The Armageddon Virus

A virus that can wipe out humanity, the so-called doomsday virus or Armageddon virus, has been the topic of many sci-fi thrillers. The question is how real is it? Or is it just that, science fiction, or are we living in the shadow of annihilation?

By JC Ryan

"Like so many epidemics before, the loss of so many lives began with a single microscopic organism. It's human nature to seek even the smallest comfort in reason, or logic for events as catastrophic as these. But a virus doesn't choose a time or place. It doesn't hate or even care. It just happens."- F**rom the 2008 movie - Doomsday**

Contents

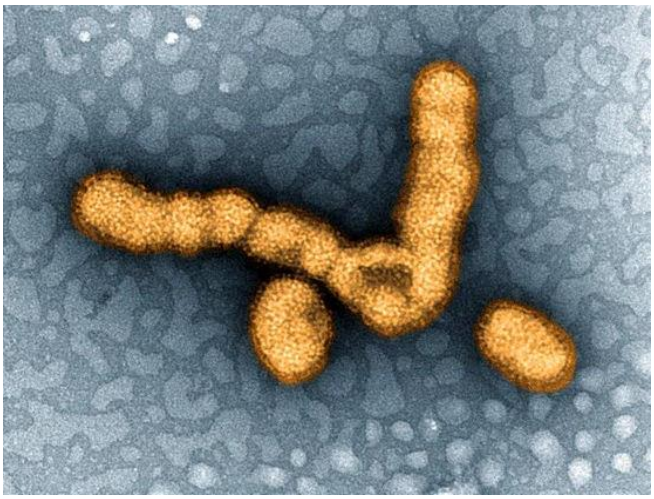
The age-old battle

Humans have been battling viruses since before our species had even evolved into its modern form. For some viral diseases, vaccines and antiviral drugs have allowed us to keep infections from spreading widely, and have helped sick people recover. For one disease — smallpox — we've been able to eradicate it, ridding the world of new cases.

But then we have to remember the Ebola virus now devastating West Africa, which demonstrates we're a long way from winning the fight against viruses.

The strain that is driving the current epidemic, Ebola Zaire, kills up to 90 percent of the people it infects, making it the most lethal member of the Ebola family. "It couldn't be worse," said Elke Muhlberger, an Ebola virus expert and associate professor of microbiology at Boston University.

What we might do to each other and ourselves now.



Imagine if a scientist created a virus that we have never seen before? Think it can’t happen? In June of 2014, it was reported that scientists in the US used fragments of avian flu found in wild ducks to create a strain of flu close to the H1N1 of 1918, to demonstrate how easily it could be done. Interestingly, the article cited the strain as ‘extinct’. I wouldn’t count on that — it came from somewhere in nature before and is likely still out there.

More importantly, the experiment has come under sharp criticism from other scientists, who cited the dangers of an engineered virus to humans if it should accidentally escape the laboratory. The genes of the laboratory virus were only

97% identical to the Spanish flu genes recovered from frozen corpses. And yet, it retained the ability to sicken experimental animals chosen for their similarity to human immune systems.

Despite the ravages of naturally occurring pandemics, the specter of bioweapons being formed from these and other deadly substances such as anthrax, smallpox, and hemorrhagic viruses are perhaps the most realistic of today's potential man-made cataclysms. These are the plots of thriller fiction and the nightmares of people whose jobs are to anticipate and prevent such things from occurring. In my book, ***Genetic Bullets***, you will find a fictionalized version of just such a scenario.

How does a government protect against a lone terrorist with a home-based laboratory capable of producing a highly toxic poison from a common castor oil plant? Or a terrorist organization, with highly sophisticated scientists who have access to controlled biologic agents?

Could our knowledge save us?

Is such a disaster even possible in this day and age of medical and scientific advances?

I am not so sure that we could rely on our medical and scientific prowess to save us. We know that to this day, despite our advances in science and medicine we have not even found a cure for the common cold — a short-lived and relatively mild illness.

Don't believe me? Take a moment and look at the extracts from the following three articles. Note the publication dates.

What is the common cold and why is there no cure for it?

In this article by Jodie Tyley Wednesday 2 December 2015 she concludes: *"While we can treat the symptoms of a cold, we cannot find a single cure as there are so many types of virus and they mutate rapidly. Therefore, in the time it takes to develop a vaccine, it is no longer useful."*

You can read the full article here:

http://www.independent.co.uk/life-style/health-and-families/features/why-is-there-no-cure-for-the-common-cold-a6756836.html

Why We Don't Have A Cure For The Common Cold

By Lauren F Friedman, Sep 29, 2014

Modern science has eradicated smallpox, extended life expectancy, and made huge gains in battling some of the world's deadliest diseases. So why can't we knock out the humble cold?

