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EDITORIAL

Fighting the Flu Threat

Pr Yasmine Belkaid,
Director General
of the Institut Pasteur

Every winter, the same story repeats itself: the flu strikes. Often dismissed as a minor illness, it is in fact a formidable adversary. In France, it affects between two and six million people every year, overwhelming our hospitals and claiming thousands of lives, especially among the most vulnerable. But behind these annual epidemics lies a more complex reality: that of constantly mutating viruses.

These pathogens have a unique ability to reinvent themselves, evading our immune defences and making the fight particularly difficult.

The danger increases considerably with the zoonotic risk: natural animal reservoirs provide fertile ground for the emergence of new, previously unknown viruses that could trigger a pandemic.

In the face of these threats, the Institut Pasteur stands as an essential bulwark. Our teams bring a dual expertise: monitoring the circulation of influenza viruses in real time and anticipating the pandemic risk posed by new viral strains. By combining high-precision epidemiological surveillance with cutting-edge research on viral evolution, our researchers are on the front line to protect public health against the constant unpredictability of influenza.

Between winter epidemics and global threats, understanding influenza is essential to protecting our health. This requires high-performance, high-security laboratories and dedicated research teams committed to decoding these viruses.

Your generosity today shapes our ability to anticipate and combat the flu threats of tomorrow, in order to protect everyone's health.



SPECIAL REPORT

Flu viruses, ever-recurring threats

Every winter, between the scarves and woolly hats, the flu virus makes its way into our respiratory tracts, confining us to bed with the classic clinical signs: coughing, high fever and aching muscles. But behind these seasonal symptoms lies a far more complex reality. This elusive virus doesn't just circulate among humans; it draws its diversity from an immense animal reservoir. It is from this interaction between humans and animals that the next major global health threat could emerge. So how do we take on a virus that is never quite the same twice?

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An infection that is never trivial

In France, according to Santé publique France, seasonal flu causes on average 20,000 hospitalisations and 10,000 deaths every year, during an epidemic lasting about three months. It is the deadliest acute respiratory infection and mainly affects older people and patients with chronic diseases. But it is more dangerous than people think: it can cause complications even in apparently healthy individuals.



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HISTORY OF MODERN INFLUENZA A PANDEMICS

1889-1890	**Russian flu** 1 million deaths *First pandemic of the modern era*
1918-1919	**Spanish flu** 50 to 100 million deaths *The deadliest pandemic in recent history*
1957-1958	**Asian flu** 1 to 4 million deaths
1968-1969	**Hong Kong flu** 1 to 4 million deaths
1977-1979	**Russian flu** 700,000 deaths
2009-2010	**A(H1N1) flu** 280,000 deaths

In its severe forms, flu causes lung damage and can affect the heart and brain. The risk of heart attack is thus increased for several years. In pregnant women, it carries a risk of premature birth or even miscarriage, while infants under six months are frequently hospitalised.

Disease factsheet
Flu

SURVEILLANCE

ACTION PASTEUR

Genomic sequencing: a sentinel for public health

At the interface between research, expertise and public health, the shared microbiology platform (P2M) has carried out high-throughput multi-pathogen sequencing since 2015. This cutting-edge technique can sequence several genes, or even the entire genome, with unmatched speed and precision. P2M receives samples from various National Reference Centres (CNR) in order to ensure genomic surveillance of pathogens and contribute to the response to health emergencies.



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As part of seasonal flu surveillance, **Vincent Enouf**, head of P2M and deputy director of the CNR for Respiratory Infection Viruses (VIR), holds regular exchanges with the European Centre for Disease Prevention and Control (ECDC) and the World Health Organization (WHO). These collaborations rely on sequencing data from influenza viruses, which allow bioinformaticians to compare the sequences obtained with those from other countries or earlier periods. ***"This comparative analysis provides a precise picture of the circulating viruses and how they are evolving, in particular in terms of resistance or sensitivity to vaccines and antivirals"***, explains the researcher. This information is then pooled internationally: ***"By sharing our data, we contribute to the twice-yearly decision on vaccine composition."***



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If a human infection with avian flu A(H5N1) were detected by the CNR VIR, the sample would be sequenced immediately by P2M ***"to determine whether the virus carries one or more of the 10 known mutations thought to facilitate human-to-human transmission"***, explains Vincent Enouf. A detailed genome analysis would then follow, together with the French Agency for Food, Environmental and Occupational Health & Safety (Anses), to trace the virus's history.

"Collaboration between national and international institutions is the key to managing a pandemic effectively."



Influenza A virus.
Colourised image.
© Institut Pasteur/C. Hannoun

The evolutionary strategy of influenza viruses

Influenza viruses are microbes that must hijack the cellular machinery of their host in order to replicate. There are four types (A, B, C and D), whose hosts, modes of circulation and health consequences differ profoundly.

• **Type A** is distinguished by its ability to trigger pandemics, thanks to its vast animal reservoir (birds, livestock, etc.) from which strains unknown to our immune system emerge.

• **Type B**, confined to humans, causes seasonal epidemics, notably in children, with two lineages (*B/Victoria* and *B/Yamagata*, the latter having disappeared since 2020).

