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VacCiencia es una publicación dirigida a investigadores y especialistas dedicados a la vacunología y temas afines, con el ojetivo de serle útil.

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Reseña de artículo publicado en *VacciMonitor*

Establecimiento de un método de cromatografía líquida de alta resolución para la cuantificación de proteína no enlazada en el conjugado de la vacuna SOBERANA®02



La enfermedad causada por el coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2, por sus siglas en inglés) ha constituido un desafío para las entidades de salud a nivel mundial. Para mitigar esa pandemia, muchas instituciones e investigadores desarrollaron diferentes vacunas. SOBERANA®02 es una vacuna basada en la plataforma de subunidades proteicas. Se obtiene a partir de la conjugación química de la proteína recombinante del dominio de unión al receptor (RBD, por sus siglas en inglés) de la proteína de la espícula del virus SARS-CoV-2 al toxoide tetánico (TT) que permite incrementar la inmunogenicidad e inducir memoria inmunológica.

Como el éxito de esa unión determina la calidad del antígeno, resulta esencial medir cuánto RBD queda sin enlazar tras la conjugación. Para ello se validó un método de cromatografía líquida de alta resolución.

Lo anterior se recoge en el artículo «*Establecimiento de un método de cromatografía líquida de alta resolución para la cuantificación de proteína no enlazada en el conjugado de la vacuna SOBERANA®02*», de Merchán-Milia y colaboradores, publicado en la revista *VacciMonitor*.

Los autores desarrollaron con ese fin un método de cromatografía líquida de alta resolución por exclusión molecular, con detección por arreglo de diodos y un material de referencia de RBD monomérico, y lo validaron con tres lotes de conjugado para demostrar que es fiable en el control de calidad, con un límite de aceptación de proteína libre inferior al 20 %.

La validación siguió la Guía del ICH Q2(R2) y las regulaciones del CECMED y abarcó las características de desempeño que se resumen a continuación.

Parámetros evaluados y su significado para el método

Idoneidad del sistema: Se evaluó mediante inyecciones repetidas de acetona y del material de referencia, observando tiempos de retención, eficiencia de la columna y asimetría del pico. Demostró un comportamiento satisfactorio del sistema, evidenciado por la consistencia de los tiempos de retención, la adecuada respuesta del detector y la reproducibilidad de las inyecciones.

Precisión: Se evaluaron seis réplicas de tres lotes por un mismo analista (intraensayo) bajo las mismas condiciones de operación y, por otro lado, fueron evaluadas tres réplicas de cada lote (interensayo) por dos analistas, con fases móviles preparadas por cada uno en días diferentes. Demostró que el método mantiene un desempeño consistente frente a las variaciones habituales del procedimiento analítico, demostrando su adecuada.

Exactitud: se evaluó mediante estudios de recuperación a tres niveles de concentración (bajo, medio, alto) con un material de referencia, dentro del rango de trabajo establecido. Demostró la idoneidad del método para la cuantificación del analito; presenta una exactitud adecuada en todo el rango evaluado, confirmando la ausencia de sesgo sistemático.

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Linealidad y rango: Se evaluó mediante curvas de calibración con cinco niveles de concentración. Los resultados confirmaron la reproducibilidad del método y su idoneidad para la cuantificación de proteína residual en el intervalo evaluado.

Especificidad: La especificidad del método se evaluó mediante estudios de degradación forzada, sometiendo la muestra a condiciones de estrés térmico. Demostró la capacidad del método para discriminar la proteína residual frente a productos de degradación.

Límites de detección y cuantificación: se realizó una extrapolación de los datos de las curvas de calibración obtenidas en el ensayo de linealidad, a partir de los cinco niveles de concentración evaluados. Los valores obtenidos evidencian una elevada sensibilidad del método HPLC-PDA para la determinación de proteína libre, permitiendo su detección y cuantificación a niveles traza dentro de matrices complejas.

En conjunto, los resultados de la validación demostraron que el método HPLC-PDA desarrollado es adecuado para la cuantificación de proteína libre en muestras de conjugados. El método presentó linealidad satisfactoria en el intervalo evaluado, alta sensibilidad analítica y adecuada precisión, junto con una especificidad comprobada frente a productos de degradación generados bajo estrés térmico. Estos hallazgos confirman la robustez del procedimiento analítico y su idoneidad para el análisis de rutina de proteína residual en matrices complejas.

Fuente:

Merchán-Milia, A., Plutin-Ocaña, Y., Chovel-Cuervo, M., Delgado-Arrieta, I., Herrera-Guada, L., & Santana-Mederos, D. (2026). Establecimiento de un método de cromatografía líquida de alta resolución para la cuantificación de proteína no enlazada en el conjugado de la vacuna SOBERANA®02. *VacciMonitor, 35*, e103526. Recuperado a partir de https://vaccimonitor.finlay.edu.cu/index.php/vaccimonitor/article/view/9311

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Noticias en la Web

The Next Chapter of mRNA

Nov 12. It's been a very good year for Stéphane Bancel. On a crisp October day, the CEO of Moderna, of COVID-vaccine fame, is sitting in his glass-walled office in the company's headquarters in Cambridge, Mass., weeks before encouraging results from the company's first mRNA cancer vaccine would become public. He's recounting the biotech's rocky road turning an unproven, scientifically dismissed approach—using messenger RNA, or mRNA, the genetic code that instructs cells to make proteins—into a platform for producing new categories of medicines.

Fifteen years ago, Bancel had his doubts. At the time, there were no approved mRNA-based products on the market, and most scientists would have agreed that mRNA was too unstable to form the basis of a new class of medical treatments. In fact, the entire biotech industry had bet—successfully—on manipulating another, more reliable genetic material: DNA.

"It was crazy to think of using mRNA as a drug," Bancel reflects. But that was before a fateful meeting forced him to look at the genetic material in a different way, and realize that with the right manipulation, mRNA provided a way to make drugs that were never possible with existing strategies. Now, he believes that nearly any protein drug made today with existing, recombinant DNA technology can also be made using mRNA.

The company's goal isn't to follow the usual road map and make one type of drug for one disease at a time, but to build a new platform from which a variety of different treatments can be developed in a plug-and-play scenario—similar to how the computer-technology industry is built on the foundational hardware and operating systems around which a whole universe of software has blossomed. "mRNA is the information molecule, so if you find the way to safely and effectively get it into the right cells, you can unlock a lot of medicines to help people's suffering," says Bancel.



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Moderna's mRNA COVID vaccine saved an estimated 2 million lives globally—while earning the company $46 billion—from 2021 to 2024. This fall, people are getting its newly approved mRNA flu shot, the first of its kind. And in October, Moderna announced with Merck that their mRNA approach also worked to stimulate the immune system to fight cancer—creating a therapeutic vaccine, rather than a preventative one. Intismeran, combined with one of Merck's drugs, successfully kept melanoma from recurring in a group of patients with mid- to late-stage disease. By the end of the year, Bancel says, he expects to unveil similarly encouraging results from Moderna's first mRNA therapy for a rare disease.

In just over a decade, mRNA has gone from molecular misfit to biomedical golden child, in no small part because of Bancel's efforts at Moderna to prove the naysayers wrong. "At the beginning, it was either zero drugs, or we find a way to climb this mRNA mountain and make a lot of drugs," says Bancel.

Born in Marseilles, Bancel grew up with a strong interest in math and science, fueled in part by his father, an engineer who was always fixing things around the house. "We used to sail in the summer, and one summer my brother and father and I sailed from Marseilles to Mallorca—a two-day trip—and the engine broke in the middle of the water in the middle of the night," he says. "I remember we were holding the flashlight above him, and he was fixing the engine by himself."

Bancel was pursuing a degree in chemical engineering at Ecole Centrale Paris when, on a whim, he took a genetics class at the university next door and "fell in love with genetics," he says. He went on to earn a master's in chemical engineering at the University of Minnesota and an M.B.A. from Harvard Business School before working at Eli Lilly in Indianapolis for six years, mostly in manufacturing.

In 2006, he became CEO of the French diagnostics company bioMérieux. He was working in the company's Boston office in 2011 when he got a call from his friend Noubar Afeyan, founder of Flagship Pioneering, a venture-capital firm and health-startup incubator. Bancel served on the boards of several of Afeyan's startups and had already turned down multiple offers to lead some of the new companies. But Afeyan thought he finally had one that might entice his friend.

Afeyan had been approached by a trio of scientists with the idea for a company to develop new treatments from mRNA. He showed Bancel data from a handful of mice that had been injected with human mRNA to make a human protein. "I'm like, 'This is impossible, because everything we learned in biology is that if you inject mRNA, you create an immune response,'" says Bancel. But what if it worked? Afeyan persisted. What would it mean? "I said, if it works, you're going to be able to make hundreds, maybe thousands of medicines that you cannot using [current] biotech technology," says Bancel.

Up to that point, the biotech industry was focused on manipulating DNA and making products to work on molecules that cells secreted—all in cell cultures using bacteria or viruses that were genetically engineered to produce the molecule in question. mRNA, on the other hand, works inside of cells, temporarily adding new genetic instructions for the cells to make new proteins, which could replace

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missing ones in certain diseases. In the case of infectious diseases or cancer, it could theoretically make proteins to stimulate the immune system.

But mRNA was too unstable to turn into a treatment formulation and too aggravating to the immune system, so the possibility of mRNA generating a new class of drugs hadn't advanced past "what if." When Bancel asked his good friends from college and business school whether he should take Afeyan's offer to helm the new company, everyone told him "Don't do it," he says. Two other biotechs—CureVac and BioNTech (which would become Moderna's competitor during COVID), both from Germany—had a head start on exploiting mRNA. But Afeyan was convinced that Moderna could lead this new field. Bancel had a choice to make, Afeyan said: Flagship would proceed with the company, with Bancel either as its head, a board member, or a regret-filled bystander.

The chance to build something in biotech from the ground up and figure it out along the way proved too tempting for the engineer in Bancel. In 2011, the company went from being called LS18—short for Life Sciences 18 in Flagship's ledger of startups—to Moderna, a mash-up of "modified RNA," with Bancel as its first CEO.

Bancel had experience in the pharmaceutical industry, but he had no playbook for starting a new company based on an unproven technology. He dived straight into every aspect of the company—even getting on the floor to build secondhand desks himself at Moderna's first headquarters in Cambridge—and pushed himself and his team hard. "The key was, how do you get to that one drug before you run out of money and investors throw in the towel on you, saying we're done?" he says.

Moderna spent its first few years in stealth mode, with no website, Bancel didn't want the world to watch Moderna's teenage years, as the company developed the technology he was convinced would change medicine.

Fuente: TIME. Disponible en https://n9.cl/5hfzn

Países de América Latina fortalecen la vacunación, el tamizaje y el acceso a tecnologías para alcanzar la eliminación del cáncer cervicouterino

13 nov. Representantes de 18 países de América Latina se reunieron esta semana en Ciudad de Panamá para fortalecer la implementación de programas de prevención y control del cáncer cervicouterino, con especial énfasis en expandir la introducción del tamizaje con pruebas de VPH (virus del papiloma humano), consolidar estrategias eficaces para aumentar las coberturas de vacunación contra el VPH y ampliar el acceso a vacunas, pruebas y tecnologías esenciales a través del Fondo Rotatorio de la OPS

La Reunión Subregional para América Latina: Acelerando la eliminación del cáncer cervicouterino en América, organizada por la Organización Panamericana de la Salud (OPS) se realizó del 11 al 13 de noviembre, en el marco de la Conferencia de Salud Global de las Américas de la Universidad Internacional de la Florida (FIU), en antelación al Día Mundial para la Eliminación del Cáncer Cervicouterino, que se conmemora el 17 de noviembre para reconocer los avances alcanzados y movilizar una mayor acción hacia las metas mundiales de eliminación para 2030.

La reunión convocó a responsables de programas nacionales de cáncer, inmunización y vigilancia de Argentina, Bolivia, Brasil, Chile, Colombia, Costa Rica, Cuba, El Salvador, Guatemala, Honduras, México,

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Nicaragua, Panamá, Paraguay, Perú, República Dominicana, Uruguay y Venezuela, junto con expertos regionales y representantes de la OPS.



