errors, so there is no excuse not to.' I think the savvy groups are already doing so."

There are two types of sequencing errors: the substitution of one base for another; and the insertion or deletion of one or more bases. Substitution errors are not particularly bothersome, say numerous sequencers, but insertions and deletions can be catastrophic. That is because of the nature of the genetic code, in which a group of three nucleotides encodes one amino acid. If an extra base is thrown in, it causes a shift in the reading frame used to translate the code, thereby confounding efforts to work out the amino acid sequence of the protein encoded by the gene.

What Roberts has come up with, in collaboration with Janos Posfai of the Institute of Biophysics at the Hungarian Academy of Science, is a simple new program called DETECT that finds these potential frameshift errors. It works by comparing all possible translations of the newly determined DNA sequence to every sequence in a protein database. The program then looks for regions of the new sequence that would resemble a protein already in the database if a base were added or removed.

Finding such a "hit" doesn't necessarily mean that the new sequence is in error, Roberts points out, but rather shows places where the data should be rechecked. Sometimes it is the database sequence that is wrong. And if no error is found, then "something biologically interesting" is likely to be going on, says Roberts. Indeed, he has already found an example of a phenomenon known as ribosomal frameshifting, in which a gene contains extra bases in the coding region that must be skipped over during translation.

Roberts and Posfai have tested their program on sequences in GenBank that flank known bacterial genes, reasoning that these regions were more likely to contain errors than the well-studied genes. They examined a total of 6000 unidentified reading frames, spanning 1.3 million bases—about 4% of the database. "In 156 cases, the program predicted what we consider clear errors," says Roberts. Based on that first run, Roberts suspects that the program might detect several thousand errors in GenBank.

Roberts is quick to point out that DETECT is just a first step in developing computer tools for sequence error detection. The program's greatest limitation is that it works only for those genes that have known relatives already in the database; only about 30% of newly determined sequences now do. But as more and more of the human genome is sequenced, as well as the genomes of other organisms, the chances of finding a match will shoot up quickly.

Reaction at the Cold Spring Harbor meeting was positive, though Sydney Brenner of the Medical Research Council Laboratory in Cambridge noted that Roberts and Posfai have simply automated what many seasoned sequencers have been doing by hand for some time. But it is the amateurs that Roberts is hoping to convert when he makes the program available in a few weeks. "Most of the people who are sequencing don't do it full time, and they make all the errors that amateurs make." What Roberts wants to instill in these occasional sequencers is "the idea that one should try to find errors *before* saying the sequence is finished," which means before publication.

Even if Roberts fails to get that message across, all is not lost, according to new work by David States of the National Library of Medicine and David Botstein of Stanford, which will be published soon in the *Proceedings of the National Academy of Sciences*. Reasoning that some error is inevitable, States and Botstein set out to determine just how flawed a sequence can be and still be useful, in terms of detecting similar proteins in the database. To their surprise, they found that relatively inaccurate data, with up to 5% substitution errors and 1% frameshift errors, could detect similarities, even to distant relatives—provided the researcher knows there are errors in the sequence and ideally knows roughly where they are. But, States and Botstein say, their findings are not a license to be sloppy: "Our view remains that the goal in molecular sequencing is as high an accuracy as can be practically and economically achieved." ■ LESLIE ROBERTS

Rhino Biology: Keeping Tabs on an Endangered Species

Since humans began taking over their territory, the rhino populations of Asia and Africa have come near extinction, plummeting from an estimated million at the turn of the century to just 11,000 now. Earlier this month, some 300 scientists and conservationists from around the world gathered at an International Conference on Rhinoceros Biology and Conservation, sponsored by the Zoological Society of San Diego, to compare notes on what can be done to save these endangered mammals.

Bursting Bottlenecks

In the 1950s the eradication of malaria in the Ganges River plain of northern India and Nepal enabled farmers and poachers to move into the tall grasslands there. The result: The intruders pushed the Indian or greater one-horned rhinoceros to the brink of extinction. By 1962 fewer than 80 of the creatures remained in what is now the Royal Chitwan National Park in Nepal.

With so few breeding animals left, the Chitwan Park rhinos have long been assumed to be doubly threatened. Like several other near-extinct species—including African rhinos—they were thought to have dramatically low genetic diversity, which would further weaken their survival chances. But when population geneticist Gary McCracken of the University of Tennessee measured genetic variability in the Chitwan Park rhinos, which now number about 400, he got a welcome surprise: It approaches the highest levels ever reported for free-ranging mammals.

"This is good news because it means we needn't expect that all large mammals that have gone through recent bottlenecks should be genetic paupers," says San Diego Zoo geneticist Oliver Ryder. It also leads McCracken and collaborator Eric Dinerstein to suggest that population bottlenecks may have been overemphasized as a cause of low genetic diversity in other threatened species.

Studies performed on more than 200 mammalian species since the early 1970s have shown that, on average, about 4% of an animal's genes are heterozygous, meaning that different variants of the genes were inherited from the mother and father. Genetic heterozygosity in the endangered African rhinos, both blacks and whites, has been measured at less than 2%. Yet similar analyses by McCracken on 23 Chitwan rhinos show an average heterozygosity of almost 10%.

To explain this unexpected finding, McCracken and Dinerstein propose that Indian rhinos acquired high levels of diversity and their African cousins, low levels, before either species suffered its precipitous decline in numbers. Dinerstein, a wildlife ecologist formerly with the Smithsonian/Nepal Terai Ecology Project and now with the World Wildlife Fund, points out that prior to the 15th century, perhaps half a million Indian rhinos ranged in a swath from northwestern Burma, across the floodplain of the Ganges, to northern Pakistan. The creature's high

density, wide distribution, and the tendency of individuals to roam over large distances would have favored the accumulation of high genetic diversity, Dinerstein says.