• **Type C**, rare and mild, is not targeted by vaccines.

•**Type D**, identified in 2011 in cattle and pigs, has not yet been associated with human disease.

Although all influenza viruses share a similar genetic structure, influenza A is the champion of rapid and unpredictable evolution, whereas types B, C and D evolve much more slowly and in a more limited way.

The evolutionary dynamics of type A, which allow it to escape our immune defences, are driven by two distinct processes: **antigenic shift (or genetic reassortment) and antigenic drift.**

The first is linked to the segmented nature of influenza viruses' genetic material. It is an abrupt evolutionary leap that occurs when two different strains infect the same cell at the same time and mix their gene segments to create a completely new virus. This rare but formidable phenomenon is what triggers global pandemics.

Antigenic drift, for its part, is a mechanism that creates variants within a single strain. It corresponds to the accumulation of small mutations that gradually modify surface proteins (such as haemagglutinin, H) and allow the virus to escape antibodies. This is why vaccines must be updated every year to remain effective.

Flu vaccine: a race against the clock

Even if the vaccine is not invincible armour, studies estimate that it reduces the risk of flu by 41% on average. In case of infection, it also reduces severity and lethality. But every year brings the same puzzle: which strains should be included in the vaccine? The WHO leads this process through its global network, GISRS (Global Influenza Surveillance and Response System). National influenza centres located around the world continuously analyse clinical samples and epidemiological data.

Continued on p. 5

FORECASTING

ACTION PASTEUR

Modelling flu to stay ahead of it

The Mathematical Modelling of Infectious Diseases Unit brings together a wide range of projects to answer several fundamental questions: how do pathogens (flu, Zika, Ebola, etc.) spread? How should public health policies be shaped to deal with them?



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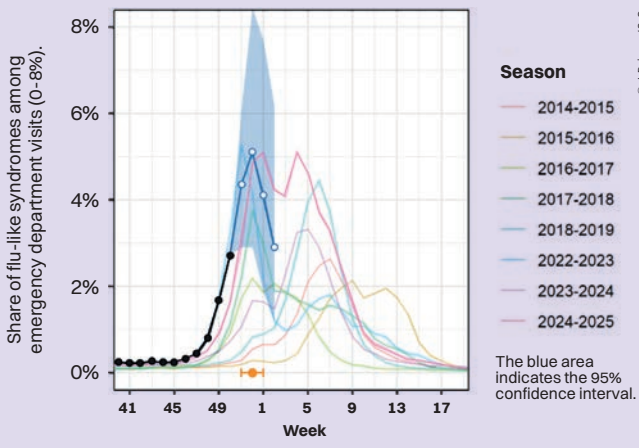
"We work closely with the French health authorities so that our work informs the public health response to epidemics", explains **Simon Cauchemez**, head of the unit.

For winter 2025-2026, his team worked alongside Santé publique France to model the dynamics of the flu epidemic. The researchers use around ten predictive models of different types: some look for similarities between past seasons and the ongoing epidemic, while others describe the mechanisms of spread within the population. ***"By building an ensemble model that aggregates the results of the different models, we improve forecasting performance,"*** says the researcher. This tool makes it possible to anticipate the epidemic trajectory four weeks ahead and to predict the epidemic peak. It will be used during upcoming seasonal epidemics. ***"Some aspects of the model could be adapted to other respiratory infections such as respiratory syncytial virus, which causes bronchiolitis"***, adds the researcher.

The unit also contributed to the recommendations of the High Council for Public Health (HCSP) on the stockpile of antivirals to build up in preparation for an influenza pandemic. By modelling different scenarios based on analysis of past pandemics, the researchers were able to advise the HCSP on the quantity of antivirals needed to treat patients who would require them.

On the basic research side, Simon Cauchemez has carried out analyses to better understand the immune response to flu. ***"By studying virus transmission data within households, we confirmed the role of certain antibodies in protecting against infection, but also in reducing the risk of transmission to other individuals"***, he explains. This is an interesting prospect for new generations of vaccines.

Four-week forecast of the flu trajectory in mainland France, 2025-2026 season.



© J. Paireau / S. Cauchemez

INTERVIEW

India **Leclercq**

University professor, researcher in the Environment and Infectious Risks Unit


© D.R

"Influenza viruses are an ideal model for studying environmental persistence."

What does environmental virology involve?

Environmental virology explores the persistence of viruses outside their host, whether in the air we breathe, on the surfaces we touch (door handles, touchscreens, etc.) or in water. These three environments, liquid, solid and gaseous, form a continuum. For example, a virus expelled in a sneeze can settle on a surface, evaporate into the air as aerosols, or be carried by air currents before infecting a new person. Understanding each link is essential for assessing transmission risks and designing appropriate prevention strategies.

How do you study the persistence of flu in the environment?

