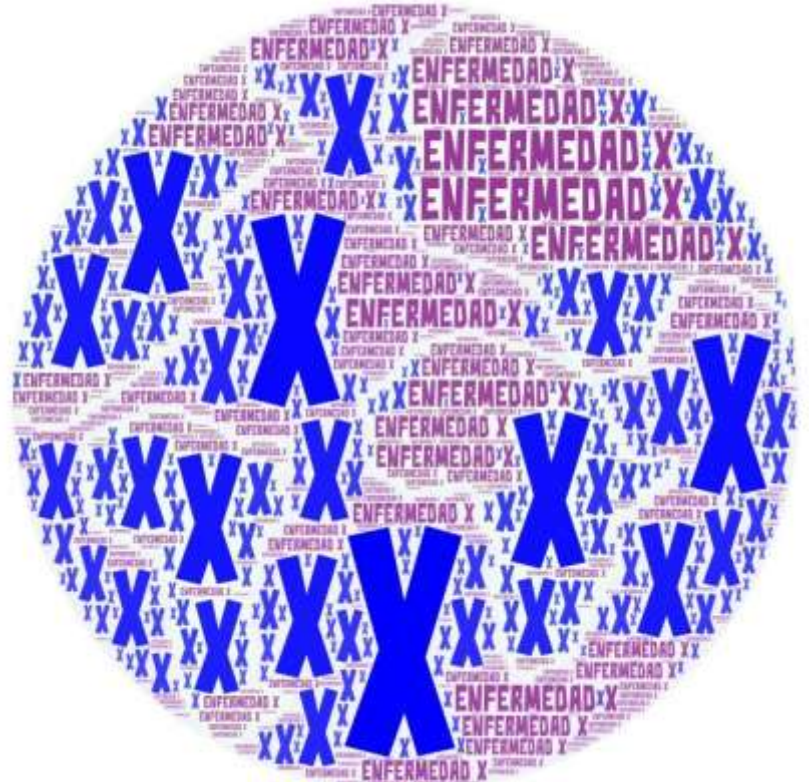


Sesiones de Maitines. Martes 4 de Febrero de 2020.

¿Vamos a morir de la ENFERMEDAD X?

**Jose Guerra Laso
Sº de M. Interna
CAULE.**



Actos terroristas



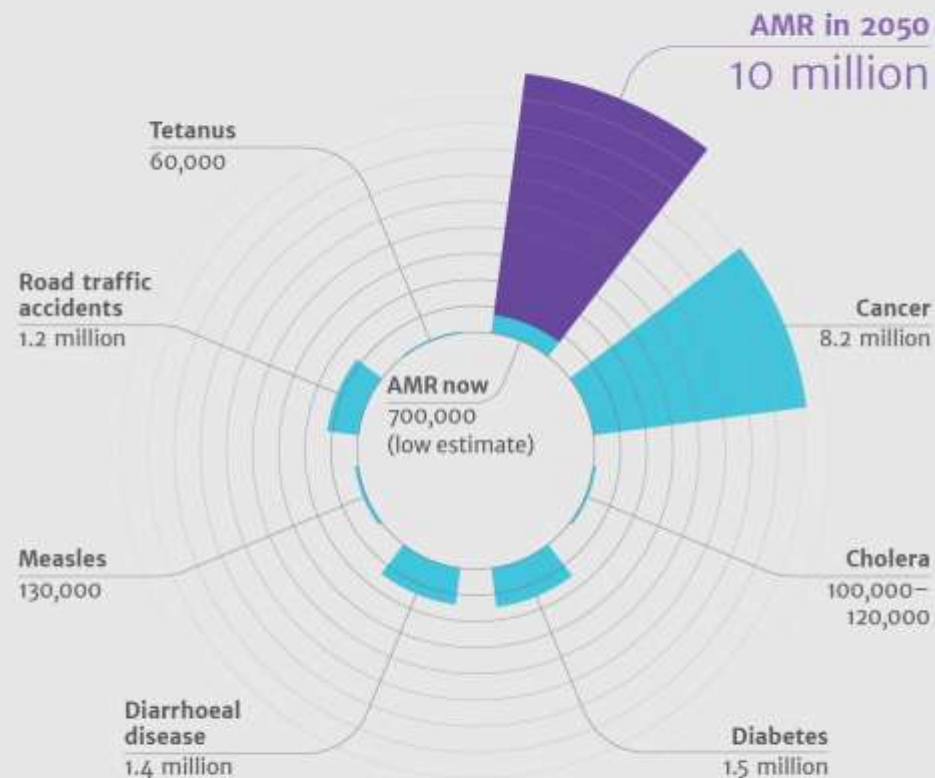
Desastres tecnológicos



Catástrofes climáticas



Deaths attributable to AMR every year compared to other major causes of death



Sources

Diabetes
Cancer
Cholera
Diarrhoeal disease

www.who.int/mediacentre/factsheets/fs037/en/
www.who.int/mediacentre/factsheets/fs037/en/
www.who.int/mediacentre/factsheets/fs037/en/
www.who.int/mediacentre/factsheets/fs037/en/

Measles
Road traffic accidents
Tetanus

www.who.int/mediacentre/factsheets/fs037/en/
www.who.int/mediacentre/factsheets/fs037/en/
www.who.int/mediacentre/factsheets/fs037/en/



Complejo Asistencial

Pre-siglo XVII

430 a. C.-429 a. C.: La Plaga de Atenas acaba con un tercio de la población, unas 150.000 personas.

426 a. C.-425 a. C.: Regreso de la Plaga de Atenas.

166: La Peste antonina llega a Roma y se extiende por todo el imperio. Dura 15 años y cobra 5 millones de víctimas.

251: La Peste de Cipriano, procedente de Etiopía, cruza Egipto, el norte de África y llega a Roma. Prevalece 20 años y causa entre 3 y 5 millones de muertes.

542: La peste bubónica, llamada la Peste de Justiniano, azota el imperio Bizantino. En cuatro meses acaba con casi 40% de la población. Se extienden a África, Asia y Europa.

735-737: El sarampión se extiende a Japón.

1346: La segunda oleada de peste bubónica (Peste Negra) cobra 34 millones de víctimas.

1518: Epidemia de baile de 1518 extraña epidemia ocurrida en julio del año 1518 en la ciudad de Estrasburgo, Francia. Se desconoce el número de muertos

1545: Los aztecas y mayas son diezmados por la Viruela, que cobra millones de vidas.

Siglo XVII al XIX

1629-1631: La gran peste de Milán, Italia, cobra 280.000 víctimas.

1649: Epidemia en Sevilla, más de 60.000 víctimas (46% de la población)

1666: Aparece la Gran plaga de Londres, entre 70.000 y 100.000 víctimas.

1679: Gran peste de Viena, 76.000 víctimas.

1707-1709: Se dispersa la viruela en Islandia.

1720-1722: Aparece la Plaga de Marsella.

1817-1824: Primera pandemia de cólera, importada de India por tropas británicas.

1827-1835: Segunda pandemia de cólera.

1852: Tercera pandemia de cólera.

1856: Cuarta pandemia de cólera.

1870-1875: Epidemia de viruela en Europa.

1881: Quinta pandemia de cólera.

1889-1890: La Gripe rusa, comenzó en Rusia y se extendió rápidamente por toda Europa, alrededor de 1 millón de personas murieron en esta pandemia.¹

Siglo XX

1918-1919: La Gripe española; 20-50 millones de víctimas.

1957-1958: La Gripe asiática; 4 millones de víctimas.

1962: La epidemia de la risa de Tanganica (hoy Tanzania) de 1962, aproximadamente 1000 personas se vieron afectadas

1968-1969: La Gripe de Hong Kong; 2 millones de víctimas.

1981 hasta hoy: pandemia del sida (más de 30 millones de muertes y sigue en aumento).

1990: Brote de difteria en la Unión Soviética; 1,500 mueren en 5 años.

Y la TBC!!!

Siglo XXI

2002: Se calcularon en 1.000 los casos de polio en la región de Uttar Pradesh, India.

2003: Epidemia de SARS. 8.000 infectados y 700 muertes en dos meses.

2005: La gripe aviar en su cepa H5N1, se convirtió en una amenaza de pandemia cuando se produjeron los primeros contagios en seres humanos.

2009-2010: La Pandemia de gripe A (H1N1) se cobró la vida de más de 18.000 personas alrededor del mundo.

2010: Un brote de cólera azotó Haití, alcanzando más de medio millón de afectados y 8.000 víctimas en el 2013.

