

## Turtle recovery could take many decades

Under current protective laws, it would take at least 70 years to achieve a 10-fold increase in populations of the loggerhead sea turtle off the coast of the southeastern United States, according to a new computer forecast. Wider use of turtle excluder devices (TEDs) — trapdoor-like mechanisms that allow sea turtles to escape shrimp-trawling nets — would reduce this recovery time by only 30 to 40 years, the forecast indicates.

Biologists consider a 10-fold population increase crucial to saving this threatened species.

The new computer model is the first to take into account the differing effects of TEDs on the survival of loggerhead turtles of various ages and sizes, says Selina Heppell, a biologist at North Carolina State University in Raleigh. Heppell described the model last week at the joint annual meeting of the American Institute of Biological Sciences and the Ecological Society of America, held in Honolulu.

Because TEDs are less effective in saving smaller, younger turtles, she says, the model suggests that fewer than anticipated numbers of loggerheads will survive to reproductive age.

Most TEDs consist of a panel of metal bars inserted into a trawling net at an angle leading up to a hole in the top of the net. The bars are designed to allow shrimp to pass through and accumulate in the sack-like end of the net, while diverting larger marine animals — such as sea turtles — up and out of the net through the hole.

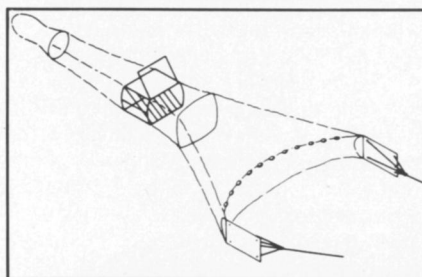
The U.S. National Marine Fisheries Service (NMFS) estimates that TEDs have slashed by 67 percent the annual mortality rate of sea turtles caught in trawling nets in U.S. coastal waters since the 1988 enactment of a federal law requiring shrimp trawlers to use the devices during selected times of the year in most offshore areas. Despite the use of TEDs, however, the NMFS projects that at least 4,360 sea turtles inhabiting U.S. coastal waters will drown in trawling nets this year.

Heppell's forecast rests on the assumption that TEDs reduce the mortality rate of net-trapped juvenile loggerheads by only 34 percent each year, because these smaller turtles sometimes get swept between the bars of the devices and become caught in the nets. This potentially fatal generation gap skews the demographics of the loggerhead population toward older turtles with fewer remaining reproductive years, Heppell says. This, in turn, slows the recovery rate of the species as a whole, she asserts.

"TEDs have had a very positive effect

on increasing the population [of loggerhead turtles]," Heppell says, "but 70 years is a longer time to see a 10-fold population recovery than we'd expected." She adds that although the number of nesting loggerheads has increased within the past three years, indicating the overall benefits of TEDs, "we have to be a little cautious in saying we've found the answer to saving the [loggerhead] turtle population. . . . It's going to take a long time."

Last April, the NMFS proposed new regulations that would expand the requirements for TED use by mandating trawlers to use TEDs year-round at all U.S. inshore and offshore locations. This would achieve a 97 percent reduction in



A turtle excluder device (slanted bars) provides an escape hatch for sea turtles accidentally swept into a shrimp-trawling net.



A loggerhead sea turtle on the beach.

trawler-related turtle mortality, according to agency estimates.

However, the proposal does not call for new TED designs less likely to trap juvenile loggerheads. Nor does it address what Heppell describes as a potential threat to all sea turtles: the harvesting of sargassum, a type of seaweed that grows in floating mats.

Commercial harvesting of these vast mats for use in pharmaceuticals or livestock feed could destroy an important habitat for "small juvenile" sea turtles, Heppell says. According to her model, this category of juveniles constitutes the second most important age group for the recovery of the loggerhead population. Increasing the mortality rate of small juveniles through sargassum harvesting could delay a 10-fold increase in loggerheads to 140 years, Heppell projects.

— C. Ezzell

## Shaking and baking to atomic positions

An expert crystallographer can take literally years to work out, largely by trial and error, the positions of atoms in a given molecule. An innovative, computer-intensive method of extracting information directly from X-ray diffraction data now offers the possibility of cutting that time to hours.

In a recent test of this new method, researchers needed only a few hours of computer time to provide the information needed to find the positions of 104 atoms in pairs of molecules of a compound related to the immune-suppressing drug cyclosporin. Using more conventional methods, Russian scientists had spent nearly a decade trying to determine its structure — without any success.

The researchers who developed the technique, led by Herbert A. Hauptman of the Medical Foundation of Buffalo and the State University of New York at Buffalo, announced their achievement at last week's American Crystallographic Association meeting, held in Pittsburgh. This success marked the first time the researchers had applied their technique to a large molecule with a previously unknown structure.

The technique has the potential to dramatically accelerate the designing of drugs for specific purposes, a process that relies on knowledge of chemical structures of molecules, Hauptman says.

In X-ray crystallography, researchers bombard a single crystal of a given substance with X-rays of a certain wavelength. The orderly rows of atoms within the crystal deflect these X-rays in particular directions to produce a distinctive pattern of spots on a photographic plate.

The positions and intensities of these spots, which could number in the thousands, provide information about the locations of atoms within molecules of the given substance. But that isn't enough to draw a complete three-dimensional portrait of the unknown molecule. Because they don't know the times when X-rays arrived at each spot, crystallographers generally lack information about the so-called phase relationships of the diffracted X-rays. And because they need both intensity and phase data to find a molecular structure, experts must often rely on informed intuition to aid in unraveling a molecule's structure.

Several years ago, Hauptman proposed a mathematical formula that he claimed could be used for zeroing in on the missing phase information. This complicated formula exploits subtle relationships between phases and measured diffraction intensities. If one could minimize the value of this complicated expression containing thousands of variables, one could solve the phase problem.