Ebola 'was passed on by breastfeeding', adding weight to fears deadly virus can lurk in bodily fluids of survivors for months

- Some final cases of Ebola could've been transmitted through breast milk
- Largest study of tail-end of West African epidemic shows cases where the deadly virus was passed on via unconventional routes, including semen
- Dr Jeremy Farrar, of the Wellcome Trust, says discovery supports theory that the virus can persist in bodily fluids of survivors for a long time

By LIZZIE PARRY FOR DAILYMAIL.COM

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Some of the final cases of the deadly Ebola virus could have been transmitted through breast milk, new research suggests.

The largest analysis to date of the tail-end of the epidemic, which swept through West Africa from late 2013 to 2015, found some of the last cases were passed on via unconventional routes, such as semen and breast milk.

An international team of researchers sequenced Ebola virus genomes in a temporary tent laboratory in Sierra Leone.

Researchers led by the University of Cambridge and Wellcome Trust Sanger Institute generated 554 complete Ebola genome sequences from samples of blood, cheek swabs, semen and breast milk.

The largest analysis to date of the tail-end of the Ebola epidemic, which swept through West Africa in 2014, found some of the last cases were passed on via unconventional routes, such as semen and breast milk.

These were collected between December 2014 and September 2015 from Ebola isolation and treatment centres in the north and west of the country.
The research, published in the journal Virus Evolution, describes a number of case studies. These include a mother who may have transmitted Ebola to her baby via breastfeeding, and an Ebola survivor who passed on the virus sexually a month after being released from quarantine.

Dr Jeremy Farrar, director of the Wellcome Trust, said: ‘Close contact with an infected individual is still by far the most common way for Ebola to spread.

‘But this study supports previous research suggesting that the virus can persist in bodily fluids for a long time after recovery.

‘These unusual modes of transmission may have contributed to isolated flare-ups of infections towards the end of the epidemic.

‘The success of this innovative project shows how important it is to carry out genome sequencing within the affected countries, and for the data to be shared in a rapid and open way as part of the epidemic response.

‘Strengthening laboratory and surveillance facilities where they are currently lacking will also aid early detection, making the world better prepared for infectious disease outbreaks.’

During the outbreak which swept Guinea, Liberia and Sierra Leone, more than 28,000 cases were reported including more than 11,000 deaths.

This new study suggests rapid sequencing of viral genomes in the midst of an epidemic could play a vital role in bringing future outbreaks under control, by allowing public health workers to quickly trace new cases back to their source.

Sierra Leone was the most widely affected of the three West African countries worst hit by the Ebola epidemic, with 14,124 cases and 3,956 deaths to date.

Without effective vaccines or treatments for the infection, bringing the epidemic under control relied largely on public health measures such as the rapid identification and isolation of Ebola patients, contact tracing and quarantine, as well as encouraging safe burial practices.

By mid-2015 cases in the three most-affected countries had declined, but isolated cases of the disease continued to appear, even though all known transmission chains were thought to be extinguished.

Researchers led by the University of Cambridge and Wellcome Trust Sanger Institute began investigating these cases in a temporary genome sequencing facility set up by Professor Ian Goodfellow.

Based in a tent at the Ebola Treatment Centre in Makeni, Sierra Leone, the facility provided in-country sequencing capability to process

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samples from patients in Makeni and surrounding areas in real time, without the need for sample shipment out of the country.

The team generated 554 complete Ebola genome sequences from samples of blood, buccal swabs, semen and breast milk collected between December 2014 and September 2015 from Ebola isolation and treatment centres in the north and west of the country.

These were combined with 1,019 samples sequenced by other groups to create a picture of the viral variants present in Sierra Leone.

They found that during 2015 at least nine different lineages of the virus were circulating in Sierra Leone, eight of which evolved from a single variant that introduced Ebola to the country in June 2014.

The remaining viruses came from a separate, geographically distinct lineage that originated in Guinea.

Starting in mid-2015 samples from all new Sierra Leone cases were rapidly sequenced in the facility.

The data, combined with the growing reference set, helped field workers locate the source of infection for some of the final Ebola cases in Sierra Leone.