Una enfermedad prevenible que continúa afectando a miles de mujeres

"Nos reunimos por una razón urgente: el cáncer cervicouterino es una enfermedad prevenible, y sin embargo sigue siendo el tercer cáncer más frecuente en las mujeres de América Latina y el Caribe", afirmó la Dra Zohra Abaakouk, asesora nacional de enfermedades no transmisibles y salud mental, en representación de la Dra Lilian Ninett Reneau Gaitan, representante interina de la OPS en Panamá.

En 2024, más de 81.000 mujeres fueron diagnosticadas y más de 38.000 murieron por esta enfermedad en la Región de las Américas. La mortalidad en América Latina y el Caribe es tres veces mayor que en Norteamérica, lo que refleja las persistentes desigualdades asociadas a la enfermedad. "Detrás de esas cifras hay madres, hijas y hermanas, y hay profundas inequidades que no podemos aceptar. Sabemos qué hay que hacer. La brecha entre lo que sabemos y lo que logramos es la que debemos cerrar juntos", agregó la Dra. Abaakouk.

La reunión buscó acelerar el avance hacia las metas 90-70-90 de la estrategia mundial de la Organización Mundial de la Salud para la Eliminación del Cáncer Cervicouterino para 2030: alcanzar un 90 % de vacunación contra el VPH en las niñas antes de los 15 años; lograr que el 70 % de las mujeres sean examinadas mediante una prueba de alto rendimiento; y asegurar que el 90 % de las mujeres con lesiones precancerosas o cáncer cervicouterino reciban tratamiento adecuado. La eliminación como problema de salud pública requiere alcanzar y mantener una incidencia inferior a cuatro casos por cada 100.000 mujeres.

"Abordar esta enfermedad es una cuestión de salud pública pero no sólo de salud también de derechos, de igualdad y de justicia social, garantizando que el lugar donde una mujer nace, vive y trabaja, no determine sus posibilidades de prevenir una enfermedad o de recibir atención de salud de

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calidad", manifestó Itziar Gonzalez Camacho, Coordinadora General de la Agencia Española de Cooperación Internacional para el Desarrollo (AECID) en Panamá, durante la apertura de la reunión.

Ampliar la vacunación y llegar a las niñas que aún no están protegidas

En la Región de las Américas, 49 países y territorios (de 51) ya han incorporado la vacuna contra el VPH a sus programas nacionales de inmunización, lo que la convierte en la región con mayor acceso. Sin embargo, aún persisten desafíos para ampliar la cobertura ya que solo dos países de la Región han alcanzado 90% de primeras dosis entre las niñas.

Durante las sesiones, los participantes revisaron la situación de la región y las nuevas recomendaciones del Grupo Asesor Estratégico de Expertos (SAGE, por sus siglas en inglés) sobre vacunación contra el VPH, que refuerza la recomendación de aplicar la dosis única en niñas de 9 a 14 años como la manera más eficiente para alcanzar la meta del 90% de vacunación.

Además, se discutieron estrategias para identificar y vacunar a las niñas que no han recibido la vacuna mediante registros nominales y compartieron experiencias de vacunación escolar, promoción y comunicación, sostenibilidad de los programas y registros nominales, y otras estrategias implementadas en países como Chile, Uruguay, Cuba, México, Brasil, Panamá y Bolivia.

Fortalecer el tamizaje con pruebas de VPH

El segundo día se orientó al fortalecimiento de los programas nacionales de tamizaje y tratamiento. Los participantes analizaron la transición desde programas basados principalmente en citología hacia el uso de pruebas de detección del VPH, así como estrategias para mejorar la planificación, el seguimiento de las mujeres y la calidad de los servicios.

La prueba de VPH es la recomendada para el tamizaje por ser más efectiva y, combinada con enfoques innovadores como “tamizar y tratar”, ha demostrado ser efectiva para prevenir el cáncer cervicouterino. De los países asistentes a la reunión, 13 ya han introducido la prueba de VPH en sus programas nacionales de tamizaje, y gracias a un acuerdo del Fondo Rotatorio de la OPS con proveedores, ahora pueden acceder a las pruebas de VPH a través de un precio preferencial y un paquete integral de apoyo.

La reunión permitió además trabajar con una novedosa herramienta de planificación para el tamizaje y tratamiento desarrollada por la OPS, que los equipos nacionales utilizaron para analizar sus necesidades y fortalecer la planificación de los servicios. Las sesiones abordaron también la recolección de datos, los registros de cáncer, el control de calidad de los laboratorios que realizan pruebas de VPH y las recomendaciones para el tamizaje y manejo de lesiones cervicouterinas.

Mejor acceso a vacunas, pruebas y equipos a través del Fondo Rotatorio

Otro componente clave de la reunión fue fortalecer el conocimiento y uso del Fondo Rotatorio Regional de la OPS como mecanismo para ampliar el acceso de los países a productos y tecnologías necesarios para prevenir, detectar y tratar el cáncer cervicouterino.

Durante una sesión práctica, los equipos nacionales conocieron el portafolio de productos disponibles, que incluye vacunas contra el VPH, pruebas de detección del VPH y equipos para diagnóstico y tratamiento, como termoabladores, colposcopios móviles y equipos para escisión electroquirúrgica con asa. También trabajaron en el proceso de previsión y adquisición de estos insumos y dispositivos.

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De las estrategias regionales a la implementación en los países

Además, los participantes revisaron también los planes nacionales de eliminación, los marcos de monitoreo y evaluación y las capacidades de los países para realizar el seguimiento de las personas con lesiones precancerosas o cáncer cervicouterino. Actualmente, siete países de la Región han finalizado sus planes nacionales de eliminación y otros nueve se encuentran desarrollándolos.

La eliminación del cáncer cervicouterino forma parte de dos iniciativas emblemáticas de la OPS: Mejor atención para las enfermedades no transmisibles, que busca ampliar el acceso equitativo a servicios integrados e integrales para las ENT desde la atención primaria de salud, y la Iniciativa de Eliminación de Enfermedades, orientada a eliminar más de 30 enfermedades y condiciones relacionadas en las Américas para 2030.

La reunión forma parte de las capacitaciones planificadas por la OPS para acelerar la eliminación del cáncer cervicouterino en la Región, que se desarrollan con el apoyo de la Agencia Española de Cooperación Internacional para el Desarrollo (AECID), así como con recursos proporcionados a través de la Conferencia de Salud Global, parte del Consorcio Global de Salud de Florida International University (FIU).

Fuente: OPS. Disponible en https://n9.cl/vaehu3

Argentina aprobó una nueva vacuna contra el neumococo: cuáles son sus características y a quiénes está destinada



14 nov. La enfermedad neumocócica continúa siendo una preocupación sanitaria, especialmente entre los adultos mayores y las personas con factores de riesgo. La aprobación se produce en un contexto de vigilancia epidemiológica que muestra la circulación de distintas variantes del neumococo en el país.

La Administración Nacional de Medicamentos, Alimentos y Tecnología Médica (ANMAT) aprobó en Argentina una nueva vacuna antineumocócica conjugada de 21 serotipos, desarrollada específicamente para la población adulta. El anuncio fue realizado por MSD Argentina y representa la incorporación de una nueva alternativa para prevenir la enfermedad neumocócica invasiva y la neumonía en personas mayores de 18 años.

La enfermedad neumocócica es causada por la bacteria *Streptococcus pneumoniae*, que puede provocar desde infecciones respiratorias hasta cuadros graves, como meningitis y bacteriemia. El riesgo de complicaciones aumenta especialmente en adultos mayores y en personas con enfermedades crónicas o inmunocompromiso.

Uno de los aspectos destacados de la nueva vacuna es la inclusión de serotipos que tienen una presencia relevante en la vigilancia epidemiológica argentina. Entre ellos se encuentran los serotipos 3, 8, 9N y 12F, identificados entre los que circulan con mayor frecuencia en la población adulta.

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Según datos del Laboratorio Nacional de Referencia, durante 2025 se analizaron 679 muestras correspondientes a casos de enfermedad neumocócica invasiva. Los serotipos 12F, 3 y 14 estuvieron entre los más frecuentes en los distintos grupos de edad, mientras que los serotipos 8 y 9N registraron una frecuencia elevada entre las personas mayores de 17 años.

Estos datos ponen de manifiesto la importancia de contar con estrategias de prevención que contemplen las características epidemiológicas de cada población y la distribución de los serotipos responsables de las infecciones.

Una cobertura relevante para Argentina

De acuerdo con estimaciones realizadas a partir de datos nacionales de vigilancia correspondientes al período 2016-2023, los serotipos incluidos en la vacuna de 21 valencias representarían una cobertura teórica del 69,8% de los serotipos asociados a enfermedad neumocócica invasiva en adultos de entre 50 y 59 años, y del 67% en personas de 60 años o más.

Es importante aclarar que estos porcentajes representan la proporción de serotipos incluidos en la formulación de la vacuna y no constituyen una medición de su efectividad clínica ni garantizan ese nivel de protección individual.

Qué se sabe sobre la evidencia clínica

La aprobación de ANMAT se sustenta en los resultados del programa clínico STRIDE, integrado por distintos ensayos de Fase 3 que evaluaron la respuesta inmunitaria y la seguridad de la vacuna en diferentes grupos de adultos.

Entre ellos se destacan STRIDE-3, que comparó la vacuna de 21 serotipos con PCV20 en adultos de 18 años o más sin vacunación neumocócica previa, y STRIDE-10, que la comparó con la vacuna polisacárida PPSV23 en personas de 50 años o más.

Según la información difundida por MSD, los estudios mostraron respuestas inmunitarias frente a los serotipos incluidos y un perfil de seguridad consistente con el observado en las vacunas comparadoras.

Desde la compañía señalaron que esta aprobación forma parte de su estrategia para contribuir a la prevención de la enfermedad neumocócica en adultos.

La importancia de la vacunación en adultos

La enfermedad neumocócica continúa siendo un problema relevante de salud pública, especialmente entre las personas mayores de 65 años y quienes presentan factores de riesgo, como enfermedades cardiovasculares, respiratorias, metabólicas o alteraciones del sistema inmunológico.

La vigilancia epidemiológica permite identificar qué serotipos circulan con mayor frecuencia y orientar las estrategias de prevención. En este escenario, la incorporación de nuevas formulaciones vacunales amplía las herramientas disponibles para abordar la enfermedad en la población adulta.

La utilización de esta nueva vacuna deberá ajustarse a su indicación aprobada por ANMAT, a las recomendaciones de las autoridades sanitarias y a la evaluación de cada paciente por parte de los profesionales de la salud.

Fuente: EQS NOTAS.com. Disponible en https://n9.cl/gm9ti

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Ebola exposes Covid's unlearnt lessons



Nov 15. The world learnt painful lessons from the COVID-19 pandemic. It showed what scientific co-operation could achieve by developing vaccines at unprecedented speed, and improving genomic sequencing and diagnostics. Yet the latest Ebola epidemic in the Democratic Republic of the Congo suggests that turning those advances into public-health protection remains unfinished business.

Six months after the outbreak was declared, a Doctors Without Borders official says it is not under control. According to the medical humanitarian organisation, many cases are appearing without known links to earlier infections, suggesting the failure of contact tracing. This is the outcome of several shortcomings, including unpaid health workers, surveillance teams lacking fuel, shortages of protective equipment and inadequate support for those treating suspected cases.

More than 11,000 people have been infected, nearly half of whom have died, making it the country's deadliest outbreak. These failures point to weaknesses in the response at a local level, primarily fragmented co-ordination and poor regulation. Hundreds of millions of dollars allocated to the response remain unaccounted for, and warrant investigation. Conflict, porous borders and distrust complicate the task, too.

Meanwhile, the coronavirus itself has not disappeared, with a new variant currently spreading around the world. Experts say there is no convincing evidence that it causes more severe disease than previous strains, yet that is not a reason for complacency. As long as the virus continues to mutate, vulnerable people will be at risk with surveillance required to detect changes.

A report by the Independent Panel for Pandemic Preparedness and Response makes a related point about Mpox and other known threats – that outbreaks become emergencies when warning signs are missed, community health care is neglected and investment dips between crises. Far too often, unfortunately, prevention is ignored once an emergency recedes.

