Epidemiología COVID-19 y caracterización viral de SARS-CoV-2:

Vías de transmisión, letalidad y panorama mundial

Dr. David Alejandro Cabrera Gaytán

Comité de Emergencias de la OMS.

Declaración sobre la segunda reunión del Comité de Emergencias del Reglamento Sanitario Internacional (2005) acerca del brote del nuevo coronavirus (2019-nCoV), celebrada el 30 de enero de 2020

30 de enero de 2020 | Declaraciones

El jueves 30 de enero de 2020, de 13.30 a 18.35 horas, hora de Ginebra (CEST), el Comité de Emergencias convocado por el Director General de la OMS en virtud del Reglamento Sanitario Internacional (RSI (2005)) se reunió para tratar sobre el brote del nuevo coronavirus (2019-nCoV) en la República Popular China y los casos exportados a otros países. La función del Comité es prestar asesoramiento al Director General, en quien recae la

- 30 de enero: ESPI.

- Sexta declaración de ESPI en menos de 10 años:

1. 2009 por la pandemia de influenza A(H1N1)pdm09.
2. 2014 por la propagación internacional del poliovirus.
3. 2014 brote de Ébola en África Occidental.
4. 2016 por la epidemia del virus Zika 2015/16.
5. Julio de 2019 por Ébola.

Fuente:
https://www.who.int/es/news-room/detail/30-01-2020-statement-on-the-second-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-outbreak-of-novel-coronavirus-(2019-ncov)

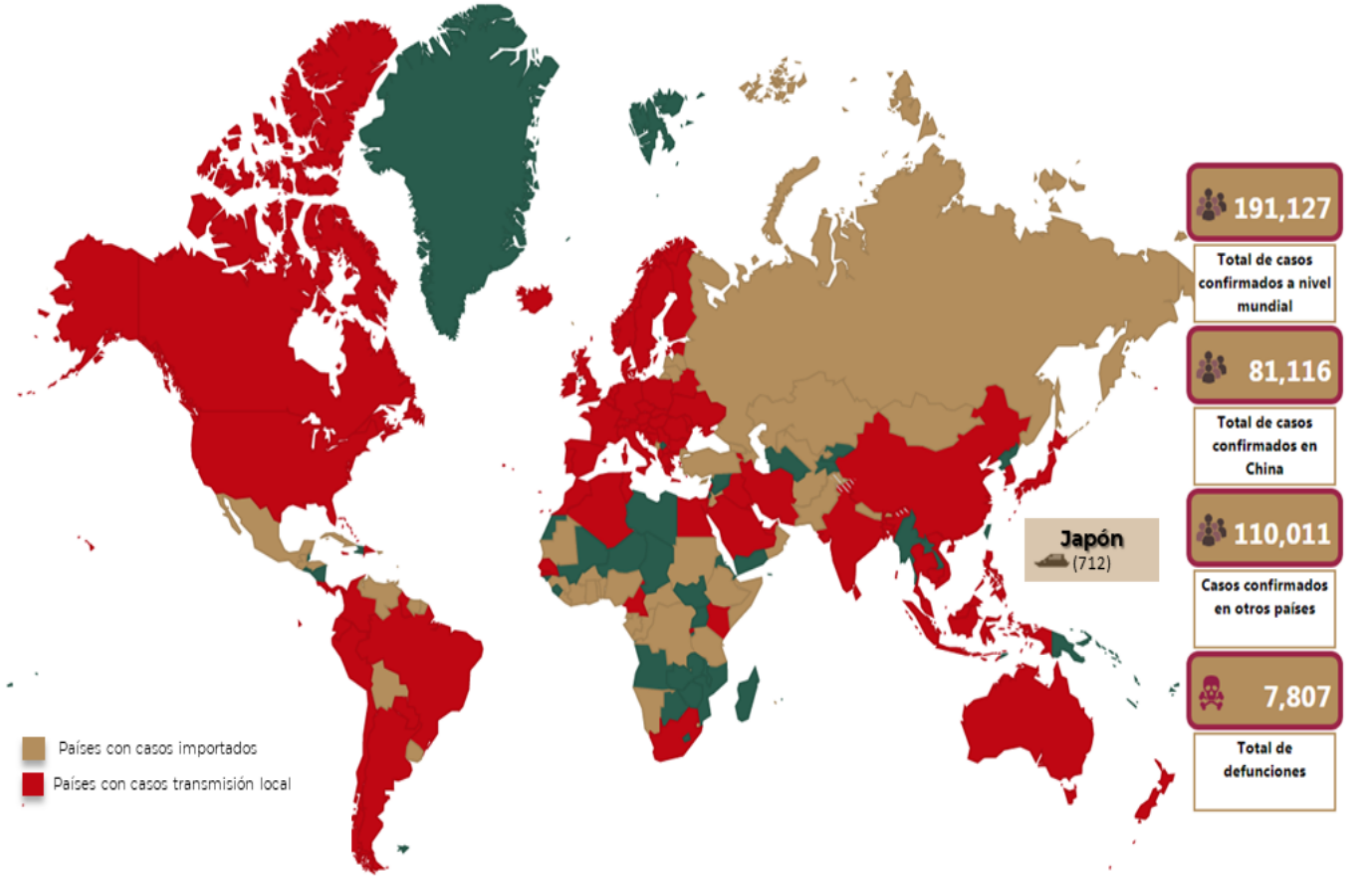
Eurosurveillance editorial team1. Note from the editors: World Health Organization declares novel coronavirus (2019-nCoV) sixth public health emergency of international concern. Euro Surveill. 2020;():pii=200131e. https://doi.org/10.2807/1560-7917.ES.2020.25.5.200131e

Situación mundial

GOBIERNO DE MÉXICO | IMSS

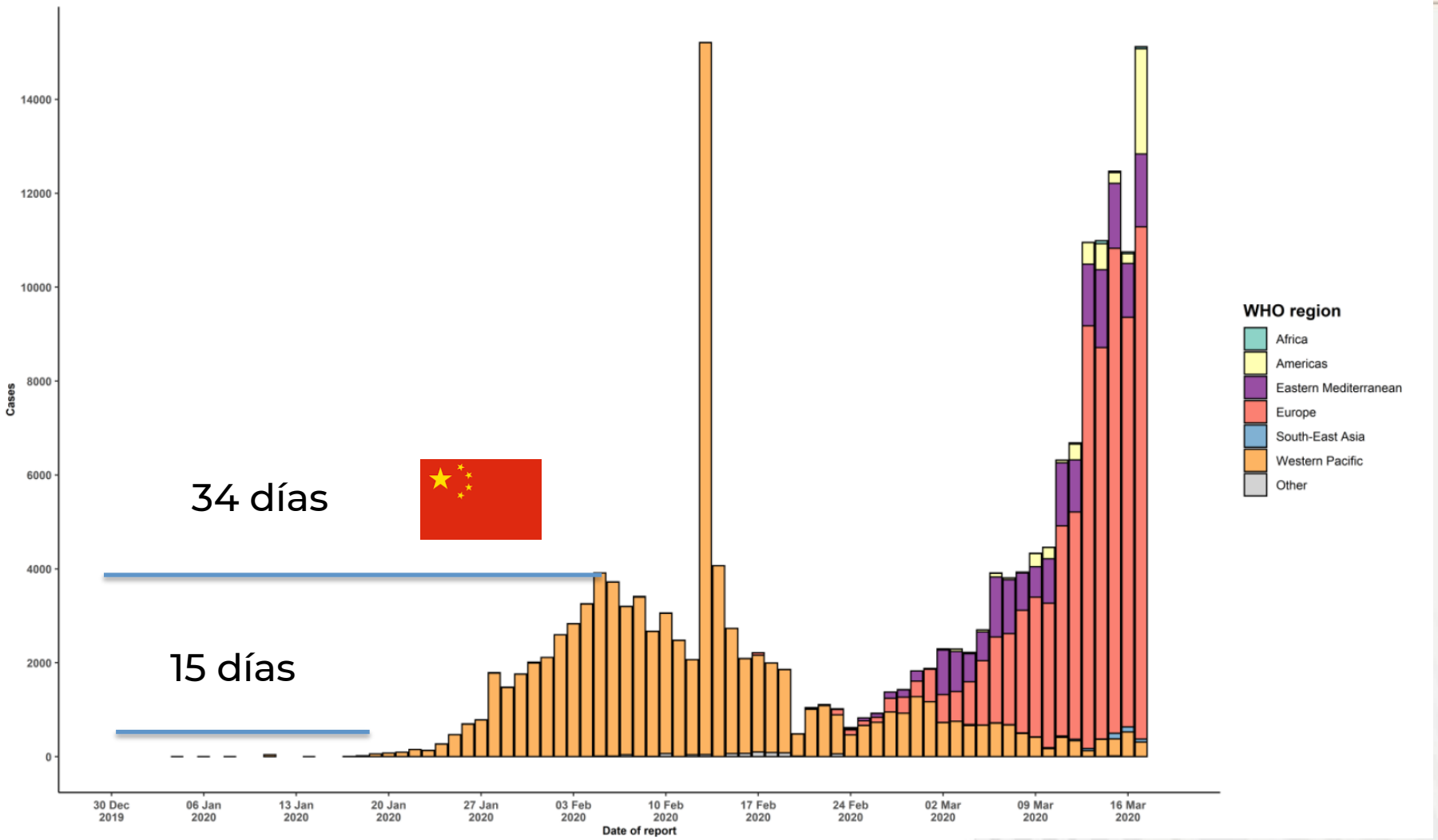
Distribución global de casos confirmados de COVID-19 por SARS-CoV-2 por laboratorio al día 18 de marzo de 2020.