Influenza viruses are an ideal model for studying environmental persistence: they are well characterised, easy to handle in the laboratory, and critical for public health. **They remain infectious for up to 48 hours on non-porous surfaces (stainless steel, plastic) and up to 12 hours on porous materials (fabric, paper).** Our first experiments were fairly conventional: by varying parameters such as temperature, humidity or salinity one at a time, we measured how long the viruses kept their infectious capacity. But very soon we needed to go further and control all these conditions simultaneously, including aerosolisation. A climate chamber was then custom-designed and installed in a high-biosafety laboratory. It allows us, for example, to test virus survival on different surfaces at 15 or 25 degrees, with 40% humidity. A new, even higher-performing chamber is expected next year and will open up new experimental possibilities.

What have your studies revealed about flu viruses?

A surprising discovery overturned our hypotheses: two flu viruses that are genetically very close, such as two A(H1N1) variants, could behave radically differently in the environment. We identified a key mechanism: **the virus's surface proteins are far more sensitive to external conditions than the viral genome.** They play a central role in infection and react to variations in their environment.

You also work on aerosols. How do you study them?

In partnership with the CSTB[1], we use a system called Albatros, based on acoustic levitation. We generate a tiny droplet, about 100 to 170 micrometres across, held in suspension by sound waves.

We can then observe under a microscope what happens, and measure whether the virus it contains is still infectious. We discovered that it is not the complete drying of the droplet that destroys the virus: it is the evaporation itself. From 30 seconds, infectious capacity drops, whereas the droplet takes about 60 seconds to dry entirely.


© C. Batéjat

Controlled-atmosphere isolator installed in the high-security laboratory of the Environment and Infectious Risks Unit.

What has Covid-19 changed in your work?

Before the pandemic, environmental virology was a marginal field of research. Covid-19 changed everything: once-academic questions, such as virus survival in the air or on surfaces, became major societal issues. Our expertise on the inactivation of SARS-CoV-2 earned us funding for the DISPERS[2] project, carried out with Anses[3], the CSTB[1] and CERTES[4]. The first results are revealing: **in trials on pigs, we detected infectious bioaerosols of flu viruses up to five days after infection, despite air renewal. This dynamic explains chain reinfections in farms.**

In a world where interactions between humans, animals and ecosystems are intensifying, environmental virology is becoming an essential discipline for anticipating tomorrow's epidemics.

> "The Covid-19 pandemic has upended environmental virology."

1. ***CSTB*** *: Scientific and Technical Centre for Building.*
2. ***DISPERS*** *: Survival dynamics of airborne pathogens in built environments.*
3. ***Anses*** *: French Agency for Food, Environmental and Occupational Health & Safety.*
4. ***CERTES*** *: Centre for Studies and Research in Thermal Science, Environment and Systems.*

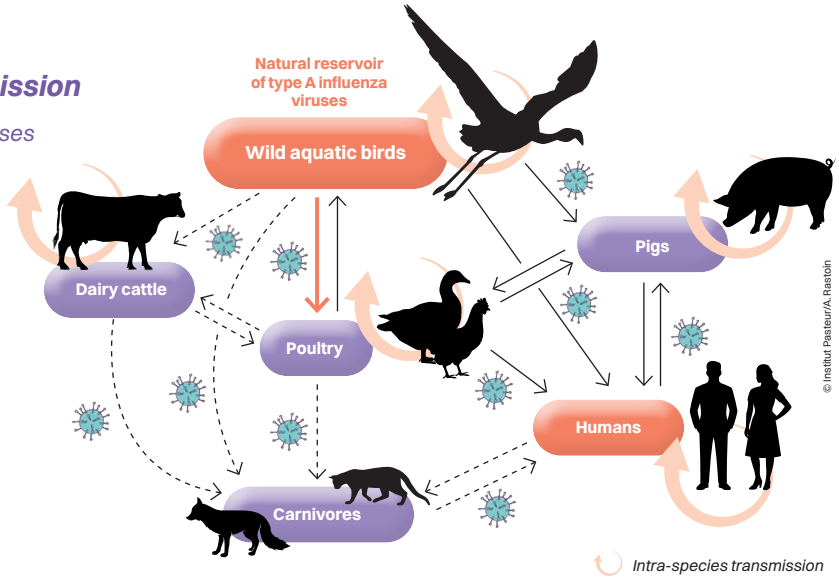
UNDERSTANDING

Influenza A viruses: ecology and transmission

Present in humans and many animals, influenza A viruses have birds (wild and farmed) as their main reservoir, with the pig as an important mammalian host.

They are identified by their surface proteins H (haemagglutinin) and N (neuraminidase), giving rise to the HxNy nomenclature.

Although these viruses cause seasonal epidemics in humans and outbreaks in animals, the two worlds generally remain separate. The passage of the virus from animal to human is a complex event that does not happen easily.



The viruses included are not chosen at random: their selection takes into account their geographical distribution, the age groups affected, the severity of cases, or the emergence of unusual subtypes. WHO collaborating centres then decode their genetic material and their antigenicity (the ability to trigger an immune response). **The goal is to draw up an identikit of the dominant viruses six months before the flu season.** In February for the Northern Hemisphere and in September for the Southern Hemisphere, a GISRS committee recommends the strains to include in the vaccine.