... trying to develop drugs to treat rhinovirus also has some particular challenges. Smith, who worked on such research in his lab at the Donald Danforth Plant Science Center, tells us that some of the approaches they were testing *"really did work,"* at least in the lab. Still, *"while these compounds were pretty good at hitting a number of different strains at once, there were still a few outlier strains."*

That's the tricky thing about rhinoviruses, says Bochkov: *"It is difficult to find an antiviral equally efficient against 160 rhinoviruses."*

Furthermore, colds are not usually life-threatening, so the Food and Drug Administration would have a very low threshold for the kind of side effects that would be considered worth it. *"It really had to be nearly as safe as water for approval for the general public,"* says Smith. Few drugs are.

The challenges did not stop there. *"Only humans show symptoms of [rhinovirus] infection,"* explains Smith, making it nearly impossible to do any testing between petri dishes and human trials. Even then, researchers would first have to find a rhinovirus that test subjects had not already been exposed to — a difficult task with so many strains circulating every year.

You can read the full article here:

http://www.businessinsider.com.au/how-to-cure-a-cold-2014-9

The first influenza pandemic in the 21st century

The first influenza pandemic in the 21st century commenced in March, 2009 causing nearly 300,000 deaths globally within the first year of the pandemic. In late 2013 and in early 2014, there was gradual increase in the reported case of H1N1 infection and according to World Health Organization (WHO) report, influenza activity increased in several areas of the Southern Hemisphere and was dominated by the H1N1 pandemic strain of 2009. In the present study, a comprehensive comparison of the global amino acid composition and the structural features of all HA gene sequences of H1N1, available in the Flu Database (NCBI), from 1918 to December, 2014 has been performed to trace out the possibility of a further H1N1 pandemic in near future. The results suggest that the increased potential to enhance pathogenicity for the H1N1 samples of 2013 (latter part) and 2014 could lead to a more severe outbreak in the near future.

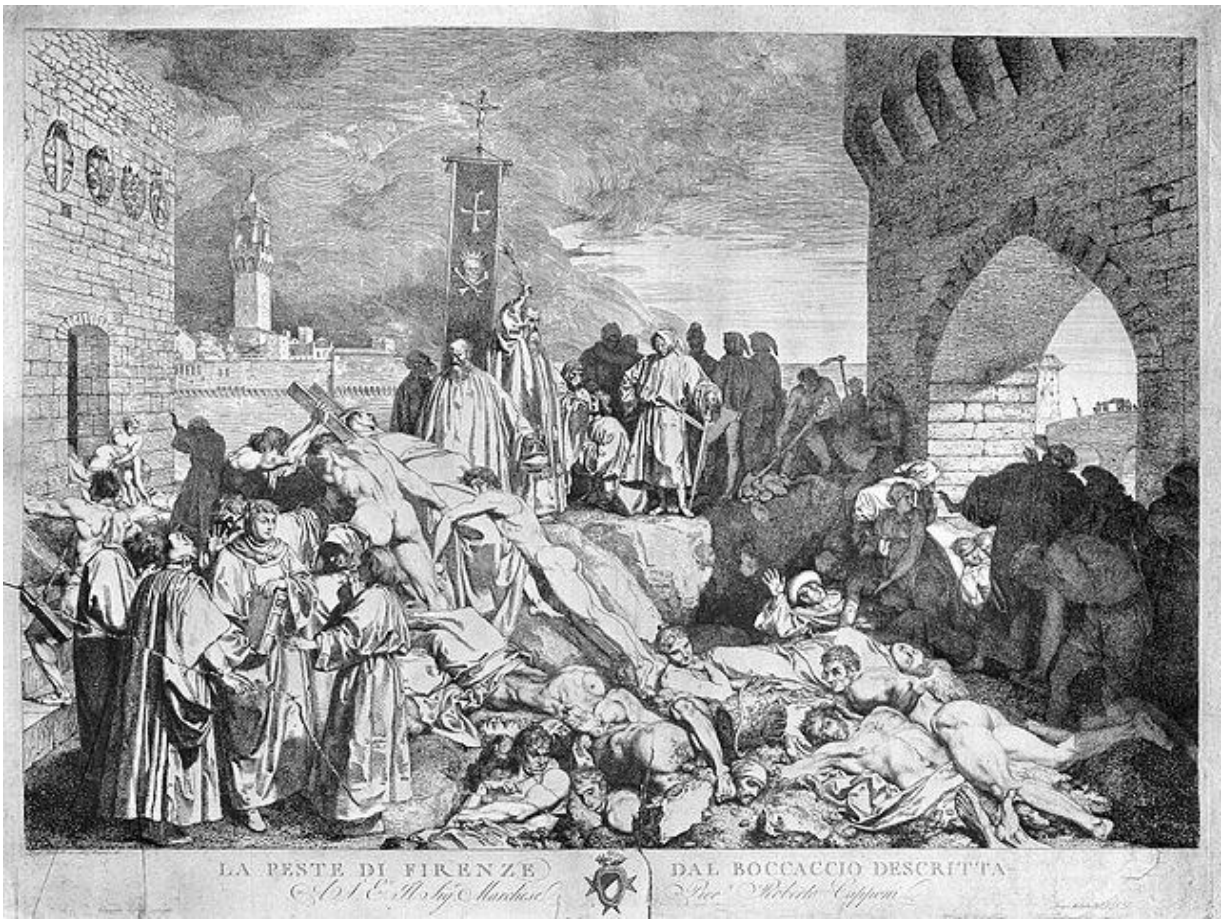
You can read the full article here:

https://www.ncbi.nlm.nih.gov/pubmed/25735729

Not too long ago

The Black Death and the Plague of Justinian both wiped out millions of people and lasted for over a century. In fact, the Black Death, the most infamous of the outbreaks, began in the late 1340s and lingered for over three hundred years, killing 25 million people including a fifth of the population of London in the epidemic of 1665-1666. The Plague of Justinian is estimated to have wiped out half of Europe's population between 541 AD and the 700s when it disappeared.

The latest outbreak, which started in China in 1855 and didn't officially end until 1959, was when scientists finally isolated the cause, a bacterial infection found in rodents and their fleas, which were the means by which the illness was transmitted to humans. Plague is found in mice, camels, chipmunks, prairie dogs, rabbits, and squirrels, but according to an article found on the National Geographic website, the most dangerous to humans are rats, 'especially the urban sort.'



Even now, plague can be found in various parts of the world, including China, India, Vietnam, Mongolia, and the United States. As recently as 2003, more than 2100 human cases and 180 deaths were recorded, mostly in Africa.

Nowadays, the illness is survivable if treated in time with the proper antibiotics; however, there are concerns that an aerosolized form could be used as a bioterror weapon.

Similar concerns exist for viral diseases. The 1918 outbreak of Spanish flu killed between 50 and 100 million of the 500 million that contracted it. The Spanish flu was caused by the H1N1 influenza virus but nicknamed the Spanish flu because Spain was neutral in World War I and had free media press without censorship so could report freely on the pandemic, which lead to the impression that Spain was particularly hard hit.

Doomsday in our DNA

Scientists have discovered that we carry viruses in our DNA. Now there is a chilling thought. They do however believe that we don't have to worry about it because it probably won't come back to life. I just wish they could be certain.

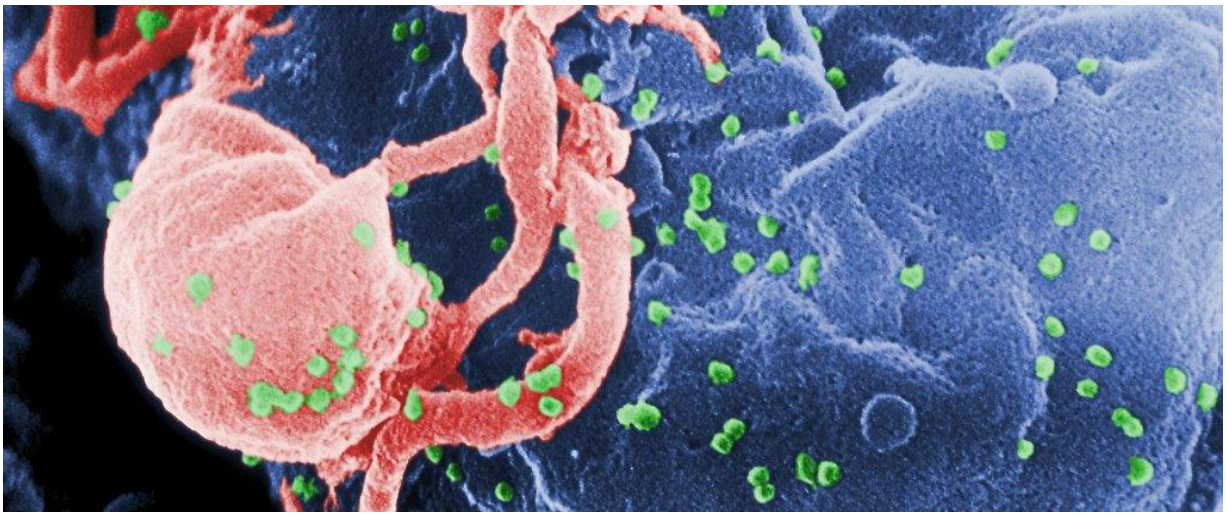
Below are a few articles which I came across during my research about this topic.

There's an intact ancient virus lying dormant in human DNA

http://www.sciencealert.com/there-s-an-intact-ancient-virus-lying-dormant-in-human-dna

Don't worry. It probably won't come back to life.

By Brendan Cole 25 Mar 2016



Research has shown that our DNA houses the ghosts of viruses fended off by your ancestors, and some of those viruses could still be dangerous if they wake up. And now scientists just found more of them.