Región	Casos Acumulados	Casos en las últimas 24 hrs
Pacífico Occidental	91,845	312
Europa	74,760	10,911
Mediterráneo Oriental	18,060	1,552
Américas	4,979	2,243
Asia Sudoriental	538	63
África	233	42



Fuente: Secretaría de Salud.

Situación mundial:
Curva epidémica por región de la OMS.



Fuente: OMS. Reporte No. 58. 18 de marzo de 2020.

Situación mundial: Defunciones

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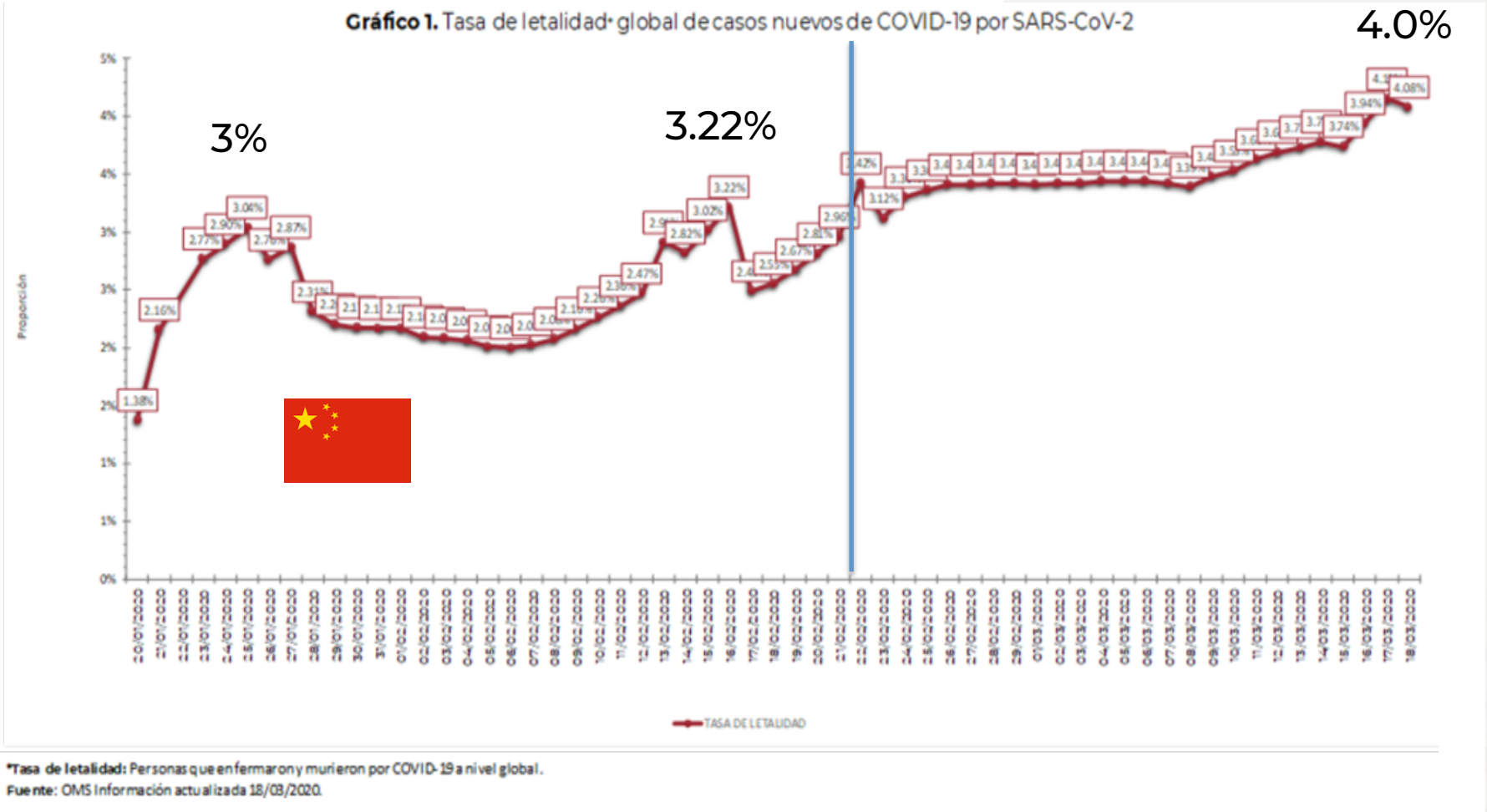

*Tasa de letalidad: Personas que enfermaron y murieron por COVID-19 a nivel global.
Fuente: OMS Información actualizada 18/03/2020.

Fuente: Secretaría de Salud.

Situación en EUA

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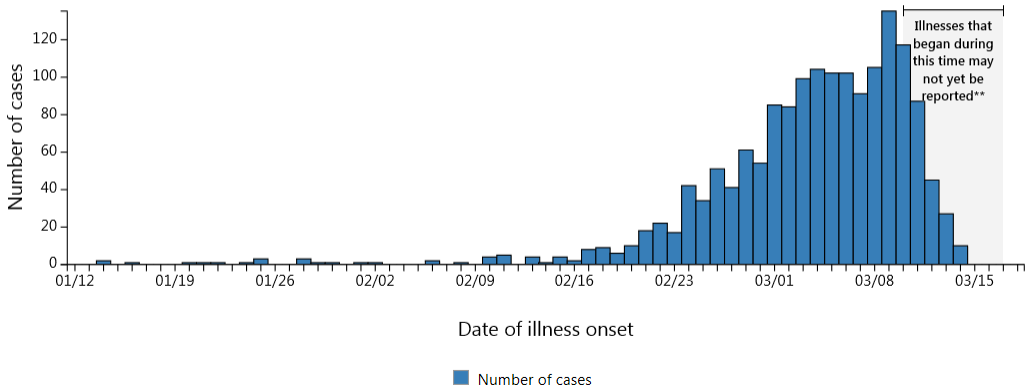
Cases of COVID-19 Reported in the US, by Source of Exposure*†	
Travel-related	269
Close contact	276
Under investigation	6,493
Total cases	7,038

COVID-19 cases in the United States by date of illness onset, January 12, 2020, to March 17, 2020, at 4pm ET (n=1,606)**