The Pandemic Agreement, adopted by the World Health Organisation's member states in May last year, was intended to address some of these inadequacies through stronger international co-operation and fairer access to vaccines, diagnostics and treatments. However, the agreement cannot be opened for signatures until its section on pathogen-sharing is adopted, no sooner than May next year, because of disagreements over who benefits when developing countries share pathogen samples that may be used to develop commercially valuable medicines. Wealthier nations and pharmaceutical companies seek reliable access to these samples, while poorer countries demand binding guarantees that the resulting vaccines and treatments will reach them too.

International collaboration alone cannot address local challenges, such as the ones mentioned above regarding the Congo. But it can provide a framework for countries to act together, if backed by resources and political commitment. This is particularly salient with imported cases of the virus having been

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confirmed in Kenya and Nigeria, reminding all that infectious diseases do not respect national boundaries, and that weaknesses in one country's health system can become a threat to others.

The measure of what the world learnt from COVID-19 will not be the speed with which it develops the next vaccine – although that is important. It will be whether it can detect, contain and stop the next outbreak before it becomes a pandemic.

Fuente: The National Editorial. Disponible en https://n9.cl/y62sj

Scientists are using AI to develop superior vaccines against viruses threatening global health

Nov 16. Their new vaccine against bird flu – a significant threat to human health – outperformed the current stockpiled jab in animal trials.

This proves that the technique could help strengthen pandemic preparedness and national biosecurity.

In a study published in the journal 'Cell Reports Medicine', the team reports that their new broad-spectrum bird flu vaccine gave complete protection against globally circulating, diverse variants of the disease in animal trials.

"A Cambridge team has had a third success with their AI-guided technique for designing vaccines against highly infectious viruses that threaten animal and human health."

The results show the vaccine is far superior to bird flu vaccines currently stockpiled by many governments for use in the event of a human outbreak. In the study, those vaccines protected only around 50% of animals exposed to multiple bird flu variants, compared with complete protection achieved by the team's new vaccine.

Developed by the University's Laboratory of Viral Zoonotics and spin-out DIOSynVax Ltd, this is the latest in a series of new vaccines made in an entirely new way. Their active ingredient is designed to give lasting protection from thousands of virus variants in a single vaccine.

The new study proves that the team's 'plug and play' approach can be used to create safe, highly effective vaccines for a plethora of infectious diseases threatening animal and human health globally.

The next step is to test the new bird flu vaccine in human clinical trials, so that it can be ready to be given to humans immediately, when needed.

Bird flu is spreading in animals around the world and currently considered a significant threat to global public health.

Although some human infections with the North American variants have been mild, other variants in south-east Asia have caused severe disease and high mortality in humans.

Like the coronaviruses that caused COVID-19, and many other emerging infectious diseases, bird flu is an RNA virus. RNA viruses represent a particular threat to human health because they can mutate rapidly into new strains that can jump from animals to humans and evade our immune systems – and our existing vaccines.

Earlier this year the team announced that their broad-spectrum coronavirus vaccine had proved safe in human trials, and published results showing their broad-spectrum influenza vaccine protects against both human and swine flu viruses.

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Current pandemic preparedness relies on stockpiling vaccines against individual virus variants that have already emerged. These require constant updating as the virus changes – increasing the cost to governments.

The Cambridge team's approach uses AI-guided engineering to create broadly protective vaccines intended to remain effective across a wide range of existing and future variants. Heeney said:

"These new-generation vaccines are a game changer for national biosecurity and more resilient public health.

"They mean we can be much better prepared to respond immediately to virus epidemics and pandemics, rather than the current scenario of always being on the back foot and responding with a strain which will have changed."

The results demonstrate the potential of AI-guided vaccine design in developing broad protective population immunity ahead of evolving biological threats. This aligns closely with the emerging national and international focus on biosecurity, following the UK government's recent £100 million investment in national AI biosecurity.

A superior bird flu vaccine

In the new study, the DIOSynVax vaccine completely protected mice and ferrets against a range of genetically distinct variants of the virus causing bird flu – all of which have caused human infections and represent potential pandemic threats. In comparison, only half the animals survived these same viruses when immunised with the World Health Organisation's existing bird flu vaccine.

The bird flu vaccine stockpiled by governments for human use is based on representative virus isolates identified through the World Health Organization's pandemic influenza preparedness programme. It was designed to protect against one specific strain of the disease, but the study found it provides minimal protection against other strains in circulation.

The decades-old vaccine technology is largely reactive, responding to pathogens after they have emerged. Traditional vaccines are designed to give protection to specific virus strains or variants that have already been detected in humans. But since viruses are constantly mutating, by the time the vaccines are manufactured and distributed, they have limited protection and must be updated regularly to try and keep up.

Collaborators at Canada's National Microbiology Laboratory (NML), and Italy's Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) independently validated the DIOSynVax vaccine against bird flu viruses from globally different sources.

An entirely new way to design vaccines

The active ingredient in a vaccine, called an antigen, triggers the body's immune system to produce a protective response. This trains the body to fight off future infection by a pathogen containing this specific antigen.

To design the bird flu vaccine, the team collected the genetic sequence data of all the bird flu viruses logged by surveillance programmes around the world, which take virus samples from wildlife, livestock and humans infected with bird flu.

They built an AI tool to integrate the huge amount of genetic data and use it to design a range of 'super-antigens', which contain the antigen features common to this whole group of viruses.

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These were screened in cells to select the best one for the vaccine, which was then tested in animal trials.

“Using AI vastly speeds up the process of vaccine design, and then we can test the vaccine candidates in the lab to make sure they’re robust and safe,” said Heeney.

Vishwanath said: “By instructing the immune system to target different stages of the viral lifecycle, we can induce an immune response blocking several crucial steps in its replication.”

This new class of universal vaccines is future-proofed. They not only protect against many variants simultaneously, but potentially against related viruses that haven’t yet emerged and spilt over to humans.

A highly adaptable technology

Emerging RNA viruses like bird flu can spread quickly between livestock, wildlife, and people. The team’s goal is to create broadly protective vaccines for both animals and humans, helping reduce opportunities for pathogens to emerge, adapt and spread.

In October the team, together with partners at the Universities of Regensburg and Southampton, received £4.28 million from UK Research and Innovation (UKRI) and Defra as part of a national biosecurity investment aimed at tackling future disease outbreaks, shortening response times and reducing risks internationally and in the UK.

The funding will enable the team to continue development of their single vaccine against the viruses causing Lassa fever, Marburg, and Ebola – some of the most dangerous in the world. Ebola has an average fatality rate of around 50%, and there is no approved Marburg vaccine or antiviral treatment.

The team is also working on a seasonal flu vaccine that would provide broad-spectrum protection over several flu seasons. Preliminary results show that the vaccine antigen they designed in 2018 is still effective after seven years.

The need for frequent reformulation is a fundamental limitation of current vaccines, and the reason why flu and Covid jabs are currently needed every year by millions around the world – at a huge cost to health services.

Bird flu: a highly mobile virus

Bird flu is carried in the guts of infected birds and, due to many species flying long distances as they migrate each year, it can easily be carried halfway across the world and deposited as infectious droppings. This year it was detected for the first time in animals in Australia and New Zealand.

“It’s when bird flu adapts to live in the airways of mammals that we start to get really nervous,” said Heeney, “not only because of the impact on animal health but because of the threat to humans. If we can make better animal vaccines, then we can better protect human health as well.”

Pigs and humans have the same receptors for the virus in their respiratory tract, which means that a bird flu virus infecting pigs could increase the virus’ ability to infect humans too. And with the speed at which humans travel across the world, a highly infectious strain emerging in one place could quickly be everywhere.

Fuente: TECHNOLOGY.ORG. Disponible en https://n9.cl/53lb8

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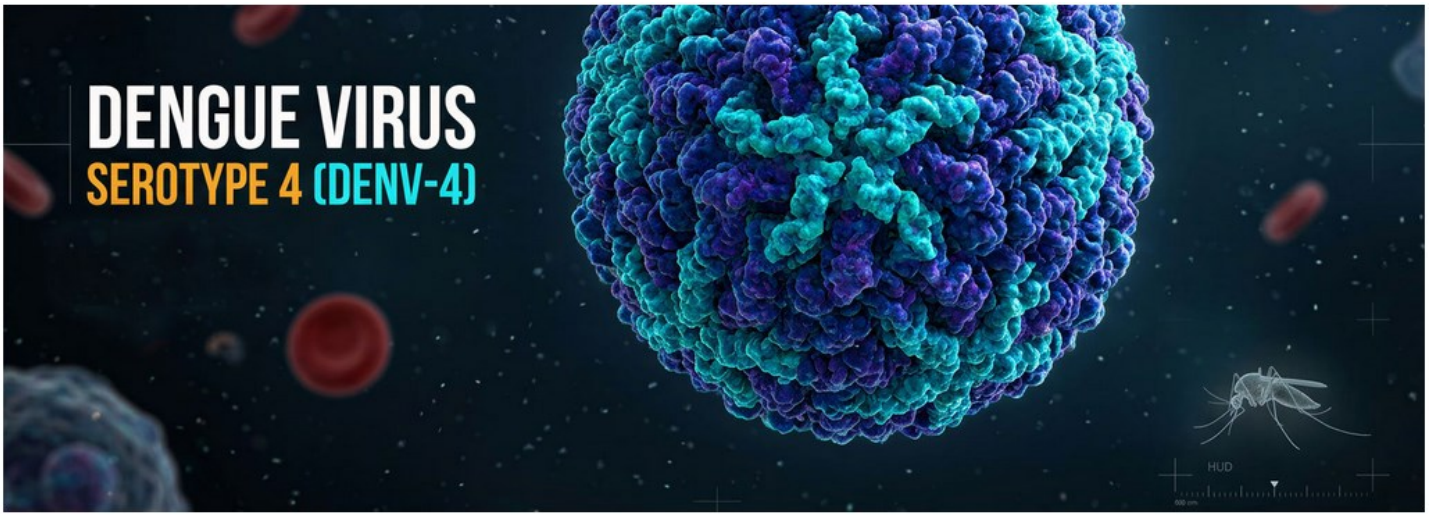
University of Maryland School of Medicine Researchers Develop New Human Challenge Model to Advance Dengue Vaccine and Treatment Research

Nov 16. Researchers at the University of Maryland School of Medicine (UMSOM) and the Institute of Human Virology (IHV) have developed the first successful human challenge model for dengue serotype 4, a major advance that could speed the development of new drugs and vaccines against a strain of the dengue virus that remains difficult to study. The findings were published this week in *The Lancet Microbe*.

Dengue is the flavivirus. Each received a single injection under the skin containing 95 plaque-forming units of the challenge virus — a very low dose by the standards of earlier dengue challenge studies, which used at least seven times more virus.

Participants were checked daily for symptoms, had blood drawn regularly, and were housed in a local hotel while the virus was detectable in their blood, so that local mosquitoes could not pick it up and spread it.

The study ran at the University of Maryland School of Medicine in Baltimore between April 2022 and December 2023.



What the researchers found

All 14 participants developed detectable virus in their blood and mild-to-moderate dengue symptoms. The most common symptoms were rash and fatigue, which every participant developed, followed by headaches. “The study also offered us a rare opportunity to examine how immunity develops and persists following dengue infection,” said Joel Chua, MD, Associate Professor of Medicine, Institute of Human Virology, UMSOM. “We gained new insights into the immune system's response at the earliest timepoints after dengue exposure and also found evidence that the immune response generated by an initial DENV-4 exposure can provide durable, serotype-specific protection at least one year later.”