Current vaccines are trivalent, made up of two type A strains and one type B strain. The annual choice of vaccine strains is scientific but also a gamble, as some strains evolve faster than others. An unexpected variant may emerge after the official decision and partially escape the vaccine during the epidemic season. Recent work suggests that a later decision, or more responsive technologies (such as mRNA vaccines), could thus improve vaccine-virus matching.

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VIROLOGY

ACTION PASTEUR

Crossing the species barrier: the adaptation strategy of influenza viruses


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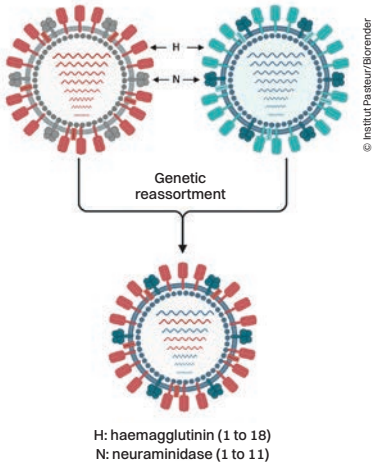
As a rule, type A influenza viruses of avian origin do not replicate in humans. Occasionally, they cross this species barrier and can cause a flu pandemic. How do they adapt to humans, replicate efficiently in our cells and get around our defence mechanisms? These are the questions that **Nadia Naffakh** and her team in the RNA Biology and Influenza Virus Unit are trying to answer: ***"At the level of the infected cell, we study how viruses hijack molecular machinery for their own benefit and escape antiviral responses"***, she explains.

To become adapted to humans, avian influenza viruses must in particular escape the action of Mx1, an antiviral protein that constitutes a major species barrier.

"We are trying to identify all the mutations that allow the virus to escape Mx1. We also want to determine which domestic species could, like the pig, promote the pre-adaptation of avian viruses to humans through the selection of such mutations", explains Nadia Naffakh.

Adaptation to humans is also facilitated by the segmented nature of the influenza virus genome. Co-infection of a single cell by two different viruses can create new "mosaic" viruses, mixing segments from their parents to acquire novel properties.

Ultimately, characterising the mutations and genetic combinations that favour the adaptation of avian-origin influenza viruses to humans aims to strengthen surveillance of viruses circulating in the animal reservoir, and to better anticipate the emergence of viruses with pandemic potential.



"Understanding the rules that govern this phenomenon of genetic reassortment is essential to determine which combinations of segments can be viable and promote species jumps."

AVIAN FLU

ACTION PASTEUR

A global expansion, a human risk that remains limited

Zoonotic flu of avian origin remains one of the most closely monitored pandemic threats, with influenza A(H5N1) virus at the forefront.



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"Flu pandemics occur about three times per century, far more frequently than coronavirus pandemics", points out **Marie-Anne Rameix-Welti**, director of the CNR for Respiratory Infection Viruses. ***"It is a permanent threat."***

In wild aquatic birds, these viruses often circulate without causing major disease. But some strains, after passing into poultry, acquire high pathogenicity. The major change of the past decade is ecological: A(H5N1) viruses, first amplified in poultry farming, are now widely dispersed by wild birds worldwide. The 2025-2026 season reached an unprecedented level, with an unparalleled die-off among wild birds. ***"The virus now affects every continent, as far as Antarctica, with continuous, non-seasonal circulation, a situation with no equivalent in the history of influenza surveillance"***, the researcher explains.

Recent data show a clear diversification of mammalian hosts, with more than 48 mammal species infected in 26 countries since 2020. Even so, the viruses currently circulating remain predominantly avian in their biology, and no sustained human-to-human transmission has been observed to date. The passage from one species to another nonetheless follows well-identified routes. ***"The pig plays a key role as an intermediate host"***, the scientist explains. ***"Susceptible to simultaneous infection by human and avian viruses, it offers ideal conditions to produce new, potentially formidable hybrid viruses."***

The WHO continuously assesses these risks through a multidimensional analysis system, to which the researcher contributes. In this matrix, which crosses emergence risk with potential impact,



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A(H5N1) stands out for its high mortality but remains relatively low on emergence risk, for lack of sufficient determinants of adaptation to humans.

"Ultimately, it is swine viruses or avian A(H7N9) viruses that pose the greatest risk in this matrix", she concludes.

Disease factsheet

Avian flu

The zoonotic threat: when the virus crosses the species barrier

While seasonal flu is a major public health issue, virologists' real concern lies in the animal reservoir, chiefly wild aquatic birds, which harbour all subtypes of influenza A virus without developing symptoms. These viruses thus circulate silently within populations, forming an unstable natural genetic bank.

Some of these viruses, such as A(H5N1) or A(H7N9), can cross the species barrier and infect a human, notably during close contact with poultry (live animal markets, farms). So far, these transmissions remain epidemiological dead ends. Although these strains cause severe, even fatal disease (A(H5N1) has a case fatality rate above 50%), they do not spread efficiently between humans. Indeed, they struggle to infect the cells of the upper respiratory tract, which are essential for airborne transmission. While the risk of direct transmission to humans currently remains very limited, underestimating it would be a serious mistake. It is therefore essential to avoid any contact with dead or sick wild animals. **The scenario most feared by the WHO and animal health agencies is that of a zoonotic virus that, through mutation or genetic reassortment in an intermediate host such as the pig, manages to acquire both efficient human-to-human transmission and high virulence.** Such a combination would be the recipe for a major pandemic. Global surveillance of animal viruses is therefore crucial to detect these changes before they become a major danger for humans.