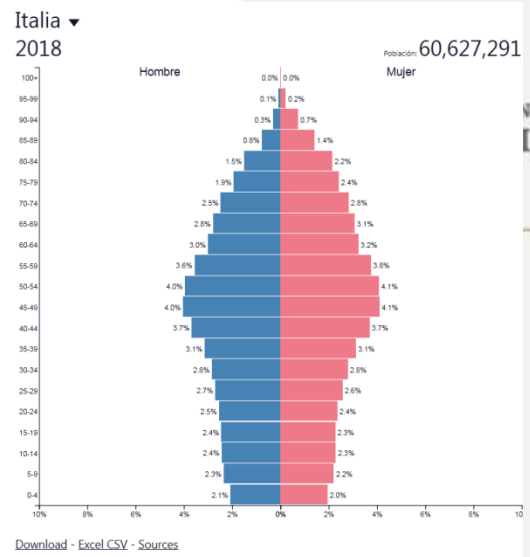


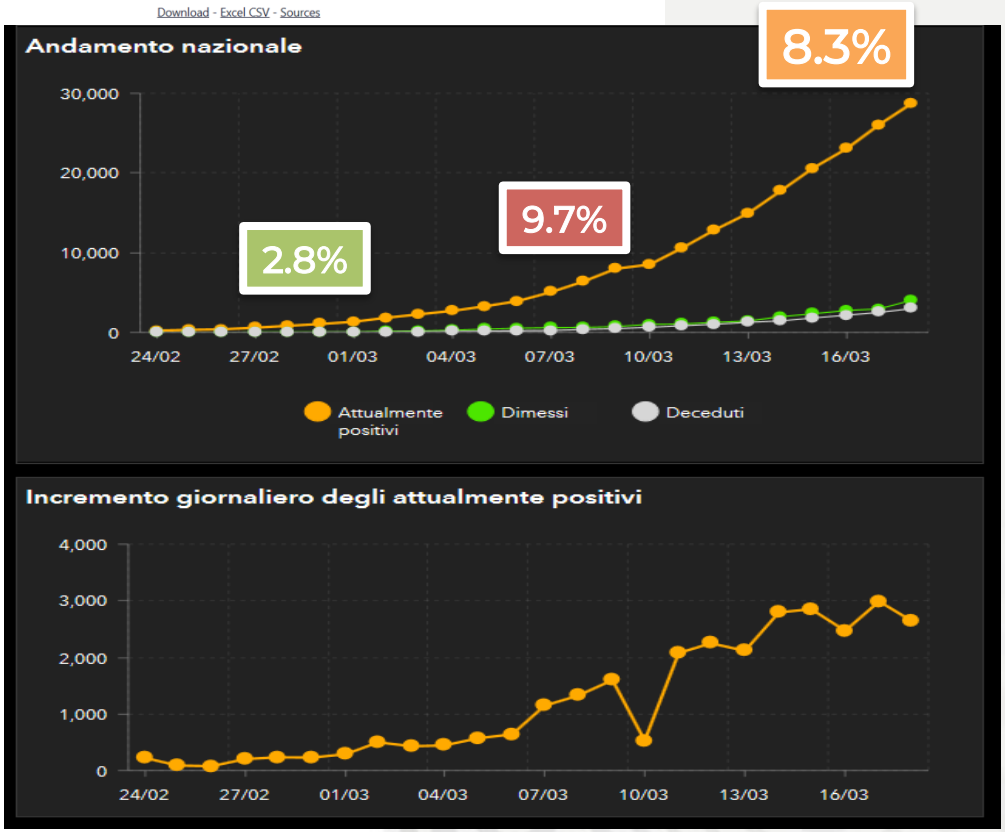
598 positivos de California (13 defunciones)
65% entre 18 y 64 años.

Fuente:
CDC. https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/cases-in-us.html#reporting-cases
CDPH. https://www.cdph.ca.gov/Programs/CID/DCDC/Pages/Immunization/ncov2019.aspx

Situación en Italia

Expectativa de vida (H/M)	80/85
Población en área urbana (2010)	68.3%
Media de edad (2012)	43.99
Población de 60 años y más	29.0%





Fuente:
http://opendatadpc.maps.arcgis.com/apps/opsdashboard/index.html#/b0c68bce2cce478eaac82fe38d4138b1

Situación en México y en el IMSS

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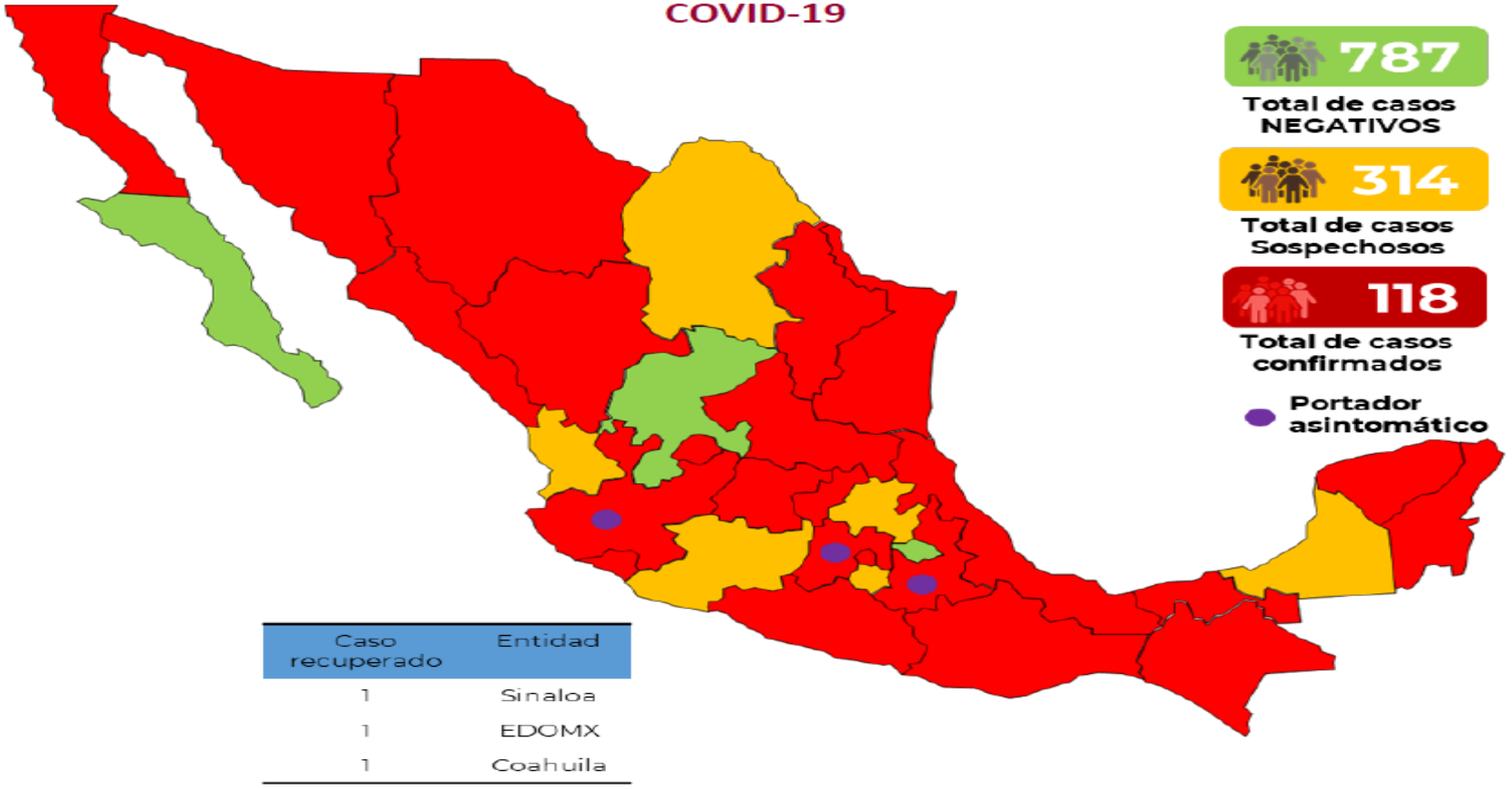
Mapa de México con los casos confirmados, negativos y sospechosos a COVID-19

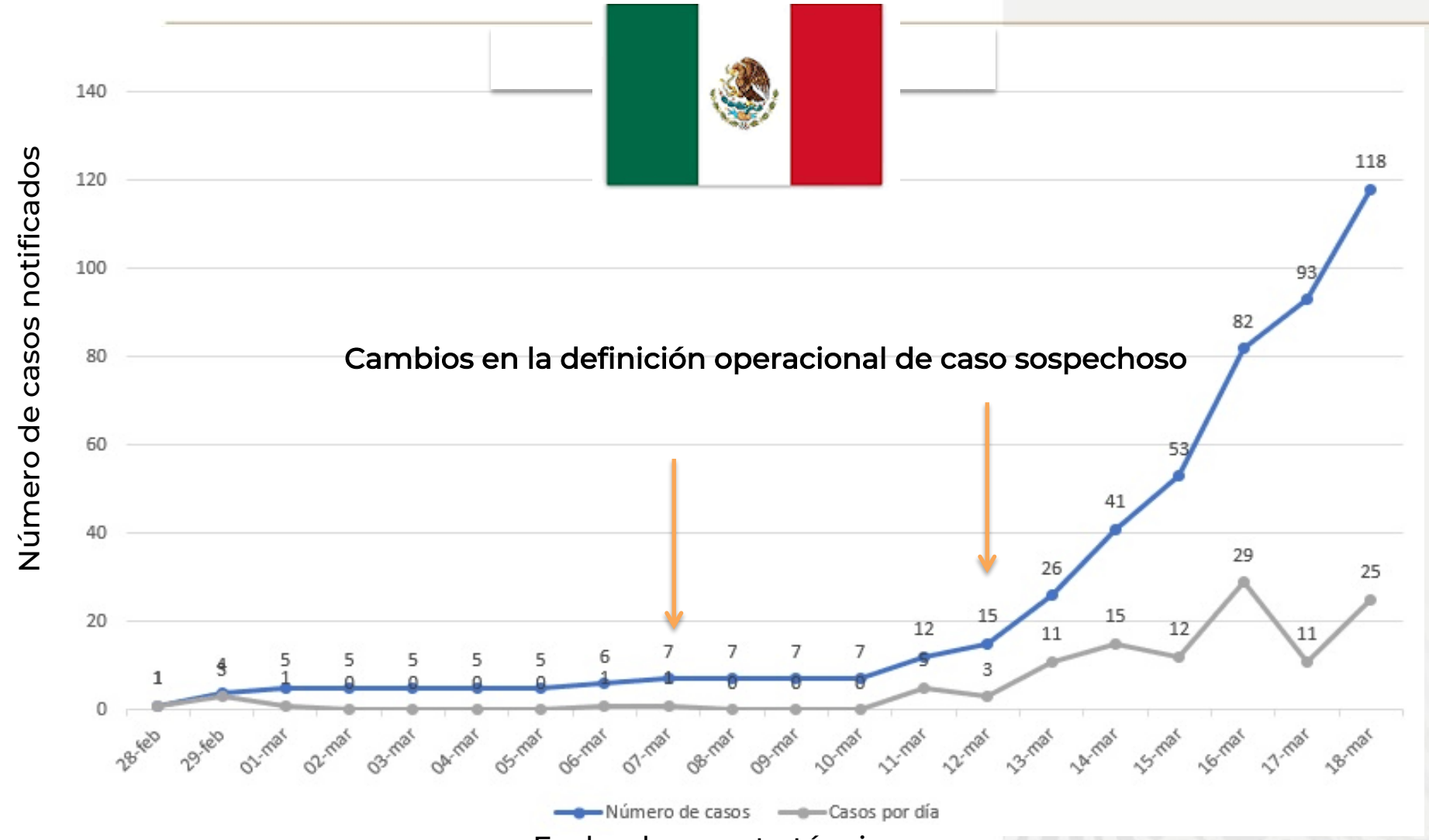


Caso recuperado	Entidad
1	Sinaloa
1	EDOMX
1	Coahuila

Fuente: SSA(SPPS/DGE/DIE/InDRE/Informe técnico.COVID-19/Mexico-18 de marzo 2020 (corte 13:00hrs)

Fuente: Secretaría de Salud.