One of the world’s most prevalent mosquito-borne infections, the Dengue virus has four distinct serotypes, known as DENV-1 through DENV-4. While infection with one serotype generally produces lasting protection against that same serotype, it does not necessarily protect against the other three. The dengue serotype 4 poses a particular challenge because, unlike other dengue types, it circulates

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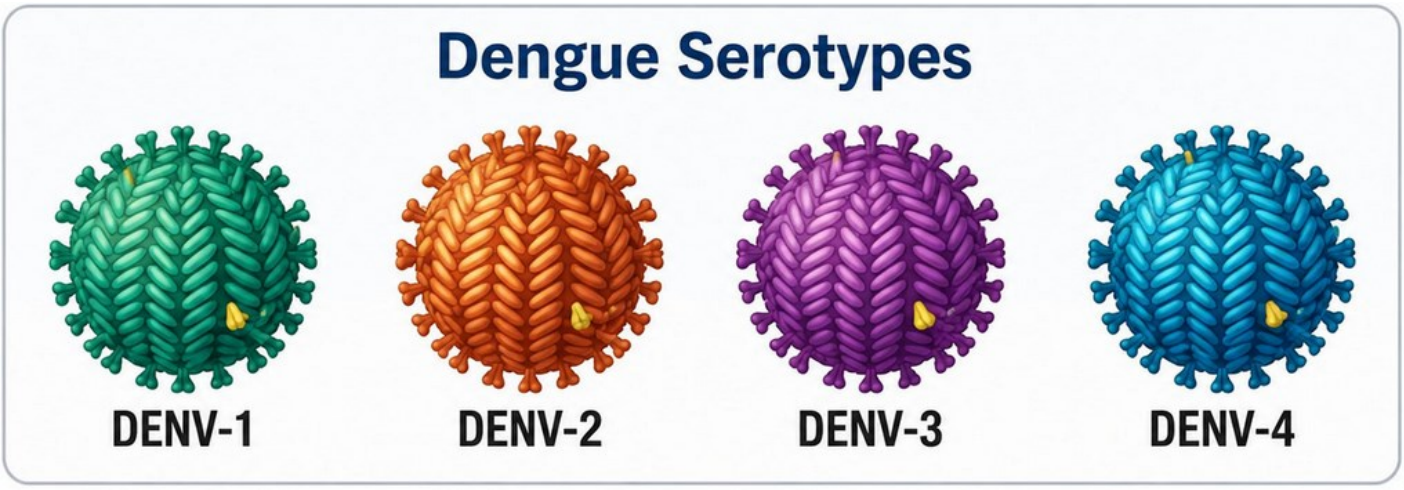
slowly and unpredictably, sometimes with decades between outbreaks. Large field trials have not been able to measure how well vaccines work against it. Recent phase 3 trials of dengue vaccines could not produce reliable efficacy estimates for dengue serotype 4.



In addition to evaluating clinical symptoms and viral activity, researchers conducted extensive immunological and transcriptomic analyses to better understand the body's response to both initial exposure and subsequent rechallenge. Following primary infection, participants demonstrated robust antibody responses, expansion of antibody-producing cells, and activation of antiviral genes. These responses were largely absent following the second exposure, consistent with the observed protection.

The findings build on previous work developing human challenge models for dengue serotypes 1 and 3. Together, these models provide researchers with additional tools to investigate the distinct characteristics of each serotype and evaluate promising vaccine and therapeutic candidates before advancing them into larger clinical trials.

“Dengue virus is one of the WHO top ten global health threats and the outbreak in Florida is only a harbinger of the spread of dengue that is expected within the United States by 2080,” said study principal investigator Kirsten E. Lyke, MD, Professor of Medicine, Center for Vaccine Development and Global Health. “We have no antiviral therapy against dengue, so the development of vaccines is critically important for protection now and into the future. Human challenge models allow us to test therapeutics, biologic agents and vaccines, in order to focus our energy development product with known efficacy. This study is part of a consortium effort to develop human challenge models for all four serotypes.”

Although the study involved a relatively small group of healthy adult volunteers and further research is needed, the results establish an important foundation for future dengue vaccine and antiviral development. The ability to reliably evaluate immune responses to DENV-4 in a controlled clinical setting could help researchers address longstanding gaps in the development of effective countermeasures against all four dengue serotypes.

The study was funded by the Military Infectious Disease Research Program and the Medical Technology Enterprise Consortium.

Fuente: UNIVERSITY OF MARYLAND SCHOOL OF MEDICINE. Disponible en https://n9.cl/z2bb0

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Bivalent RSVpreF Vaccine Protects Older Adults Against Severe Disease Across Three Seasons



Nov 20. A single dose of the bivalent RSVpreF protein subunit vaccine provided sustained protection against respiratory syncytial virus-related hospitalizations and emergency department encounters in older adults across three consecutive respiratory illness seasons, according to a major retrospective test-negative case-control study conducted within Kaiser Permanente Southern California. The clinical research, published in Infectious Diseases and Therapy, evaluates real-world vaccine effectiveness among individuals aged sixty years and older between November 24, 2023, and April 18, 2026. Prior clinical investigations demonstrated that respiratory syncytial virus protein subunit immunizations significantly decrease severe clinical outcomes including hospital admissions and emergency department visits for at least two respiratory syncytial virus seasons following administration. However, published observational data evaluating real-world vaccine performance beyond the second season remained entirely absent until this clinical evaluation, which extends surveillance through a third full epidemiological cycle to understand immunological durability and public health utility in routine healthcare operations.

Respiratory syncytial virus causes substantial morbidity and mortality annually among older demographic cohorts in high-income settings, precipitating hundreds of thousands of inpatient hospitalizations and tens of thousands of recorded fatalities. The current observational study tracked clinical encounters across a comprehensive managed care consortium in Southern California, examining whether protection afforded by the bivalent formulation marketed as Abrysvo remains robust across extended time horizons in aging patients exhibiting complex medical histories.

The study sample was drawn from individuals aged sixty years or older presenting with lower respiratory tract disease or acute respiratory illness who required an emergency department visit or hospital admission across the monitored study period. Eligible clinical events were defined as an initial acute respiratory presentation within each respective respiratory syncytial virus season associated with at least one documented lower respiratory tract disease or acute respiratory illness diagnostic discharge code under the International Classification of Diseases, Tenth Revision, in any diagnostic position. To ensure definitive microbiological verification, every qualifying presentation required concurrent multiplex polymerase chain reaction testing of a nasal or nasopharyngeal swab collected within a window extending from fourteen days prior to three days following clinical admission.

Because diagnostic laboratory testing for respiratory syncytial virus can be underutilized in routine clinical practice for hospitalized adults exhibiting lower respiratory tract conditions, the investigative team implemented systematic salvage protocols. Standard-of-care laboratory testing was supplemented by study-initiated salvage and respiratory syncytial virus polymerase chain reaction evaluation of swabs originally collected solely for influenza or SARS-CoV-2 screening, using the identical Cobas eplex RP2 multiplex testing platform.

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Within the study design, confirmed cases were patients testing positive for respiratory syncytial virus without concurrent viral coinfection. To establish an unbiased control cohort, controls were strictly defined as symptomatic patients testing negative for respiratory syncytial virus, human metapneumovirus, influenza, and SARS-CoV-2, while simultaneously testing positive for a non-vaccine-preventable respiratory pathogen. This strict control definition was adopted to reduce potential bias arising from single-specimen sensitivity limitations or correlated viral vaccination uptake behaviors.

Vaccination exposure was rigorously classified as documented electronic health record receipt of the bivalent RSVpreF formulation at least twenty-one days prior to the acute lower respiratory tract disease or acute respiratory illness admission date. The health system verified immunization records through internal clinical documentation augmented by bi-directional electronic data exchange with the California Immunization Registry. Over the multi-year study window, investigators screened 6,813 lower respiratory tract disease events and 10,296 acute respiratory illness events occurring among adults aged sixty years and older. Following application of strict inclusion and exclusion criteria, 3,131 lower respiratory tract disease encounters and 4,797 acute respiratory illness encounters qualified for final statistical evaluation, comprising 46.0 percent and 46.6 percent of screened presentations, respectively. Inpatient hospital admissions accounted for 70.5 percent of the eligible lower respiratory tract disease cohort and 56.7 percent of the acute respiratory illness cohort.

The demographic and clinical profile of the analyzed patient populations demonstrated high baseline vulnerability and comorbidity. Across the lower respiratory tract disease and acute respiratory illness cohorts, median patient age was 78 years and 77 years, with interquartile ranges spanning 70 to 85 years and 69 to 84 years, respectively. The median Charlson comorbidity index across both evaluated disease groups was 4, reflecting widespread chronic systemic disease. In addition, 22.8 percent of individuals in the lower respiratory tract disease group and 22.1 percent in the acute respiratory illness group met formal clinical definitions for immunocompromising medical conditions. Within the evaluated cohorts, 637 lower respiratory tract disease presentations and 967 acute respiratory illness presentations occurred in individuals vaccinated with bivalent RSVpreF, representing 20.3 percent and 20.2 percent of qualifying presentations. Microbiological analyses identified 911 respiratory syncytial virus cases among lower respiratory tract disease encounters and 1,261 cases among acute respiratory illness encounters.

Adjusted vaccine effectiveness was calculated from odds ratios generated via multivariable logistic regression models or generalized estimating equations when individual participants contributed multiple sequential clinical events. Statistical models incorporated extensive pre-specified baseline confounders, including patient age, sex, race and ethnicity, Charlson comorbidity index scores, encounter calendar month, specific encounter facility, and receipt of influenza vaccination within the year preceding the index encounter date. Additional model-specific variables included body mass index categories, cigarette smoking status, presence of diabetes mellitus, prior annual inpatient encounters, prior virtual care encounters, neighborhood deprivation indices, and immunocompromised status. Primary evaluations were modeled separately for each post-vaccination season to account for temporal cohort evolution and varying baseline characteristics across sequential respiratory seasons...

Fuente: Bioengineer.org. Disponible en https://n9.cl/gtpgx

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Incorpora IMSS vacuna contra COVID-19 al esquema infantil para menores de cinco años



20 nov. La campaña está dirigida a niñas y niños de 6 a 59 meses que reciben el biológico por primera vez; el esquema contempla dos dosis, con un intervalo de un mes entre aplicaciones.

El Instituto Mexicano del Seguro Social (IMSS) en Quintana Roo invita a madres y padres de familia a llevar a vacunar contra COVID-19 a niñas y niños de 6 a 59 meses de edad, como parte de las acciones para fortalecer la protección de la población infantil ante posibles complicaciones respiratorias.

La coordinadora de Enfermería en Salud Pública del Instituto en Quintana Roo, Anabel Martínez Benítez, destacó que este año la vacuna contra COVID-19 se incorpora por primera vez al esquema básico de vacunación para este grupo de edad, por lo que representa una nueva medida de prevención para proteger la salud de niñas y niños.

Explicó que el esquema contempla dos dosis: una inicial y una segunda aplicación un mes después, sin que sea necesaria una revacunación anual.

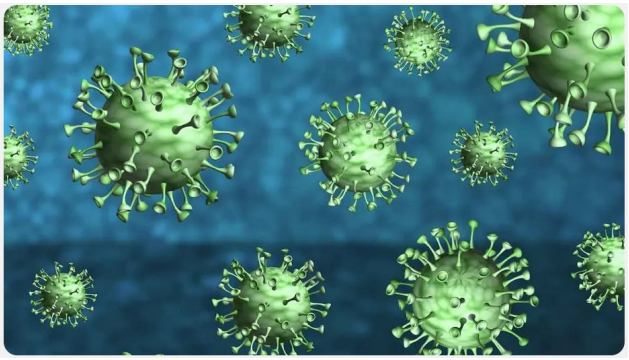
Martínez Benítez Indicó que, para facilitar el acceso a este servicio, el IMSS cuenta con módulos de vacunación en sus unidades médicas y en puntos estratégicos de la comunidad, como centros comerciales, plazas, parques y ferias de salud, además de las guarderías del Instituto.

Martínez Benítez subrayó que la vacuna es segura y cumple con los estándares establecidos para su transporte, conservación y resguardo, por lo que invitó a las familias a acudir con confianza a los puntos de vacunación.

Señaló que, aunque la aplicación es voluntaria, la participación de madres y padres de familia es fundamental para fortalecer la prevención y proteger la salud de las niñas y los niños.

Fuente: Periódico Quequi. Disponible en https://n9.cl/hqu03

Llegó a Argentina una nueva variante de COVID-19: qué se sabe y por qué aumentan los casos



21 nov. Se trata de PJ.2.1, un linaje descendiente de Ómicron que ya fue detectado en pacientes de la provincia de Buenos Aires. Las vacunas disponibles continúan ofreciendo protección.