2014: La epidemia de ébola de 2014 comenzó con un brote en Guinea en marzo y se extendió en los meses siguientes a Liberia y Sierra Leona, fallecieron más de 4.500 personas en medio año.

2012-2015: El Síndrome respiratorio por coronavirus de Oriente Medio fue detectado en el 2012 en Arabia Saudí. El virus ya ha infectado a casi 2494 personas y ha matado casi más de 858.

2014: El Virus Zika azota toda Latinoamérica. Con varios millones de infectados y miles de bebés nacidos con microcefalia y otros miles de muertos, la cifra sigue en aumento.

Prioritizing diseases for research and development in emergency contexts



The first list of prioritized diseases was released in December 2015. Using a published prioritization methodology (2016), the list was first reviewed in January 2017 and a second time in 2018. An updated methodology and a new list are anticipated before the end of 2019. The Blueprint list of priority diseases is not an exhaustive list, nor does it indicate the most likely causes of the next epidemic:

- Crimean-Congo haemorrhagic fever (CCHF)
- Ebola virus disease and Marburg virus disease
- Lassa fever
- Middle East respiratory syndrome coronavirus (MERS-CoV) and Severe Acute Respiratory Syndrome (SARS)
- Nipah and henipaviral diseases
- Rift Valley fever (RVF)
- Zika
- Disease X (*Disease X represents the knowledge that a serious international epidemic could be caused by a pathogen currently unknown to cause human disease, and so the R&D Blueprint explicitly seeks to enable cross-cutting R&D preparedness that is also relevant for an unknown "Disease X" as far as possible*)

Factors to consider when prioritizing diseases

Agent-based factors

Agent-based factors are connected to properties of the pathogen causing the disease. Those agents posing the greatest risk of epidemic or pandemic potential might include agents:

1. Which are particularly pathogenic;
2. Where the mechanism of transmission are likely to result in high levels of human to human transmission;
3. Which can infect humans;
4. Which exhibited any human to human transmission;
5. Which exhibited efficient human to human transmission or efficient vector-mediated transmission to humans;
6. With a natural reservoir that can spill over into humans;
7. With a close relative with a medical countermeasures;
8. Resistant to the use of medical countermeasures;
9. Without medical countermeasures;
10. With robust environmental survival capabilities;
11. With similar phenotypic characteristics to those responsible for historical epidemics and pandemics;
12. Which can rapidly evolve;
13. Which can easily take up relevant characteristics from other pathogens (such as horizontal gene transfer); and
14. Agents which elude detection and diagnosis

Host-based factors

Host-based factors are connected to properties of the host, often associated with the immunopathology of the disease. Those diseases posing the greatest risk of epidemic or pandemic potential might include those which:

1. Can evade the host's immune system;
2. Can disrupt the host's immune system;
3. There is a deleterious and severe host response;
4. Involve immunologically privileged locations within the host;
5. There is little or no cross-immunity;
6. There was no population immunity; and
7. Natural protective immunity after infection is not robust.

Health factors

Health factors include those related to the clinical presentation of the disease, public health capacity, and epidemiological factors.

Clinical presentation

Clinical presentation factors are connected to how medical personnel and public health infrastructure will experience the disease. Diseases posing the greatest risk of epidemic or pandemic potential might include those:

1. Which are difficult to recognise - including those with non-specific early features or easily confused with more common diseases (e.g. pneumonias);
2. Which result in large number of deaths;
3. Which have a prolonged infectious prodrome;
4. With prolonged infectivity;
5. With a long duration;
6. With evidence of increasing severity;
7. With evidence of increasing transmissibility; and
8. Which cause complications or sequelae.

Public health capacity

Public health capacity factors are connected to the existence of the necessary resources to respond to the disease. Diseases posing the greatest risk of epidemic or pandemic potential might include those requiring:

1. Specialised detection or diagnostics;
2. Specialised surveillance;
3. Specialised interventions - including things not used on a regular basis, or are not available to most countries, or which are not regularly used in other species (including highly skilled personnel, equipment, availability of isolation units, respirators, PPE, etc) and infection control measures;
4. The investment of significant public health resources; and
5. Capability to employ and emergency response.

Epidemiological factors

Epidemiological factors are connected to how the disease spreads. Diseases posing the greatest risk of epidemic or pandemic potential might include those:

1. Which typically infect health personnel;
2. Which carry a high risk of occupational exposure (including for culling, vets, burial details, lab workers, first responders)
3. Which cause clusters of cases;
4. Which disproportionately affect special populations;
5. Where epidemiological links might hidden or difficult to discern;
6. With certain modes of transmission, such as airborne transmission; and
7. With evidence of increasing geographic range.

4. Context-based factors

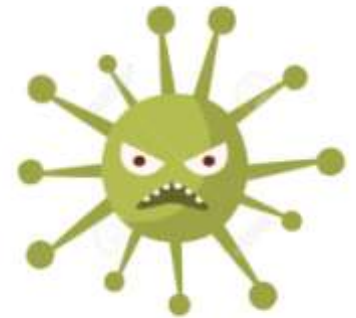
Impacts, other than those felt directly in a health setting, can influence whether a disease should be prioritized. Diseases which might need to be prioritized could include those which:

1. Cause major disruptions to food and water supply (including Production, distribution, alternative sources, ability to readily decontaminate);
2. Cause major economic impacts;
3. Cause major social disruptions (including Stigma, DALY);
4. Cause major environmental impacts;
5. Are traditionally associated with deliberate outbreaks;
6. Cause health care system disruption;
7. Are present in high density and or highly inter-connected human populations;
8. Affect people whose behaviour is likely to increase transmission; and
9. Occur in places with poor public health infrastructure.

Prioritization elements

In order to be able to determine those pathogens and diseases to be prioritized under the R&D Blueprint, the following nine elements were identified:

1. Human transmissibility (including population immunity, behavioural factors, etc.)
2. Severity or case fatality rate
3. Spillover potential
4. Evolutionary potential
5. Available countermeasures
6. Difficulty of detection or control
7. Public health context of the affected area(s)
8. Potential scope of outbreak (risk of international spread)
9. Potential societal impacts



***Fácilmente transmisible entre humanos.
Severo, alta mortalidad.
Potenciales efectos indirectos/secundarios.
Capacidad de transformación.
Posibilidad de adaptación.
Difícil de detectar/controlar.
Alta capacidad de diseminación.
Alto impacto social.***

Enfermedad por el virus del Ebola



Organización
Mundial de la Salud

30 de mayo de 2019

Cronología de los brotes del virus del Ebola

Año	País	Especie del virus	Casos	Defunciones	Tasa de letalidad
2015	Italia	Zaire	1	0	0%
2014	República Democrática del Congo	Zaire	66	49	74%
2014	España	Zaire	1	0	0%
2014	Reino Unido	Zaire	1	0	0%
2014	Estados Unidos	Zaire	4	1	25%
2014	Senegal	Zaire	1	0	0%
2014	Mali	Zaire	8	6	75%
2014	Nigeria	Zaire	20	8	40%
2014-2016	Sierra Leona	Zaire	14124*	3956*	28%
2014-2016	Liberia	Zaire	10675*	4809*	45%
2014-2016	Guinea	Zaire	3811*	2543*	67%
2012	República Democrática del Congo	Bundibugyo	57	29	51%
2012	Uganda	Sudán	7	4	57%
2012	Uganda	Sudán	24	17	71%
2011	Uganda	Sudán	1	1	100%
2008	República Democrática del Congo	Zaire	32	14	44%
2007	Uganda	Bundibugyo	149	37	25%
2007	República Democrática del Congo	Zaire	264	187	71%
2005	Congo	Zaire	12	10	83%
2004	Sudan	Sudán	17	7	41%
2003	Congo	Zaire	35	29	83%
(Nov-dic)					
2003	Congo	Zaire	143	128	90%
(Ene-abr)					
2001-2002	Congo	Zaire	59	44	75%
2001-2002	Gabón	Zaire	65	53	82%
2000	Uganda	Sudán	425	224	53%