Situación en México



Fuente: Secretaría de Salud.

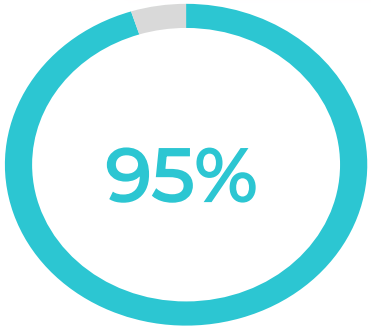
Casos sospechosos y confirmados COVID-19

17:00 hrs

Del 27 de febrero al 18 de marzo 2020

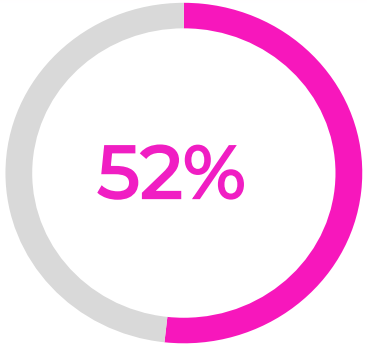
346 Casos notificados que cumplen definición operacional

Antecedente epidemiológico



Ambulatorios

329



Femenino

179

contact

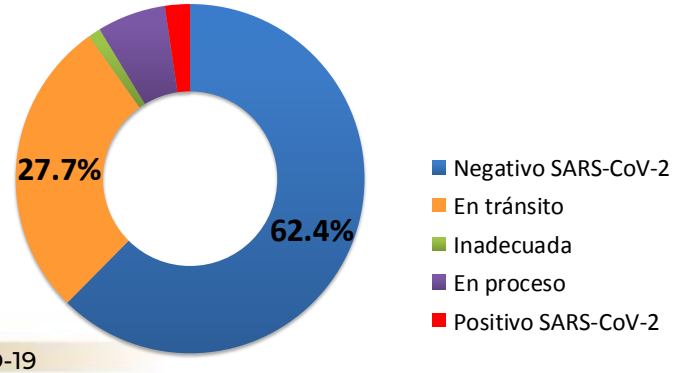
64 (18.5)%

Paises visitados	Casos	Porcentaje
EUA	95	27.5
Italia	51	14.7
España	31	9.0
España, Francia, Italia	19	5.5
España, Francia	13	3.8
España, Italia	11	3.2
Francia	11	3.2
Alemania	7	2.0
Japón	7	2.0
Alemania, Francia	6	1.7
Corea del Sur	4	1.2
Alemania, España	3	0.9
Alemania, España, Francia	2	0.6
Alemania, Francia, Italia	2	0.6
España, Alemania	2	0.6
España, Italia, Francia	2	0.6
EUA, Francia	2	0.6
EUA, Italia, Francia	2	0.6
Francia, Italia	2	0.6
Alemania, España, Italia	1	0.3
Alemania, España, EUA	1	0.3
Alemania, España, Francia, Italia	1	0.3
Alemania, España, Italia	1	0.3
China	1	0.3
EUA, España	1	0.3
EUA, Japón	1	0.3
Francia, Alemania	1	0.3
Francia, Alemania, España	1	0.3
Italia, España	1	0.3
Total	282	81.5

- Notificación de casos sospechosos en 31 Delegaciones
- Mediana de edad= 33 años (3-91)
- 7 menores de 10 años de los cuales 3 Negativos a SARS-CoV-2 y 4 en estudio.

Distribución de muestras de casos sospechosos de COVID-19 n=346

Resultado	No	%
Negativo SARS-COV2	216	62.4
En tránsito	96	27.7
En proceso	22	6.4
Inadecuada	4	1.2
Positivo SARS-COV2	8	2.3
Total	346	100.0



Fuente: Censo casos notificados COVID-19 17:00hrs

Distribución de casos sospechosos y confirmados COVID-19 por Delegación

17:00 hrs

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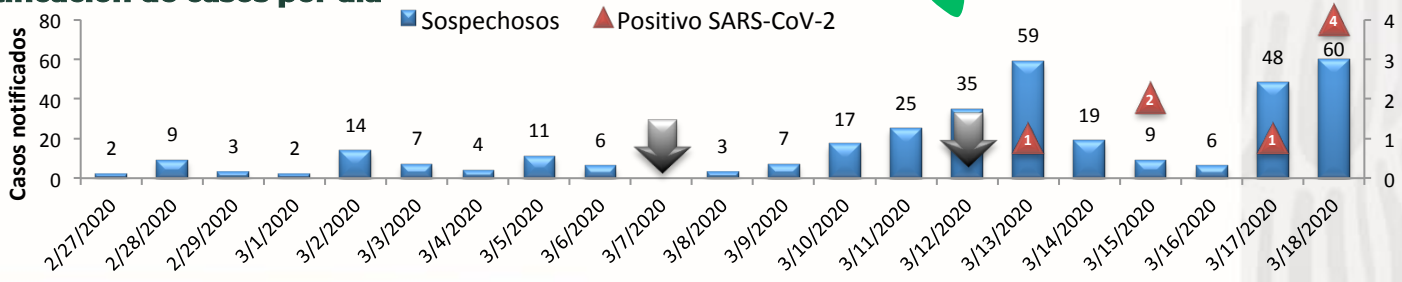
En estudio	
Aguascalientes	5
Baja California	14
Campeche	2
CDMX Norte	25
CDMX Sur	16
Chihuahua	2
Colima	3
Durango	2
Guanajuato	1
Guerrero	4
Hidalgo	6
Jalisco	7
México Oriente	5
México Poniente	6
Michoacan	6
Morelos	1
Puebla	5
Querétaro	3
San Luis Potosí	2
Sinaloa	1
Sonora	1
Tamaulipas	1
Tlaxcala	2
Veracruz Norte	1
Total	**121**

Casos confirmados			
Entidad	F	M	Total
CDMX Norte		1	1
CDMX Sur*	2	2	4
Chihuahua		1	1
Durango		1	1
México Oriente		1	1
Total	**2**	**6**	**8**

*Contacto (1)
&Un paciente hospitalizado

Delegación	Casos sospechosos
Aguascalientes	10
Baja California	30
Baja California Sur	6
Campeche	2
CDMX Norte	67
CDMX Sur	55
Chiapas	1
Chihuahua	5
Coahuila	5
Colima	5
Durango	7
Guanajuato	6
Guerrero	7
Hidalgo	9
Jalisco	20
México Oriente	10
México Poniente	17
Michoacan	6
Morelos	2
Nuevo León	14
Oaxaca	3
Puebla	17
Querétaro	11
Quintana Roo	8
San Luis Potosí	4
Sinaloa	5
Sonora	1
Tamaulipas	2
Tlaxcala	3
Veracruz Norte	7
Veracruz Sur	1
Total	**346**

Notificación de casos por día



Cambio en definición operacional

Fuente: Censo casos notificados COVID-19 17:00hrs

Empezando a conocer al enemigo. ¿Qué tan infeccioso es?

Enfermedad	R_0
Sarampión	12–18
Difteria	6-7
Viruela	5–7
Poliomielitis	5–7
Rubéola	5–7
Parotiditis	4–7
Tos ferina	5.5
VIH	2–5
SARS	2–5
COVID-19	1.4–3.9
Influenza A(H1N1)pdm09	1.4-2.0
Ebola (brote de 2014)	1.5-2.5
MERS	0.7

Fuente:
European Centre for Disease Prevention and Control. Rapid Risk Assessment: Outbreak of acute respiratory syndrome associated with a novel coronavirus, Wuhan, China; second update – 26 January 2020. ECDC: Stockholm; 2020.
La Gestión De Riesgos Ante Una Pandemia De Gripe: Guía De La Oms Para Fundamentar Y Armonizar Las Medidas Nacionales E Internacionales De Preparación Y Respuesta Ante Una Pandemia .Geneva: Organización Mundial de la Salud;2017. Licencia: CC BY-NC-SA 3.0 IGO.
Baldo, et al. J Prev Med Hyg. 2016 Mar; 57(1): E19–E22.