Una nueva variante de COVID-19 comenzó a ganar terreno en distintos países y ya fue detectada en Argentina. Se trata de PJ.2.1, un linaje descendiente de Ómicron que, según expertos y organismos

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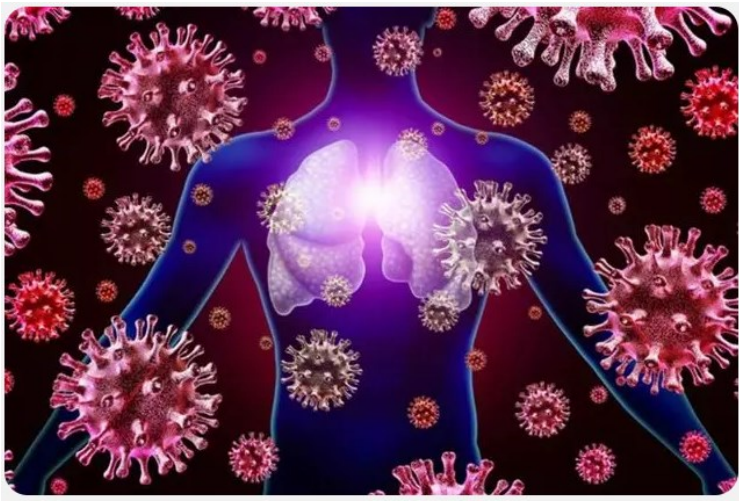
internacionales, presenta una mayor capacidad de transmisión y coincide con un incremento reciente de casos en el país.

La presencia de esta variante fue confirmada tras la secuenciación de muestras realizada por investigadores de la Universidad Nacional de La Plata. De acuerdo con los datos difundidos por Clarín, los primeros casos identificados corresponden a tres pacientes internados en hospitales de la provincia de Buenos Aires.

La Organización Mundial de la Salud (OMS) catalogó a PJ.2.1 como una "variante bajo vigilancia" debido a su crecimiento sostenido en distintas regiones del mundo, especialmente en América del Norte. También fueron reportados casos en Brasil durante las últimas semanas.

Qué se sabe sobre la nueva variante



Según especialistas, PJ.2.1 acumula numerosas modificaciones genéticas respecto de variantes anteriores, una característica que podría favorecer su capacidad de propagación.

La viróloga Paola Resende, integrante del Grupo Asesor Técnico de la OMS sobre la evolución de los virus, explicó que esta variante posee mutaciones que aumentan la afinidad con los receptores celulares, lo que se traduce en una mayor transmisibilidad.

Sin embargo, hasta el momento no existen evidencias suficientes para concluir que provoque cuadros más graves. La propia OMS señaló que los datos clínicos disponibles todavía son limitados para determinar si está asociada con una mayor severidad de la enfermedad.

Las vacunas siguen siendo efectivas

Uno de los principales mensajes de los especialistas es que las vacunas continúan ofreciendo protección frente a este nuevo linaje.

Ensayos de laboratorio citados por la OMS mostraron que los anticuerpos generados por las vacunas actualizadas lograron neutralizar la variante PJ.2.1. En Argentina, las opciones disponibles incluyen la vacuna de ARN mensajero que se aplica en el sistema público y la vacuna nacional ARVAC, disponible en farmacias.

Los síntomas asociados a esta variante son similares a los observados en otras versiones recientes del coronavirus. Entre los más frecuentes se encuentran fiebre, tos, dolor de garganta y secreción nasal.

Crecen los casos y preocupa la baja vacunación

Especialistas advirtieron que en las últimas semanas se registra un aumento de contagios.

El infectólogo Roberto Debbag, presidente de la Sociedad Latinoamericana de Vacunología, sostuvo que los casos "definitivamente están subiendo" y remarcó la importancia de completar los esquemas de vacunación, especialmente en embarazadas, adultos mayores e inmunosuprimidos.

También señaló que la cobertura de las vacunas contra COVID-19 se encuentra muy por debajo de otras campañas recientes, particularmente entre las embarazadas, un grupo clave para transmitir protección a los bebés durante los primeros meses de vida.

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En paralelo, algunas jurisdicciones comenzaron a reforzar la vigilancia epidemiológica. En Formosa, por ejemplo, las autoridades sanitarias dispusieron retomar los hisopados y pruebas PCR ante lo que calificaron como un incremento brusco de los casos registrados durante la última semana.

Los especialistas coinciden en que la aparición de PJ.2.1 no implica un regreso al escenario de la pandemia, aunque recomiendan mantener actualizados los esquemas de vacunación y extremar los cuidados en personas con mayor riesgo de desarrollar complicaciones.

Fuente: LA VOZ. Disponible en https://n9.cl/vxq64x

Engineered Vaccine Platforms Transform Disease Prevention and Targeted Immunotherapy Across Clinical Applications

Nov 22. Vaccine technology is undergoing a fundamental paradigm shift from conventional formulations that passively deliver microbial antigens into modular, engineered platforms capable of programming specific immune responses. In a comprehensive review published in *Molecular Biomedicine*, an international team led by researchers Gustavo Cabral-Miranda, Jaqueline D. Q. Silva, and Jose E. Krieger evaluated how integrating antigen architecture, innate receptor sensing, cellular targeting, platform design, and delivery routes dictates protective and therapeutic outcomes. Traditional vaccinology historically defined vaccines as biological preparations exposing the host to an antigenic representation of a pathogen to establish immunological memory before exposure. While that principle remains foundational for prophylactic applications, modern clinical demands increasingly require therapeutic vaccines to intervene in existing pathologies. The authors emphasize that contemporary vaccines function as programmable multi-component systems, wherein each molecular constituent provides distinct instructions to the host immune system to elicit tailored cellular, humoral, or regulatory programs matched against specific disease-associated biological barriers.

Prophylactic and therapeutic vaccination operate under fundamentally divergent biological constraints and therefore require distinct immunological design criteria. Prophylactic immunizations are administered prior to pathogen encounter, within an uncompromised host environment characterized by intact tissue architecture and preserved immunological homeostasis. Under these physiological conditions, vaccine-induced signaling can be systematically optimized to generate long-lived protective memory through the coordinated engagement of innate and adaptive compartments. This orchestration promotes germinal center formation, antibody affinity maturation, class-switch recombination, long-lived plasma cell differentiation, and memory B-cell expansion. Simultaneously, prophylactic regimens generate durable helper and cytotoxic memory T-cell populations, as well as mucosal immunoglobulin A and tissue-resident memory cells capable of intercepting invading pathogens at mucosal entry portals. Early innate sensing by dendritic cells and other antigen-presenting cells via pattern recognition receptors initiates this sequence by upregulating co-stimulatory molecules, inflammatory cytokines, and interferons that guide lineage polarization and ensure rapid recall protection upon subsequent exposure.

Conversely, therapeutic vaccination confronts hostile immune landscapes reshaped by established disease, continuous antigen exposure, systemic immune suppression, and extensive tissue remodeling. Administered after disease manifestation, therapeutic interventions cannot simply generate immune memory de novo; instead, they must redirect, restore, or amplify ongoing immune

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responses within dysfunctional microenvironments. Persistent antigen exposure drives antigen-specific T cells into functional exhaustion, a progressive impairment marked by diminished proliferative potential, reduced effector cytokine synthesis, metabolic dysregulation, and high expression of inhibitory checkpoints including programmed cell death protein 1, cytotoxic T-lymphocyte-associated protein 4, T-cell immunoglobulin and mucin-domain containing-3, and lymphocyte activation gene 3. Importantly, persistent stimulation does not generate a uniform exhausted population, as progenitor-like cells expressing the transcription factor TCF1 retain proliferative capacity whereas terminally exhausted subsets resist reinvigoration. Therapeutic efficacy consequently hinges upon activating responsive precursor populations, reversing antigen-presenting cell dysfunction, and directing effector lymphocytes into diseased compartments.

The biological bottlenecks confronting therapeutic immunization become especially pronounced in oncology, where expanding peripheral tumor-reactive T cells is rarely sufficient to halt disease progression. Effective cancer vaccines must successfully execute an intricate cascade spanning precise antigen selection, dendritic cell cross-presentation, functional cytotoxic T-cell priming, systemic trafficking, dense infiltration across abnormal tumor vasculature, and sustained survival within immunosuppressive tumor ecosystems. Tumors actively counter cytotoxic responses by mobilizing regulatory T cells, myeloid-derived suppressor cells, and tumor-associated macrophages, alongside suppressive cytokine cascades and severe metabolic competition. Furthermore, malignant clones exploit genomic instability to escape immune destruction through antigen loss and human leukocyte antigen loss of heterozygosity, which abrogates peptide presentation. Although personalized neoantigen vaccines, such as mRNA-4157 combined with programmed cell death protein 1 blockade, have demonstrated significant improvements in recurrence-free survival in randomized phase IIb trials for resected melanoma, broad clinical validation remains under phase III evaluation, demonstrating that overcoming tumor escape mechanisms requires multifaceted interventions.

Chronic viral infections and fibrotic disorders present similarly distinct technological hurdles that preclude universal vaccine architectures. In chronic viral settings, sustained antigen expression reshapes antiviral immunity, requiring therapeutic platforms to restore helper T-cell function, reverse cytotoxic exhaustion, and deliver targeted immunogens into anatomically secluded viral reservoirs rather than merely amplifying circulating antibody titers. In pathological fibrosis, the primary target is neither a foreign pathogen nor a malignant clone, but an activated endogenous cellular state embedded within vital organs. Fibroblasts and myofibroblasts are critical for physiological wound healing, yet their persistent activation drives pathological extracellular-matrix deposition. Precision immunization against fibroblast activation protein in murine cardiac fibrosis models demonstrated that active vaccination can selectively attenuate myofibroblast accumulation and improve tissue remodeling. However, because target pathways overlap with normal repair, therapeutic success requires precise discrimination between disease-associated cell states and healthy stromal homeostasis, demonstrating the therapeutic utility of active immunization combined with passive monoclonal antibodies.

The capacity of modular vaccine technologies to program specialized immune responses depends intrinsically on innate immune sensing and dendritic cell specialization. Vaccine formulations activate diverse pattern recognition receptors, including Toll-like receptors, RIG-I-like receptors, NOD-like

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receptors, C-type lectin receptors, and cyclic GMP-AMP synthase-stimulator of interferon genes complexes, triggering transcription programs that determine whether responses become cytotoxic, humoral, or mucosal. Crucially, the responding dendritic cell subset governs adaptive polarization: conventional type 1 dendritic cells, distinguished by surface expression of chemokine receptor XCR1, specialize in antigen cross-presentation through major histocompatibility complex class I molecules to prime cytotoxic CD8-positive T cells. In contrast, conventional type 2 dendritic cells predominantly coordinate major histocompatibility complex class II presentation and helper CD4-positive T-cell differentiation. Engineering delivery systems that selectively target XCR1 or modulate intracellular cargo trafficking allows researchers to steer immunogens toward designated presentation pathways, ensuring that endocytosed antigens escape lysosomal degradation and access cytosolic proteasomal processing machinery.

Adjuvant formulation represents an equally decisive design node for calibrating the intensity, durability, and qualitative trajectory of vaccine-induced immunity. While classical aluminum salts effectively elicit antibody responses, contemporary adjuvant systems deliberately steer cellular and humoral trajectories to match disease requirements. Oil-in-water emulsions such as MF59 and AS03 amplify immune-cell recruitment and antigen capture, whereas defined innate agonists provide targeted pathway activation. CpG oligodeoxynucleotides engage Toll-like receptor 9 to favor type 1 helper T-cell polarization, and the AS01 liposomal adjuvant system couples monophosphoryl lipid A with saponin QS-21 to trigger robust cellular immunity. Newer agonists targeting Toll-like receptors 3, 7, and 8, as well as the stimulator of interferon genes axis, enhance type I interferon secretion and cytotoxic expansion. Nevertheless, the authors caution that maximizing inflammatory potency can cause counterproductive reactogenicity or trigger regulatory feedback; formulation engineering must therefore balance immune stimulation against tissue tolerability to sustain productive lymphocyte differentiation.