This work revealed that some cases were acquired through unconventional transmission chains and supports a growing body of evidence that the Ebola virus can be found in fluids such as semen or breast milk and may persist beyond the standard quarantine times.

Senior author Professor Goodfellow, from the University of Cambridge, said: 'During the initial part of the Ebola epidemic several teams were sequencing samples, but the delays caused by shipping the samples out of West Africa made it difficult to use the sequence data for investigating new chains of transmission.

'Often by the time the data was published the samples were six months old.

'To be able to rapidly identify the source of new cases we need to sequence samples and release data in real-time, share samples and share data as it's produced.'

Dr Matthew Cotten, joint senior author, from the Wellcome Trust Sanger Institute added: 'During the epidemic combining our Ebola virus genome sequences with data from other groups provided insight into how the virus was evolving and contributed to an important reference for tracking the source of new cases.

'As the outbreak progressed, our data also show that quarantines, border control and checking methods were effective, as movement of the virus within and between countries ceased.'
At the beginning of the West African Ebola epidemic, around March 2014, the virus mostly spread through the sharing of bodily fluids from human-to-human, such as between broken skin or the eyes or nose. Improper burial practices, and people’s desire to hold
onto dead bodies that were infected with the virus, quickly sped up the outbreak.

Now that the epidemic has largely come to an end and is no longer a WHO-designated public health emergency, however, scientists have begun piecing together the ways it spread in more “unconventional” ways. In a new study, researchers have mapped out the tail end of the West African Ebola epidemic, and through detailed genome sequencing have managed to create a bigger picture of how the last few cases were caused mainly by sexual transmission. That includes semen, or even breast milk.

It’s not news that sexual transmission played a role in the outbreak, particularly at the end. In a 2015 study, researchers found that the Ebola virus was able to remain in semen for much longer than previously believed. It was because of this that several cases kept appearing even at the end of the epidemic. Recovered Ebola patients were still able to transmit the virus sexually even though the virus had been eradicated from the rest of their body.

But the latest study is the first to examine in detail how exactly this happened, in the hopes of learning better ways to prevent future outbreaks. In the study, the researchers tried to piece together an image of viral variants that were present during the epidemic in Sierra Leone. They examined 554 Ebola genome sequences taken from blood, buccal swab, semen, and breast milk samples, all of which were gathered between December 2014 and September 2015. In order to create a more detailed picture of how the virus spread during this time, the researchers used real-time sequencing of Ebola virus genomes.

The researchers found more evidence to support the notion that the Ebola virus remains in certain bodily fluids — like semen and breast milk — long after a
patient has recovered. Being able to use genome sequencing to predict that would help health workers tackle future viral outbreaks.

“To be able to rapidly identify the source of new cases we need to sequence samples and release data in real-time, share samples and share data as it’s produced,” said Ian Goodfellow of the University of Cambridge, an author of the study, in a press release. Dr. Jeremy Farrar, Director of the Wellcome Trust, added: “The success of this innovative project shows how important it is to carry out genome sequencing within the affected countries, and for the data to be shared in a rapid and open way as part of the epidemic response.”

The CDC provides guidelines for mothers who have been infected by Ebola or who have somehow been exposed to it and potentially in danger of infection, firstly noting that if there are safe alternatives to breastfeeding, they should use those options instead. In fact, a mother with Ebola or “under investigation” for the disease shouldn’t have close contact with the infant at all, and to be safe, shouldn’t breastfeed the child even months after recovery.

“Although Ebola virus has been detected in breast milk, it is not known whether the virus can be transmitted from a mother to her infant through breastfeeding,” the CDC states. “However, given what is known about the transmission of Ebola virus, regardless of breastfeeding status, an infant whose mother has Ebola is already at high risk of getting infected from close contact with the mother, and is at high risk of death overall.”

There is still not enough research to provide confirmation on when it’s safe for a recovered or infected mother to breastfeed again — or for a patient to resume sexual relations, either. Research has
shown that the virus can be found in semen up to 82 days after the symptoms first appeared. The WHO recommends that patients should be tested for Ebola in semen every month after their illness, until their semen tests negative for the virus twice. Even then, the individual should practice safe sex with a condom for at least a year afterwards.