After surveying 2,500 human genomes, a team discovered evidence of 36 different viruses that had accumulated in there over the course of our evolution, including 19 that had never been found before, and one that might still be infectious if it was turned on.

So how does viral DNA get in our cells in the first place? To reproduce, viruses need to use your own DNA against you. They start by getting inside of your cells and shoving their genes in between yours. That way, when your cells make copies of their DNA - like they do when they're about to replicate - they make copies of the virus's genes, too.

The virus's genes then switch on once they're in the new cell and turn it into a virus-making factory. These new viruses go on to shove their genes into other cells, and the process repeats.

Eventually (hopefully), your body fights off the viruses that are floating around and infecting new cells, but it can't get rid of the bits of virus that are already stuck in your DNA. So, it does the next-best thing and switches those bits of DNA off.

But once they're switched off, the segments of viral DNA don't go anywhere; they're just stuck in the middle of your genome, getting copied every time your cells divide. That means if some cells with altered genomes get passed on to your child, then the virus's genes get passed down the generations - switched off, but still potentially infectious.

These bits of DNA aren't doing anything, so mutations can accumulate in them without it having any real effects on how your body works, and eventually, all of these mutations make the DNA unable to switch back on and make an infectious virus, even if it wanted to.

But mutations or no mutations, these are bits of DNA that humans didn't evolve to have in there, so they can still cause other problems. For example, parts of the viral DNA can become activated and contribute to diseases, or they can just wreak havoc in the normal function of individual cells.

In their new study, a team led by Jeffrey Kidd of the University of Michigan and John Coffin of Tufts University found 18 of these mutants that had never been seen before. Some of them were pretty rare, appearing in only a couple of the 2,500 genomes surveyed. But others were widespread, popping up over 75 percent of the time.

Interestingly, the researchers also found one virus that was more intact. This happens when an infection is recent enough - or, by chance, the bits of DNA won't have mutated very much since it happened - and it means that the dormant DNA could still produce an infectious virus if it were turned back on.

As of last year, only one such protovirus, as it's known, had been discovered. Now we know of two.

Not much is known about the newly found protovirus, named Xq21.33 after its location on the X chromosome, and the teams are still working to see if they can figure out what kind of virus it came from and what the virus did. But what they do know is that it infected the ancestors of 44 of the people whose genomes were examined, and the team is confident that it has mutated so little since then that it could still be infectious today.

The researchers don't think there's much of a chance of this virus suddenly coming back to life, since our bodies have ways of keeping quiet the genes that it wants silenced. But still, it's disconcerting to think about the ghost of a virus our ancestors fought off coming back to haunt us.

The study has been published in the *Proceedings of the National Academy of Sciences.*

More ancient viruses lurk in our DNA than we thought

http://now.tufts.edu/news-releases/more-ancient-viruses-lurk-our-dna-we-thought-0

One whole endogenous retrovirus genome -- and bits of 17 others -- were spotted in a study of 2,500 human genomes

March 22, 2016. For More Information or to Request a Photo from this News Release, Contact: **Siobhan Gallagher** siobhan.gallagher@tufts.edu

BOSTON and ANN ARBOR, Mich. (March 22, 2016)—Think your DNA is all human? Think again. And a new discovery suggests it's even less human than scientists previously thought.

Nineteen new pieces of non-human DNA -- left by viruses that first infected our ancestors hundreds of thousands of years ago -- have just been found, lurking between our own genes.

And one stretch of newfound DNA, found in about 50 of the 2,500 people studied, contains an intact, full genetic recipe for an entire virus, say the scientists who published their findings in the Proceedings of the National Academy of Sciences.

Whether or not it can replicate, or reproduce, it isn't yet known. But other studies of ancient virus DNA have shown it can affect the humans who carry it.

In addition to finding these new stretches, the scientists also confirmed 17 other pieces of virus DNA found in human genomes by other scientists in recent years.

The study looked at the entire span of DNA, or genome, from people from around the world, including a large number from Africa -- where the ancestors of modern humans originated before migrating around the world. The team used sophisticated techniques to compare key areas of each person's genome to the "reference" human genome.

Working at Tufts University School of Medicine and the University of Michigan Medical School, the researchers made the findings with funding from the National Institutes of Health.

HERV-enly find

The findings add to what science already knows about human endogenous retroviruses, or HERVs. That's the name for the ancient infectious viruses that inserted a DNA-based copy of their own RNA genetic material into our ancestors' genomes. They're part of the same type of virus that includes the modern human immunodeficiency virus, which causes AIDS.

Over generations, the virus-generated DNA kept getting copied and handed down when humans reproduced. That's how it ended up in our DNA today. In fact, about 8 percent of what we think of as our "human" DNA actually came from viruses. In some cases, HERV sequences have been adopted by the human body to serve a useful purpose, such as one that helps pregnant women's bodies build a cell layer around a developing fetus to protect it from toxins in the mother's blood.