Empezando a conocer al enemigo.

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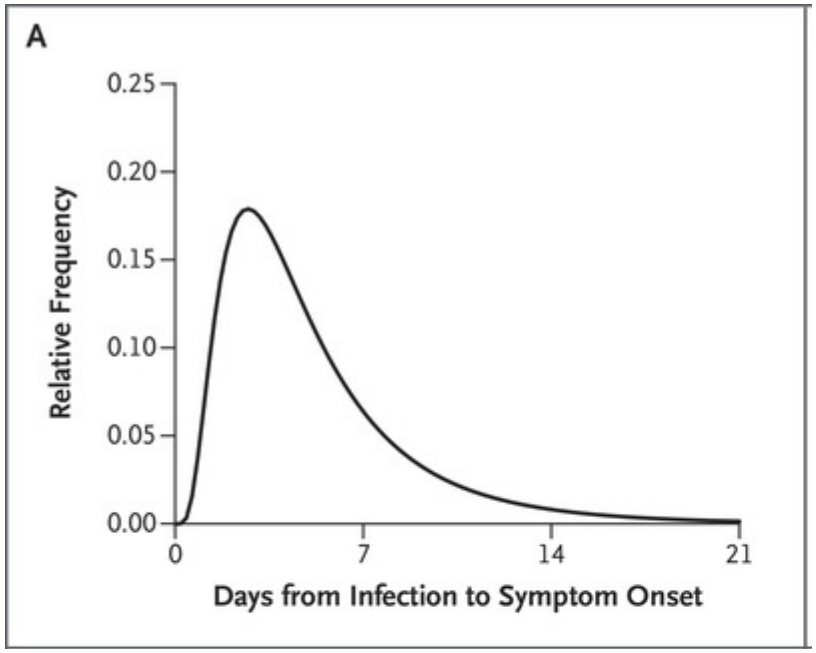
Enfermedad	COVID-19	MERS	SARS
Casos confirmados	191,127	2,494 (al 30 de noviembre de 2019)	8,098
Defunciones	7,807	858	774
Letalidad	4.08%	34.4%	9.6%

Empezando a conocer al enemigo. El brote en China.

- Periodo de incubación: 5.2 días (IC95% 4.1 a 7.0).



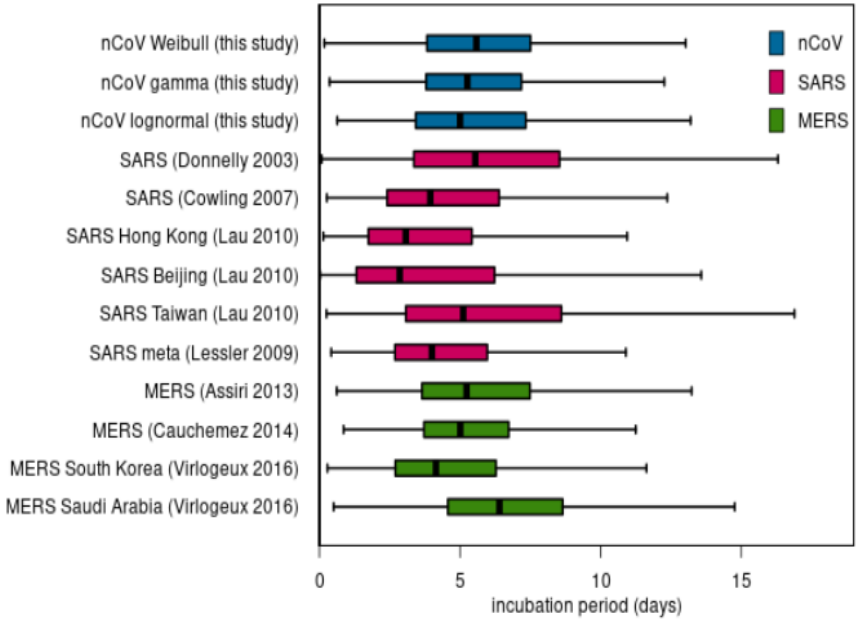


Fig. 3 Box-and-whisker-plots of estimated incubation periods for coronaviruses from different studies; median (black point), interquartile range (box), and maximum of 1.5 times the interquartile range (whiskers).

Fuente:
Li, et al,2020. NEJM. https://www.nejm.org/doi/full/10.1056/NEJMoa2001316?query=featured_home

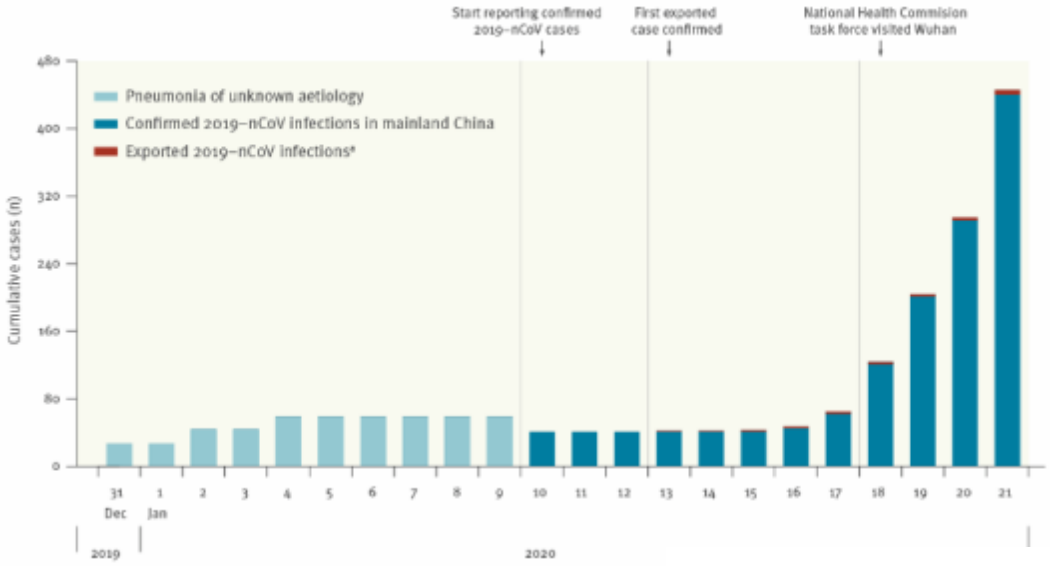
Empezando a conocer al enemigo. El brote en China.

- Duración desde el inicio de la enfermedad hasta la primera visita médica para 45 pacientes: 5,8 días (IC del 95%, 4,3 a 7,5).

- Duración media desde el inicio hasta el ingreso hospitalario se estimó en 12.5 días (IC 95%, 10.3 a 14.8) entre 44 casos.

Fuente:
Li, et al,2020. NEJM. https://www.nejm.org/doi/full/10.1056/NEJMoa2001316?query=featured_home

Empezando a conocer al enemigo. El brote en China.



- Tendencia al incremento y propagación a otras áreas.
- El 70% reportó acudir al Southern China Seafood Wholesale Market

- Al inicio, la letalidad muy alta.

Fuente:
Wu, e tal, 2020. Eurosurveillance. https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.3.2000044

Empezando a conocer al enemigo. El brote en China.