“Close contact with an infected individual is still by far the most common way for Ebola to spread, but this study supports previous research suggesting that the virus can persist in bodily fluids for a long time after recovery,” Farrar said in the press release. “These unusual modes of transmission may have contributed to isolated flare-ups of infections towards the end of the epidemic.”

Scientists to Share Real-time Genetic Data on MERS, Ebola

LONDON—Genetic sequence data on two of the deadliest yet most poorly understood viruses are to be made available to researchers worldwide in real time as scientists seek to speed up understanding of Ebola and MERS infections.

The project, led by British scientists with West African and Saudi Arabian collaboration, hopes to encourage laboratories around the world to use the live data - updated as new cases emerge - to find new ways to diagnose and treat the killer diseases, and ideally, ultimately, prevent them.

"The collective expertise of the world's infectious disease experts is more powerful than any single lab, and the best way of tapping into this ... is to make data freely available as soon as possible," said Jeremy Farrar, director of the Wellcome Trust global health charity which is funding the work.

The gene sequences, already available for MERS cases and soon to come in the case of Ebola, will be posted on the website virological.org for anyone to see, access and use.

Middle East Respiratory Syndrome (MERS) is a viral disease which first emerged in humans in 2012 and has been spreading in Saudi Arabia and neighboring countries since then. It is caused by a coronavirus and has already killed more than 430 people.
An unprecedented epidemic of Ebola virus in West Africa has killed more than 10,000 people in the past year and infected more than 25,000 mainly in Guinea, Sierra Leone and Liberia.

Despite the many deaths caused by Ebola and MERS, researchers still know relatively little about the viruses - including what animals might be acting as "viral reservoirs" - and scientists are battling to develop safe and effective cures or vaccines against them.

Genetic changes

Paul Kellam, a professor at Britain's Sanger Institute, said mapping the gene structure, or sequencing the genome, of a virus can tell scientists a lot about how it is spreading and changing, and help in the search for better ways to diagnose, treat and prevent infections.

"With more genetic surveillance we can spot things that are potential areas of concern - such as [genetic] changes that might mean our diagnostics might not work so well any more, or changes that suggest a virus is becoming able to transmit more easily," he explained in a telephone interview.

Yet while this kind of data is invaluable to researchers, it is rarely shared swiftly or freely enough among them. Saudi Arabia was widely criticized at the start of the MERS outbreak for being slow to cooperate with experts around the world wanting to conduct crucial research on the disease.

Kellam said Saudi authorities are now committed to sharing viral data widely and immediately, keen to enlist the help of international scientists in controlling MERS.

As part of the same gene sequencing project, Ian Goodfellow from the University of Cambridge is in Sierra Leone working with the government there to make similar data on the Ebola virus available on virological.org as soon as possible.

He plans to collect samples from Ebola patients, sequence them in a matter of hours and process the data to make the viral genome sequences in weeks - a process that could take months if samples were to be bought back to Britain for analysis.
Sexual transmission involved in tail end of Ebola epidemic

Some of the final cases of Ebola in Sierra Leone were transmitted via unconventional routes, such as semen and breastmilk, according to the largest analysis to date of the tail-end of the epidemic.

An international team of researchers has produced a detailed picture of the latter stages of the outbreak in Sierra Leone, using real-time sequencing of Ebola virus genomes carried out in a temporary laboratory in the country.

While the study did not suggest that unconventional transmission was more common than previously thought, the authors describe several instances including a mother who may have transmitted Ebola to her baby via breastfeeding, and an Ebola survivor who passed on the virus sexually a month after being released from quarantine. [More details of cases in the notes to editors].

The research, published today in the journal Virus Evolution, suggests that rapid sequencing of viral genomes in the midst of an epidemic could play a vital role in bringing future outbreaks under control, by allowing public health workers to quickly trace new cases back to their source.

Sierra Leone was the most widely affected of the three West African countries worst hit by the Ebola epidemic, with 14,124 cases and 3,956 deaths to date. Without effective vaccines or treatments for the infection, bringing the epidemic under control relied largely on public health measures such as the rapid identification and isolation of Ebola patients, contact tracing and quarantine, as well as encouraging safe burial practices.