Nucleic acid technologies represent a highly versatile foundation for programmable vaccinology, offering exceptional sequence agility and endogenous intracellular antigen expression. Both messenger RNA and DNA platforms enable simultaneous processing across major histocompatibility complex class I and class II pathways, facilitating comprehensive cellular and humoral priming. While DNA vaccines demonstrated favorable stability, historical applications showed limited potency in humans due to intracellular delivery barriers. Lipid nanoparticle-formulated messenger RNA platforms resolved critical delivery bottlenecks during the COVID-19 pandemic, demonstrating rapid antigen redesign and scalable manufacturing. The structural design space is further expanding with self-amplifying RNA, which incorporates replicase machinery to achieve sustained antigen expression at reduced doses as validated in late-stage clinical trials, and circular RNA, whose covalently closed architecture confers exonuclease resistance. However, nucleic acid deployment has revealed platform -specific constraints, including transient systemic reactogenicity, rare post-vaccination myocarditis, and the ongoing necessity to chemically optimize ionizable lipids to reduce off-target hepatic accumulation while enhancing lymph node localization.

Complementary delivery platforms and anatomical administration routes critically influence tissue distribution, drainage kinetics, and localized immunological imprinting. Recombinant viral vectors achieve efficient intracellular transduction and potent cytotoxic T-cell priming, though neutralizing anti-vector immunity often limits repeated homologous dosing, necessitating heterologous prime-boost

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schedules or capsid engineering. Conversely, virus-like particles display highly dense, repetitively ordered epitopes that effectively cross-link B-cell surface receptors to induce durable neutralizing humoral titers. Meanwhile, administration routes establish local tissue microenvironments that govern immune outcomes: intramuscular and subcutaneous injections prioritize systemic immunoglobulin G and circulating lymphocytes, whereas intradermal delivery engages dense dermal dendritic cell networks to achieve dose-sparing immune activation. Mucosal administration via oral or intranasal delivery uniquely induces secretory immunoglobulin A and lung-resident memory T cells capable of blocking pathogen entry, highlighting that matching delivery technology to anatomical administration routes is essential for conferring localized and systemic protection.

To overcome stubborn therapeutic barriers, contemporary vaccinology increasingly relies on multidimensional combination regimens that integrate active immunization with passive monoclonal antibodies, targeted immunomodulators, and engineered vesicles. Monoclonal antibodies provide immediate neutralizing or cytotoxic activity, bridging temporal gaps while active vaccination establishes durable adaptive memory. In oncology, combining vaccines with immune checkpoint inhibitors targeting programmed death-1, programmed death-ligand 1, or cytotoxic T-lymphocyte-associated protein 4 counteracts immunosuppression and restores cytotoxic function. Similarly, functionalized nanoparticles and stem cell-derived extracellular vesicles, such as adipose-derived exosomes carrying microRNA-196a-5p that activate protective GATA6 signaling, provide targeted delivery of therapeutic RNAs to fibrotic stroma. The authors highlight that assessing such integrated strategies requires moving beyond simple peripheral blood titers toward tissue-level pharmacodynamic biomarkers, including intratumoral T-cell infiltration, receptor clonality, human leukocyte antigen expression, and spatial microenvironmental remodeling, to confirm genuine target engagement within diseased tissues.

Translating engineered immune programs into reproducible clinical benefit requires integrating multi-omics systems vaccinology with predictive artificial intelligence. High-throughput profiling across transcriptomics, proteomics, metabolomics, and single-cell sequencing reveals early molecular signatures that predict downstream antibody durability and cellular protection well before conventional clinical endpoints manifest. Deep learning and machine learning algorithms leverage these datasets to model complex antigen-antibody interactions, predict protective epitopes, optimize messenger RNA translation and secondary structure, and simulate lipid nanoparticle membrane dynamics. However, computational models remain vulnerable to population variability and incomplete dataset representations, requiring iterative validation through closed experimental-computational feedback loops. The authors conclude that clinical success ultimately depends on rigorous translational realism: vaccine formulations must satisfy safety, reactogenicity, manufacturing feasibility, stability, and equitable access, establishing a verified causal continuum extending directly from initial immune activation to target engagement, tissue modification, and meaningful clinical survival.

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Patentes registradas en Patentscope

Estrategia de búqueda: *(Vaccine) AND DP:([12.11.2026 TO 22.11.2026]) as the publication date 37 records.*

1.WO/2026/235483NOVEL RSV PREVENTION VACCINE ANTIGEN WITH IMPROVED STABILITY OF PREFUSION F (PRE-F)
WO - 12.11.2026
Clasificación Internacional C07K 14/005 Nº de solicitud PCT/KR2026/096646 Solicitante KOREA NATIONAL INSTITUTE OF HEALTH Inventor/a GWAK, Won Seok
The present invention relates to a recombinant respiratory syncytial virus (RSV) F protein with improved stability of a pre-F form, and a vaccine composition for the prevention or treatment of RSV infection, comprising same. The recombinant RSV F protein of the present invention introduces an independent amino acid mutation on the basis of the amino acid sequences of a domestic epidemic RSV B strain, thereby enhancing pre-F protein stability to improve vaccine persistence in the human body, and thus may be widely used as a RSV infection prevention vaccine in various formulations such as a subunit vaccine, mRNA vaccine, VLP vaccine, and the like.

2.WO/2026/235319NOVEL RSV VACCINE ANTIGEN WITH IMPROVED PREFUSION F (PRE-F) STABILITY
WO - 12.11.2026
Clasificación Internacional C07K 14/005 Nº de solicitud PCT/KR2026/005741 Solicitante KOREA NATIONAL INSTITUTE OF HEALTH Inventor/a GWAK, Won Seok
The present invention relates to a recombinant respiratory syncytial virus (RSV) F protein having improved stability in a prefusion F (pre-F) conformation, and to a vaccine composition comprising the recombinant RSV F protein for preventing or treating RSV infection. The recombinant RSV F protein of the present invention has unique amino acid mutations introduced therein on the basis of the amino acid sequence of an RSV A strain circulating in Korea, such that the stability of the pre-F protein is enhanced to improve the in vivo persistence of the vaccine, and thus, the recombinant RSV F protein can be widely used in vaccines of various formulations, such as a subunit vaccine, an mRNA vaccine, and a VLP vaccine for preventing RSV infection.

3.WO/2026/237634VACCINE PROTECTIVE AGENT, PREPARATION METHOD THEREFOR AND USE THEREOF
WO - 19.11.2026
Clasificación Internacional A61K 47/42 Nº de solicitud PCT/CN2026/090682 Solicitante CHANGCHUN BCHT BIOTECHNOLOGY CO. Inventor/a LU, Jingcai
A vaccine protective agent for a live attenuated influenza vaccine, a preparation method therefor and the use thereof. The vaccine protective agent comprises recombinant human albumin, gelatin, sucrose, sodium glutamate, and arginine. The use of recombinant human albumin instead of human serum albumin can avoid the potential safety hazard of plasma-derived viruses existing in conventional human serum albumin protective agents, and reduce the incidence of adverse reactions after vaccination. A live attenuated influenza vaccine prepared using the vaccine protective agent of the present invention does not require lyophilization and enables long-term stable storage.

4.WO/2026/238167H1N1 BROAD-SPECTRUM MRNA VACCINE TARGETING TANDEM HA-NA PROTEIN BASED ON KEY AMINO ACID MUTATIONS, AND PREPARATION METHOD THEREFOR
WO - 19.11.2026

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Clasificación Internacional A61K 39/145 Nº de solicitud PCT/CN2026/110930 Solicitante INSTITUTE OF MEDICAL BIOLOGY, CHINESE ACADEMY OF MEDICAL SCIENCES AND PEKING UNION MEDICAL COLLEGE Inventor/a LU, Shuaiyao
The present invention relates to the technical field of vaccine preparation. Provided are an H1N1 broad-spectrum mRNA vaccine formed from a tandem HA-NA protein based on key amino acid mutations, and a preparation method therefor. The amino acid sequence of the mRNA vaccine is as set forth in SEQ ID NO: 1, and the nucleotide sequence is as set forth in SEQ ID NO: 2. The amino acid sequence of the mRNA vaccine is obtained by means of retaining, on the basis of an HA conserved sequence, mutation sites with amino acid property transitions that occur near major antigenic sites of an HA head and a receptor binding site, so as to obtain an HA' amino acid sequence containing key mutation sites, and linking the HA' and NA conserved amino acid sequences by means of using a flexible peptide.

5.WO/2026/233479MRNA-MV2 VACCINE AGAINST MPOX VIRUS AND PREPARATION METHOD THEREFOR
WO - 12.11.2026
Clasificación Internacional C12N 15/39 Nº de solicitud PCT/CN2026/111072 Solicitante INSTITUTE OF MEDICAL BIOLOGY, CHINESE ACADEMY OF MEDICAL SCIENCES AND PEKING UNION MEDICAL COLLEGE Inventor/a LU, Shuaiyao
Provided in the present invention are an mRNA vaccine against an mpox virus and a preparation method therefor. The mRNA vaccine has an amino acid sequence as shown in SEQ ID NO. 1, and a nucleic acid sequence as shown in SEQ ID NO. 2. The vaccine forms a single-chain dimeric conformation by means of rational cleavage and reassembly, and is obtained by means of linking two conserved antigens A35R and M1R in tandem via cleavage sequence P2A. The vaccine provides a good preventive efficacy against MPXV infection, and is safe and stable.

6.20260360465METHOD TO EVALUATE THE CONSPICUOUSNESS OF AN EPITOPE TOWARDS THE REPERTOIRE OF T-CELL RECEPTORS
US - 12.11.2026
Clasificación Internacional G16B 20/00 Nº de solicitud 19133136 Solicitante IMMUNEWATCH BV Inventor/a Pieter MEYSMAN

The current invention relates to a method of predicting T-cell response to a query epitope with a known epitope-TCR binding comprising calculating conspicuousness score of said epitope based on the number of known TCR sequences or TCR clusters responsive to said epitopes or by a centrality metric for each said epitopes in the epitope-TCR graph. The invention further relates to a second method to predict T-Cell response of any arbitrary epitopes using a machine learning algorithm. The T-cell response of epitopes can be used for the selection of molecules for vaccine and/or non-immunogenic compositions. The invention further relates to a third method for producing vaccine, to a vaccine, a biological and a data base.

7.3330695ENGINEERED NUCLEIC ACID MOLECULE, MRNA VACCINE FOR HPV-RELATED DISEASES, AND USE THEREOF
CA - 12.11.2026
Clasificación Internacional A61K 35/76 Nº de solicitud 3330695 Solicitante CSPC MEGALITH BIOPHARMACEUTICAL CO., LTD. Inventor/a DONG Yunxia
The present invention relates to an engineered nucleic acid molecule, an mRNA vaccine for HPV-related diseases, and the use thereof. The obtained mRNA vaccine for the treatment of HPV can fully activate the in-vivo specific T-cell reaction, and has a potent tumor inhibition activity in an HPV-related mouse CDX tumor model.

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8.WO/2026/239160NUCLEIC ACID VACCINE AGAINST MALARIA BASED ON HBSAG FUSIONS WITH CSP ANTIGENS
WO - 19.11.2026
Clasificación Internacional C12N 15/30 Nº de solicitud PCT/IB2026/000244 Solicitante INSTITUT PASTEUR Inventor/a CHITNIS, Chaitanya
The invention relates to a recombinant polynucleotide construct, preferably RNA, encoding at least a surface antigen of hepatitis B virus (HBsAg) or a fragment thereof fused to a circumsporozoite protein (CSP) of a Plasmodium, or an immunogenic fragment thereof. The invention further relates to uses of the construct, compositions comprising the construct, methods of making and using the construct to produce proteins and VLPs, and the encoded proteins and VLPs and their use as a vaccine. The invention also relates to a recombinant polynucleotide construct, preferably RNA, encoding at least a signal sequence (SS) of influenza virus hemagglutinin fused to a blood stage (BS) antigenic protein of a Plasmodium or a fragment thereof fused to transmembrane domain (TM) of influenza virus hemagglutinin and uses thereof, notably as a vaccine.

9.WO/2026/238264A METHOD TO PREDICT VACCINE INDUCED RESPONSIVENESS
WO - 19.11.2026
Clasificación Internacional G01N 33/50 Nº de solicitud PCT/EP2025/063632 Solicitante INSTITUT PASTEUR Inventor/a DUFFY, Darragh
The invention provides a method for predicting the response of subjects to a vaccine and for selecting subjects for administration of a vaccine, based on the detection of at least one predictive biomarker. The invention provides also a screening method for the predictive biomarkers.