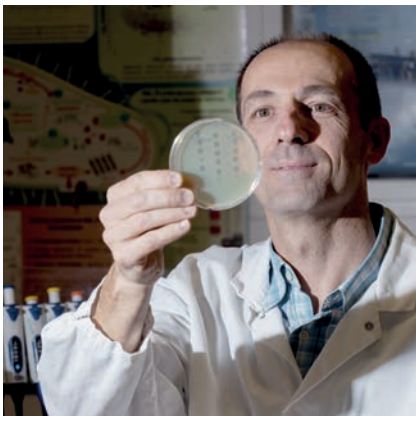
Research on the front line against influenza

Flu remains a biological adversary of formidable sophistication. While the vaccine, renewed every year, symbolises our ability to respond to an ever-evolving enemy, it is above all tangible proof of a collective victory. **Each vaccine update crowns the efforts of epidemiological surveillance and research, thereby saving millions of lives.**

Behind this feat lies a human and scientific mobilisation. Virologists, epidemiologists and modellers combine their expertise in an approach of permanent anticipation: tracking circulating viruses, decoding their evolution and anticipating their spread in order to protect us better.

REPORT BY THE EDITORIAL TEAM

MEETING


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Laurent Debarbieux

Head of the Bacteriophage, Bacterium, Host Unit

Antibiotic resistance: setting course for phage therapy

On the occasion of World Antimicrobial Resistance Awareness Week *(every year from 18 to 24 November)*, **we meet the researcher who is studying the use of phage therapy to combat antibiotic resistance.**

Laurent Debarbieux graduated in molecular biology in 1995 and completed his training at Harvard Medical School over four years before joining the Institut Pasteur in 2000. *"I followed the classic path of the French academic system"*, he says with some modesty. In 2004, while reading a short note in a prestigious journal, he learned about phage therapy. Two years later, he began a research project on bacteriophages and their use in medicine. *"Phage therapy is an opportunity to counter antibiotic resistance"*, argues the researcher. His expertise earned him, in 2022, the creation of his own research unit at the Institut Pasteur, called **Bacteriophage, Bacterium, Host.**

The "lung-on-a-chip": a miniature laboratory

The unit's work revealed a major discovery: the effectiveness of phage therapy depends closely on the patient's immune system. Indeed, neutrophils, white blood cells that are key to anti-infectious defence, are essential. In their absence, the therapy is ineffective. ***"These results call into question current protocols, in which treatments are administered without taking the patients' immune profile into account"***, stresses Laurent Debarbieux. For him, the future of phage therapy lies in personalised medicine, in which each patient would be characterised by their immune response before any treatment.

Laurent and his team are currently developing an innovative "lung-on-a-chip" model reproducing human alveolar architecture. This device makes it possible to study the interactions between pathogenic bacteria and bacteriophages, with the aim of proposing targeted therapies against *Pseudomonas aeruginosa* and *Acinetobacter baumannii*, two bacteria that are often resistant to multiple antibiotics and responsible for lung infections.

Phage therapy: a fundamentally Pasteurian discovery

"The father of phage therapy was also a Pasteurian", Laurent Debarbieux points out. This heritage goes back to 1917, when Félix d'Hérelle published the first scientific evidence of the use of bacteriophages as a therapeutic tool. After a brief golden age, the discovery of antibiotics eclipsed phage therapy in the West. *"It was relegated to the shadows"*, the researcher laments. Today, in the face of the inexorable rise of antibiotic resistance, this therapeutic approach is enjoying renewed interest. ***"With my team, we have advanced knowledge to make better use of bacteriophages in medicine"***, he says.

The Institut Pasteur has recently become home to the only national collection of bacteriophages, an essential tool in the fight against antibiotic-resistant bacteria. *"This bank came into being thanks to the drive of several teams, and our unit is its main contributor"*, says Laurent Debarbieux. Designed as a resource of characterised biological products, this collection aims to secure access to bacteriophages of therapeutic value. Soon, its opening to deposits by French and European teams will allow it to become a pillar of phage therapy research.

A decisive milestone reached in France

Laurent Debarbieux welcomes a major advance: this summer, the French National Agency for the Safety of Medicines (ANSM) authorised the *Hospices Civils de Lyon* to produce bacteriophages for therapeutic use. This decision is part of a broader movement, marked by the European Commission's funding of three clinical trials in 2026. It follows the compassionate use treatment* of some 200 European patients (Belgium, France, Portugal, etc.). ***"The results show that phage therapy is effective for more than 70% of patients who had reached a therapeutic dead end. In twenty years, we have gone from theory to practice!"*** says the researcher with delight, who expects significant expansion over the next five years.