Junta de
Castilla y León
Consejería de Sanidad

SPECIAL REPORT

The Ongoing Ebola Epidemic in the Democratic Republic of Congo, 2018–2019

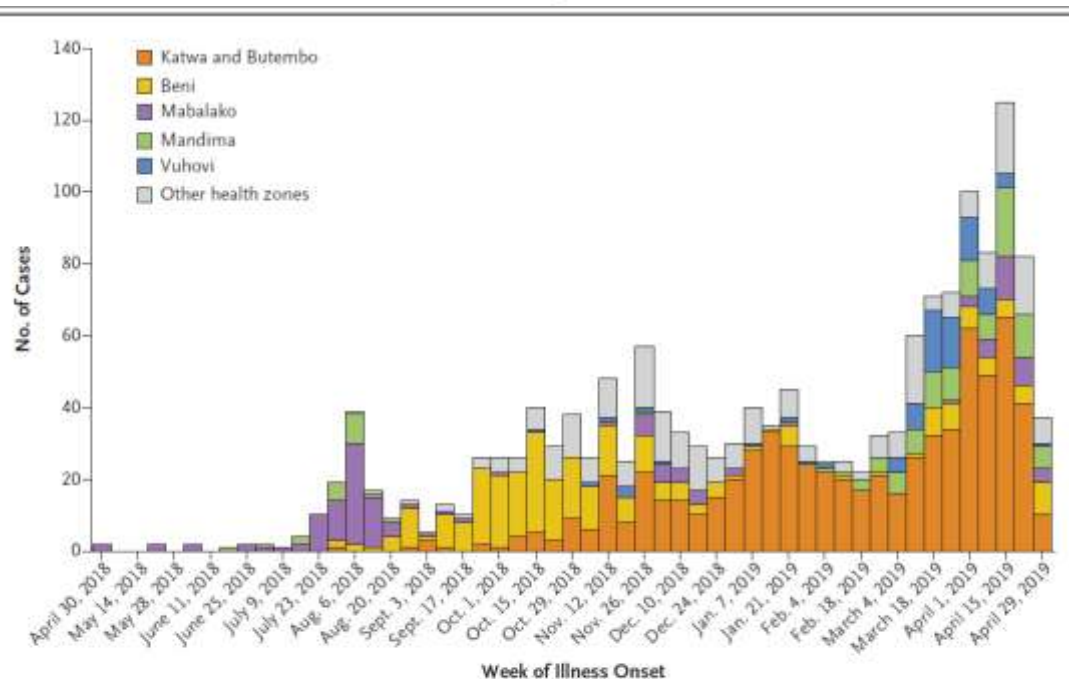


Figure 1. Confirmed and Probable Cases of Ebola Virus Disease (EVD) by Week of Onset and Health Zone, Democratic Republic of Congo.

Data are as of May 7, 2019. Data for recent weeks are subject to delays in case confirmation and reporting, as well as ongoing data cleaning. Adapted with permission from the World Health Organization and the Ministry of Health, Democratic Republic of Congo, 2019.²

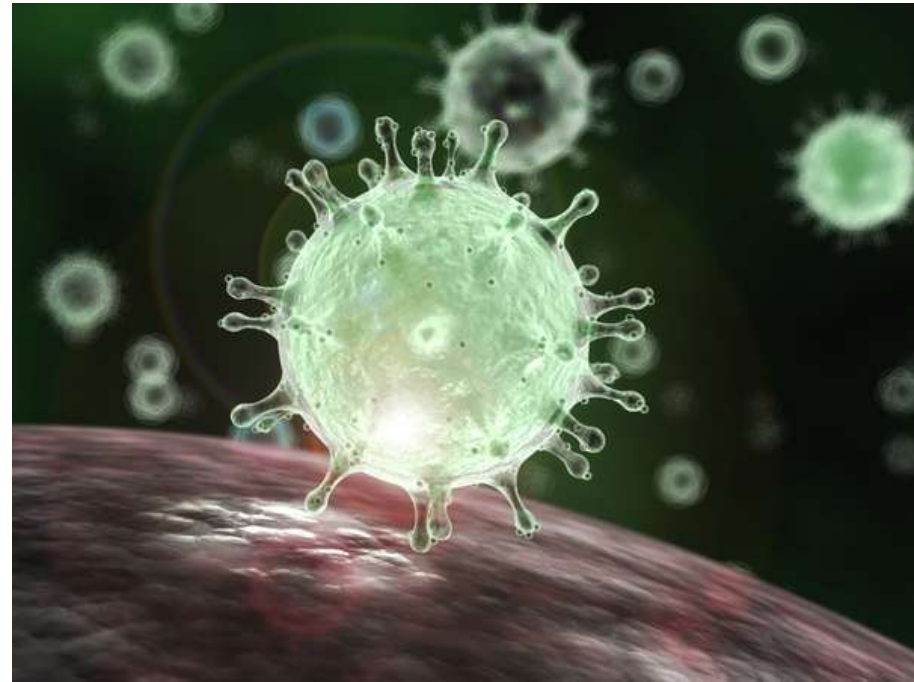
1600 casos.
Mortalidad 67%.



Sesiones de Maitines. Martes 4 de Febrero de 2020.

¿Vamos a morir de una infección por coronavirus

**Jose Guerra Laso
Sº de M. Interna
CAULE.**



Chinese Authorities Say Viral Pneumonia Outbreak Is Not SARS, MERS or Bird Flu

By Reuters Staff

January 07, 2020

BEIJING (Reuters) - Chinese healthcare authorities in Wuhan said an outbreak of viral pneumonia was not Severe Acute Respiratory Syndrome (SARS), Middle East respiratory syndrome (MERS) or bird flu, and that they were still working to identify the cause and source.

In a statement posted on its website Sunday night, the Wuhan Municipal Health Commission said a total of 59 cases of unknown viral pneumonia had been reported as of Sunday, including seven in a critical condition. It also said it had put 163 people who had had contacts with the patients under medical observation.

The viral pneumonia started in the central city of Wuhan late last month, prompting fears of a possible SARS epidemic.

Reuters Health Information © 2020

Cite this: Chinese Authorities Say Viral Pneumonia Outbreak Is Not SARS, MERS or Bird Flu - *Medscape* - Jan 06, 2020.

WHO Says New Virus May Have Caused China Pneumonia Outbreak

By Kate Kelland and Se Young Lee

January 09, 2020

LONDON/BEIJING (Reuters) - A cluster of more than 50 pneumonia cases in China's central city of Wuhan may be due to a newly emerging member of the family of viruses that caused the deadly SARS and MERS outbreaks, World Health Organization (WHO) said on Wednesday.

While the United Nations health agency said it needed more comprehensive information to confirm precisely the type of pathogen causing the infections, it said a new coronavirus was a possibility.

On Thursday, China's official Xinhua news agency said preliminary lab results conducted by a team of experts showed a new type of coronavirus caused the outbreak that began in December.

Xu Jianguo, an academic at the Chinese Academy of Engineering who led the team, told Xinhua that tests on samples from patients found 15 positive results of the new coronavirus. Fifty nine cases of the pneumonia have been reported as of Sunday.

"It may take years for researchers to develop medicines and vaccines," the Xinhua report said.

The outbreak comes ahead of the Lunar New Year holidays in late January, when many of China's 1.4 billion people will be traveling to their home towns or abroad. The Chinese government expects passengers to make 440 million trips via rail and another 79 million trips via airplanes, officials said during a briefing on Thursday.

Wang Yang, the Chinese transport ministry's chief engineer, said at the briefing that authorities will step up efforts to prevent the pneumonia outbreak from spreading further during the holiday period, including ensuring proper disinfection in major public transportation hubs.

Coronaviruses are a large family of viruses that can cause infections ranging from the common cold to Severe Acute Respiratory Syndrome (SARS). Some of the virus types cause less severe disease, while some - like the one that causes Middle East Respiratory Syndrome (MERS) - are far more severe.

The WHO noted that coronaviruses emerge periodically - including in 2002 to cause SARS and in 2012 to cause MERS.

EDITORIAL



Medical Journals and the 2019-nCoV Outbreak

Eric J. Rubin, M.D., Ph.D., Lindsey R. Baden, M.D., Stephen Morrissey, Ph.D.,
and Edward W. Campion, M.D.

This editorial was published on January 27, 2020, at NEJM.org.