10.WO/2026/233112CARBOHYDRATE-BASED PLANT VACCINE LEAD COMPOUND, AND SYNTHESIS METHOD THEREFOR AND USE THEREOF
WO - 12.11.2026
Clasificación Internacional C07H 15/04 Nº de solicitud PCT/CN2026/092260 Solicitante INNER MONGOLIA UNIVERSITY Inventor/a ZHANG, Yongmin
Provided in the present application are a carbohydrate-based plant vaccine lead compound and a synthesis method therefor, wherein a glucosamine group is modified by means of an organic synthesis process, and a tetrasaccharide-structured derivative having an inducing activity, namely compound 12, is obtained by means of a glycosylation reaction; and some functional groups of compound 12 are then removed to obtain a chitosan oligosaccharide analog with a clear structure and a single component, namely compound 14. The technique for inducing disease resistance in plants using chitosan oligosaccharides is optimized through experimental studies. The results show that the plant vaccine lead compound of the present application can significantly promote the growth and development of plants at a relatively low concentration. Therefore, the product of the present application has good promotion and application prospects in agriculture-related fields.

11.20260355307PLASMA MEMBRANE-PERMEABILIZED INACTIVATED ORAL VACCINE
US - 12.11.2026
Clasificación Internacional A61K 39/39 Nº de solicitud 19123724 Solicitante NINGBO MINGYI BIOTECHNOLOGY CO., LTD. Inventor/a Yiwei JIANG

The present invention provides a plasma membrane-permeabilized inactivated oral vaccine and a preparation method therefor. The inactivated oral vaccine includes a pathogen inactivated by permeabilization by a permeabilizer, a plasma membrane, and an integral membrane protein thereof,

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wherein the pathogen is selected from the group consisting of an enveloped virus, a bacterium, a fungus, an endoparasite, and a cancer cell, and the permeabilizer includes a lipopeptide as a surfactant.

12.WO/2026/232823IMMUNE CARRIER MICROSPHERES LOADED WITH INDIVIDUALIZED MHC-II BINDING POLYPEPTIDE, AND PREPARATION AND USE OF VACCINE THEREOF
WO - 12.11.2026
Clasificación Internacional A61K 38/08 Nº de solicitud PCT/CN2025/144207 Solicitante SHANGHAI MICROSPHERE BIOTECHNOLOGY CO, LTD Inventor/a TAN, Lisong
The present invention relates to the technical field of immune carriers and particularly to immune carrier microspheres loaded with an individualized MHC-II binding polypeptide, and preparation and use of a vaccine thereof. The microspheres are of a shell-core structure comprising a core and an outer shell. The core microspheres are loaded with the individualized MHC-II binding polypeptide. The MHC-II binding polypeptide sequence is obtained by means of prediction and screening on the basis of HLA genotyping results, and each HLA allele corresponds to at least one high-affinity MHC-II binding polypeptide. The outer shell is a coating layer of a glucan or another high molecular weight polymer. The advantage is that T and B epitopes are positioned inside and outside the microspheres, respectively, which leads to separated immune competition inhibition and achieves a better immune effect. Antibodies are prevented from cross-reactions that lead to side effects. The diversity of carrier molecules is reduced to avoid T cell overactivation that leads to side effects. Th1 and Th2 epitopes can be contained in the microspheres, so that both antibody immunity and T cell immune functions are produced. The particle size of the microspheres is controllable, and immune functions can also be fulfilled without adjuvants.

13.WO/2026/236648MONKEYPOX VIRUS OPG153 GLOBULAR DOMAIN VACCINE
WO - 12.11.2026
Clasificación Internacional A61K 39/12 Nº de solicitud PCT/US2026/027339 Solicitante BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM Inventor/a MCLELLAN, Jason
Provided herein are engineered OPG153 globular domain-containing proteins that exhibit enhanced stability and/or antigenicity. Methods are also provided for use of the engineered OPG153 globular domain-containing proteins as diagnostics, in screening platforms, and/or in vaccine compositions.

14.20260355308ORAL-ADMINISTRATION-TYPE VACCINE COMPOSITION CONTAINING FIBROIN-CONTAINING NANOPARTICLES
US - 12.11.2026
Clasificación Internacional A61K 39/39 Nº de solicitud 19123890 Solicitante NATIONAL AGRICULTURE AND FOOD RESEARCH ORGANIZATION Inventor/a Mitsuru SATO

A composition for an oral vaccine comprises nanoparticles containing an antigen and fibroin.

15.20260355300AFRICAN SWINE FEVER VIRUS ASFV-KOR.INJE.MEC-01.2022 ATTENUATED BY CELL ADAPTATION AND USES THEREOF
US - 12.11.2026
Clasificación Internacional A61K 39/12 Nº de solicitud 19486181 Solicitante CHOONGANG VACCINE LABORATORIES CO., LTD (CAVAC) Inventor/a IN-JOONG YOON

An attenuated African swine fever virus ASFV-KOR.INJE.MEC-01.2022 is obtained by passaging the African swine fever virus (ASFV) in a rhesus monkey kidney cell-derived cell line. The African swine fever virus ASFV-KOR.INJE.MEC-01.2022 naturally attenuated by cell adaptation possesses both safety and efficacy, and therefore it can be effectively utilized as an antigen in vaccine compositions for the prevention of African swine fever.

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16.20260355301CELL LINE FOR CULTURING AFRICAN SWINE FEVER VIRUS AND VACCINE USING THE SAME
US - 12.11.2026
Clasificación Internacional A61K 39/12 Nº de solicitud 19487923 Solicitante CHOONGANG VACCINE LABORATORIES CO., LTD (CAVAC) Inventor/a IN-JOONG YOON

A CA-CAS-01-A cell line deposited under Accession Number KCTC14568BP is capable of mass propagation of African swine fever virus (ASFV). The cell line and the ASFV produced therefrom can be advantageously utilized for the prevention of African swine fever and the mitigation of its impact. A method for mass production of African swine fever virus includes infecting the CA-CAS-01-A cell line with an African swine fever virus isolate, followed by culturing; and purifying African swine fever virus from a culture medium of the culturing.

17.WO/2026/241758VACCINE AGAINST SEVERE FEVER WITH THROMBOCYTOPENIA SYNDROME VIRUS
WO - 19.11.2026
Clasificación Internacional C07K 14/175 Nº de solicitud PCT/US2026/028693 Solicitante THE RESEARCH FOUNDATION FOR THE STATE UNIVERSITY OF NEW YORK Inventor/a LOVELL, Jonathan
The present disclosure provides immunogenic and vaccine compositions for inducing an immune response against Severe Fever with Thrombocytopenia Syndrome virus (SFTSV). The compositions comprise liposomes comprising cobalt-porphyrin-phospholipid and a recombinant SFTSV antigen associated with the liposomes. The recombinant SFTSV antigen may comprise an SFTSV Gn or Gc antigen, or an immunogenic fragment, domain, or subdomain thereof, and may include a polyhistidine tag that associates with cobalt in the liposome to display the antigen on the liposome surface. In some examples, the antigen comprises an SFTSV Gn subdomain III-containing antigen. The compositions may further comprise one or more adjuvants, including PHAD, MPLA, QS-21, or combinations thereof. Methods of making and using the compositions to elicit antigen-specific or SFTSV-neutralizing antibodies and to inhibit, reduce, or prevent SFTSV infection or Severe Fever with Thrombocytopenia Syndrome are also provided.

18.WO/2026/233435RABIES VIRUS GLYCOPROTEIN G, POLYNUCLEOTIDE, AND INFECTIOUS DISEASE VACCINE CONTAINING SAME
WO - 12.11.2026
Clasificación Internacional C12N 15/47 Nº de solicitud PCT/CN2026/095698 Solicitante ENCUREGEN PHARMA GUANGZHOU LIMITED Inventor/a XIA, Jingya
Provided are a rabies virus glycoprotein G, a polynucleotide, and an infectious disease vaccine containing the same. The rabies virus glycoprotein G is a mutant protein, which tends to form a dimer compared with the wild type, and can induce a higher level of neutralizing antibody titer in vivo. The polynucleotide encodes the rabies virus glycoprotein G. The polynucleotide has been subjected to codon optimization design of a coding sequence, and the ORF sequences thereof are as set forth in SEQ ID NOs: 3-13. The polynucleotide exhibits longer-lasting cell surface expression compared with a coding sequence having non-optimized codons, can induce sustained high levels of binding antibodies and neutralizing antibodies against the rabies virus G protein in a subject, and thus has broad prospects for clinical application.

19.WO/2026/237803PROTEIN CONJUGATE AND LNP VACCINE FOR INDUCING ANTI-ALLERGEN IMMUNE RESPONSE IN PETS
WO - 19.11.2026
Clasificación Internacional A61K 39/35 Nº de solicitud PCT/CN2026/095365 Solicitante GYOTTA BIOTECHNOLOGIES, INC. Inventor/a LI, Xuan

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Provided is a protein conjugate. The protein conjugate comprises a fusion protein and a lipid conjugated to the fusion protein via a covalent bond, particularly a cat Fel d 1 fusion protein covalently bound to a lipid. The present invention also relates to a lipid nanoparticle (LNP) formulation comprising the protein conjugate, preferably for use as a vaccine platform, for generating an immune response, in particular an antibody response, against the cat Fel d 1 antigen. The Th cell epitope, especially the universal Th epitope, fused into the fusion protein results in further enhancement of the generated immune response. The immunization of pets with these LNP vaccines may result in reduced antigen levels in pet secretions.

20.3084522VACCINE COMPOSITION FOR PREVENTING PORCINE MYCOPLASMA INFECTION, COMPRISING RECOMBINANT PROTEIN
ES - 13.11.2026
Clasificación Internacional C12N 15/74 Nº de solicitud 17839895 Solicitante Innovac Inventor/a HAHN, Tae Wook

21.WO/2026/234261NOVEL LIPID NANOPARTICLE FORMULATIONS FOR DELIVERY OF NUCLEIC ACIDS, HAVING A PIPERIDINE RING AND TWO CHAINS WITH TWO CARBOXYL GROUPS EACH
WO - 12.11.2026
Clasificación Internacional C07D 211/20 Nº de solicitud PCT/EP2026/063477 Solicitante CUREVAC SE Inventor/a IBRAHIMHOVA, Vusala
The present invention provides novel ionizable lipids and novel lipid nanoparticles useful for the delivery of nucleic acids, related pharmaceutical compositions or vaccines as defined herein for use as a medicament, preferably a vaccine, for use in the treatment and/or prophylaxis of diseases, preferably cancer diseases.

22.20260357191SALMONELLA STRAIN WITH CHROMOSOMALLY INTEGRATED LANDING PAD
US - 12.11.2026
Clasificación Internacional C12N 1/20 Nº de solicitud 19112206 Solicitante PROKARIUM LIMITED Inventor/a Marc Biarnes Carrera

The present invention relates to a modified live attenuated strain of *Salmonella*, said strain comprising at least one chromosomally integrated synthetic polynucleotide sequence inserted into a pre-determined pseudogenomic location, said sequence comprising at least one defined recombination site for the introduction of a heterologous polynucleotide sequence encoding a polypeptide, wherein said chromosomally integrated synthetic polynucleotide sequence is located within at least one genomic locus as defined by any one of SEQ ID NOs: 1-30, or a sequence comprising at least 70% identity to any one of SEQ ID NOs: 1-30. The present invention also relates to a vaccine composition comprising the modified strain and various uses and methods thereof.

23.20260356920A HUMAN VH-BASED SCAFFOLD FOR THE PRODUCTION SINGLE DOMAIN ANTIBODIES AND THEIR USE
US - 12.11.2026
Clasificación Internacional C07K 16/104 Nº de solicitud 19102044 Solicitante THE SCRIPPS RESEARCH INSTITUTE Inventor/a Joseph JARDINE

Provided herein are a human VH-based scaffold for the production of single domain antibodies and their use.