Phage therapy is definitively emerging from the shadows to establish itself as a national medical priority, with the creation of an interdisciplinary expert group. *"We are witnessing the construction of a complete ecosystem"*, he explains, *"where basic research, academic production of bacteriophages and clinical trials fit together coherently"*. He highlights the Institut Pasteur's competitive advantage, unique in its position at the interface between fundamental science and clinical applications. For him, extending access to phage therapy has ***"become imperative to counter antibiotic resistance."***

What is phage therapy?

Phage therapy uses bacteriophages, natural viruses that specifically infect and destroy bacteria without affecting human cells. The main advantage of bacteriophages is their ability to target a small number of pathogenic bacteria while sparing the beneficial bacteria of the microbiota.

Generally well tolerated in humans, they are eliminated from the body within a few days after the infection ends. Bacteriophages can be used alone, in cocktails or in combination with antibiotics.

* Compassionate use (or compassionate access) is a medical scheme that allows the prescription of a drug that is not authorised, or is used outside its official indications, to treat patients with a serious, rare or disabling condition when no other solution exists.

Escherichia coli bacteriophages under an electron microscope. © Institut Pasteur/A. Ryter.



© Projet Madeleine

WOMEN'S HEALTH

An intergenerational citizen study on the vaginal microbiota

The Institut Pasteur*, Pasteur Lille and the Pileje Foundation are joining forces to launch the Madeleine project, a groundbreaking citizen study dedicated to women's health. This innovative project aims to study daughter-mother-grandmother triads within different families and answer a central question: what role does the vaginal microbiota play in their health?

With the ambition of collecting 210 samples, the study will explore the influence of heredity and lifestyle on the composition of this microbiota, as well as its link with the occurrence of vaginal infections. The intergenerational approach is a real added value, making it possible to better understand the respective share of genetic and environmental factors.

By launching Madeleine, France joins a global network of "sister" studies, all inspired by the pioneering Belgian project Isala (2020). Alongside the research, a prevention campaign will be rolled out to raise public awareness of the importance of the vaginal microbiota and of good hygiene practices that help preserve it.

** Work led by Sean Kennedy, head of the Metagenomic Signatures group at the Institut Pasteur.*

To sign up for the study:
form.dragnsurvey.com/survey/r/d3414d65

NEWS

PAEDIATRIC HEALTH

Preventing bronchiolitis: rising resistance, but protection maintained

Nirsevimab is a monoclonal antibody, marketed in 2023, indicated for the prevention of respiratory syncytial virus (RSV) infections, the main cause of bronchiolitis in infants. While its effectiveness has been widely demonstrated, both in clinical trials and in real-world use, concerns persist about the emergence of viral resistance.



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The Institut Pasteur*, in partnership with Henri Mondor Hospital (Créteil) and the ANRS-Emerging Infectious Diseases network, conducted a study based on real-life data from the 2024-2025 winter season. The study aimed to analyse the viral genome in infants infected despite treatment. The results show that resistance to nirsevimab was detected in 12.5% of RSV type B infections in children who had received the treatment. In total, 23 distinct mutations were identified across all sequenced genomes, compared with only two in the previous season (2023-2024). Mutations remain rare for RSV type A. No mutation was detected in RSV from untreated children, indicating that resistant viruses are not spreading and that prevention remains effective. This significant increase nevertheless underlines the need to strengthen genomic surveillance of RSV.

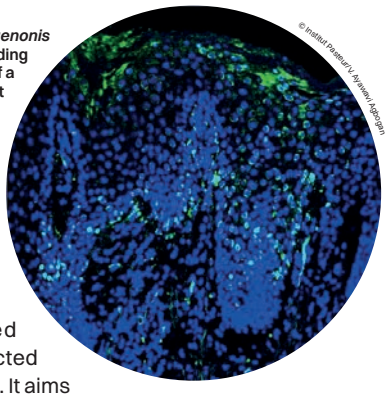
** Work led by Marie-Anne Rameix-Welti, director of the National Reference Centre for Respiratory Infection Viruses at the Institut Pasteur; Slim Fourati, virology laboratory of Henri Mondor Hospital (AP-HP), the teams of the ANRS-MIE virology network, Inserm, and the universities Paris-Est-Créteil and Paris-Saclay-Versailles-Saint-Quentin.*

DERMATOLOGY

A skin bacterium plays a role in Verneuil's disease

Verneuil's disease is an extremely painful chronic skin condition characterised by abscesses, inflammatory nodules and deep scars. Affecting up to 4% of the world's population, mostly women, it remains incurable to date. Researchers at the Institut Pasteur* have characterised the role of a bacterium in triggering this disease.

Porphyromonas uenonis is a bacterium naturally present on the skin, where it is usually harmless. In severe forms of Verneuil's disease, its behaviour changes: it crosses the patients' skin barrier. There it causes local inflammation and actively participates in triggering autoimmune reactions, in which the immune system turns against the body's own skin cells, worsening the lesions.



