polyacrylamide gel electrophoresis, revealing a single main polypeptide of $M_r$ about 130,000, considerably greater than that found previously using crosslinking studies[1]. Leung *et al.* synthesized an oligonucleotide probe which they used to identify clones in a rabbit liver cDNA library. From these they determined the sequence of a full-length cDNA corresponding to GH receptor messenger (m) RNA, from which they showed that the amino-acid sequence of the receptor comprises 620 residues plus an 18-residue signal peptide (see figure). A hydrophobic region from residues 247–270 probably represents a transmembrane domain, leaving 246 residues at the amino-terminal end as an extracellular domain, which presumably binds GH, and 350 residues on the cytoplasmic side of the plasma membrane, presumably involved with signal transduction. The $M_r$ derived from the sequence (~ 65,000) is less than that observed for the receptor purified from liver, which can be largely accounted for by glycosylations (there are five potential glycosylation sites in the extracellular domain). Some of the liver-derived receptor molecules are linked to ubiquitin ($M_r$ ~ 9,000), a protein that may be involved in regulation of receptor turnover.

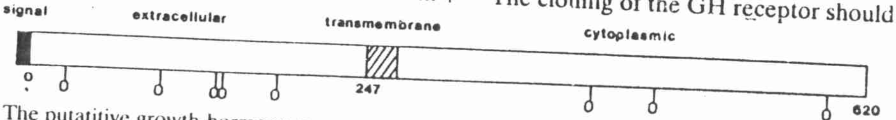
Using fragments of the rabbit cDNA as probes, Leung *et al.* identified clones in a human liver cDNA library, from which they derived the sequence of a full-length cDNA for a putative human GH receptor. The human and rabbit receptors are very similar, showing about 84 per cent identity in amino-acid sequence; this homology is considerably greater than shown by the corresponding GHs, and is surprising in view of the species specificity of biological responses to GH.

To establish whether the cDNA sequences obtained correspond to the complete receptors, Leung *et al.* constructed expression plasmids containing the full coding sequence of the rabbit receptor and a coding sequence for the extracellular domain of the human receptor, and introduced them into monkey COS-7 cells, which normally do not express GH receptors. They found expression of a membrane-associated GH-binding protein in cells transfected with the rabbit receptor cDNA and secretion of a soluble GH-binding protein by cells transfected with human receptor cDNA. These binding proteins have specificities similar to those of receptors derived from normal tissues in that the rabbit protein can bind human GH, bovine GH and to a lesser extent ovine prolactin, whereas the human protein can bind human GH but not bovine GH or ovine prolactin. This observed species specificity for receptor binding is very similar to that seen in the biological actions on growth promotion, providing strong evidence that the cDNAs cloned correspond to receptors that mediate the growth-promoting effects of GH.

Leung *et al.* also show that the amino-terminal sequence of the soluble GH-binding protein found in rabbit serum is identical to that of the GH receptor in liver. The soluble binding protein probably represents the extracellular domain of the receptor produced either by proteolytic cleavage or altered processing of a precursor of the receptor mRNA. The studies on cDNAs do suggest that some of the mRNA in liver could encode a variant form of the receptor lacking most of the intracelluar domain, but it is not clear whether this is the secreted binding protein.

The work of Leung *et al.* will have a significant impact on our view of the GH receptor. It provides a definitive sequence for the membrane-bound GH-binding proteins in rabbit and human liver and demonstrates that the differences between species are less than previously suspected. This single polypeptide (after glycosylation) is all that is needed for GH binding, although it is not yet established whether other subunits are needed for biological activity. It is likely that these binding proteins really are the biological receptors for the growth-promoting actions of GH, because the species specificity for hormone binding clearly matches that for biologial activity. The paper also clarifies the relationship between the GH receptor and the GH-binding protein in serum. It provides few clues, however, about the mechanism of signal transduction. The receptor sequence is not related to known tyrosine-kinase growth-factor receptors, or indeed to any other known protein.

The cloning of the GH receptor should



The putatitive growth-hormone receptor precursor is a polypeptide chain of 620 residues plus an 18-residue signal peptide. A hydrophobic region (residues 247–270) probably constitutes a single transmembrane domain. Eight asparagine residues (circles) are potential glycosylation sites.