The new HERVs are part of the family called HERV-K. The intact whole viral genome, or provirus, just found was on the X chromosome; it's been dubbed Xq21. It's only the second intact provirus found to be hiding in human DNA.

In the researchers' own words:

"This one looks like it is capable of making infectious virus, which would be very exciting if true, as it would allow us to study a viral epidemic that took place long ago," says senior author and virologist John Coffin, Ph.D. of the Tufts University School of Medicine. "This research provides important information necessary for understanding how retroviruses and humans have evolved together in relatively recent times."

“Many studies have tried to link these endogenous viral elements to cancer and other diseases, but a major difficulty has been that we haven't actually found all of them yet,” says co-first author Zachary H. Williams, a Ph.D. student at the Sackler School of Graduate Biomedical Sciences at Tufts in Boston. “A lot of the most interesting elements are only found in a small percentage of people, which means you have to screen a large number of people to find them.”

“This is a thrilling discovery,” says co-first author Julia Wildschutte, Ph.D., who began the work as a Ph.D. student in Coffin’s lab at Tufts. “It will open up many doors to research. What’s more, we have confirmed in this paper that we can use genomic data from multiple individuals compared to the reference human genome to detect new HERVs. But this has also shown us that some people carry insertions that we can’t map back to the reference.”

U-M genetics researcher Jeffrey Kidd, Ph.D., worked with Wildschutte when she was a member of his laboratory team. “These are remnants of ancient events that have not been fixed in the population as a whole, but rather happened in the ancestors of some people alive today,” Kidd says. “There have been a number of examples of other HERVs that insert themselves next to human genes or near them, and have impact on their expression. We’re interested in applying these methods to find other types of viral or mobile element insertions.”

Genetic teamwork

The Michigan team used methods for characterizing repetitive DNA sequences that Kidd and his team had developed, while Coffin and Williams used complementary techniques. Wildschutte is now at Bowling Green State University.

Many of the genomes they examined were from the 1000 Genomes Project, an international collaboration. Another set of genomes came from work Kidd and colleagues at Stanford University had done as part of the Human Genome Diversity Project, with a focus on DNA samples from African volunteers.

These latter samples showed more signs of HERVs, in line with the high level of genetic diversity in African populations. That diversity stems from the longtime stability and intermixing of the continent’s population – as opposed to other populations in Europe, Asia and the Americas that stem from specific out-migrations in ancient times.

Cataloging all the HERV insertions in humans will require even more scanning of whole human genomes, which are becoming easier to come by as technology improves and becomes less expensive. And although intact proviruses lurking in our DNA may be rare, the impact of other HERV sequences on our health or disease is probably not.

The research was funded by the National Institutes of Health (OD009154, CA089441, GM112339) as well as the American Cancer Society and the F.M. Kirby Foundation.

PNAS, early online publication, www.pnas.org/cgi/doi/10.1073/pnas.1602336113

About Tufts University School of Medicine and the Sackler School of Graduate Biomedical Sciences

Tufts University School of Medicine and the Sackler School of Graduate Biomedical Sciences are international leaders in medical and population health education and advanced research. Tufts University School of Medicine emphasizes rigorous fundamentals in a dynamic learning environment to educate physicians, scientists, and public health professionals to become leaders in their fields. The School of Medicine and the Sackler School are renowned for excellence in education in general medicine, the biomedical sciences, and public health, as well as for innovative research at the cellular, molecular, and population health level. The School of Medicine is affiliated with six major teaching hospitals and more than 30 health care facilities. Tufts University School of Medicine and the Sackler School undertake research that is consistently rated among the highest in the nation for its effect on the advancement of medical and prevention science.

About the University of Michigan Health System

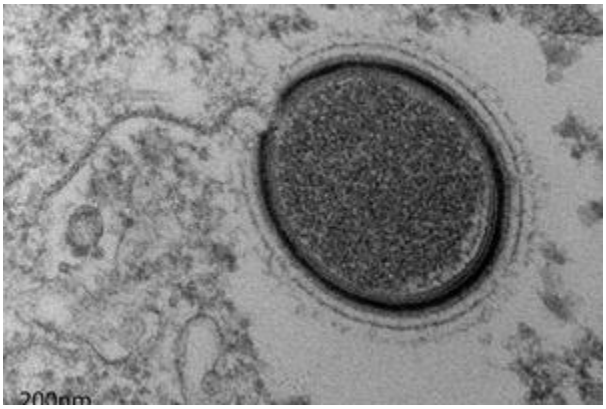
The University of Michigan Health System is a national leader in advanced patient care, innovative research to improve human health and comprehensive education of physicians, health professionals and medical scientists. UMHS includes a 1,000-bed hospital complex and more than 40 clinical care locations, and the U-M Medical School with its 1,900-physician faculty group practice, numerous research laboratories and projects funded by more than $470 million in research grants, and highly regarded training programs. UMHS has earned recognition for quality & safety from U.S. News & World Report, the Leapfrog Group and beyond. More information: www.uofmhealth.org

Frozen Giant Virus Still Infectious After 30,000 Years

http://www.livescience.com/52175-ancient-giant-virus-revived-siberia.html

By Stephanie Pappas, Live Science Contributor | September 15, 2015

The new virus, called *Mollivirus sibericum*, was found in Siberian permafrost.