© Institut Pasteur/V. Aujoulat, Adocyam

Porphyromonas uenonis **(in green) invading skin cells (in blue) of a Verneuil's disease patient at a severe stage.**

This discovery sheds new light on this painful skin condition, which could result from an overall imbalance of the skin microbiota. It opens promising therapeutic prospects. A clinical trial named ABCESS2 is currently being conducted at the Institut Pasteur Medical Centre. It aims to evaluate the effectiveness of a combination of four antibiotics with the goal of inducing prolonged remission in patients at stage 2 of the disease. Recruitment is still under way and results are expected during 2028.

** Work led by Caroline Demangel, head of the Immunobiology and Therapy Unit at the Institut Pasteur, in collaboration with Olivier Join-Lambert (University of Caen) and Maia Delage and Aude Nassif, dermatologists at the Institut Pasteur Medical Centre.*

STUDY

Why does the heart so rarely develop cancer?

A recent study suggests that heartbeats slow the growth of cancer cells. The researchers suggest that the mechanical forces exerted on cells slow the activation of genes involved in cell proliferation.

Cardiac tumours are extremely rare: they are estimated to affect between 0.001 and 0.03% of the population, and in 80% of cases they are benign. Cardiac metastases, arising from a cancer that developed in another organ, are 40 to 100 times more frequent but remain equally exceptional.

How can such rarity be explained? A study carried out on mice provides some answers: the phenomenon appears to be linked to the heart's continuous beating. Constantly subjected to intense mechanical stress, heart cells renew themselves very little, at a rate of only about 1% per year. This is a striking difference from other tissues: skin regenerates completely in a few weeks, while the stomach or intestine renew themselves in a few days.

Yet it is precisely this cell renewal that lies at the heart of cancer risk: with each division, a cell can accumulate DNA mutations that may disrupt its normal functioning and lead to uncontrolled proliferation, in other words a cancer.

This discovery opens promising therapeutic prospects. It does, however, raise a fundamental question: what makes the heart so special? The lungs, also subject to incessant movement, do not escape cancer. That leaves the mechanisms specific to cardiac tissue. Once elucidated, they could be exploited in the treatment of other cancers, notably through targeted mechanical stimulation of tumour sites.


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Quarantine: the history of a public health measure

FOCUS

The recent Hantavirus crisis has forcefully reminded us of the need for strict, coordinated health measures. Among them, quarantine holds a central place: a look back at the origins and meaning of a measure against the spread of epidemics that is more than six centuries old.



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The first documented quarantine was introduced at the port of Dubrovnik, Croatia, on 27 July 1377, some twenty years after the great Black Death epidemic that had devastated Europe. Travellers were then required to stay for a month on the island of Mrkan or in the town of Cavtat before being allowed to enter Dubrovnik. The practice gradually spread across Europe: Venice was one of the first cities to codify it legally, in 1423, by building a dedicated lazaretto on an island in its lagoon.

In modern epidemiology, quarantine means a total restriction of movement, prescribed or recommended on a temporary basis for apparently healthy people who may have been exposed to a contagious disease. While the forty-day duration became established during the 15th century, giving the term its name, it is now adapted to the pathogen concerned.

Quarantine should also be distinguished from isolation. The former applies to people coming from at-risk areas who have no symptoms. It aims to monitor their health throughout the pathogen's known incubation period, to confirm or rule out that they are well. The latter, for its part, concerns individuals whose infection is confirmed, whether symptomatic or asymptomatic carriers, with the sole aim of preventing any transmission of the pathogen to other people.

SYMPOSIUM

The Institut Pasteur and the Institut Pasteur Korea strengthen their partnership

The Institut Pasteur and the Institut Pasteur Korea co-organised a symposium on 5 June entitled *"Crossroads of Basic and Translational Research in Biomedical Science."* Supported by the French Embassy in Korea, it was part of the celebrations of 140 years of diplomatic relations between the two countries. The event was organised in honour of the signing of a cooperation agreement between the two institutions, which aims to modernise their relationship and strengthen their research collaborations.



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The two institutions reaffirmed their desire to cooperate in research and development, technological innovation and education, with a focus on applications related to diagnostics and drug discovery.

On the occasion of the symposium, a delegation of Institut Pasteur researchers travelled to exchange with their Korean peers on translational research for the discovery of therapeutic solutions, advances in vaccine development and technological innovations. One of the plenary lectures was given by Carla Saleh, head of the Institut Pasteur's Department of Virology, on the links between infection and ageing. A closing session was also organised on equity, diversity and inclusion, to discuss the impact of the lack of diversity on research.

A transatlantic alliance against antibiotic resistance

Following a fruitful partnership on SARS-CoV-2, the Institut Pasteur and the University of California, San Francisco (UCSF) are renewing their alliance to tackle a major health challenge: the emergence of antibiotic-resistant bacteria.


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Led by Mélanie Hamon (head of the Chromatin and Infection Unit at the Institut Pasteur) and Nevan Krogan (director of the UCSF Quantitative Biosciences Institute), this new virtual unit is embarking on an ambitious five-year project: using artificial intelligence to build an atlas of the interactions between human cells and bacterial proteins.

In time, these data could allow the repurposing of existing drugs, originally designed for other conditions, as new antibiotics.