DOI: 10.1056/NEJMe2001329

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TABLA 134-1 Clasificación de los virus

FAMILIA	EJEMPLO	TIPO DE ÁCIDO NUCLEICO	TAMAÑO DEL GENOMA (kb o kpb)	CUBIERTA	SIMETRÍA DE CÁPSIDE
Virus de ARN					
Picornaviridae	Poliovirus	ARN (+) MC	7-9	No	I
Astroviridae	Astrovirus	ARN (+) MC	6-7	No	I
Caliciviridae	Virus Norwalk	ARN (+) MC	7-8	No	I
Togaviridae	Virus de la rubéola	ARN (+) MC	10-12	Sí	I
Flaviviridae	Virus de la fiebre amarilla	ARN (+) MC	10-12	Sí	E
Coronaviridae	Coronavirus	ARN (+) MC	28-31	Sí	H
Rhabdoviridae	Virus de la rabia	ARN (-) MC	11-15	Sí	H
Paramyxoviridae	Virus del sarampión	ARN (-) MC	13-18	Sí	H
Filoviridae	Virus Ébola	ARN (-) MC	19	Sí	H
Arenaviridae	Virus de la coriomeningitis linfocítica	2 segmentos de ARN circulares MC (ambos sentidos)	11	Sí	E
Bunyaviridae	Virus de la encefalitis de California	3 segmentos de ARN circulares MC (ambos sentidos)	11-19	Sí	H
Orthomyxoviridae	Virus de la gripe	6-8 segmentos de ARN (-) MC*	10-15	Sí	H
Reoviridae	Rotavirus	10-12 segmentos de ARN BC *	19-32	No	I
Retroviridae	VIH	2 segmentos de ARN (+) MC idénticos	7-13	Sí	E

Virus de ADN

Hepadnaviridae	Virus de la hepatitis B	ADN BC circular con porciones MC	3-4	Sí	I
Parvoviridae	Parvovirus humano B19	ADN (+) o (-) MC	4-6	No	I
Polyomaviridae	Virus JC	ADN circular BC	5	No	I
Papillomaviridae	Virus del papiloma humano	ADN circular BC	7-8	No	I
Adenoviridae	Adenovirus	ADN lineal BC	26-45	No	I
Herpesviridae	Virus del herpes simple	ADN lineal BC	125-240	Sí	I
Poxviridae	Virus vaccinia	ADN lineal BC	130-375	Sí	Compleja

*Reovirus y orbivirus: 10 segmentos; rotavirus: 11 segmentos; virus de la fiebre de Colorado por garrapatas: 12 segmentos.

(+), transcripción en sentido positivo; (-), transcripción en sentido negativo; BC, bicatenario; E, esférica; H, helicoidal; I, icosaédrica; MC, monocatenario.
 Datos de Condit RC. Principles of virology. En: Knipe DM, Howley PM, eds. Fields Virology. 5ª ed. Filadelfia: Lippincott-Raven Press; 2007:25-57.

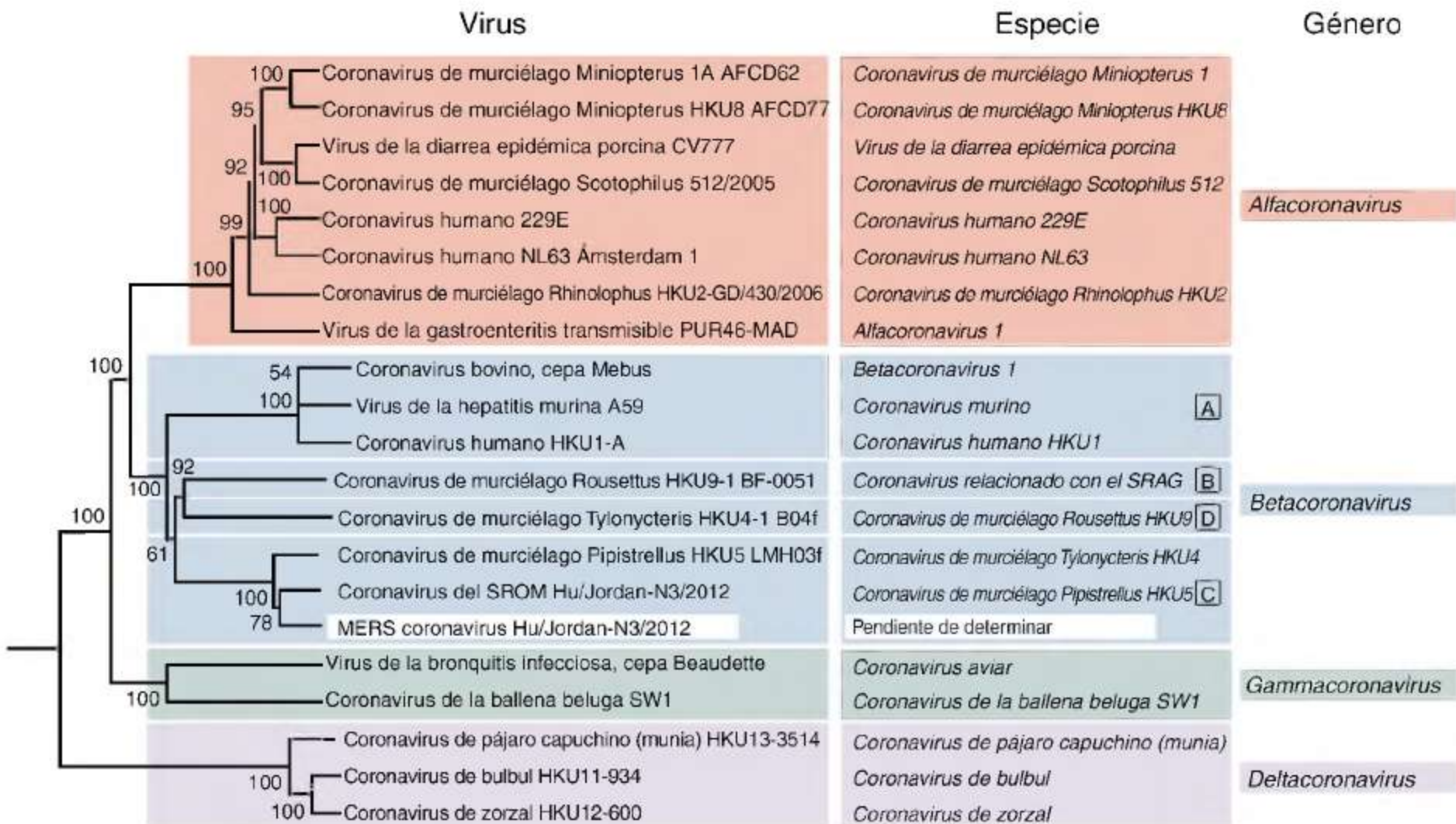
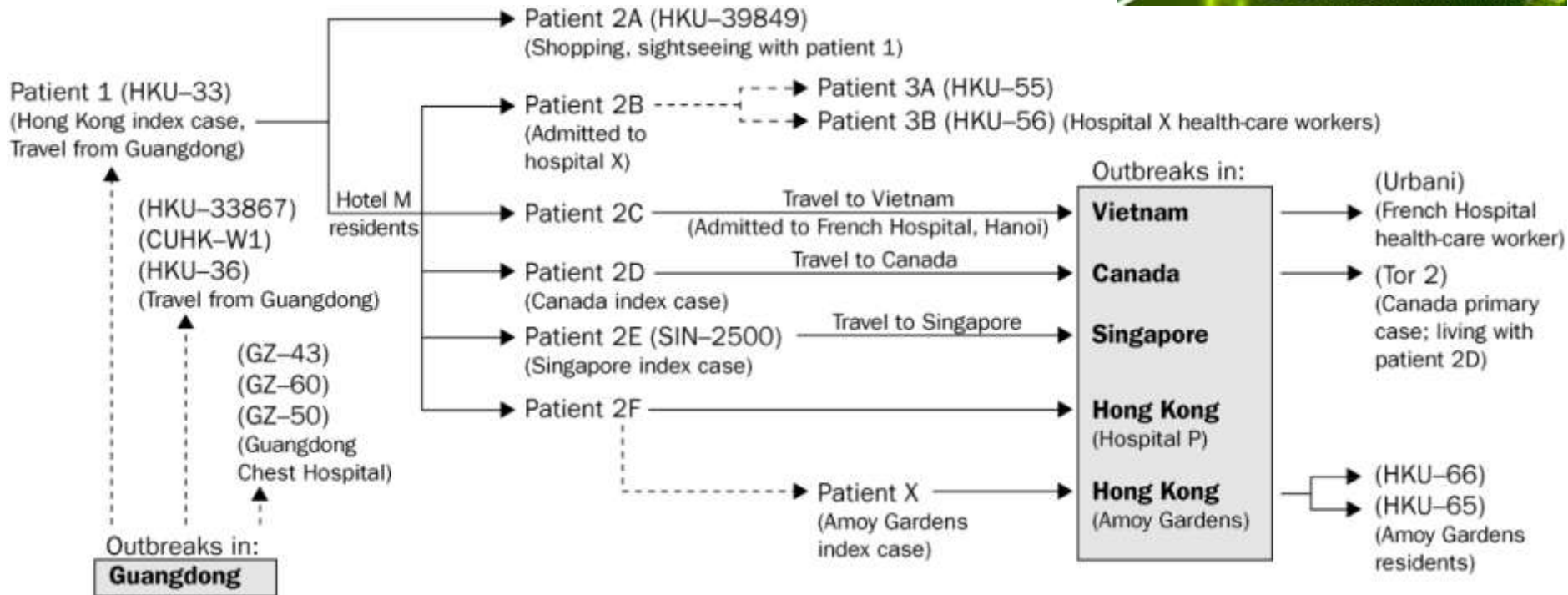
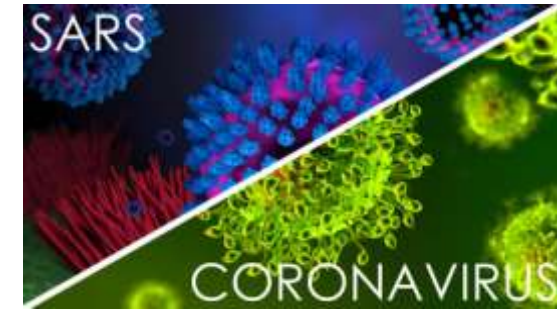