It's 30,000 years old and still ticking: A giant virus recently discovered deep in the Siberian permafrost reveals that huge ancient viruses are much more diverse than scientists had ever known.

They're also potentially infectious if thawed from their Siberian deep freeze, though they pose no danger to humans, said Chantal Abergel, a scientist at the National Center for Scientific Research at Aix-Marseille University in France and co-author of a new study announcing the discovery of the new virus. As the globe warms and the region thaws, mining and drilling will likely penetrate previously inaccessible areas, Abergel said.

"Safety precautions should be taken when moving that amount of frozen earth," she told Live Science. (Though viruses can't be said to be "alive," the Siberian virus is functional and capable of infecting its host.)

Discovering giants

The new virus isn't a threat to humans; it infected single-celled amoebas during the Upper Paleolithic, or late Stone Age. Dubbed *Mollivirus sibericum*, the virus was found in a soil sample from about 98 feet (30 meters) below the surface.

These scanning electron microscopy images show particles of the four families of giant viruses now known: from the largest, spanning 0.6 microns (Mollivirus) to the smallest, at 1.5 microns (pandoravirus).

M. sibericum is a member of a new viral family, the fourth such family ever found. Until about a decade ago, viruses were thought of as universally tiny, Abergel said, and they were isolated by filtration techniques that strained out larger particles. But after the discovery of an amoeba-infecting giant virus called *Mimivirus*, first reported in the journal Science in 2003, researchers widened their search for bigger viruses. *Mimivirus* and its ilk are so large that they can be seen under an ordinary light microscope. The largest of this group, *Megavirus chilensis,* has a diameter of about 500 nanometers. Typical viruses range in size from 20 nanometers up to a few hundred nanometers.

Since the discovery of the *Mimivirus* family, researchers have discovered the Pandoraviridae and Pithoviridae families — the latter discovered in the same soil sample as *M. sibericum* and reported by Abergel and her colleague Jean-Michel Claverie, the head of the Structural and Genomic Information Laboratory at the National Center for Scientific Research at Aix-Marseille University, in 2014.

Unusual evolution

M. sibericum is wider in diameter than the other giant viruses discovered, at 600 nanometers versus 500. It has a genome of 600,000 base pairs (picture the "rungs" on the DNA "ladder"), which hold the genetic instructions to create 500 proteins. Viruses are snippets of RNA or DNA that work by hijacking a cell's machinery to carry out these instructions. [Tiny Grandeur: Stunning Images of the Very Small]

Abergel and her team are interested in studying resurrected giant viruses to understand how this group evolved and how viral genetics could have influenced the evolution of cells. Viruses are incorporated into cells, and viral DNA sometimes becomes a permanent part of a cell's genome.

"Viruses played a role in making the cell evolve in a very good way," Abergel said. The researchers don't know when giant viruses emerged on Earth, but they probably have roots in the very origins of DNA and RNA, she said.

"We are now at the stage where there are four families of giant viruses, and we can say that they are much more diverse [than previously known]," Abergel said.

The researchers' technique to isolate and study these viruses doesn't pose a threat to humans or animals, Abergel said, but it's possible that dangerous viruses do lurk in suspended animation deep belowground, she said. These viruses are buried deep, so it's likely that only human activities — such as mining and drilling for minerals, oil and natural gas — would disturb them. The discoveries of the giant viruses reveal that they can remain infectious for at least tens of thousands of years, Abergel said. So far, however, scientists have yet to discover any ancient human-infecting giant viruses.

Deeper study of the viruses will help clarify the risk, Abergel and Claverie wrote in a statement in 2014. But the research has the potential to answer basic questions as well, Abergel said.

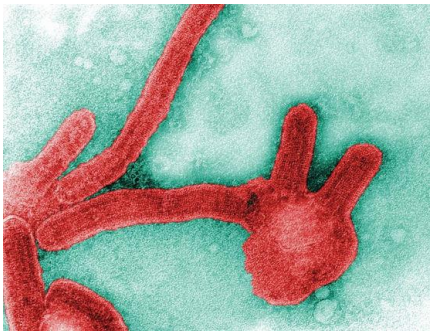
"We do think that these giant viruses will help us understand how life appeared on Earth," she said. "We think there are so many genes which are unique to those genomes, and there are many things to learn from the study of those genes."