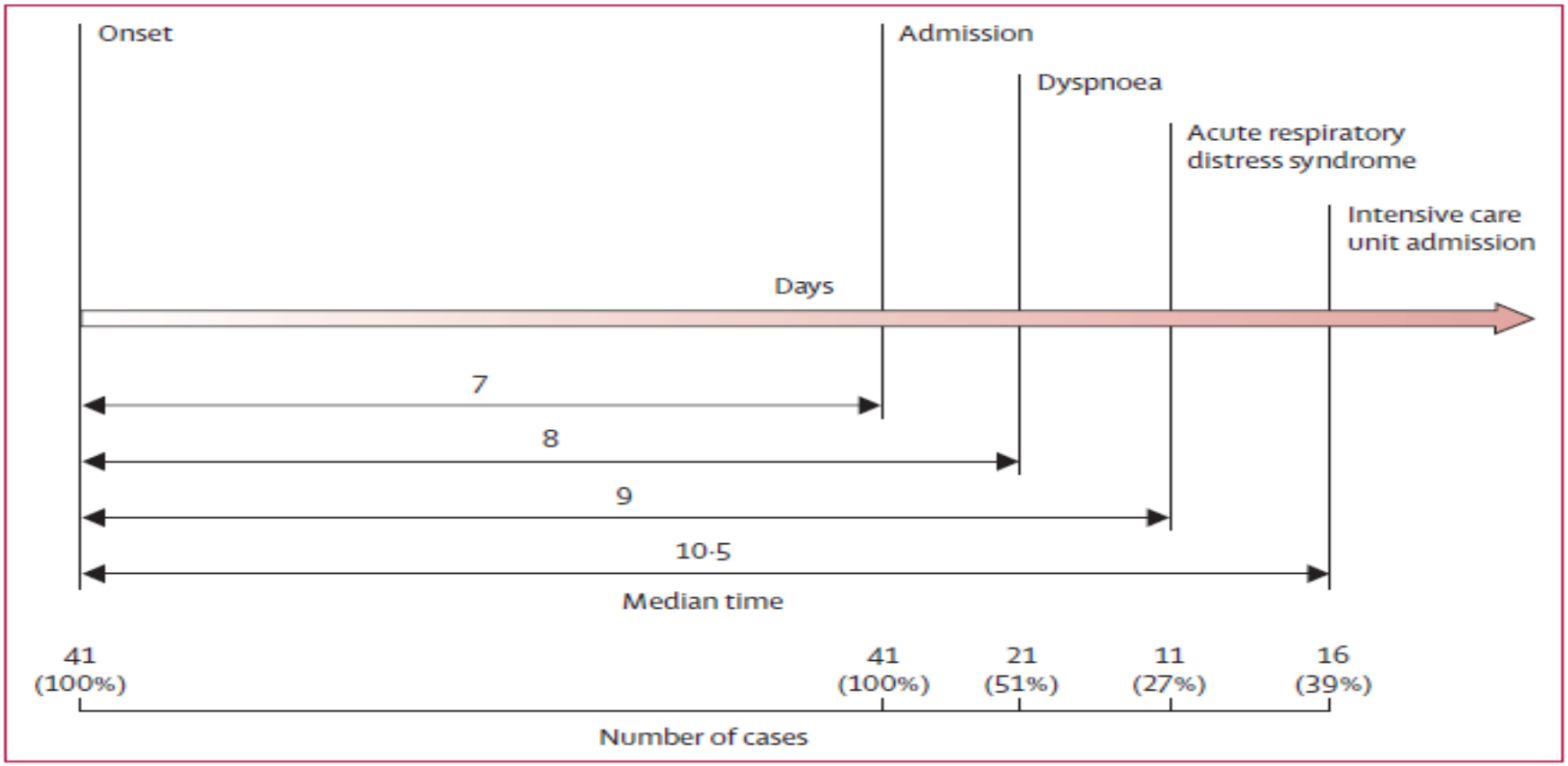


Figure 2: Timeline of 2019-nCoV cases after onset of illness

- Disnea en el 55% de los pacientes.
- 8 días con disnea [IQR 5·0–13·0]).
- 63% con linfopenia.

Fuente:
Huang, et. Al, 2020. The Lancet.

Caracterización

- 72,314 pacientes.
- 44,672 confirmados (61%).
- 889 asintomáticos (1.2%).
- 1,023 defunciones.
- 39 a 79 años (86.6%).
- Dispersión rápida.
- Severidad:
  - Leve: Sin neumonía
  - Moderado: Disnea, FR>30, O_2 ≤93%, infiltrados >50%.
  - Grave: choque séptico, SIRA, FOM.
- HAS: 12.8% y 39.7% entre decesos.

China CDC Weekly

Vital Surveillances

The Epidemiological Characteristics of an Outbreak of 2019 Novel Coronavirus Diseases (COVID-19) — China, 2020

The Novel Coronavirus Pneumonia Emergency Response Epidemiology Team

Abstract

Background: An outbreak of 2019 novel coronavirus diseases (COVID-19) in Wuhan, Hubei Province, China has spread quickly nationwide. Here, we report results of a descriptive, exploratory analysis of all cases diagnosed as of February 11, 2020.

Methods: All COVID-19 cases reported through February 11, 2020 were extracted from China's Infectious Disease Information System. Analyses included the following: 1) summary of patient characteristics; 2) examination of age distributions and sex ratios; 3) calculation of case fatality and mortality rates; 4) geo-temporal analysis of viral spread; 5) epidemiological curve construction; and 6) subgroup analysis.

Results: A total of 72,314 patient records—44,672 (61.8%) confirmed cases, 16,186 (22.4%) suspected cases, 10,567 (14.6%) clinically diagnosed cases (Hubei Province only), and 889 asymptomatic cases (1.2%)—contributed data for the analysis. Among confirmed cases, most were aged 30–79 years (86.6%), diagnosed in Hubei (74.7%), and considered mild (80.9%). A total of 1,023 deaths occurred among confirmed cases for an overall case fatality rate of 2.3%. The COVID-19 spread outward from Hubei Province sometime after December 2019, and by February 11, 2020, 1,386 counties across all 31 provinces were affected. The epidemic curve of onset of symptoms peaked around January 23–26, then began to decline leading up to February 11. A total of 1,716 health workers have become infected and 5 have died (0.3%).

Conclusions: COVID-19 epidemic has spread very quickly taking only 30 days to expand from Hubei to the rest of Mainland China. With many people returning from a long holiday, China needs to prepare for the possible rebound of the epidemic.

Introduction

A cluster of pneumonia cases of unknown origin in Wuhan, China caused concern among health officials in late December 2019. On December 31, an alert was issued by the Wuhan Municipal Health Commission, a rapid response team was sent to Wuhan by the Chinese Center for Disease Control and Prevention (China CDC), and a notification was made to the World Health Organization (WHO) (*1–6*). Likely potential causes including influenza, avian influenza, adenovirus, severe acute respiratory syndrome coronavirus (SARS-CoV), and Middle East respiratory syndrome coronavirus (MERS-CoV) were ruled out. Epidemiological investigation implicated Wuhan's Huanan Seafood Wholesale Market, which was shut down and disinfected, and active case finding was initiated and vigorously pursued (*2,4–5*).

On January 7, 2020, the causative pathogen was identified as a novel coronavirus, and genomic characterization and test method development ensued (*2–6*). Now named 2019-nCoV, the virus is distinct from both SARS-CoV and MERS-CoV, yet closely related (*5,7*). Early cases suggested that COVID-19 (i.e. the new name for disease caused by the novel coronavirus) may be less severe than SARS and MERS. However, illness onset among rapidly increasing numbers of people and mounting evidence of human-to-human transmission suggests that 2019-nCoV is more contagious than both SARS-CoV and MERS-CoV (*3,8–11*).

On January 20, China's "*National Infectious Diseases Law*" was amended to make 2019-novel coronavirus diseases (COVID-19) a Class B notifiable disease and its "*Frontier Health and Quarantine Law*" was amended to support the COVID-19 outbreak response effort. Then, on January 23, the Chinese Government began to limit movement of people in and out of Wuhan, and two days later, it announced its highest-level commitment and mobilized all sectors to respond to the epidemic and prevent further spread of COVID-19. Characterization of the epidemiological features of COVID-19 is crucial for the development and implementation of effective control strategies. Here, we report the results of a descriptive, exploratory analysis of all cases found through February 11, 2020.

Chinese Center for Disease Control and Prevention

CCDC Weekly / Vol. 2 / No. x 1

Fuente:
The Novel Coronavirus Pneumonia Emergency Response Epidemiology Team. The Epidemiological Characteristics of an Outbreak of 2019 Novel Coronavirus Diseases (COVID-19) — China, 2020. Chinese Center for Disease Control and Prevention.

Caracterización

- 3,019 personal de salud.
- 1,716 casos confirmados en personal de salud (3.8%)

TABLE 1. Patients, deaths, and case fatality rates, as well as observed time and mortality for n=44,672 confirmed COVID-19 cases in Mainland China as of February 11, 2020.

Baseline Characteristics	Confirmed Cases, N (%)	Deaths, N (%)	Case Fatality Rate, %	Observed Time, PD	Mortality, per 10 PD
Overall	44,672	1,023	2.3	661,609	0.015
Age, years					
0–9	416 (0.9)	–	–	4,383	–
10–19	549 (1.2)	1 (0.1)	0.2	6,625	0.002
20–29	3,619 (8.1)	7 (0.7)	0.2	53,953	0.001
30–39	7,600 (17.0)	18 (1.8)	0.2	114,550	0.002
40–49	8,571 (19.2)	38 (3.7)	0.4	128,448	0.003
50–59	10,008 (22.4)	130 (12.7)	1.3	151,059	0.009
60–69	8,583 (19.2)	309 (30.2)	3.6	128,088	0.024
70–79	3,918 (8.8)	312 (30.5)	8.0	55,832	0.056
≥80	1,408 (3.2)	208 (20.3)	14.8	18,671	0.111
Sex					
Male	22,981 (51.4)	653 (63.8)	2.8	342,063	0.019
Female	21,691 (48.6)	370 (36.2)	1.7	319,546	0.012
Occupation					
Service industry	3,449 (7.7)	23 (2.2)	0.7	54,484	0.004
Farmer/laborer	9,811 (22.0)	139 (13.6)	1.4	137,992	0.010
Health worker	1,716 (3.8)	5 (0.5)	0.3	28,069	0.002
Retiree	9,193 (20.6)	472 (46.1)	5.1	137,118	0.034
Other/none	20,503 (45.9)	384 (37.5)	1.9	303,946	0.013

Fuente:
The Novel Coronavirus Pneumonia Emergency Response Epidemiology Team. The Epidemiological Characteristics of an Outbreak of 2019 Novel Coronavirus Diseases (COVID-19) — China, 2020. Chinese Center for Disease Control and Prevention.