FIGURA 157-2 Relaciones filogenéticas entre miembros de la subfamilia Coronavirinae. Se ha elaborado un árbol de vecinos cercanos con raíces a partir de las alineaciones de secuencia de aminoácidos de los dominios conservados a nivel de toda la familia Coronaviridae de la poliproteína replicasa 1 (ADRP, nsp3; Mpro, nsp5; RdRP, nsp12; Hel, nsp13; ExoN, nsp14; NendoU, nsp15; O-MT, nsp16) para 21 coronavirus, cada uno de los cuales es un representante de una especie de coronavirus conocida actualmente. Se indican cinco de los seis coronavirus humanos conocidos (HCoV-229E, HCoV-NL63, HCoV-HKU1, SRAG-CoV y SROM-CoV). El HCoV-OC43 se relaciona estrechamente con el coronavirus bovino, que se muestra en la figura. El torovirus equino Berne sirvió como exogrupo. Los nombres de los virus se muestran con especificaciones de cepa; los nombres de especie y género están en cursiva por convención. El árbol muestra los cuatro grupos monofiléticos principales, que corresponden a los géneros *Alfa*, *Beta*, *Gamma* y *Deltacoronavirus* (codificados por color). También se indican las estirpes de betacoronavirus A a D (correspondientes a los antiguos subgrupos de CoV 2A a D). Los valores de bootstrap (1.000 réplicas) se indican en los puntos de ramificación. El árbol está dibujado a escala (barra de escala, 0,2 sustituciones de aminoácidos por sitio). (De de Groot RJ, Baker SC, Baric RS, y cols. Middle East respiratory syndrome coronavirus [MERS-CoV]: announcement of the Coronavirus Study Group. J Virol. 2013;14:7790-7792.)

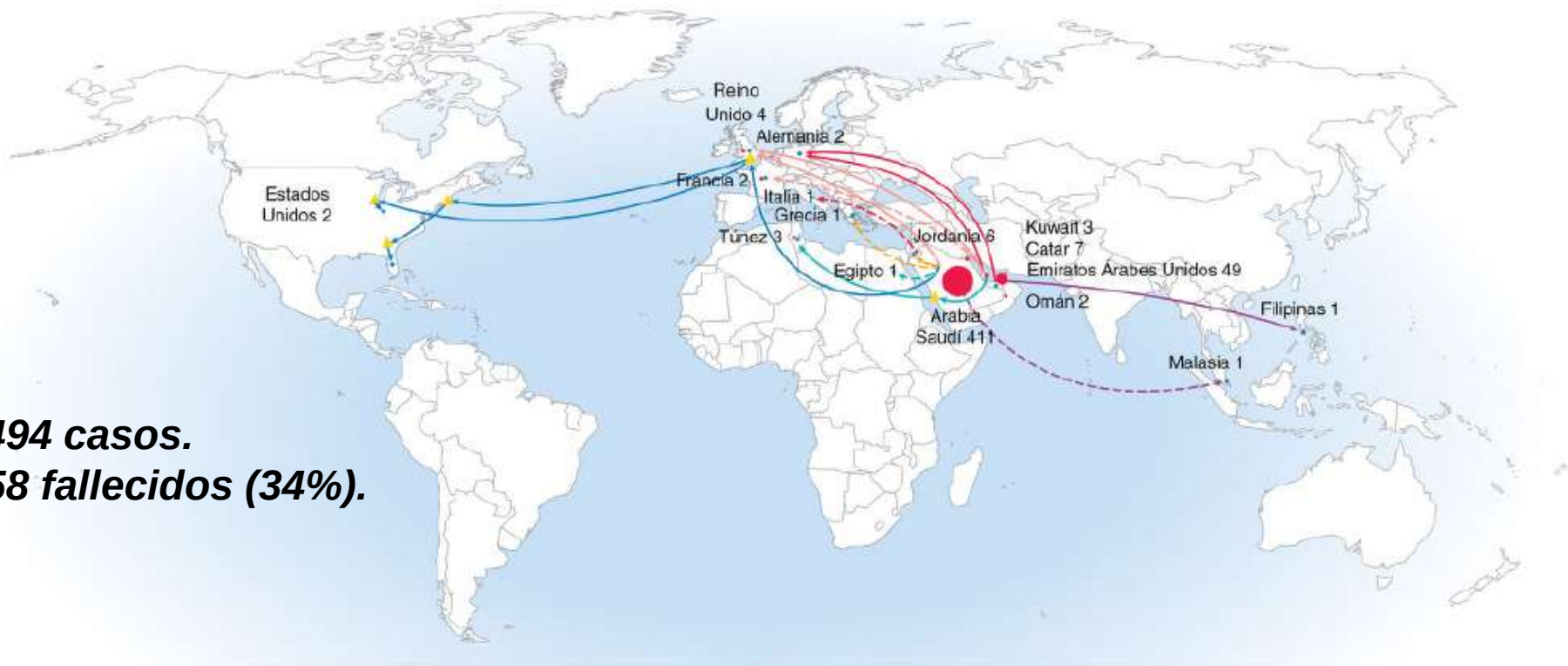
Molecular epidemiology of the novel coronavirus that causes severe acute respiratory syndrome

Lancet 2004; 363: 99–104



Desde Hong Kong. 2002-2004.
Afectó a 30 países.
8098 afectados, 744 muertes (9,2%).

**2494 casos.
858 fallecidos (34%).**



Tipo	Número de casos	Lugares de exposición por países notificantes			
● Local	• 1	← Egipto	← Grecia	← Malasia	← Estados Unidos
● Importado	• 10	← Francia	← Italia	← Filipinas	← Reino Unido
▲ Escala	● 100	← Alemania	← Jordania	← Túnez	

FIGURA 157-5 Distribución de los casos confirmados de síndrome respiratorio de Oriente Medio por país notificador, de marzo de 2012 a mayo de 2014. Este mapa se basa en uno publicado por el European Centre for Disease Prevention and Control y muestra el predominio de casos notificados por Arabia Saudí, con otros casos originados en Oriente Medio, así como las rutas de viaje durante la importación a otros países (flechas de color). Se ha añadido el segundo caso importado a Estados Unidos. El número total de casos mostrado es algo menor que el número notificado por la OMS varios días después⁷, lo que refleja el rápido incremento de casos notificados durante mayo de 2014. (Modificada del European Centre for Disease Prevention and Control. Epidemiological Update: Middle East Respiratory Syndrome Coronavirus [MERS-CoV]. Disponible en http://www.ecdc.europa.eu/en/press/news/_layouts/forms/News_DispatchForm.aspx?List=8db7286c-fe2d-476c-9133-18ff4cb1b568&ID=998. Consultado el 6 de mayo de 2014.)



Short communication

Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event

D. Paraskevis^{a,*}, E.G. Kostaki^a, G. Magiorkinis^a, G. Panayiotakopoulos^b, G. Sourvinos^c, S. Tsiodras^d

^a Department of Hygiene Epidemiology and Medical Statistics, Medical School, National and Kapodistrian University of Athens, Athens, Greece

^b National Public Health Organisation (NPHO), Athens, Greece

^c Laboratory of Clinical Virology, School of Medicine, University of Crete, Heraklion, Greece

^d Medical School, National and Kapodistrian University of Athens, Athens, Greece



Conclusions: The levels of genetic similarity between the 2019-nCoV and RaTG13 suggest that the latter does not provide the exact variant that caused the outbreak in humans, but the hypothesis that 2019-nCoV has originated from bats is very likely. We show evidence that the novel coronavirus (2019-nCoV) is not-mosaic consisting in almost half of its genome of a distinct lineage within the betacoronavirus. These genomic features and their potential association with virus characteristics and virulence in humans need further attention.

Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study

Nanshan Chen*, Min Zhou*, Xuan Dong*, Jieming Qu*, Fengyun Gong, Yang Han, Yang Qiu, Jingli Wang, Ying Liu, Yuan Wei, Jia'an Xia, Ting Yu, Xinxin Zhang, Li Zhang



Published **Online**
January 29, 2020
[https://doi.org/10.1016/S0140-6736\(20\)30211-7](https://doi.org/10.1016/S0140-6736(20)30211-7)

Patients (n=99)	
Age, years	
Mean (SD)	55.5 (13.1)
Range	21-82
≤39	10 (10%)
40-49	22 (22%)
50-59	30 (30%)
60-69	22 (22%)
≥70	15 (15%)
Sex	
Female	32 (32%)
Male	67 (68%)

Chronic medical illness	50 (51%)
Cardiovascular and cerebrovascular diseases	40 (40%)
Digestive system disease	11 (11%)
Endocrine system disease†	13 (13%)
Malignant tumour	1 (1%)
Nervous system disease	1 (1%)
Respiratory system disease	1 (1%)
Admission to intensive care unit	23 (23%)
Clinical outcome	
Remained in hospital	57 (58%)
Discharged	31 (31%)
Died	11 (11%)

Patients (n=99)	
Signs and symptoms at admission	
Fever	82 (83%)
Cough	81 (82%)
Shortness of breath	31 (31%)
Muscle ache	11 (11%)

Treatment

Oxygen therapy	75 (76%)
Mechanical ventilation	
Non-invasive (ie, face mask)	13 (13%)
Invasive	4 (4%)
CRRT	9 (9%)
ECMO	3 (3%)
Antibiotic treatment	70 (71%)
Antifungal treatment	15 (15%)
Antiviral treatment	75 (76%)
Glucocorticoids	19 (19%)
Intravenous immunoglobulin therapy	27 (27%)

2019-nCoV=2019 novel coronavirus. ARDS=acute respiratory distress syndrome. ECMO=extracorporeal membrane oxygenation. CRRT=continuous renal replacement therapy.

Table 2: Clinical characteristics and treatment of patients with 2019-nCoV pneumonia

ORIGINAL ARTICLE

Early Transmission Dynamics in Wuhan, China,
of Novel Coronavirus–Infected Pneumonia

This article was published on January 29, 2020, and last updated on January 31, 2020, at NEJM.org.

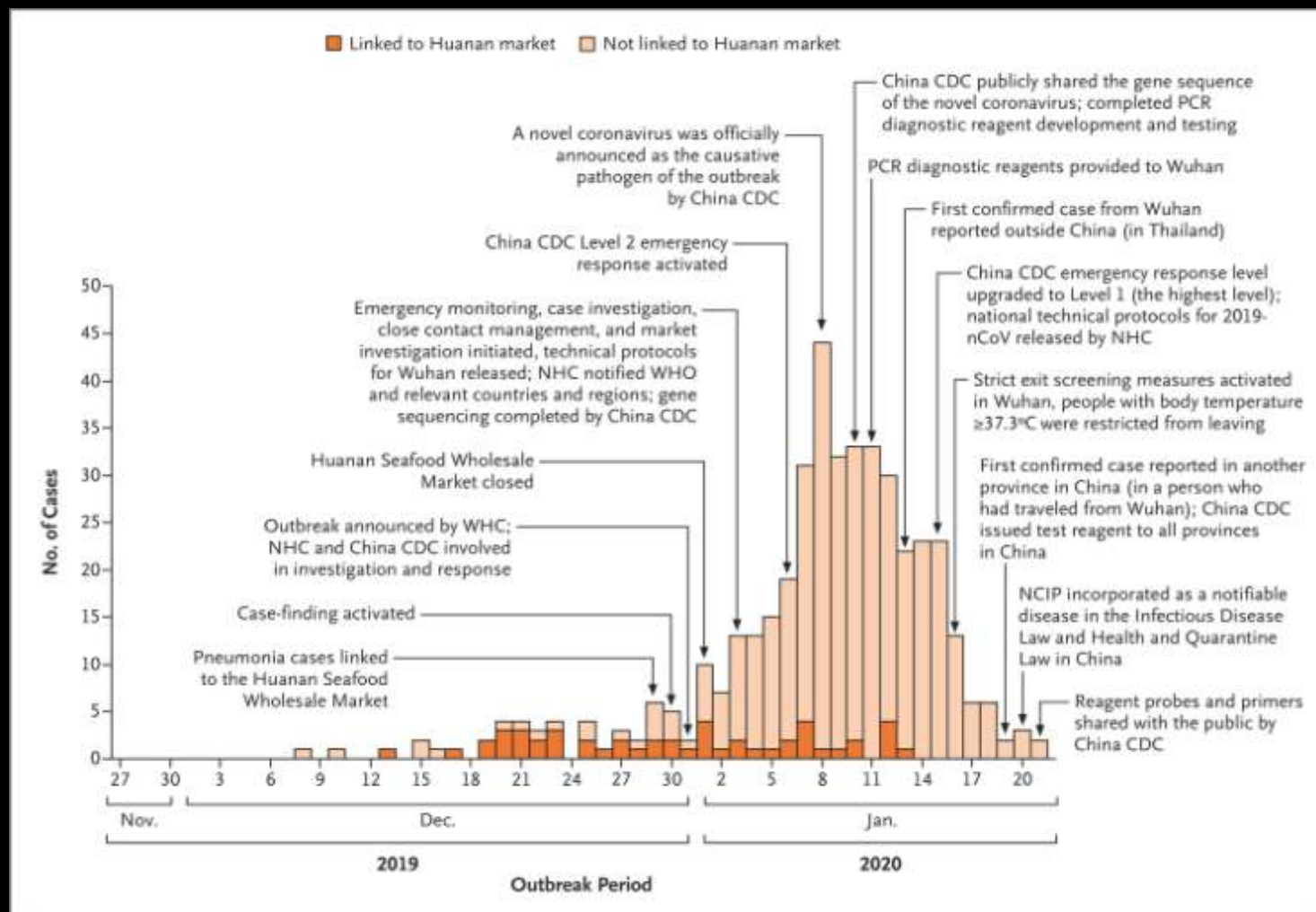
Dic-2019 a Enero-2020.

425 casos, todos de la ciudad de Wuhan.

Definición de caso: Fiebre + infiltrado pulmonar + no leucocitosis + no mejoría a los 3 días de tratamiento antibiótico adecuado.

Diagnóstico por PCR en muestras respiratorias.

Onset of Illness among the First 425 Confirmed Cases of Novel Coronavirus (2019-nCoV)-Infected Pneumonia (NCIP) in Wuhan, China.



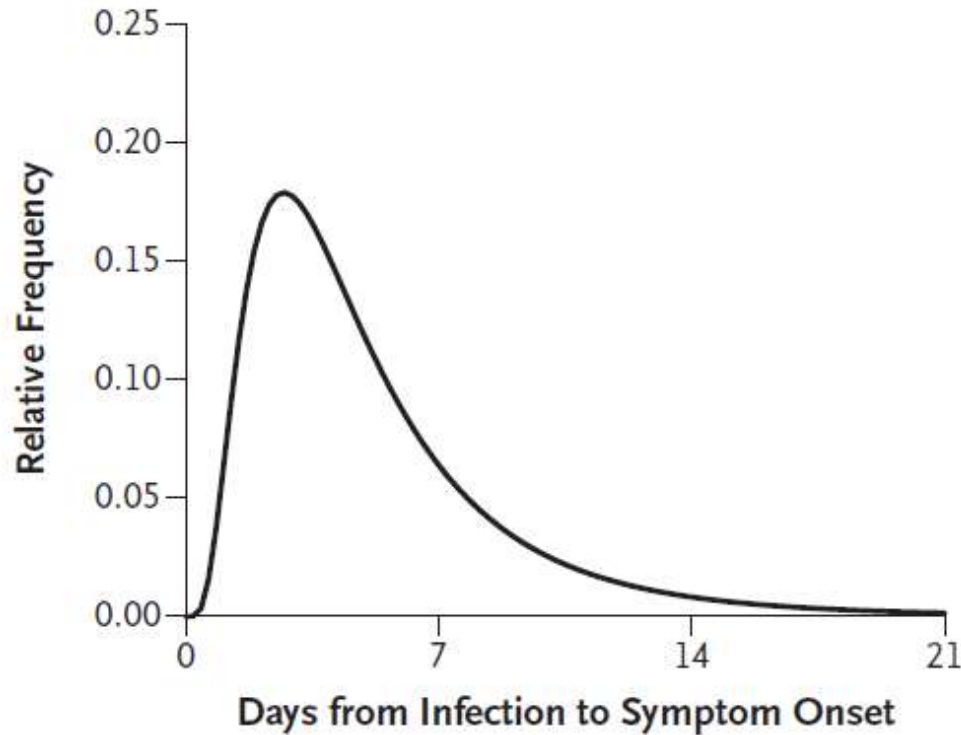
Characteristics of Patients with Novel Coronavirus–Infected Pneumonia in Wuhan as of January 22, 2020.*