The research appeared online Sept. 8 in the journal Proceedings of the National Academy of Sciences. *Follow Stephanie Pappas on Twitter and Google+. Follow us @livescience, Facebook & Google+. Original article on Live Science.*

The 9 Deadliest Viruses on Earth

http://www.livescience.com/56598-deadliest-viruses-on-earth.html

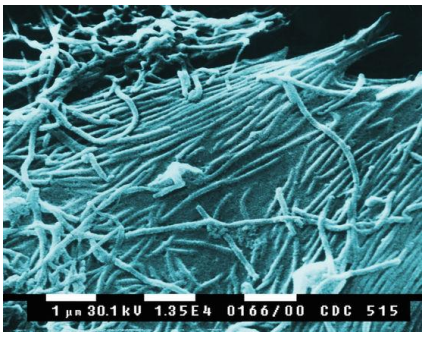
Marburg virus



Scientists identified Marburg virus in 1967, when small outbreaks occurred among lab workers in Germany who were exposed to infected monkeys imported from Uganda. Marburg virus is similar to Ebola in that both can cause hemorrhagic fever, meaning that infected people develop high fevers and bleeding throughout the body that can lead to shock, organ failure and death.

The mortality rate in the first outbreak was 25 percent, but it was more than 80 percent in the 1998-2000 outbreak in the Democratic Republic of Congo, as well as in the 2005 outbreak in Angola, according to the World Health Organization (WHO).

Ebola virus

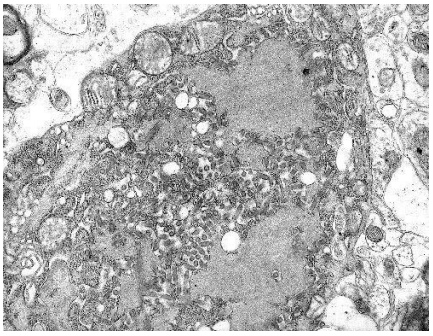


The first known Ebola outbreaks in humans struck simultaneously in the Sudan and the Democratic Republic of Congo in 1976. Ebola is spread through contact with blood or other body fluids, or tissue from infected people or animals. The known strains vary dramatically in their deadliness, Muhlberger said.

One strain, Ebola Reston, doesn't even make people sick. But for the Bundibugyo strain, the fatality rate is up to 50 percent, and it is up to 71 percent for the Sudan strain, according to WHO.

The outbreak underway in West Africa began in early 2014, and is the largest and most complex outbreak of the disease to date, according to WHO.

Rabies

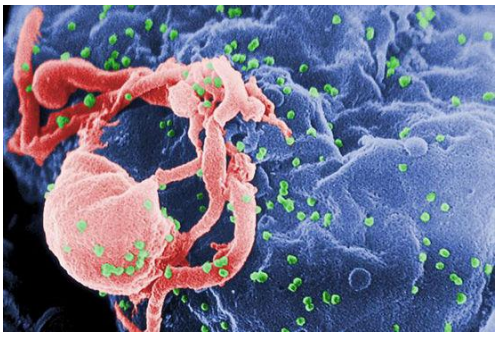


Although rabies vaccines for pets, which were introduced in the 1920s, have helped make the disease exceedingly rare in the developed world, this condition remains a serious problem in India and parts of Africa.

"It destroys the brain, it's a really, really bad disease," Muhlberger said. "We have a vaccine against rabies, and we have antibodies that work against rabies, so if someone gets bitten by a rabid animal we can treat this person," she said.

However, she said, "if you don't get treatment, there's a 100 percent possibility you will die."

HIV

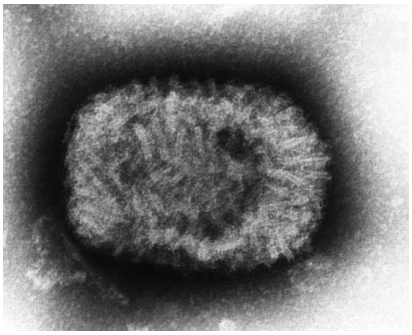


In the modern world, the deadliest virus of all may be HIV. "It is still the one that is the biggest killer," said Dr. Amesh Adalja, an infectious disease physician and spokesman for the Infectious Disease Society of America.

An estimated 36 million people have died from HIV since the disease was first recognized in the early 1980s. "The infectious disease that takes the biggest toll on mankind right now is HIV," Adalja said.

Powerful antiviral drugs have made it possible for people to live for years with HIV. But the disease continues to devastate many low- and middle-income countries, where 95 percent of new HIV infections occur. Nearly 1 in every 20 adults in Sub-Saharan Africa is HIV-positive, according to WHO.

Smallpox

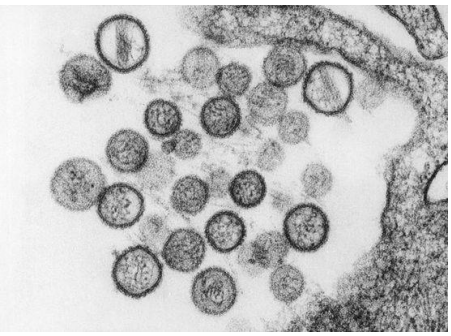


In 1980, the World Health Assembly declared the world free of smallpox. But before that, humans battled smallpox for thousands of years, and the disease killed about 1 in 3 of those it infected. It left survivors with deep, permanent scars and, often, blindness.