Caracterización

- Letalidad: hombre 2.8% y mujer 1.7%.

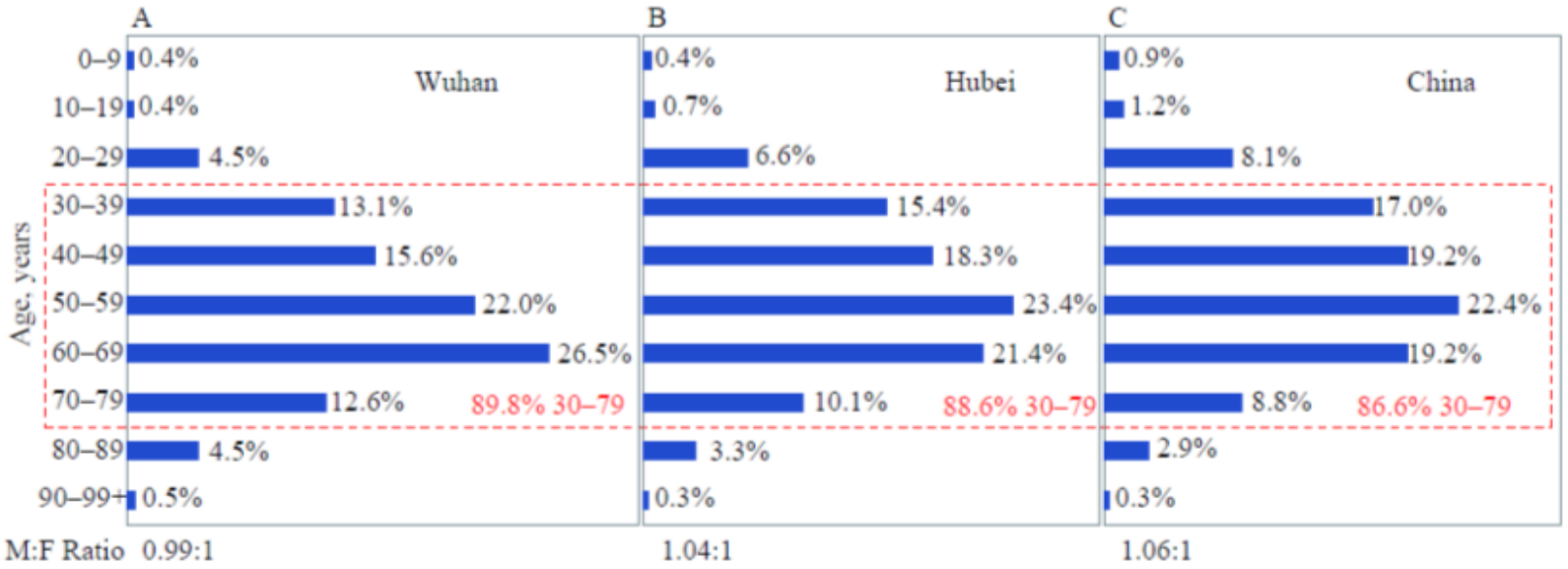
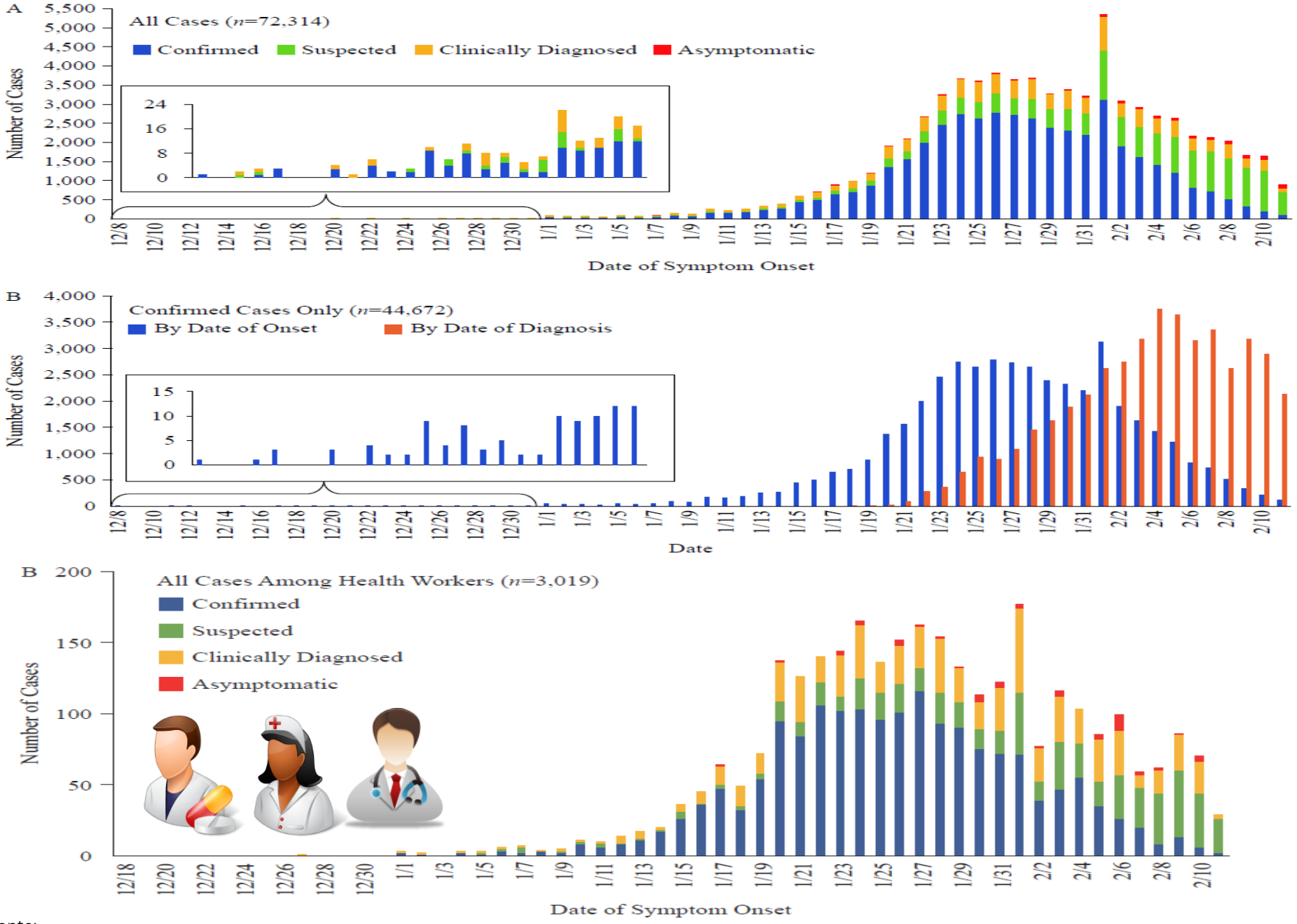


FIGURE 1. Age distribution and sex ratio of all confirmed COVID-19 cases in China through February 11, 2020. (A) patients diagnosed in the city of Wuhan only; (B) patients diagnosed in Hubei Province, which includes Wuhan as its capital city; and (C) patients diagnosed in China overall, including Hubei Province and all 30 other provincial-level administrative divisions (PLADs). Dashed red line highlights the proportion of patients in the 30–79 years age range. Sex ratio (i.e. male-to-female [M:F] ratio) is shown below each graph.

Fuente:
The Novel Coronavirus Pneumonia Emergency Response Epidemiology Team. The Epidemiological Characteristics of an Outbreak of 2019 Novel Coronavirus Diseases (COVID-19) — China, 2020. Chinese Center for Disease Control and Prevention.

Caracterización



Fuente:
The Novel Coronavirus Pneumonia Emergency Response Epidemiology Team. The Epidemiological Characteristics of an Outbreak of 2019 Novel Coronavirus Diseases (COVID-19) — China, 2020. Chinese Center for Disease Control and Prevention.

¿Transmisión vertical?

Clinical characteristics and intrauterine vertical transmission potential of COVID-19 infection in nine pregnant women: a retrospective review of medical records

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Summary

Background Previous studies on the pneumonia outbreak caused by the 2019 novel coronavirus disease (COVID-19) were based on information from the general population. Limited data are available for pregnant women with COVID-19 pneumonia. This study aimed to evaluate the clinical characteristics of COVID-19 in pregnancy and the intrauterine vertical transmission potential of COVID-19 infection.

Research in context

Evidence before this study

We searched PubMed and the China National Knowledge Infrastructure database for articles published up to Feb 6, 2020, using the keywords "novel coronavirus", "2019 novel coronavirus", "2019-nCoV", "pneumonia", "coronavirus", "Wuhan", AND "novel" ,"pregnancy", "maternal infection", AND "fetal infection" for articles published in both Chinese and English. We found two articles: one titled *Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China*, published in *The Lancet*, and another titled *Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia*, published in the *New England Journal of Medicine*. We identified no published studies on pregnant women with the 2019 novel coronavirus disease (COVID-19) infection.