Then when land-clearing and human settlement began to fragment and destroy the habitat in the 19th century, the rhinos sought refuge in the unpopulated Chitwan valley, perhaps moving in from corridors along malaria-infested riverine systems. "It is possible," McCracken says, "that because of this compression the Chitwan population currently has higher levels of variability than the original populations."

When the drastic population decline occurred in Chitwan, it was rapid and brief, lasting only a single rhino generation—from 1950, when there were at least 1000 animals, to 1962, when there were only 60 to 80—before recovery began. That's not enough time, McCracken says, for significant loss of genetic variability to occur. For that, species must survive population bottlenecks that are very small and repeated or sustained over several generations. Indeed, McCracken and Dinerstein calculate that the Chitwan rhinos have lost less than 3% of their genetic variability from 1950 to the present.

So why then is the genetic variability of the African species so much lower than that of their Indian cousins? McCracken theorizes that their low heterozygosity may have evolved at least in part as a consequence of a series of climatic fluctuations in the Pliocene and Pleistocene that caused repeated contractions and expansions of their range, and thus repeated fragmentation and then coalescing of rhino populations. He suggests that the lower densities and more highly structured social organization of African rhinos may have played a part in their lower genetic variation, too. The reductions in African rhino numbers caused by human poaching may have nothing to do with their low heterozygosity, McCracken says.

Geneticist George Amato of the New York Zoological Society says McCracken and Dinerstein have performed "a very valuable service by pointing out that low variability could quite frankly be just a characteristic of the species." It's important, Amato adds, not to write off conservation of such species as a no-win situation: "People need to recognize that these animals may have been very successful for a long time without having a lot of genetic variation."

Isotopic IDs for Rhino Horn

Trade in rhino horn, valued as a folk medicine in Asia, has long been banned in an effort to protect declining rhinoceros populations. But now the countries of southern Africa, where the rhino herds are stable, want to reopen the trade. Is there a way to do that without providing a laundering place for horns poached from the more endangered Asian and East African populations? There might be, given a foolproof system for determining the origin of any chunk of horn brought to market. Now, archeologist Nikolaas van de Merwe, a professor at both Harvard and the University of Cape Town, says he's found just such a system, similar to the one he devised 2 years ago for tracing the origins of elephant ivory (*Science*, 1 December 1989, p. 1120).

By using a mass spectrometer to analyze the isotopic composition of a horn sample the size of a fingernail paring, van de Merwe can, he says, pinpoint both the donor's species and the park in which it lived. Since black rhinos browse on leaves and twigs while whites graze on grasses, the ratio of carbon-13 to carbon-12 in horn easily delineates the two species. By analyzing for isotopes of three additional elements—nitrogen, which reflects the relative aridity of a region, and strontium and lead, which are clues to the age of the geological substrate—van de Merwe says he can place an animal into a specific park.

Animals Animals

On the brink. *The Indian rhino has come near extinction, but that has apparently not lead to its genetic impoverishment.*

A good way to pinpoint the source of rhino horn may soon be needed if South Africa, Zimbabwe, and Namibia get their way. The three countries, which harbor 75% of the remaining black rhinos and almost 90% of the remaining whites, have stockpiled undisclosed tons of horn since trade was banned in the 1970s. In his country, says Rowan Martin of Zimbabwe's Department of National Parks and Wildlife Management, the costs of protecting rhinos is perceived as "a bottomless pit with little economic return." To take advantage of "the inherent economic value of rhinos" to support their conservation efforts, Zimbabwe and its neighbors plan to propose that they be allowed to sell their stockpiled horn when the member nations of the Convention on International Trade in Endangered Species (CITES) meet next March.

But according to geographer Esmond Bradley Martin of the World Wildlife Fund, who has documented and battled the horn trade for a dozen years, the southern African countries can expect a fight.

Rhino Rumbles

Whales do it. Elephants do it. Now it seems that even syncopated rhinos do it. What they all do is generate infrasonic rumbles—noises too low in frequency to be detected by the human ear.

Elizabeth von Muggenthaler, a senior honors student in animal behavior at Old Dominion University in Norfolk, Virginia, made the discovery last fall while using a sensitive portable recording system borrowed from NASA to capture vocalizations from a female African elephant named Monica at the Virginia Zoological Park. The student got more than she bargained for when she began to pick up an odd sound pattern. Rufus, a male white rhino in the neighboring enclosure, turned out to be the source.

Since then, von Muggenthaler and her supervisor, reproductive biologist Joseph C. Daniel Jr., with the aid of electrical and computer engineer John Stoughton, have made recordings from a dozen more rhinos, of all four captive species (Sumatran, Indian, black, and white) in five U.S. zoos. All the animals produce infrasound in the 5 to 75 hertz range, along with audible moans and grunts. Von Muggenthaler reports preliminary evidence that individuals may have distinctive "infrasonic signatures," with vocalization patterns differing between the sexes. Exchanges between two animals may also have a "conversational quality," she says.

Whether rhinos actually use their infrasonic abilities to communicate over long distances as elephants do remains to be tested. Some researchers at the meeting were skeptical, but wildlife ecologist Kes Hillman Smith of Zaire's Garamba National Park, which shelters the last 28 northern white rhinos, was intrigued by von Muggenthaler's finding. Despite the low rhino density in Garamba, it's not unusual to find several female groups gathered in proximity but out of sight and human hearing from one another, Smith notes. Infrasonic signaling is "something we sort of suspected." ■ YVONNE BASKIN