Table 1. Characteristics of Patients with Novel Coronavirus–Infected Pneumonia in Wuhan as of January 22, 2020.*

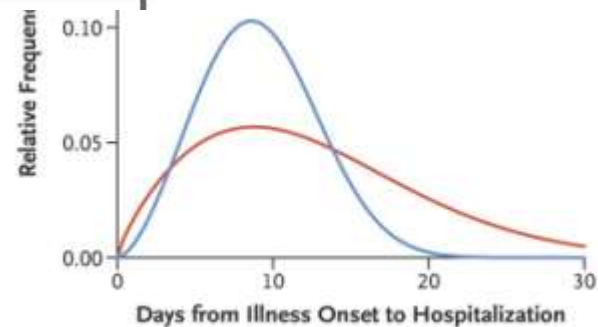
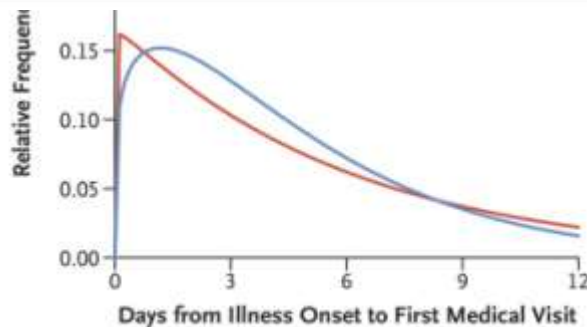
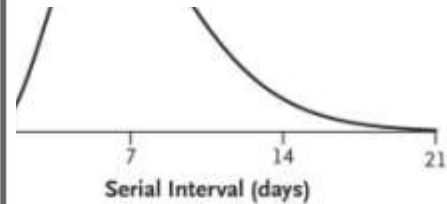
Characteristic	Before January 1 (N=47)	January 1 –January 11 (N=248)	January 12 –January 22 (N=130)
Median age (range) — yr	56 (26–82)	60 (21–89)	61 (15–89)
Age group — no./total no. (%)			
<15 yr	0/47	0/248	0/130
15–44 yr	12/47 (26)	39/248 (16)	33/130 (25)
45–64 yr	24/47 (51)	106/248 (43)	49/130 (38)
≥65 yr	11/47 (23)	103/248 (42)	48/130 (37)
Male sex — no./total no. (%)	31/47 (66)	147/248 (59)	62/130 (48)
Exposure history — no./total no. (%)			
Wet market exposure	30/47 (64)	32/196 (16)	5/81 (6)
Huanan Seafood Wholesale Market	26/47 (55)	19/196 (10)	5/81 (6)
Other wet market but not Huanan Seafood Wholesale Market	4/47 (9)	13/196 (7)	0/81
Contact with another person with respiratory symptoms	14/47 (30)	30/196 (15)	21/83 (25)
No exposure to either market or person with respiratory symptoms	12/27 (26)	141/196 (72)	59/81 (73)
Health care worker — no./total no. (%)	0/47	7/248 (3)	8/122 (7)

* Reduced denominators indicate missing data. Percentages may not total 100 because of rounding.

A



We examined data on exposures among 10 confirmed cases, and we estimated the mean incubation period to be 5.2 days (95% confidence interval [CI], 4.1 to 7.0); the 95th percentile of the distribution was 12.5 days (95% CI, 9.2 to 18) (Fig. 2A).



EDITORIAL



Another Decade, Another Coronavirus

Stanley Perlman, M.D., Ph.D.

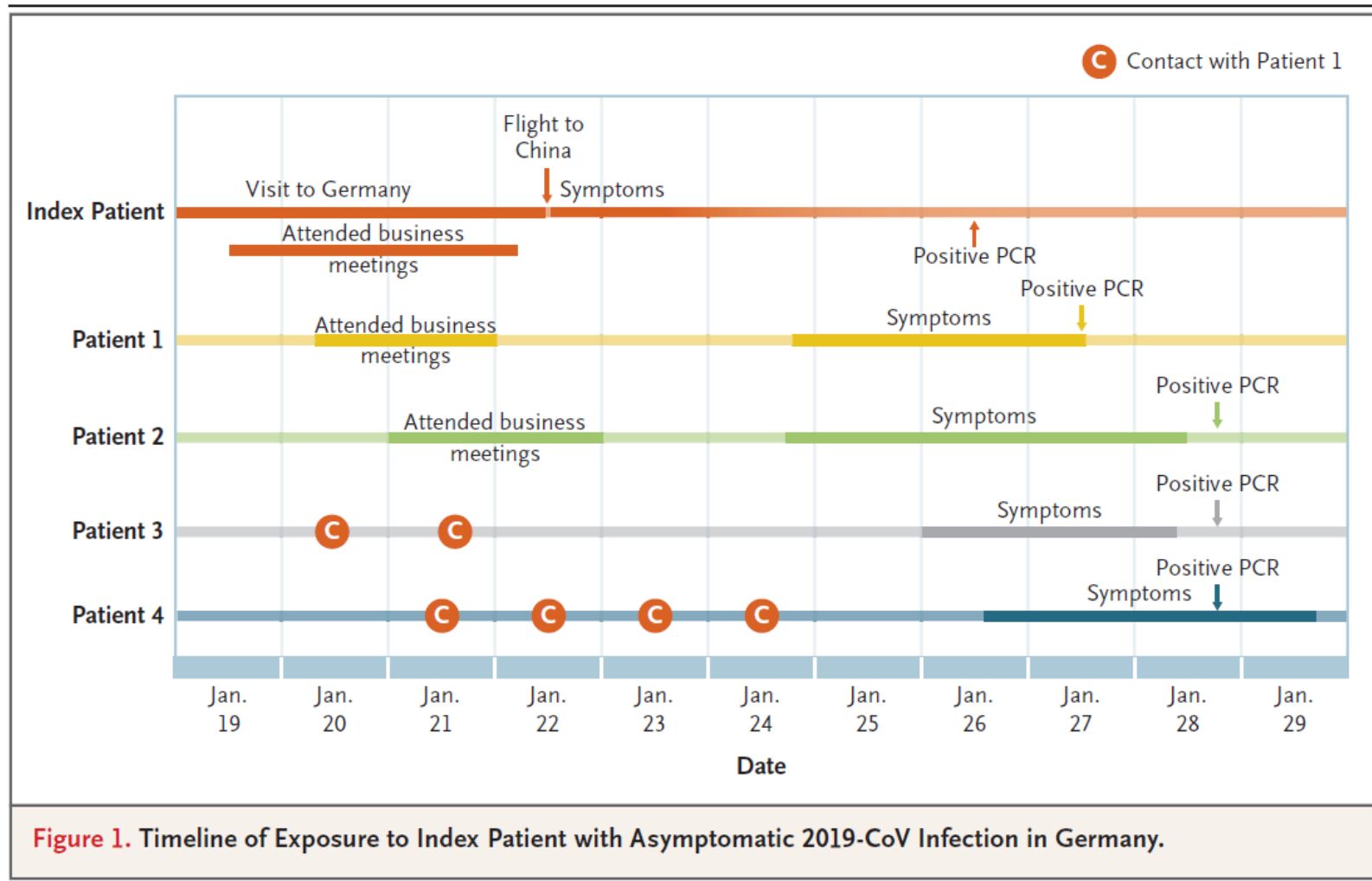
This editorial was published on January 24, 2020, at NEJM.org.