Added value of this study

We retrospectively reviewed clinical records, laboratory findings, and chest CT scans for nine pregnant women with laboratory-confirmed COVID-19 pneumonia. Evidence of vertical transmission was assessed by testing for the presence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in amniotic fluid, cord blood, breastmilk, and neonatal throat swab samples from six of nine patients. All nine women were in the third trimester. Seven presented with fever without chill. Other symptoms included cough (in four of nine patients), myalgia (in three), sore throat (in two), and malaise (in two). Fetal distress occurred in two cases. Five of the nine patients had lymphopenia (<1·0 × 10^9 cells per L). Three patients had increased aminotransferase concentrations. None of the patients developed severe COVID-19 pneumonia or died. Nine livebirths were recorded. No severe neonatal asphyxia was observed. All nine livebirths had a 1-min Apgar score of 8–10 and 5-min Apgar score of 9–10. Amniotic fluid, cord blood, neonatal throat swab, and breastmilk samples from six of the nine patients were tested for SARS-CoV-2, and all results were negative.

Implications of all the available evidence

The clinical characteristics of COVID-19 pneumonia in pregnant women were similar to those of non-pregnant adult patients with COVID-19 pneumonia. Based on data from this small group of patients, there is currently no evidence of vertical transmission in pregnant women who develop COVID-19 pneumonia in the third trimester.

- 9 pacientes.
- Sin identificar al virus en:
  - Líquido amniótico
  - Leche materna
  - Cordón umbilical

	Patient 1	Patient 2	Patient 3	Patient 4	Patient 5	Patient 6	Patient 7	Patient 8	Patient 9	n (%)
Gestational age at delivery	37 weeks, 2 days	38 weeks, 3 days	36 weeks	36 weeks, 2 days	38 weeks, 1 day	36 weeks, 3 days	36 weeks, 2 days	38 weeks	39 weeks, 4 days	..
Birthweight (g)	2870	3730	3820	1880	2970	3040	2460	2800	3530	..
Low birthweight (<2500 g)	No	No	No	Yes	No	No	Yes	No	No	2 (22%)
Premature delivery	No	No	Yes	Yes	No	Yes	Yes	No	No	4 (44%)
Apgar score (1 min, 5 min)	8, 9	9, 10	9, 10	8, 9	9, 10	9, 10	9, 10	9, 10	8, 10	..
Severe neonatal asphyxia	No	No	No	No	No	No	No	No	No	0
Neonatal death	No	No	No	No	No	No	No	No	No	0
Fetal death or stillbirth	No	No	No	No	No	No	No	No	No	0

Table 2: **Neonatal outcomes**

Fuente: Chen H, et al. Clinical characteristics and intrauterine vertical transmission potential of COVID-19 infection in nine pregnant women: a retrospective review of medical records. The Lancet, 2020. https://doi.org/10.1016/S0140-6736(20)30360-3

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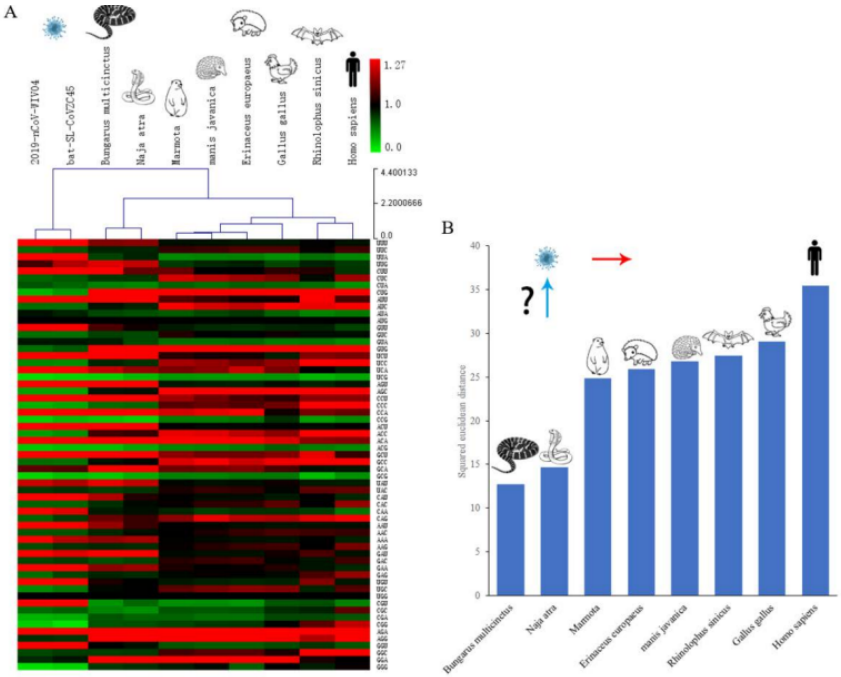
- Las serpientes de China tienen la mayor similitud entre los codones en comparación con los de marmota, manis, quiróptero, ave y humano (Fig.3B).

- Se utilizaron dos tipos de serpientes, que contienen *Bungarus multicinctus* Naja Atra (cobra china).



Fuente:
Wei Ji, et al , 2020. En prensa. doi: 10.1002/jmv.25682

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Homologous recombination within the spike glycoprotein of the newly identified coronavirus may boost cross-species transmission from snake to human.

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NEWS · 23 JANUARY 2020

Why snakes probably aren't spreading the new China virus

One genetic analysis suggests reptilian reservoir — but researchers doubt that the coronavirus could have originated in animals other than birds or mammals.

Evidence gap

"They have no evidence snakes can be infected by this new coronavirus and serve as a host for it," says Paulo Eduardo Brandão, a virologist at the University of São Paulo who is investigating whether coronaviruses can infect snakes at all. "There's no consistent evidence of coronaviruses in hosts other than mammals and Aves (birds)."

RELATED

Stop the Wuhan virus

Wei's team has not yet responded to e-mails from *Nature*'s news team seeking comment on the paper and the criticism it has received.

Many researchers are sceptical that the animal host or hosts of 2019-nCoV can be identified without further field and laboratory work. Many hope that genetic tests of animals or environmental sources, such as cages and containers, from the Wuhan market will turn up clues.

- En un artículo de difusión de la revista *Nature*.
- Escepticismo entre reservorios.
- Una forma en que los virus se adaptan es mediante la codificación de proteínas utilizando la misma elección de codones que su huésped. El equipo de Wei comparó los codones favorecidos por 2019-nCoV con los preferidos por posibles anfitriones, incluidos erizos, pangolines, murciélagos, pollos, humanos y

Fuente:
Callaway E, Cyranoski D. Why snakes probably aren't spreading the new China virus. Nature. doi: 10.1038/d41586-020-00180-8

¿Reservorio?

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A good candidate

Previously, researchers have noted that coronaviruses are a possible cause of death in pangolins[1], and that nCoV-2019 and coronaviruses from pangolins use receptors with similar molecular structures to infect cells.

Even before today's announcement, pangolins were a good candidate for being an intermediate species for the virus, so it's very interesting that the researchers have found such a close sequence, says David Robertson, a computational virologist at the University of Glasgow, UK.

Pangolins are protected animals, but illegal trafficking is widespread, and some species are critically endangered. They are sold, controversially, for their meat and scales, and for use in traditional Chinese medicine, in which parts of the animal are used to treat ailments such as skin diseases, menstrual disorders and arthritis. Chinese law states that people selling pangolins can be punished by 10 years or more in prison.

What you need to know about the novel coronavirus

The coronavirus emerged in the Chinese city of Wuhan in December, and is thought to have leapt to humans at a seafood and wild-animal market, where many of the first people to become infected worked. Pangolins were not listed on an inventory of items sold at the market – although the illegality of trading pangolins could explain this omission.

viruses MDPI

Article

Viral Metagenomics Revealed Sendai Virus and Coronavirus Infection of Malayan Pangolins (*Manis javanica*)

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Abstract: Pangolins are endangered animals in urgent need of protection. Identifying and cataloguing the viruses carried by pangolins is a logical approach to evaluate the range of potential pathogens and help with conservation. This study provides insight into viral communities of Malayan Pangolins (*Manis javanica*) as well as the molecular epidemiology of dominant pathogenic viruses between Malayan Pangolin and other hosts. A total of 62,508 *de novo* assembled contigs were constructed, and a BLAST search revealed 3600 ones (≥300 nt) were related to viral sequences, of which 68 contigs had a high level of sequence similarity to known viruses, while dominant viruses were the Sendai virus and Coronavirus. This is the first report on the viral diversity of pangolins, expanding our understanding of the virome in endangered species, and providing insight into the overall diversity of viruses that may be capable of directly or indirectly crossing over into other mammals.

Fuente:
Viruses 2019, 11, 979; doi:10.3390/v11110979