In addition, Raphaël Laurenceau, of the Institut Pasteur's Synthetic Biology Unit, spent two months at the Gladstone Institutes (affiliated with UCSF) to develop a molecular tool capable of accelerating the evolution of proteins of interest for biomedical research. A transatlantic collaboration that combines expertise and innovation to prepare for tomorrow's health challenges.

SCIENTIFIC COOPERATION

An unprecedented Franco-British alliance in health and artificial intelligence

The Institut Pasteur, the University of Oxford, Université Paris Cité, Diamond Light Source and the SOLEIL Synchrotron signed a historic agreement on 27 May 2026, creating the Franco-British Interdisciplinary Strategic Alliance in Health and Artificial Intelligence (Health Alliance).


© British Department for Science, Innovation and Technology

French and British representatives at COMIX in Paris, 27 May 2026, at the signing at the British Embassy in Paris. From left to right: **Martin Walsh,** *Deputy Director of Life Sciences at Diamond Light Source;* **Richard Cornall,** *Nuffield Professor of Clinical Medicine at the University of Oxford;* **Matthieu Resche-Rigon,** *Dean of the Faculty of Health at Université Paris Cité;* **Odette Tomescu-Hatto,** *Director of International Affairs at the Institut Pasteur;* **Jean Susini,** Director General of the SOLEIL Synchrotron.

This partnership opens a new chapter in scientific cooperation between the two countries. It responds to a major challenge: converting the unprecedented quantities of biological and clinical data generated by scientific advances into faster diagnostics, more effective treatments and improved prevention strategies. To achieve this, the Alliance networks world-class expertise and national infrastructures, bringing together molecular biology, advanced imaging, data science, artificial intelligence and translational medicine.

The Institut Pasteur contributes through its recognised expertise in pathogen biology and genetics, within the framework of three priority programmes: pandemic preparedness, the fight against antibiotic resistance, and women's gynaecological health.

"This partnership fits fully within our international cooperation strategy," said Odette Tomescu-Hatto, Director of International Affairs at the Institut Pasteur. *"By strengthening our collective capacity to better understand infectious diseases and to harness the potential of health data, this collaboration will benefit patients and global health."*

Pasteur and you

PasteurDon

20 YEARS of exceptional mobilisation!

For 20 years, the Pasteurdon has brought people together around a single ambition: advancing research to protect and improve our lives. Over the editions, it has become a major, deeply collective event in support of our researchers.

Thank you to everyone who accompanies and supports us, in particular during this 20th edition:

our patron and godmother Kad Merad and Julia Vignali,

our ambassadors Françoise Barré-Sinoussi, Erik Orsenna, Julian Bugier, Marc Levy, Alexandra Lamy, and many others,

our 50 media partners TV and radio,

the ambassador cities, which helped the movement grow and carried the voice of science to new audiences,

our researchers and the whole Pasteurian community, who embodied this mobilisation: charity runs, challenges, open days for young people to discover the work done at the heart of the laboratories,

our loyal patrons Fondation Le Roch-Les Mousquetaires, Groupe Pasteur Mutualité and AG2R la Mondiale,

and all of our donors.


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PasteurDon.fr 20 ANS

Catch up on the PasteurDon conferences, available on replay!

Researchers **Virginie Sauvage**, **Marion Guérin** and **Capucine Grandjean** share their work on infectious threats and cancer research, two flagship themes of this 20th edition.


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A captivating event for everyone on the challenges of research and public health.

Access the replay of the conferences:
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GENEROSITY

Thank you to ZEvent for its support of research!

In 2019, the ZEvent community rallied alongside the Institut Pasteur to support research and advance science. From 3 to 6 September 2026, for the tenth and final edition of ZEvent, the Institut Pasteur was once again among the supported charities. The funds raised will help advance our research on the microbiota.

Thanks to the generosity of streamers and their communities, these waves of solidarity contribute concretely to our research and public health missions. A huge thank you to everyone who took part in this collective adventure, and especially to the creators who publicised our projects to their communities.

Thank you for your trust, your energy and your commitment alongside science!

PASTEUR.FR

Welcome to the Institut Pasteur's new website

Every year, more than 10 million visitors consult our content: from disease fact sheets to health recommendations, including scientific news.





The new ***Pasteur.fr*** offers a more accessible and fluid experience for exploring both our practical information and the richness of our research. Our goal: to open windows onto the collective scientific adventure and help you understand how our research contributes to improving health.

We have also simplified your donation area, with a secure form allowing you to support our researchers and projects in just a few clicks. You benefit from the same security guarantees and contribution options.

To find out more, visit ***www.pasteur.fr/en***

CONFERENCES on stem cells

We are pleased to invite you to the Institut Pasteur **on Tuesday 15 December 2026** from 2:30 pm to 4:30 pm.

INTRODUCTION

by **Romain Levayer**
Director of the Department of Developmental and Stem Cell Biology



"The promise of stem cells in regenerative medicine"

by **Michel Cohen-Tannoudji**
Epigenomics, Proliferation and Cellular Identity Unit



"Stem cells: when research unlocks the mysteries of ageing"

by **Miria Ricchetti**
Head of the Molecular Mechanisms of Pathological and Physiological Ageing Unit



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