Both SARS-CoV and MERS-CoV infect intrapulmonary epithelial cells more than cells of the upper airways. Consequently, transmission occurs primarily from patients with recognized illness and not from patients with mild, nonspecific signs. It appears that 2019-nCoV uses the same cellular receptor as SARS-CoV (human angiotensin-converting enzyme 2 [hACE2]), so transmission is expected only after signs of lower respiratory tract disease develop.

CORRESPONDENCE

Transmission of 2019-nCoV Infection from an Asymptomatic Contact in Germany

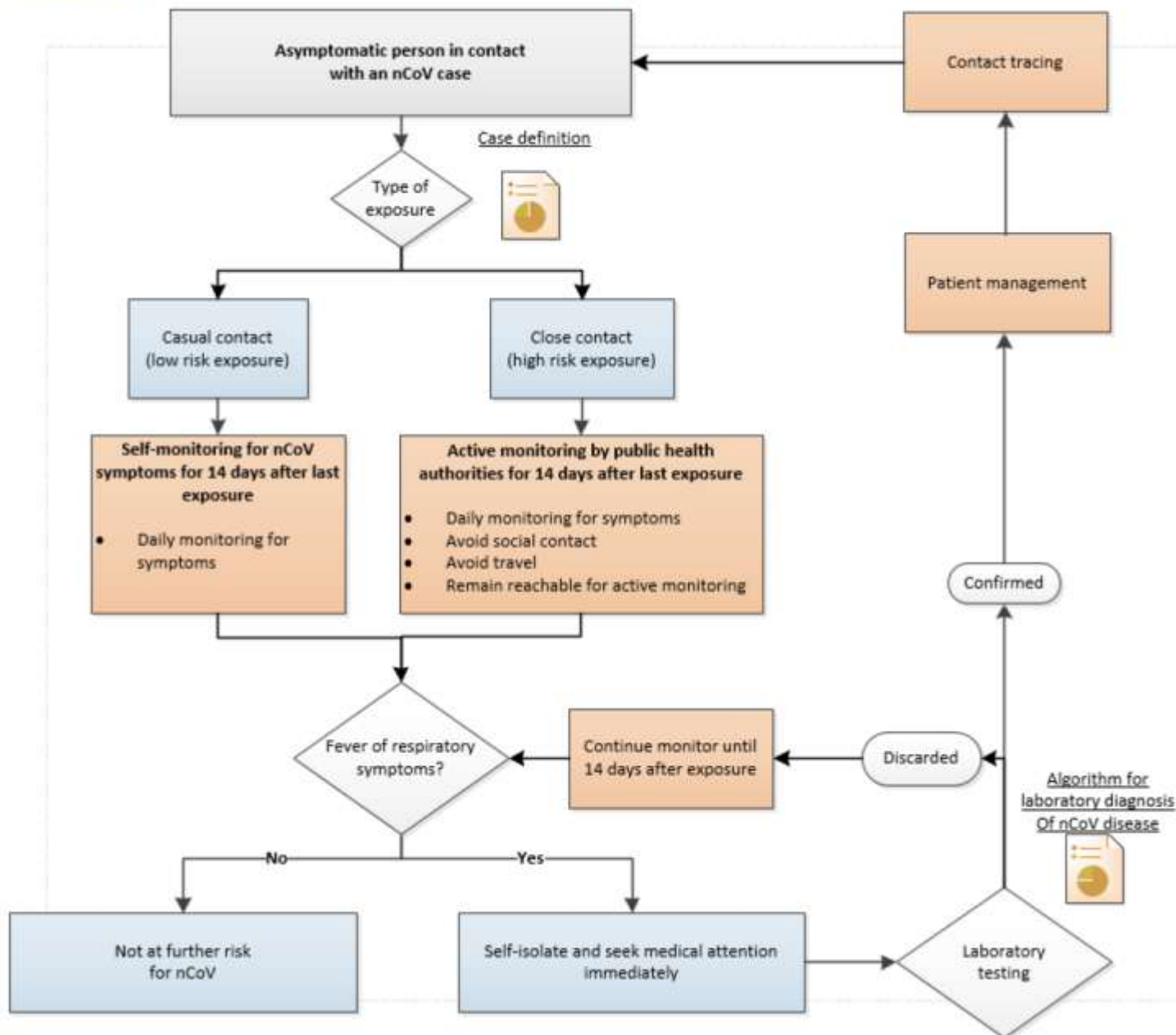
This letter was published on January 30, 2020, at NEJM.org.





Date of production: 03/02/2020

Figure 1. Algorithm for management of contacts of probable or confirmed 2019-nCoV cases





The NEW ENGLAND JOURNAL of MEDICINE

This article was published on January 24, 2020, at NEJM.org.

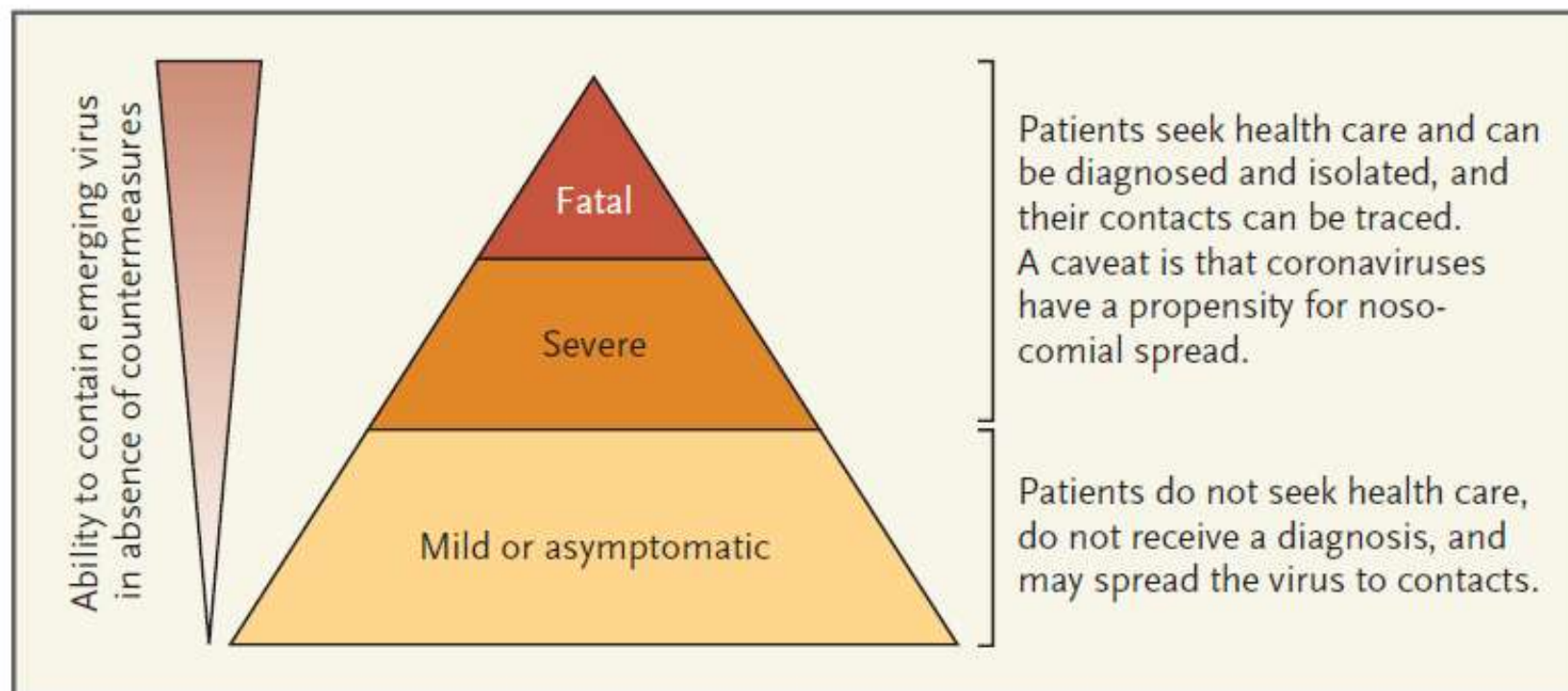


Figure 1. Surveillance Pyramid and Its Relation to Outbreak Containment.

The proportion of mild and asymptomatic cases versus severe and fatal cases is currently unknown for 2019-nCoV — a knowledge gap that hampers realistic assessment of the virus's epidemic potential and complicates the outbreak response.

El mundo actual está más intercomunicado que nunca.

Hay un entorno con numerosos microorganismos potencialmente muy peligrosos. Enfermedad X.

Ante grandes pandemias, las estructuras organizativas habituales son limitadas.

Debemos mantener la calma y colaborar de acuerdo con nuestras capacidades.