Mortality rates were far higher in populations outside of Europe, where people had little contact with the virus before visitors brought it to their regions. For example, historians estimate 90 percent of the native population of the Americas died from smallpox introduced by European explorers. In the 20th century alone, smallpox killed 300 million people.

"It was something that had a huge burden on the planet, not just death but also blindness, and that's what spurred the campaign to eradicate from the Earth," Adalja said.

Hantavirus



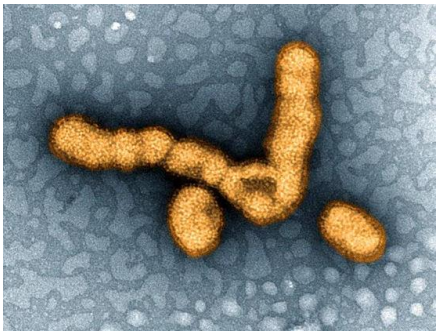
Hantavirus pulmonary syndrome (HPS) first gained wide attention in the U.S. in 1993, when a healthy, young Navajo man and his fiancée living in the Four Corners area of the United States died within days of developing shortness of breath. A few months later, health authorities isolated hantavirus from a deer mouse living in the home of one of the infected people. More than 600 people in the U.S. have now contracted HPS, and 36 percent have died from the disease, according to the Centers for Disease Control and Prevention.

The virus is not transmitted from one person to another, rather, people contract the disease from exposure to the droppings of infected mice.

Previously, a different hantavirus caused an outbreak in the early 1950s, during the Korean War, according to a 2010 paper in the journal Clinical Microbiology Reviews. More than 3,000 troops became infected, and about 12 percent of them died.

While the virus was new to Western medicine when it was discovered in the U.S., researchers realized later that Navajo medical traditions describe a similar illness, and linked the disease to mice.

Influenza

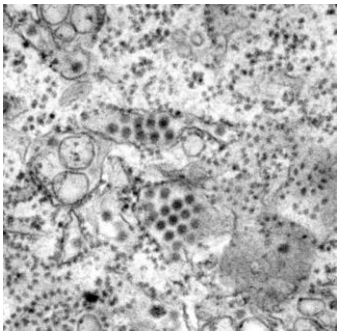


During a typical flu season, up to 500,000 people worldwide will die from the illness, according to WHO. But occasionally, when a new flu strain emerges, a pandemic results with a faster spread of disease and, often, higher mortality rates.

The most deadly flu pandemic, sometimes called the Spanish flu, began in 1918 and sickened up to 40 percent of the world's population, killing an estimated 50 million people.

"I think that it is possible that something like the 1918 flu outbreak could occur again," Muhlberger said. "If a new influenza strain found its way in the human population,*and* could be transmitted easily between humans, *and* caused severe illness, we would have a big problem."

Dengue

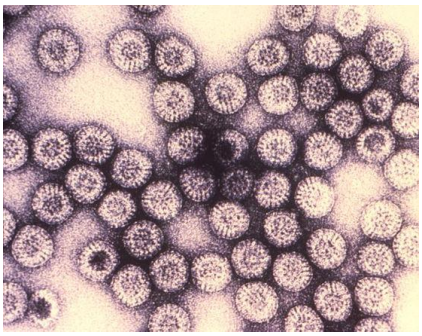


Dengue virus first appeared in the 1950s in the Philippines and Thailand, and has since spread throughout the tropical and subtropical regions of the globe. Up to 40 percent of the world's population now lives in areas where dengue is endemic, and the disease — with the mosquitoes that carry it — is likely to spread farther as the world warms.

Dengue sickens 50 to 100 million people a year, according to WHO. Although the mortality rate for dengue fever is lower than some other viruses, at 2.5 percent, the virus can cause an Ebola-like disease called dengue hemorrhagic fever, and that condition has a mortality rate of 20 percent if left untreated.

"We really need to think more about dengue virus because it is a real threat to us," Muhlberger said. There is no current vaccine against dengue, but large clinical trials of an experimental vaccine developed by French drug maker Sanofi have had promising results.

Rotavirus



Two vaccines are now available to protect children from rotavirus, the leading cause of severe diarrheal illness among babies and young children. The virus can spread rapidly, through what researchers call the fecal-oral route (meaning that small particles of feces end up being consumed).

Although children in the developed world rarely die from rotavirus infection, the disease is a killer in the developing world, where rehydration treatments are not widely available.

The WHO estimates that worldwide, 453,000 children younger than age 5 died from rotavirus infection in 2008. But countries that have introduced the vaccine have reported sharp declines in rotavirus hospitalizations and deaths.