By mid-2015 cases in the three most-affected countries had declined, but isolated cases of the disease continued to appear, even though all known transmission chains were thought to be extinguished.

Researchers led by the University of Cambridge and Wellcome Trust Sanger Institute began investigating these cases in a temporary genome sequencing facility set up by Professor Ian Goodfellow. Based in a tent at the Ebola Treatment Centre in Makeni, Sierra Leone, the facility provided in-country sequencing capability to process samples from patients in Makeni and surrounding areas in real time, without the need for sample shipment out of the country.

The team generated 554 complete Ebola genome sequences from samples of blood, buccal swabs, semen and breast milk collected between December 2014 and September 2015 from Ebola isolation and treatment centres in the north and west of the country. These were combined with 1019 samples sequenced by other groups to create a picture of the viral variants present in Sierra Leone.

They found that during 2015 at least nine different lineages of the virus were circulating in Sierra Leone, eight of which evolved from a single variant that introduced Ebola to the country in June 2014. The remaining viruses came from a separate, geographically distinct lineage that originated in Guinea.

Starting in mid-2015 samples from all new Sierra Leone cases were rapidly sequenced in the facility. The data, combined with the growing reference set, helped field workers locate the source of infection for some of the final Ebola cases in Sierra Leone. This work revealed that some cases were acquired through unconventional transmission chains and supports a growing body of evidence that the Ebola virus can be found in fluids such as semen or breast milk and may persist beyond the standard quarantine times.

Senior author Prof Ian Goodfellow, from the University of Cambridge, said: “During the initial part of the Ebola epidemic several teams were sequencing samples, but the delays caused by shipping the samples out of West Africa made it difficult to use the sequence data for investigating new chains of transmission. Often by the time the data was published the samples were six months old. To be able to rapidly identify the source of new cases we need to sequence samples and release data in real-time, share samples and share data as it’s produced.”

Dr Matthew Cotten, joint senior author, from the Wellcome Trust Sanger Institute added: “During the epidemic combining our Ebola virus genome sequences with data from other groups provided insight into how the virus was evolving and contributed to an important reference for tracking the source of new cases. As the outbreak progressed, our data also show that quarantines, border control and checking methods were effective, as movement of the virus within and between countries ceased.”
Examples of Ebola transmission between July and September 2015.

Case 1 – re-introduction of the virus in an Ebola-free town
In July 2015 a patient became ill after travelling from the Magazine Wharf district of Freetown, where Ebola was still active, to Tonkolili, which had been Ebola-free for 130 days. The patient’s brother and aunt subsequently became ill. Genome sequencing revealed that the virus acquired by the patient and his family matched the variant that was still actively being transmitted in Magazine Wharf. This established that the case was linked to Freetown, and was not a re-emergence of the Ebola virus that had been circulating previously in Tonkolili or another zoonotic introduction of the virus.

Case 2 – possible transmission from mother to baby via breastmilk
One case the researchers looked at involved a woman who may have passed Ebola to her 13th month old baby through her breastmilk. The woman was exposed to Ebola when her niece, who had fled quarantine, died at her house during childbirth. The niece’s body and that of her baby subsequently tested positive for Ebola and those present at the birth (including the woman and her 13th month old baby) were quarantined. Three days after they were released, the woman’s own baby became ill. The woman had no symptoms, and her blood tested negative for Ebola, but the virus was detected in her breastmilk. Genome sequencing showed that the same variant of virus was found in samples taken from the baby, but was different to the virus that infected the original patient (the woman’s niece).

The researchers suggest that the most likely route of transmission was between the woman and her baby via breastfeeding, but could not say with certainty that this was the case.

Case 3 – sexual transmission after recovery
A woman in Kambia died in August 2015, 50 days after the last reported case in the region. The virus she was carrying closely resembled another sample taken eight weeks earlier from a male Ebola survivor, who had sexual contact with the women not long before she died. The man’s semen was tested in September and traces of the same virus were found, suggesting that he may have inadvertently passed the virus to her sexually.