24.20260356894HETERODIMER OF POXVIRUS A16 AND G9 PROTEINS AS AN IMMUNOGEN
US - 12.11.2026

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Clasificación Internacional C07K 14/005 Nº de solicitud 19483795 Solicitante INSTITUT PASTEUR Inventor/a Annalisa MEOLA

The invention relates to an isolated heterodimer of poxvirus A16 and G9 proteins as an immunogen in a subunit or nucleic acid vaccine against poxvirus. The invention provides an engineered heterodimer, nucleic acid encoding the heterodimer, neutralizing antibodies directed against said heterodimer and their use for the prevention, treatment and diagnostics of poxvirus infections and related diseases.

25.WO/2026/234068IMMUNOGENIC FUSION PROTEIN
WO - 12.11.2026
Clasificación Internacional A61K 39/09 Nº de solicitud PCT/EP2026/063052 Solicitante MINERVAX APS Inventor/a FISCHER, Per
The proposed technology relates to an immunogenic fusion protein comprising or consisting of an amino acid sequence consisting of: i. a first amino acid sequence part consisting of 170 to 178 amino acids, preferably 174 to 175 amino acids, and having at least 90% sequence identity with the amino acid sequence shown in SEQ ID NO: 7; ii. a second amino acid sequence part consisting of 170 to 178 amino acids, preferably 174 to 175 amino acids, and having at least 90% sequence identity with the amino acid sequence shown in SEQ ID NO: 7; and optionally: iii. a linker amino acid sequence part consisting of 1 to 20 amino acids and separating the first amino acid sequence part from the second amino acid part. The immunogenic fusion protein preferably consists of 340 to 376 amino acids, preferably 348 to 370 amino acids, more preferably 349 to 351 amino acids. The proposed technology further pertains to nucleic acid molecule encoding the immunogenic fusion protein; a vector; a host cell; a vaccine; and a use of any of the foregoing in a vaccination against, or treating, a group B streptococcus infection.

26.WO/2026/241420INDIVIDUALIZED HUMAN PAPILLOMAVIRUS VACCINES AND METHODS FOR THEIR USE
WO - 19.11.2026
Clasificación Internacional C07K 14/025 Nº de solicitud PCT/US2026/028040 Solicitante MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH Inventor/a OH, SangKon
Methods and materials related to selected human papillomavirus (HPV) polypeptides are provided herein. For example, vaccine compositions that contain one or more selected HPV polypeptides and that have the ability to increase immune responses against human papillomaviruses such as HPV6 and/or HPV11 within a mammal (e.g., a human) are provided herein.

27.WO/2026/240680ANTI-AGING VACCINE
WO - 19.11.2026
Clasificación Internacional C12N 15/12 Nº de solicitud PCT/RU2026/050095 Solicitante DUKHOVLINOV, Ilia Vladimirovich Inventor/a DUKHOVLINOV, Ilia Vladimirovich
Claimed are: a recombinant nucleic acid molecule comprising a nucleic acid which codes for an immunologically relevant protein, wherein the protein contains, separated from one another by linkers, an HbhA fragment, PADRE (a pan-HLA DR-binding epitope), a group of HTL epitopes of CD87, GPNMB, CD9, CD153 and KLRG1, a group of CTL epitopes of CD87, GPNMB, CD9, CD153 and KLRG1, a WT33 epitope, and a signal mediating retrograde transport to the endoplasmic reticulum; a pharmaceutical composition containing said molecule; a host cell and method for producing said molecule; a senotherapy method; and a use of said molecule. The invention can be used for vaccination, and makes it possible to extend lifespan and to combat the senescence-associated phenotype.

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28.WO/2026/241475A CANINE-OPTIMIZED ADJUVANT FOR VETERINARY TUMOR VACCINES AND MODIFICATIONS TO ENHANCE TUMOR-SPECIFIC IMMUNE RESPONSES IN TUMOR-BEARING ANIMALS
WO - 19.11.2026
Clasificación Internacional A61K 39/39 Nº de solicitud PCT/US2026/028115 Solicitante ARDENT ANIMAL HEALTH, LLC Inventor/a COHEN, Donald A.
The present invention provides synthetic vaccine adjuvants and combination adjuvant and vaccination modalities that are optimized for canine species to induce anti-tumor immune responses when combined with canine cancer vaccines or with canine vaccines to infectious agents. The adjuvants may be broadly described as a single chain oligodeoxynucleotide (ODN) containing multiple dinucleotide CpG motifs of cytosine triphosphate deoxynucleotide ("C") linked via a phosphorothioate bond ("p") to a guanine triphosphate deoxynucleotide ("G"). The CpG motifs are positioned within the sequence in a manner that improves immunologic and biologic responses in dogs when physically or temporally combined with vaccines.

29.WO/2026/232229ENTEROCOCCUS CECORUM GLYCANS IN VACCINE AND THERAPEUTIC APPLICATIONS
WO - 12.11.2026
Clasificación Internacional C12N 1/21 Nº de solicitud PCT/CA2026/050655 Solicitante VAXALTA INC. Inventor/a SZYMANSKI, Christine
Disclosed examples generally relate to surface glycans from Enterococcus cecorum, glycan expression in a heterologous system, and methods for using the glycans to prevent, treat, and diagnose disease caused by pathogenic E. cecorum.

30.WO/2026/241684ATTENUATED HUMAN CYTOMEGALOVIRUS AND METHODS OF USE AS A VACCINE OR VECTOR
WO - 19.11.2026
Clasificación Internacional A61K 39/12 Nº de solicitud PCT/US2026/028442 Solicitante HOWARD UNIVERSITY Inventor/a TANG, Qiyi
Provided is a pp150 tegument protein of human cytomegalovirus (HCMV) containing one or more mutations that weaken association of pp150 and small capsid protein (SCP), including a missense mutation K255E. Also provided are viral particles and attenuated HCMV containing said pp150 tegument protein, constructs encoding said pp150 tegument protein, viral particles or attenuated HCMV, and vaccines containing said viral particles or attenuated HCMV. Also provided are methods of producing said constructs and vaccines, and methods of vaccination using said vaccines.

31.20260355247PEPTIDES AND COMBINATION OF PEPTIDES OF NON-CANONICAL ORIGIN FOR USE IN IMMUNOTHERAPY AGAINST DIFFERENT TYPES OF CANCERS
US - 12.11.2026
Clasificación Internacional A61K 35/17 Nº de solicitud 19669261 Solicitante Immatics Biotechnologies GmbH Inventor/a Heiko SCHUSTER

The present invention relates to peptides, proteins, nucleic acids and cells for use in immunotherapeutic methods. In particular, the present invention relates to the immunotherapy of cancer. The present invention furthermore relates to tumor-associated T-cell peptide epitopes, alone or in combination with other tumor-associated peptides that can for example serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses, or to stimulate T cells ex vivo and transfer into

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patients. Peptides bound to molecules of the major histocompatibility complex (MHC), or peptides as such, can also be targets of antibodies, soluble T-cell receptors, and other binding molecules.

32.20260355305VACCINE USING M2/BM2-DEFICIENT INFLUENZA VECTORS
US - 12.11.2026
Clasificación Internacional A61K 39/215 Nº de solicitud 19744738 Solicitante FluGen, Inc. Inventor/a Michael J. MOSER

The invention provides a recombinant virus comprising an influenza viral backbone, wherein the influenza viral backbone comprises PB1, PB2, PA, NP, M, NS, HA, and NA gene segments, wherein at least one of the PB1, PB2, PA, NP, M, NS, HA, and NA gene segments comprises at least one nucleotide sequence that encodes one or more antigens. The invention provides a recombinant virus wherein the antigen is an immunogenic fragment of SARS-COV-2 spike glycoprotein. The invention also provides a pharmaceutical formulation and a method of eliciting an immune response.

33.WO/2026/240587LIPID NANOPARTICLES CAPABLE OF SIMULTANEOUSLY DELIVERING ANTIGENS TO CANCER AND DENDRITIC CELLS, AND ANTICANCER COMPOSITION CONTAINING SAME
WO - 19.11.2026
Clasificación Internacional A61K 9/51 Nº de solicitud PCT/KR2026/096883 Solicitante RESEARCH & BUSINESS FOUNDATION SUNGKYUNKWAN UNIVERSITY Inventor/a KWEON, Dae Hyuk
The present invention relates to lipid nanoparticles capable of simultaneously delivering antigens to cancer and dendritic cells (DCs), and an anticancer composition containing same. By developing a dual-targeting mRNA vaccine targeting DEC-205, the present invention enables simultaneous antigen expression in dendritic cells and tumor cells, thereby inducing a potent anticancer immune response.

34.20260355121LIPID NANOPARTICLES FOR ENHANCED PULMONARY DELIVERY OF NUCLEIC ACID-BASED THERAPIES
US - 12.11.2026
Clasificación Internacional A61K 9/51 Nº de solicitud 19671888 Solicitante University of Maryland, College Park Inventor/a Gregg Duncan

The current disclosure provides novel lipid nanoparticles comprising lung surfactants (Surf-LNPs) wherein said Surf-LNPs are useful for providing transfer of genetic material, i.e., nucleic acids, into cells and/or tissues of the lung or potentially other organs/tissues. Surf-LNPs comprise one or more biocompatible lipid components, one or more lung surfactants, and one or more nucleic acids encoding therapeutic agents, prophylactic agents or a combination thereof. The present disclosure further provides pharmaceutical compositions comprising said Surf-LNPs and their use in the treatment of lung disease. Said Surf-LNPs may also serve as vaccine compositions through the incorporation of nucleic acids therein which encode an immunogen or antigen of interest.

35.20260355313HYPOALLOGENIC-IMMUNOGENIC PLURIPOTENT STEM CELLS AS ANTI-CANCER VACCINE
US - 12.11.2026
Clasificación Internacional A61K 40/10 Nº de solicitud 19121772 Solicitante The Board of Trustees of the Leland Stanford Junior University Inventor/a Lin Wang

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Compositions and methods are provided for immunization against cancer cells, by the administration of non-self, hypoallogenic iPSCs. To reduce host rejections against the iPSCs after vaccination, the cells are engineered to knock out or otherwise reduce expression of MHC class I and MHC class II proteins. To further reduce rejection responses against the iPSCs after vaccination, the cells are engineered to over-express CD47. The tumor-associated antigens (TAAs) and tumor-specific antigens (TSAs) expressed by the engineered cells can activate both specific cellular immunity and humoral immune response to prevent tumor growth and/or eradicate tumor cells, in the absence of undesirable graft-versus-host diseases.

36.WO/2026/236689INTRANASAL ADENOVIRUS-5 INFLUENZA VACCINE
WO - 12.11.2026
Clasificación Internacional A61K 39/12 Nº de solicitud PCT/US2026/027409 Solicitante IMMUNITYBIO, INC. Inventor/a GABITZSCH, Elizabeth
Methods are disclosed herein for stimulating an antigen-specific immune response in a subject through intranasal administration of a replication defective adenoviral vector comprising deletions in the E2b region and nucleic acid sequences encoding one or more target antigens derived from infectious disease-associated proteins or cancer-associated proteins. Administration generates both systemic and mucosal immunity, including antigen-specific IgG and IgA antibodies, CD8+ T cells, and B cells in various compartments including the lungs and mediastinal lymph nodes. These methods may be useful for treatment and preventing influenza by stimulating mucosal immunity in the upper respiratory tract, generating antibodies that bind to past, present, and potential pandemic influenza strains. These methods inhibit viral transmission within a population, conferring protection even to unvaccinated subjects.

37.WO/2026/236635PREFUSION-STABILIZED RSV F PROTEIN ECTODOMAINS
WO - 12.11.2026
Clasificación Internacional A61K 39/155 Nº de solicitud PCT/US2026/027314 Solicitante BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM Inventor/a MCLELLAN, Jason
Provided herein are engineered RSV F ectodomain polypeptides that exhibit enhanced conformational stability and/or antigenicity of the prefusion conformation. Methods are also provided for use of the engineered RSV F ectodomain polypeptides as diagnostics, in screening platforms, and/or in vaccine compositions.

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Patentes registradas en United States Patent and Trademark Office (USPTO)

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Document ID	Title	Inventor	Applicant Name
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US 20260355301 A1	Cell Line for Culturing African Swine Fever Virus and Vaccine Using the Same	YOON; IN-JOONG et al.	Choongang Vaccine Laboratories Co., Ltd (Cavac)

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