pologist Eric Delson of the American Museum of Natural History in New York City.

But the rudimentary toolkit prompts other paleoanthropologists to wonder about that road trip itself, and how such ill-equipped Atapuercan ancestors could have ventured so far in the world. "I fail to see how tools like that could give anyone an edge over a sabertooth!" says Clive Gamble of the University of Southampton, U.K.

The tools are not the only Atapuercan puzzle: the affinities of the hominids themselves are somewhat murky. Carbonell says anatomical details of the face suggest that the fossils are distinct from their only known non-African contemporaries, Asian hominids of the species *Homo erectus*. Instead, the researchers say, the fossils appear closer kin to finds from East Africa sometimes called *Homo ergaster*, although the Atapuercans had larger brains. Their teeth, however, share primitive traits with both the African and Asian forms. It may be necessary, Carbonell suggests, to name an entirely new species when more complete material emerges.

The bones also show some connection to later European fossils, although probably not to modern Europeans. Speaking from the field in July, Carbonell noted that while the Gran Dolina fossils are "very primitive, we think they are possibly related to later Europeans such as *H. heidelbergensis*." This is a group, about 400,000 years old, commonly thought to be ancestral to the better-known Neandertals, who appeared in Europe about 160,000 years ago and disappeared about 35,000 years ago, coincident with the advent of fully anatomically modern humans.

Howell, however, suggests it may be a bit early to place the Gran Dolina hominds in the Neandertal family album. If they are "somewhere between 700,000 and 1 million years old, and the next oldest humans in Europe are at 500,000," says Howell, "an awful lot can happen in half a million years." Early local populations such as the Atapuercans can go extinct, to name just one possibility, he notes.

More light on these relationships may be forthcoming, if omens are to be believed. Carbonell's team called the hominid-bearing stratum "Aurora" in honor of the name of the archaeology student who found the fossils. "But this word also means 'dawn' in Spanish," says Carbonell. "Perhaps these fossils represent a new dawn in the Paleolithic archaeology of Europe."

–JoAnn C. Gutin

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MALARIA

How the Parasite Disguises Itself

Like any protracted battle, the fight between the human immune system and the parasites that trigger malaria is fraught with sneak attacks and counterattacks. Sometimes, the immune system wins out. All too often, however, the malaria parasites sneak past the immune defenses and reach the blood vessels in the brain, where they kill their victim by blockading the brain's oxygen supply. Now, new intelligence from the trenches has uncovered the genes responsible for a key strategy that enables the malaria parasite to outsmart the immune system.

Work by three independent teams, one led by Russell Howard of the Santa Clara biotech company Affymax Research Institute, another by Thomas Wellems of the National Institute of Allergy and Infectious Diseases (NIAID), and the third by NIAID's Louis Miller, shows that the malaria parasite avoids detection by the immune system by switching between as many as 150 genes, each encoding a different version of a protein known as EMP-1 (for erythrocyte membrane protein 1). EMP-1, which is made by the parasite after it infects red blood cells, ends up on the surfaces of the cells, and anchors them to blood vessels in the brain and elsewhere. But the EMP-1's surface location also signals the parasite's presence to the immune system, so synthesizing new variants should help the parasite avoid detection. (The results appear in the 14 July issue of *Cell*.)

"Genetic, immunological, and biological data from three different labs have converged on the same group of proteins," says parasitologist Victor Nussenzweig of the New York University Medical Center in New York City. "It's important," he says, because "if you understand the mechanisms that cause cerebral malaria, perhaps you can find a way of preventing it." Such treatments are urgently needed; malaria kills more than two million people each year, often as a result of brain complications. And in many parts of the world, *Plasmodium falciparum*—the parasite that causes the most deadly form of malaria—is resistant to chloroquine, once the mainstay of malarial drug therapy.

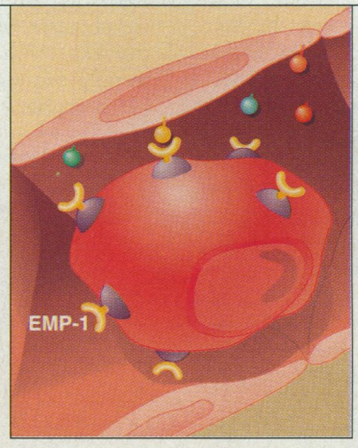

ILLUSTRATION: K. SUTLIFF

Blocking agent. EMP-1 anchors red blood cells to vessel wall.

In fact, the Wellems team originally stumbled on the new genes several years ago while searching for a gene responsible for chloroquine resistance. Three of their candidate genes turned out to be structurally similar, and further work showed they are members of a superfamily of up to 150 related genes scattered across the *P. falciparum* genome. While it soon became obvious that the genes had nothing to do with chloroquine resistance, they nonetheless piqued the Wellems team's interest, in part because they were peculiarly variable—so much so that Wellems and his colleagues dubbed the family the *var* (for variation) family.

The mystery of the *var* genes' function was eventually solved, in part, by Howard and his colleagues at Affymax. Howard has spent 10 years searching for the *P. falciparum* EMP-1 genes under the conviction that EMP-1 proteins—which have yet to be fully characterized—are central to the malaria parasite's disease-causing capabilities. By last August, the Affymax workers had finally identified two candidate genes and shown that, when inserted into bacteria, they synthesized EMP-1 as expected. When the Affymax and Wellems teams compared their genes' sequences, they found that they were looking at the same ones.

"We showed that the genes correspond to the EMP-1 proteins," says Howard, "and [Wellems] provides very nice evidence of a large family of genes, which means that the parasite has a great capacity for variation to evade the immune response." Other evidence that the *P. falciparum var* genes encode the EMP proteins came when Miller and Chris Newbold of the University of Oxford, U.K., showed that different *var* genes are turned on in malaria parasites that synthesize different types of EMP-1.

Indeed, earlier work from the Newbold laboratory had shown that about one in every 50 of a new generation of parasites secretes a different EMP-1 protein, although at that time the genes responsible for the changes were unknown. As a result, these altered parasites can dodge the immune responses that had been mounted against the original parasites, allowing them to set off a new wave of infection, and to lodge in the blood vessels of the brain and other organs.

Now that the genes responsible for that variation have been found, it's back to "the trenches," says Howard. The hope is that the *var* genes and the EMP-1 proteins they encode will eventually lead to some much-needed new anti-malarial drugs that can keep EMP-1 from attaching red blood cells to blood vessels.

–Rachel Nowak